



BOOK OF ABSTRACTS



13th International Epidemiology Workshop

Foz do Iguaçu - Brazil

9 to 12 April 2024

Interludium Iguassu Convention

Organizers:

Emerson M. Del Ponte

Eduardo S. G. Mizubuti

Armando Bergamin Filho

Lilian Amorim

Louise Larissa May De Mio

Book of Abstracts

13th International Epidemiology Workshop

Foz do Iguaçu, Brazil

9 to 12 April 2024

Organizing Committee

Emerson M. Del Ponte¹
Eduardo S. G. Mizubuti¹
Armando Bergamin Filho²
Lilian Amorim²
Louise Larissa May De Mio³

¹ Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa, MG, Brazil

² Departamento de Fitopatologia e Nematologia, Escola Superior de Agricultura “Luiz de Queiroz”, Universidade de São Paulo, Piracicaba, SP, Brazil

³ Departamento de Fitotecnia e Fitossanidade, Universidade Federal do Paraná, Curitiba, PR, Brazil

Hosted and promoted by



Sociedade Brasileira de
Fitopatologia

Sponsored by



This work is licensed under CC BY-NC 4.0 

Contents

	Page
Preface	4
Workshop program	5
Index of Invited Lectures	9
Index of Oral Talks	27
Index of Poster Presentations	57
Index of Delegates	120

Preface

The Epidemiology Committee of the International Society of Plant Pathology (ISPP) and the Brazilian Phytopathological Society (SBF) are delighted to introduce the Book of Abstracts for the 13th International Epidemiology Workshop (IEW13). This pivotal event was hosted in the city of Foz do Iguaçu, Brazil, from April 9th to 12th, 2024, at the Interludium Iguassu Convention Hotel. The conference's organization and scientific direction were handled by Emerson M. Del Ponte, Eduardo S. G. Mizubuti, Armando Bergamin Filho, Lilian Amorim, and Louise Larissa May De Mio, who also contributed as members of the scientific committee. Demonstrating a worldwide dedication to the advancement of plant disease epidemiology, the workshop saw the participation of 122 attendees from 26 different countries. The agenda was carefully structured into six main sessions featuring invited speakers, along with seven oral sessions that showcased presentations selected from the submitted abstracts. Altogether, the workshop boasted 17 invited lectures, which included a keynote speech, alongside 28 oral presentations and 60 posters. This compilation of abstracts not only bears witness to the profound scientific dialogue that distinguished the workshop but also stands as an invaluable asset for the ongoing enhancement of epidemiology research. The IEW13 was made possible through financial support from CAPES and CNPq.

Workshop Program

Monday 8 April 2024	
17:00	Registration and welcome reception
Tuesday 9 April 2024	
Keynote Session	
Moderator: Emerson Del Ponte	
7:30	Registration continues
8:15	Welcoming: Emerson Del Ponte
8:30	KL: Laurence Madden - Some reflections on plant disease epidemiology since the first international workshop
Main Session 1	
Artificial Intelligence and remote sensing in plant disease epidemiology	
Moderator: Robin Choudhury	
9:30	IL1: Christian Cruz - Modernizing plant disease monitoring: Integrating UAV and ground-based imaging in epidemiological research
10:00	IL2: Maria Rocío Madrid - Global risk of Fusarium wilt mapped by remote sensing and aerosol transport modeling in a changing climate
10:30	Coffee break
11:00	IL3 - Juan Navas-Cortéz - Prioritizing surveillance: Use of remote sensing for the early detection and monitoring of <i>Xylella fastidiosa</i> in woody crops
Oral Session 1	
Moderator: Felipe Dalla Lana	
11:30	O1: Zhanhong Ma - The Application of remote sensing in plant disease monitoring
11:45	O2: Joaquin Ramirez-Gil - Development of digital platforms for data management and analysis for evidence-based decision-making of plant epidemics
12:00	O3: Paul Melloy - Utilizing an application programming interface (API) for delivering spatial risk of blackspot to growers through commercial third-party farm management platforms.
12:15	O4: Berea Etherton - Disaster plant pathology: smart solutions for natural and human-driven cataclysms threatening global plant health
12:30	Lunch
Main Session 2	
Plant disease surveillance and monitoring	
Moderator: Peter Ojiambo	
14:00	IL4: Neil McRoberts - Surveillance in systems with vectored diseases: gathering information to inform intervention
14:30	IL5: David Gent - What explains growers' fungicide use and management: From monitoring to causal inference
Oral Session 2	
Moderator: Kelsey Andersen Onofre	
15:00	O5: Matt Combes - Examining the effect of ash dieback disease on the spread and

	detection of Emerald ash borer beetle in the UK
15:15	O6: Borba - <i>Colletotrichum</i> species infecting apples in Mid-Atlantic United States: identification, infection sources, geographical distribution, ecology and spore trapping with qPCR
15:30	O7 - Andreas von Tiedemann - Role of seed infection for the near and far distance spread of wheat blast caused by <i>Magnaporthe oryzae</i> pathotype <i>Triticum</i>
15:45	O8: Alice Inoue-Nagata - Enhancing geminivirus detection in plants: unveiling hidden threats with a cost-efficient RCA-RFLP method
16:00	Coffee break
Oral Session 3	
Moderator: Marcelo Canteri	
16:30	O9: Lisa Rothmann - Sorghum disease surveillance to understand South African producer perceptions and inform disease management and industry needs.
16:45	O10: Silvio Lopes - Variation in the potential of diseased citrus trees in backyard as sources of Candidatus <i>Liberibacter asiaticus</i> to commercial groves
17:00	O11: Aaron Plex Sulá - Global host-pathogen infection networks in major terrestrial agroecosystems
17:15	O12: Cristina Canale - Natural infectivity of the corn leafhopper, <i>Dalbulus maidis</i> , with the corn stunting complex pathogens in Santa Catarina, Brazil
17:30	Poster viewing - odd numbers
19:30	Cocktail dinner at the Interludium Hotel
Wednesday 10 April 2024	
Main Session 3	
Plant Disease Modeling and Forecasting	
Moderator: Damon Smith	
8:00	IL6: Robert Beresford - Pathogen process models: versatile tools for disease risk prediction
8:30	IL7: Irene Salotti - Disease models for decision-making in crop protection
9:00	IL8: Alexey Mikaberidze - Economic analysis of plant disease epidemics across multiple fields: estimating the economic cost of pathogen adaptation to control measures
Oral Session 4	
Chairperson: Natalia L. Peres	
9:30	O13: Zvezdomir Jeleu - A model to predict spore maturation of <i>Blumeriella jaapii</i> in cherry
9:45	O14: Vinicius Garnica - Novel weather variables associated with epidemics of <i>Stagonospora nodorum</i> blotch of winter wheat
10:00	O15: Damon Smith - Predicting tar spot of corn in the U.S. – developing the infrastructure for corn disease modeling
10:15	O16: José F. González-Acuña - Using environmental variables for the development of Logistic regressions to predict frog-eye leaf spot in soybean in the United States
10:30	Coffee break - Group photo

Oral Session 5	
Moderator: Lilian Amorim	
11:00	O17: Vinicius Cerbaro - Influence of the El Niño Southern Oscillation on the risk of Botrytis fruit rot occurrence in Florida
11:15	O18: Elin Falla - A mathematical model centred on aphid vector feeding behaviour has implications for plant host manipulation by non-persistently transmitted viruses
11:30	O19: J. Maurício Fernandes - Mitigating the impact of drought and wheat Blast on rainfed wheat production in the Brazilian Cerrado based on the selection of sowing dates and varieties
11:45	O20: Maria Chiara Rosace - Spatial modelling of hotspots for plant pests introductions in the EU using regionalized data
12:00	Lunch
Main Session 4	
Climate Change and Plant Disease Epidemiology	
Moderator: José Maurício C. Fernandes	
14:00	IL9: Karen Garret - Adapting global plant health management to global change: Opportunities for contributions from epidemiology
14:30	IL10: Adam Sparks - Tools, data resources and methods for modeling climate change effects on plant disease
Oral Session 6	
Moderator: Murillo Lobo	
15:00	O21: Israel Chedjou - Combining masculinizing resistance, rotation and biocontrol to achieve durable suppression of the potato pale cyst nematode: a model
15:15	O22: Carlos Gongora-Canul - Comparative epidemiology of tar spot as an endemic and emerging disease in the Americas
15:30	O23: Belachew Asalf - Effect of cover crops and green manuring on Sclerotinia white rot disease development and yield in carrot
15:45	O24 - Ayalsew Zerihun - What happens to the durability of disease control in fields of growers who run a resistance management programme when neighbours use only one component of the resistance management?
16:00	Coffee break
16:30	Poster viewing - even numbers
19:00	Dinner at Rafain Churrascaria Show
Thursday 11 April 2024	
8:00	Tour Iguassu Falls
Main Session 5	
Pathogen Evolution and Fungicide Resistance Management	
Moderator: Louise Larissa May De Mio	
14:00	IL11: Sydney Everhart - Epidemiology and etiology of Alternaria leaf blight and head rot caused by multiple species of <i>Alternaria</i> in the Eastern United States
14:30	IL12: Nik Cunniffe - Modelling fungicide resistance management strategies: progress and challenges
15:00	IL13: Arne Stensvand - Managing fungicide resistance in <i>Botrytis</i>

Oral Session 7	
Moderator: Juan Pablo Edwards Molina	
15:30	O25: Juan Paredes - Analysis of the field-scale spatial pattern of peanut smut in Argentina
15:45	O26: Sara Thomas-Sharma - One brick at a time: Building on epidemiological insights for improved management of Cercospora leaf blight on soybean in the mid-South.
16:00	Coffee break
16:30	O27: Vincent Phillion - Combining foliar deposit distribution and dose-response curve data to predict fungicide efficacy against scab in apple orchards, and practical implementation in the AOS43 dosing system
16:45	O28: David Gadoury - A review of pathogen biology, ecology, epidemiology, and the use of germicidal ultraviolet light to suppress plant pathogens
19:00	Dinner at 277 Craft Beer
Friday 12 April 2024	
Main Session 6	
Epidemiology-based management strategies	
Moderator: Armando Bergamin Filho	
8:30	IL14: Mary Ruth McDonald - Epidemiology- based management of vegetable diseases
9:00	IL15: Paul Esker - Exploring causal relationships to improve the development of production and management scenarios
9:30	IL16: Renato Bassanezi - Epidemiology-based management strategies for citrus Huanglongbing
10:00	Coffee break
Closing session	
Moderator: David Gadoury	
10:30	Concluding remarks and planning for IEW14
12:00	Adjourn

INDEX OF KEYNOTE AND INVITED LECTURES			
Number	Presenting author	Title	Page
KL	Laurence V. Madden	Some reflections on plant disease epidemiology since the first international workshop	10
IL1	Christian Cruz	Modernizing plant disease monitoring: Integrating UAV and ground-based imaging in epidemiological research	11
IL2	Rocío Calderón	Global risk of Fusarium wilt mapped by remote sensing and aerosol transport modeling in a changing climate	12
IL3	Juan Navas-Cortés	Prioritizing surveillance: Use of remote sensing for the early detection and monitoring of <i>Xylella fastidiosa</i> in woody crops	13
IL4	Neil McRoberts	Surveillance in systems with vectored diseases: gathering information to inform intervention	14
IL5	David H. Gent	What explains growers' fungicide use and management: From monitoring to causal inference	15
IL6	Robert M. Beresford	Pathogen process models: versatile tools for disease risk prediction	16
IL7	Irene Salotti	Disease models for decision-making in crop protection	17
IL8	Alexey Mikaberidze	Economic analysis of plant disease epidemics across multiple fields: estimating the economic cost of pathogen adaptation to control measures	18
IL9	Karen A. Garrett	Adapting global plant health management to global change: Opportunities for contributions from epidemiology	19
IL10	Adam Sparks	Tools, data resources and methods for modelling climate change effects on plant disease	20
IL11	Sydney Everhart	Epidemiology and etiology of <i>Alternaria</i> leaf blight and head rot caused by multiple species of <i>Alternaria</i> in the Eastern United States	21
IL12	Nik Cunniffe	Modelling fungicide resistance management strategies: progress and challenges	22
IL13	Arne Stensvand	Managing fungicide resistance in <i>Botrytis</i>	23
IL14	Mary Ruth McDonald	Epidemiology- based management of vegetable diseases	24
IL15	Paul Esker	Exploring causal relationships to improve the development of production and management scenarios	25
IL16	Renato Bassanezi	Epidemiology-based management strategies for citrus Huanglongbing	26



Some reflections on plant disease epidemiology since the first international workshop

Laurence V. Madden

Department of Plant Pathology, The Ohio State University, Wooster, OH 44691 (USA)

Email: madden.1@osu.edu

The year 1963 was monumental for plant disease epidemiologists. The year saw the publication of the landmark book “Plant Diseases: Epidemics and Control” by J.E. Vanderplank and also the gathering of plant pathologists from around the world at the first International Epidemiology Workshop. Vanderplank’s treatise firmly established the field as one centered on the principles of population dynamics and “...epidemiological analysis based largely on infection rates and on the relation between the amount of inoculum and the amount of disease it produces”. Many of the scientists at that first workshop would make innumerable contributions extending the discipline, applying epidemiological principles in disease prediction and management, and inspiring future generations of botanical epidemiologists, including many participants of the later international workshops. Over the past six decades, two broad subdivisions of the discipline can be seen, sometimes involving different researchers: 1) theoretical and empirical modeling of the temporal, spatial, and spatio-temporal dynamics of disease, commonly involving SEIR (or related) models or mechanistic computer simulators; and 2) prediction or forecasting of epidemics (or disease outbreaks, or the need for control interventions) on a real-time basis based on environmental (and other) data, using a range of analytical methods. The data collection and methodology often are different (or very different) between these two approaches, with some exceptions such as when population-dynamic modeling is explicitly used for real-time predictions. Many disease forecasting systems are empirically based. Statistical analysis is a fundamental tool for both approaches, except for some purely theoretical work, and there is no doubt that modern epidemiology relies very heavily on statistical analysis and modeling. The field of statistics has also been growing tremendously over the past six decades, with developments in linear mixed modeling, generalized linear and nonlinear mixed modeling, meta-analysis, Bayesian modeling and decision theory, information theory, prediction, and machine learning (statistical learning) and other computational methods. Epidemiologists have either struggled to keep up with the growing field of statistics, or have embraced the statistical advances in order to make new and innovative contributions in epidemiology, disease management, and sometimes in statistics. In addition to covering some of the history of plant disease epidemiology and the international workshops, my presentation will elaborate on the role of statistics in our field, and discuss recent research on characterizing (and modeling) variability in addition to modeling mean responses. Applications include, among other things, quantitative research synthesis for disease management.

Modernizing plant disease monitoring: Integrating UAV and ground-based imaging in epidemiological research

Da-Young Lee^{1,2}, Sungchan Oh³, Chongyuan Zhang¹, Mariela Fernandez-Campos¹, Andrés Cruz-Sancan¹, Carlos Góngora-Canul^{1,4}, and C. D. Cruz¹

¹ Department of Botany and Plant Pathology, College of Agriculture, Purdue University, West Lafayette, IN 47907, USA

² Department of Electrical Engineering, Pohang University of Science and Technology, Pohang, Gyeongsangbuk-do, 37673, South Korea

³ Institute for Plant Sciences, Purdue University, West Lafayette, IN 47907, USA

⁴ Tecnológico Nacional de México/IT de Ciudad Valles. Calle Al Ingenio 2, Ciudad Valles, San Luis Potosí, 79033, México

E-mail: cruz113@purdue.edu

Recent advancements in plant disease epidemiology have been characterized by the integration of ground-based Red-Green-Blue (RGB) imaging and Uncrewed Aerial Vehicle (UAV)-based remote sensing. These cutting-edge methods provide fresh perspectives for the detection, quantification, and monitoring of diseases, such as wheat blast and tar spot in corn. The employment of optical imaging sensors and the development of disease detection algorithms, including contour-based tar spot stomata detection through proximal RGB imaging and UAV-based multispectral imaging for wheat blast and tar spot, have shown substantial promise in digitizing disease assessments, as well as the potential to deliver detailed and comprehensive disease intensity data. Although these methods represent innovative approaches to disease monitoring, challenges remain. These include the complexity of data collection and analysis, adaptation to environmental variability, and ultimate implementation. Future research should focus on overcoming these limitations, thereby increasing the reliability and practicality of these methods across diverse agricultural settings and promoting the integration of artificial intelligence or advanced statistical techniques for data processing and interpretation. Such developments could make a significant contribution to the evolution of disease monitoring practices, with a focus on real-time disease detection, surveillance, and management in precision agriculture.

Financial support: Indiana Corn Marketing Council, USDA-ARS [5020-21220-014-016-S], USDA-NIFA [2023-67013-39300], USDA-NIFA [1016253], Purdue AG-ENG



Global risk of Fusarium wilt mapped by remote sensing and aerosol transport modeling in a changing climate

Rocío Calderón¹, Hannah K. Brodsky², Chad Vosburg³, Jaclyn A. Eller¹, Andrew D. Miles³, Natalie Mahowald², Sharifa G. Crandall³, Ryan Pavlick⁴ and Kaitlin M. Gold¹

¹Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Sciences, Cornell AgriTech, Cornell University, Geneva NY, USA.

²Department of Earth and Atmospheric Sciences, Atkinson Center for a Sustainable Future, Cornell University, Ithaca NY, USA.

³Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, University Park PA, USA.

⁴Jet Propulsion Laboratory, California Institute of Technology, Pasadena CA, USA.

E-mail: mc2283@cornell.edu

Soilborne plant diseases produce long-lasting survival spores that challenge food security by compromising annual yields and removing suitable land from agricultural production. Historical use of remote sensing (RS) to monitor plant disease has been limited to local and sub-regional scales with sub-orbital platforms. The forthcoming global imaging spectroscopy era offers an exciting opportunity to optimize surveillance at a heretofore unseen scale. The goal of our NASA IDS project is to integrate RS, aerosol transport modeling, and comparative genomics into a global disease surveillance system for the economically devastating soilborne disease, Fusarium wilt (FW), and assess *Fusarium oxysporum* (*Fo*) dispersal in aerosolized agricultural dust. As foundation, we released an interactive, global web map documenting 4500+ FW incidences reported in peer-reviewed literature over the past 30 years. Here, we developed a global susceptibility assessment built from RS data streams that uses the plant disease triangle as a theoretical framework (environment-host-pathogen interactions). We identified agricultural production zones with conducive environmental conditions for FW by overlapping Landsat-based cropland products with our incidence map. We then used species distribution modeling to map FW risk at 1km resolution to develop a first of its kind global disease suitability map. This approach, which we call Pathosystem Distribution Modeling (PDM), describes patterns between FW and long-term spectroscopy and thermal satellite measurements (e.g., MODIS, ESA-CCI, GOME-2), by identifying convergent environmental factors, crop host distribution, and plant traits impacted by biotic stress. We also implemented PDM using simulations from CMIP6 to study climate change implications on FW distribution. The CAM6-MIMI climate model was fed by this FW risk map and modified to incorporate *Fo* spore traits that influence dispersal and atmospheric survival. We found modeling evidence of transoceanic and intercontinental atmospheric transport of viable *Fo* spores. This integrated approach provides key insights about drivers for FW distribution and the spread of *Fo* on global dust currents, while laying the foundation for future use of SBG integrated with other RS tools as a global surveillance system for crop disease.

Financial support: NASA-ROSES Interdisciplinary Grant #80NSSC20K1533

Prioritizing surveillance: Use of remote sensing for the early detection and monitoring of *Xylella fastidiosa* in woody crops

Navas-Cortes J.A.¹, Poblete T.², Hornero A.^{1,2}, Camino C.³, Calderon R.⁴, Landa B.B.², Zarco-Tejada P.J.^{1,2}

1. Instituto de Agricultura Sostenible, Consejo Superior de Investigaciones Científicas, Córdoba, Spain
2. The University of Melbourne, Melbourne, Australia
3. European Commission, Joint Research Centre
4. Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell AgriTech, Geneva, United States

E-mail: j.navas@csic.es

Managing diseases caused by *Xylella fastidiosa* (*Xf*) presents unique challenges, especially in economically and historically significant woody trees. Key issues include the high costs and productivity losses associated with removing and replacing mature infected trees, difficulties in thoroughly sampling large canopies for pathogen detection, and the uncertain incubation period, which complicates timely assessment of the bacterium's spread. These factors hinder the implementation of effective eradication or containment measures. Emerging advanced imaging technologies, notably high-resolution hyperspectral and thermal imaging, are proving crucial in identifying *Xf* infections before visible symptoms appear. Such technologies, often deployed from airborne platforms, detect early physiological changes in plants indicative of infection. Pioneering research conducted in the *Xf* outbreak in Southern Italy demonstrated the potential of these methods for pre-visual detection of *Xf* infection in olive trees. Subsequent studies have further validated the use of spectrally constrained machine-learning algorithms and multispectral and thermal imaging for extensive monitoring efforts of *Xf* outbreaks. The shift towards utilizing multispectral satellite imagery for large-scale operational models marks a significant advancement. However, challenges remain, particularly in the early stages of disease progression, due to limitations in spectral band sensitivity. Previous research has explored these challenges, highlighting the critical role of tree temperature to address the vascular nature of *Xf* and its symptoms similar to water stress. While commercial multispectral imagery has proven effective for detecting advanced disease stages, the lack of high-spatial-resolution hyperspectral and thermal imaging limits early detection capabilities. Future developments in hyperspectral sensor technology and analytical frameworks are expected to enhance real-time global monitoring of plant diseases and stress conditions. Achieving this goal requires the development of accurate, sensitive, user-friendly, and affordable remote sensing techniques. Such advancements could significantly improve early detection capabilities for *Xf* epidemics, enabling timely and effective management responses.

Financial support: Projects XF-ACTORS and BeXyl (H2020 and Horizon, EU), KODA (CDTI; Spain)

Surveillance in systems with vectored diseases: gathering information to inform intervention

Sandra Olkowski¹, Weiqi Lui², Neil McRoberts¹

¹Quantitative Biology & Epidemiology group, University of California, Davis, CA 95616 USA.

²North Carolina State University/USDA-ARS USHRL, Ft Pierce FL 34945.

E-mail: nmcroberts@ucdavis.edu

We discuss several topics of interest in the use of surveillance data in the management of plant diseases at large scales. Our discussion is motivated by our experience with regulatory programs in public and plant health, aimed at disease eradication or suppression, in providing scientific support to government agencies and industry stakeholders in key decision making roles. We focus particularly on situations where data are sparse, at least initially, and current trends towards data-dependent AI approaches are therefore unlikely to succeed. The analysis is divided into three main topics. In the first section we address the question of how to initiate surveillance at large scales, focusing on methods for designing surveys that account for known risk factors. For invasive pests and pathogens which escape initial efforts at eradication or containment, an increase in the spatial extent of developing epidemics is likely to lead to the need for re-evaluation of initial parameter estimates or scores in risk models. We discuss the process of iterative re-evaluation of risk models in response to accumulating detection data from surveillance and comment on commonly-encountered shortcomings in regulatory data for modeling purposes. This section highlights potential inter-domain differences that might have to be crossed by epidemiologists who want their work to have practical impact on regulatory practice. In the third area of discussion we examine the thorny issue of trying to give decision makers improved situational awareness of the severity of the epidemic by providing estimates of disease (or pathogen) prevalence from sparse surveillance data. This question has been of considerable interest among public health epidemiologists for several years and the concept of *expansion factors* has become established in that domain as one way to achieve estimates of disease prevalence from sparse data. Since the term *expansion factors* has not found its way into plant disease epidemiology we describe their basis and use in public health contexts and discuss how the concept is related to existing ideas in plant disease epidemiology. The discussion will be illustrated by work on citrus huanglongbing (HLB) in the USA and a number of other high profile plant disease examples.

Financial support: USDA-NIFA; USDA-APHIS; California Department of Food & Agriculture; California Citrus Research Board

What explains growers' fungicide use and management: From monitoring to causal inference

David H. Gent¹, Jae Young Hwang¹, Sharmodeep Bhattacharyya², Shirshendu Chatterjee³, Thomas L. Marsh⁴, and Joshua Pedro³

¹U.S. Department of Agriculture-Agricultural Research Service, Forage Seed and Cereal Research Unit, Corvallis, Oregon 97331

²Department of Statistics, Oregon State University, Corvallis, OR 97331

³Department of Mathematics, City University of New York, New York City, New York 10031

⁴School of Economic Sciences, Washington State University, Pullman, Washington 99163

E-mail: dave.gent@usda.gov

Plant disease monitoring data is collected routinely for many purposes. Such datasets may be a rich source of information for understanding determinants of disease or management outcomes when appropriate covariates are available. Causal inference from such data sets require careful consideration of endogeneity between predictor variables and residuals to mitigate bias and appropriate covariate balancing to minimize spurious relationships caused by confounding. Methods for causal inference from observational data are applied routinely in human disease epidemiology, economics, and other social sciences yet are used relatively little in plant pathology contexts. In this research, we draw upon an extensive data set of the incidence of hop plants with powdery mildew (caused by *Podosphaera macularis*) collected from yards in the U.S. state of Oregon during 2014 to 2017, and associated metadata, to understand variation in and causes of growers' fungicide use intensity and their associated costs. A generalized random forest model identified growers' spring pruning thoroughness, cultivar susceptibility to two of the dominant pathogenic races of *P. macularis*, network centrality of a yard during May-June and June-July time transitions, and the initial strain of the fungus detected as important variables determining the number of pesticide active constituents applied and resulting costs incurred in response to powdery mildew. We confirmed the results of the generalized random forest by fitting exposure-response functions after covariate balancing. Exposure-response functions indicate that both the number of pesticide active constituents that growers applied and costs scaled linearly with the seasonal mean incidence of plants with powdery mildew. While the causes of pesticide use intensity are multifaceted, these factors collectively influence the incidence of powdery mildew, which has a direct exposure-response relationship on the number of pesticide active constituents and ultimately the annual costs of disease management. Our analyses point to several potential strategies for reducing pesticide use and costs for powdery mildew on hop. We also highlight the utility of these methods in other plant pathology contexts where large, observational data sets are available.

Financial support: U.S. Department of Agriculture (CRIS 2072-21000-061-000-D) and National Institute of Food and Agriculture Specialty Crop Research Initiative (2021-51181-35901)

Pathogen process models: versatile tools for disease risk prediction

Robert M. Beresford

The New Zealand Institute for Plant and Food Research, Auckland

E-mail: Robert.beresford@plantandfood.co.nz

Disease prediction or forecasting relies on models that predict disease risk, or potential disease, rather than disease itself. The disease triangle tells us disease develops when a virulent pathogen, a susceptible host and a favorable environment all occur together. In the real world it is rare for all three components to be sufficiently well understood to allow actual disease to be predicted. Disease risk is the probability disease will develop when a model's risk indicator predicts it will. There are always uncertainties in the prediction that the model user must be happy to accept and there are always components affecting disease that the model does not consider that the user must make their own interpretation about. The uncertainties and missing components should be unimportant in relation to the reliability of the model's risk indicator. The risk indicator may be empirically derived using statistical relationships between disease and predictive variables (usually weather). Alternatively, the risk indicator may be derived from controlled experiment data on pathogen or disease processes in response to environmental or other variables. These process models need to be thoroughly tested (validated) to ensure they accurately represent pathogen and disease behavior in the real world. The process model approach has proved useful for myrtle rust (*Austropuccinia psidii*), which is an invasive pathogen affecting the myrtle family (Myrtaceae) that has recently spread throughout the Southern Hemisphere. It arrived in New Zealand in 2017 and threatens several native species there with local extinction. The Myrtle Rust Process Model (MRPM) was initially developed during the government incursion response to predict how climate would affect the regional and seasonal risk of disease establishment. It predicts epidemiological parameters of infection risk, latent period, and spore production risk from gridded hourly data at 1.5 km spatial resolution generated by the New Zealand Convective Scale Model (NZCSM) numerical weather model. The hourly resolution output is processed into weekly risk maps, which are publicly available and used for planning disease surveillance and management. The model predicts three epidemiological parameters: 1) **Infection risk**, modelled as a 3-D surface using temperature and high relative humidity duration. Field validation of this has been done in New Zealand's temperate climate for the low temperature end of the response. The high temperature end is to be investigated in a Brazilian collaboration with the University of Sao Paulo. 2) **Latent period**, modelled as a function of temperature, initially using data for other rust species, it now uses *A. psidii* data from an Australian collaboration with the Queensland Department of Agriculture. 3) **Spore availability** risk is modelled as a function of temperature using the pathogen development rate derived from the latent period study and the effect of intense rainfall on spore removal. The MRPM has been adapted as a decision support tool with a weather station network for timing fungicides against myrtle rust in plant nurseries, for predicting climate change impacts on myrtle rust and for identifying ecological refugia in natural areas, where the climate is suitable for susceptible Myrtaceae host species but less so for the pathogen. Compared with empirical models, the process modelling approach provides a theoretical basis that allows ongoing model improvement over time and adaptation to new purposes.

Financial support: New Zealand Government, Biological Heritage National Science Challenge, Nga Raku Taketake.

Disease models for decision-making in crop protection

Irene Salotti¹, Vittorio Rossi¹

¹ Department of Sustainable Crop Production (DI.PRO.VES.), Università Cattolica del Sacro Cuore, Piacenza, Italy.

E-mail: irene.salotti1@unicatt.it ; vittorio.rossi@unicatt.it

The call for agricultural sustainability makes of paramount importance the reduction of negative effects on human health and the environment due to a large use of chemical pesticides for plant disease control. In this frame, pesticides should be used only when really needed, so switching from calendar- to risk-based applications. Plant disease prediction models support tactical decisions about whether and when crop protection interventions are needed to control the outbreak or progress of a disease. Given the number of pathogens that affect cultivated crops, with different lifestyles and infection cycles, multiple models and modeling approaches have been developed to synthesize the effect of environmental conditions and/or host growth stages on disease prediction for the implementation of risk-based management options. These models, alone or in a modelling ensemble approach, aim to predict infection periods during the crop growing season and their severity, or the disease progress to predict when the disease incidence/severity will increase to a threshold causing an economic loss. Four representative examples are provided here, which provide an overview of main applications and implications of disease models for improving crop protection sustainability. In a first example, the control of tomato late blight (caused by *Phytophthora infestans*) was organized by combining the predictions of infection events provided by diverse models, i.e., Infection Potential Index (IPI), Main Infection and Sporulation Period (MISP) and Fry's model, which consider different aspects of the disease cycle and the effect of diverse weather conditions. This combination made it possible to define the first seasonal spray and the following risk-based schedule of plant protection products during the tomato growing season by saving 30 to 55% depending on the season. In a second example, the fungicide application frequency for the control of secondary infections of grape powdery mildew (caused by *Erysiphe necator*) was based on the accumulation over the incubation period of an infection risk provided by a mechanistic model that accounts for both weather conditions and ontogenic resistance of clusters. In this approach, the interval between treatments in affected vineyards can be longer or shorter based on the risk, so leading to a reduction in the number of sprays and of their dosage as well. In a third example, the usual scheduling of plant protection products against *Botrytis cinerea* on grapevine, which is based on the host growth stages, was integrated with a model accounting for the multiple infection pathways that mainly occur in two periods (i.e., between flowering and fruit set, and after version) and cause blossom blight, latently infected berries, and berry rots. The model use made it possible to avoid unnecessary interventions while providing efficient control of the disease at harvest by using either chemical fungicides, botanicals, or biocontrol agents (BCAs). Modelling of BCAs is also part of this approach. In a fourth example, a model simulating the disease severity progress of powdery mildew on wheat (caused by *Blumeria graminis*) was used to accurately predict the intervention threshold, which is usually assessed through disease assessments in the field.

Economic analysis of plant disease epidemics across multiple fields: estimating the economic cost of pathogen adaptation to control measures

Alexey Mikaberidze¹, Chaitanya S. Gokhale^{2,3}, Maria Bargues-Ribera^{2,4}, Prateek Verma^{5,6,7}

¹ School of Agriculture, Policy and Development, University of Reading, Reading, United Kingdom

² Research Group for Theoretical Models of Eco-evolutionary Dynamics, Department of Theoretical Biology, Max Planck Institute for Evolutionary Biology, Ploen, Germany

³ Center for Computational and Theoretical Biology, Julius-Maximilians-Universitaet, Wuerzburg, Germany

⁴ Cambridge Infectious Diseases IRC - Department for Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom

⁵ Helmholtz-Institute for Functional Marine Biodiversity, University of Oldenburg, Oldenburg, Germany

⁶ Institute for Chemistry and Biology of the Marine Environment, University of Oldenburg, Oldenburg, Germany

⁷ Faculty of Business Administration and Economics, Bielefeld University, Bielefeld, Germany

E-mail: a.mikaberidze@reading.ac.uk

Epidemics of plant diseases are estimated to cause significant economic losses in crop production. Fungicide applications are widely used to control crop diseases but incur substantial costs that consist of direct and indirect costs. One essential class of indirect costs arises due to the evolution of fungicide resistance. This indirect cost must be estimated reliably to design economic policy for more sustainable use of fungicides. Such estimation is difficult because the cost depends on economic parameters and the epidemiological/evolutionary properties of crop pathogens. Even a conceptual framework for such estimation is missing. To address this problem, we combined a spatially implicit mathematical model of crop epidemics with an economic analysis at the landscape scale. We investigated how the net economic return from a landscape depends on the proportion of fungicide-treated fields. We discovered a pattern of accelerating (or decelerating) returns, contrary to expected diminishing returns. Next, we calculated the economic cost of the evolution of fungicide resistance as the difference between the optimal net return of the landscape in the absence and presence of resistance. We found that this cost depends strongly on the fungicide price, the degree of resistance, the pathogen's basic reproduction number and the yield loss due to disease. Surprisingly, the cost declines with the fungicide price and exhibits a non-monotonic pattern as a function of the basic reproduction number. Hence, to calculate the cost of resistance evolution, we must estimate these parameters robustly, incorporating variations in environmental conditions, crop varieties and the genetic composition of pathogen populations. Appropriate estimation of the cost of resistance evolution can inform economic policy and encourage more sustainable use of fungicides.



Adapting global plant health management to global change: Opportunities for contributions from epidemiology

Karen A. Garrett

Plant Pathology Department, Global Food Systems Institute, and Emerging Pathogens Institute, University of Florida, USA

E-mail: karengarrett@ufl.edu

Protecting plant health contributes to several of the UN Sustainable Development Goals, including ending poverty (Goal 1), ending hunger (Goal 2), and protecting terrestrial ecosystems (Goal 15). Perspectives such as ‘disaster plant pathology’ (Etherton et al., in review) can help to focus translation of epidemiological ideas to provide the most useful information in the face of climate change and disruptions by human epidemics and wars. Epidemiologists can contribute to global change adaptation by building better systems for decision support, from on-farm management by smallholders to global management. **The developmental stages of national programs for plant health protection.** One compelling vision for global systems supporting plant health is the proposed global surveillance system for plant disease (Carvajal Yepes et al. 2019). A ‘global epidemiology system’ would be a key component. Of course, there are currently many individual components of a global epidemiology system, driven by many individual projects and dedicated individuals and teams. One approach to improving systems is for epidemiologists to consider the developmental stages of national programs for plant health protection, in terms of the ‘core’ epidemiological needs of even a small program, and the most important epidemiological components to add when a program adds new resources and capacity. Core components can be evaluated in terms of the value of information generated and the corresponding cost of information. **Open-source ecosystems for epidemiological tools.** Identifying core epidemiological tools furthers the development of open-source ecosystems for software and databases, facilitating analyses and developing synergies among research programs. For example, our lab is advancing the R2M toolbox (garrettlab.com/r2m) including (a) software to evaluate habitat connectivity for pathogen invasions (the geohabnet package in R), (b) tools for expert knowledge elicitation to synthesize expert knowledge, and (c) software to implement scenario analysis for regional management options (the INA package in R). These tools are designed for applications ‘early in the developmental stages of national programs’ because they can be applied to make the most of currently available information and knowledge. There are also exciting possibilities for new synergies across applications of artificial Intelligence. **Global communities of practice in epidemiology.** Realizing these possibilities globally will depend on the development of global communities of practice supporting capacity development. Projects like Open Plant Pathology and the Global Plant Health Assessment help to strengthen these communities. New approaches for linked teaching and research, such as global research collaboration workshops (GRCWs), offer other opportunities for strengthening communities that leverage new options for online development of global communities and projects.

Financial support: USDA NIFA, NSF, USDA APHIS, CGIAR, USAID, Keck Foundation, FFAR

Tools, data resources and methods for modelling climate change effects on plant disease

Adam H. Sparks¹

¹ Curtin Biometry and Agriculture Data Analytics, Centre for Crop and Disease Management, Curtin University, Bentley, WA 6102, Australia.

E-mail: adam.sparks@curtin.edu.au

Modelling the effects of climate change on plant disease has been and continues to be an important part of the work of plant disease experts. An important piece of the work is to choose the right methods, tools and data. There are several freely open source (FOSS) tools available which do not require purchases and help make the work more widely shareable as anyone can download and install them without purchase. The programming languages, Julia, R and Python are all FOSS, and widely used in science which makes them ideal for this type of work. Good quality historical and future climate data is the main ingredient to do this type of modelling work. There are several freely available historical, current and future climate and weather data sources that are easily accessible through any of these three languages, *e.g.*, NASA POWER, GSOD, WORLDCLIM, but all have advantages and disadvantages depending upon the type of work being conducted. Several approaches have been used for modelling the effects of climate change on plant disease, ranging from mechanistic to statistical or empirical models with linkages between different types of models being used as well at geographic scales ranging from local to global and all scales in between. Due to the flexible nature of these tools, it is possible to use only one end-to-end to create whole pipelines to carry out the work or combine them to use the best packages available for the task now that it is much easier to seamlessly use these three languages together. All three languages offer user-contributed packages that make this work easier, whether it is acquiring weather and climate data, processing data statistical methods or even providing plant disease models. All can also easily handle modelling the effects of climate change on plant disease. The choices made will largely come down to the researcher's comfort with any of the three first, and secondly, the availability of the desired models or methods. I will discuss the support that all three languages provide for these activities and provide a brief overview of climate and weather data sources and some of the modelling approaches that have been used as a primer to get started in this area.

Financial support: Analytics for the Australian Grains Industry (AAGI) provided support for Adam Sparks' registration and travel to IEW13 through the project [CUR2210-005OPX](#).

Epidemiology and etiology of *Alternaria* leaf blight and head rot caused by multiple species of *Alternaria* in the Eastern United States

Sydney Everhart¹, Roy L. Davis Jr. II¹, Daniel Cerritos Garcia¹, Amelia Martin¹, Hirut Betaw, Christine D. Smart, Christy Hoepting, David Langston, Mychele Batista da Silva, Steven Rideout, Karan Patel, and Babesh Dutta

¹ University of Connecticut, Storrs, CT, ² Cornell University, Geneva, NY, ³ Virginia Tech University, Blacksburg / Suffolk, VA, ⁴ University of Georgia, Tifton, GA.

E-mail: everhart@uconn.edu

Alternaria leaf blight and head rot is one of the major fungal diseases causing pre- and post-harvest yield loss in commercial broccoli production in the Eastern United States. In recent years, producers have reported a lack of disease control after the application of QoI fungicides. Suspecting emergence of fungicide resistance as the driver, we conducted a multi-state survey of the pathogen from the states of Georgia, Virginia, New York, and Connecticut. Initial findings revealed the presence of two species: *Alternaria brassicicola*, the typical causal agent, and *A. japonica*, which had previously only been reported in the states of California and South Carolina; these two species were initially identified by a differential ability to sporulate in culture. Examining the fungicide sensitivity profiles of a selection of isolates showed *A. japonica* is 10X less sensitive to azoxystrobin, but sequencing revealed no mutations conferring heritable fungicide resistance. In a subsequent multi-state survey to collect symptomatic leaves from cruciferous crops and weeds in the same area in 2021 and 2022, we obtained 525 *Alternaria* spp. isolates. Although no *A. japonica* were identified, several isolates were identified as *A. alternata*, which were found to be less sensitive to azoxystrobin and contained the G143A mutation known to confer qualitative resistance to QoI fungicides. Taken together, these results have yielded a number of questions related to the epidemiology and management of this disease that we are investigating, such as: 1) how significant is the seedborne disease pathway? 2) are *A. japonica* or *A. alternata* significant yield-limiting pathogens? 3) are cruciferous weeds a potential source of the pathogen? 4) what are the optimal conditions for disease development of the different species? Currently underway are controlled studies to better understand how humidity and temperature affect development of disease caused by each of these species and population genetic studies to understand the biology and epidemiology of disease caused by *A. brassicicola*. These studies aim to fill a significant gap in our knowledge of this disease, especially as related to the different species and differences in response to fungicides.

Financial support: USDA-SCRI 2020-51181-32062

Modelling fungicide resistance management strategies: progress and challengesJames A. D. Elderfield¹, Nick Taylor¹, Nik J. Cunniffe¹¹ Department of Plant Sciences, University of Cambridge, United Kingdom

E-mail: njc1001@cam.ac.uk

Fungicide resistance management – optimising deployment of agrochemicals to delay the emergence and/or spread of resistant pathogen strains – has been studied for many decades. There is an equally long-standing modelling literature, in which various tactics have been compared. Many aspects of spray programmes can – and have – been modelled, from doses, to timing, to spatial patterns, to numbers of sprays per season. Modellers have paid particular attention to how a chemical “at risk” of resistance can be protected by combining fungicides with different modes of action. The key distinction has been between mixtures (applying two or more chemicals in a single spray) *versus* alternations (applying different chemicals sequentially). I will start by describing work showing why mixtures are expected to always outperform alternations, and how two at-risk chemicals can optimally be combined. However, almost all modelling studies focus on qualitative resistance, characterising fungicide resistance as a single monogenetic trait. This is attractive mathematically – since it allows models to track only two classes of pathogen – but is a significant simplification. For many fungicide/pathogen combinations, resistance is instead polygenic, characterised by gradual qualitative shifts in sensitivity of the pathogen population over time. Models also tend to assume disease pressures that remain constant from season to season (although yields vary as control efficacy is lost due to the spread of resistant pathogen). I will describe recent work focusing on polygenic resistance, focusing on septoria leaf blotch of winter wheat. The model is fitted to data from field trials in Denmark and allows quantitative fungicide resistance to be modelled. The model also captures the between-year fluctuations in disease pressure that characterise real field situations. Of course, challenges remain. Dispersal of inoculum means that resistance management decisions made by a single grower affect all other growers at regional scales, but models have not addressed this so far. And rich genetic data sets are becoming ever more commonplace, leading to opportunities to better inform models of resistance dynamics using field data. I will conclude my talk by briefly outlining a few open areas, intending to spark discussion of what, precisely, should be included in models, and how this can be done.

Financial support: BBSRC

Managing fungicide resistance in *Botrytis*

Katherine Ann Gredvig Nielsen^{1,2}, Magne Nordang Skårn¹, May Bente Brurberg^{1,2}, Arne Stensvand^{1,2}

¹Division of Biotechnology and Plant Health, Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway

²Department of Plant Sciences, Faculty of Biosciences (BIOVIT), Norwegian University of Life Sciences (NMBU), Ås, Norway

E-mail: arne.stensvand@nibio.no

Grey mould caused by *Botrytis* spp. is an important disease in numerous crops, and intensive fungicide treatments are often carried out, not just in production plantings but also in plant nurseries. The widespread use of single-site fungicides exerts strong selection pressure on pathogens already prone to development of fungicide resistance due to biological characteristics, such as a polycyclic life cycle. Consequently, several species of *Botrytis* are ranked as being at high risk for the development of fungicide resistance by the Fungicide Resistance Action Committee (FRAC). Numerous mutations leading to fungicide resistance have been described in populations of *Botrytis*, with reduced or poor control of grey mould as a result. Strains of *Botrytis* carrying mutations for resistance to several fungicides are described from many countries, and in Norway strains with resistance to 5 to 6 different fungicide groups have been found in several crops. In commercial perennial plantings of raspberry with high frequencies of multiresistant *Botrytis* strains, eliminating the use of one fungicide (fenhexamid) over a 3-year period with the purpose of restoring efficacy, had no or limited effect. Continued use of other fungicides during this period likely selected for multiresistant strains, thus maintaining resistance to fenhexamid. On the other hand, in a perennial strawberry field where there was a high frequency of resistance to fenhexamid, resistance decreased gradually if fungicide applications ceased. In several cropping systems, it is common to buy transplants from specialized plant nurseries, and planting material is frequently transported between countries. For example, in strawberry, fungicide-resistant strains of *Botrytis* were commonly found in both domestically produced and imported transplants. For certain samples, up to 100% of the strains isolated from imported planting material were resistant to fungicides commonly used in strawberry fruit production. Resistance to a fungicide only recently approved in Norway was also detected. These findings illustrate how trade with planting material may reduce the efficacy and/or life expectancy of available fungicides. In an area of Norway where fungicide resistance was suspected to have caused reduced disease control of grey mould in strawberry, the problem with grey mould experienced by the growers did not necessarily coincide with fungicide resistance frequencies. Other aspects of production, such as row width, use of fertilizers and watering, probably affected disease control in addition to fungicide resistance. Access to new classes of chemicals for disease management is likely very limited in the future. To continue using available fungicides, strict fungicide resistance management schemes should be followed in both plant nurseries and production fields. Plant nurseries should avoid using fungicides needed for fruit production. Non-chemical alternatives should be utilized to reduce inoculum (e.g., steaming or hot water treatments of planting material) and for control in periods of low disease pressure (e.g., biological control agents and biopesticides). If available, the number of fungicide applications may be limited by following advice from disease warning systems. Furthermore, it may be possible to develop models to predict efficacy of fungicide treatments based on the frequency of fungicide resistant mutants and the frequency of subsequent treatments of fungicides in the different FRAC groups.

Epidemiology- based management of vegetable diseases

Mary Ruth McDonald, Kevin Vander Kooi and Tyler Blauel

Department of Plant Agriculture, University of Guelph, Guelph, ON Canada

E-mail: mrmcdona@uoguelph.ca

An integrated pest management (IPM) program for onions and carrots began in the Holland Marsh, Ontario, Canada, in 1980 and has continued, with a few breaks, since that time. The 'Marsh' is an intensive area of vegetable production with family owned farms. Individual grower fields are monitored twice a week and the scouting information is provided to the grower immediately after the field is scouted. For onions, disease forecasting and spray recommendations are done for Botrytis leaf blight (*Botrytis squamosa*), onion downy mildew (*Peronospora destructor*) and since 2013, Stemphylium leaf blight (*Stemphylium vesicarium*). There is also pest monitoring that provides spray recommendations for onion thrips (*Thrips tabaci*). BOTcast is used to forecast Botrytis leaf blight. This uses temperature and leaf wetness information plus field scouting to determine when a spray threshold of one lesion per leaf is reached. Forecasting for onion downy mildew is done with Downcast, which incorporates temperature, leaf wetness, other environmental parameters, and the presence of sporangia on spore traps. The forecasting program for Stemphylium leaf blight (SLB) is still under development but incorporates temperature, leaf wetness and the presence of conidia. Growers were faster to adopt spray timing based on insect monitoring than for disease forecasting, probably because they can see the insects, or early insect damage, while conidia or sporangia are microscopic. They have experienced diseases that can be difficult to manage once the symptoms are easy to see. Also, it is easy to understand that there is no point in spraying for an insect pest if it is not there. Adoption of spray timing for Botrytis leaf blight was fairly rapid, possibly because risk of disease (disease severity units) developed slowly over time and the spray threshold worked well once effective fungicides were registered. Onion downy mildew only occurs in the region about one in every four years, and most growers follow disease management recommendations, holding off on Oomycete specific fungicides when there is low risk and spraying immediately when there is disease risk. Grower acceptance probably developed over years of trial and error and observing what their neighbours were doing. Growers mostly apply more fungicide sprays for SLB than needed, but the forecasting program also triggers too many sprays. In carrots, there are disease forecasting programs for Cercospora leaf spot (*Cercospora carotae*) and Alternaria leaf blight (*Alternaria dauci*) but spray decisions are mostly based on monitoring for threshold levels of symptoms in the field. The system has been used for decades and is mostly followed by growers, although a fungicide spray is also recommended just before the canopy closes over the rows. There is a forecasting program for white mold on carrot (*Sclerotinia sclerotiorum*) based on weather variables, but it is largely ignored. Growers in Eastern Canada routinely trim the carrot foliage to reduce white mold because the disease develops to a level that could cause economic losses almost every year. In the Marsh, white mold is less frequent; losses develop one year in four, or less frequently. Growers are not interested in trimming the foliage to prevent white mold and only express interest in spraying when symptoms are extensive. Some growers say 'just tell me what and when to spray and I'll do it'. Others take longer to adopt disease forecasting. Past experience, effective fungicides and spray thresholds based on visible symptoms contribute to grower confidence in epidemiology- based disease management for onion and carrot.

Financial support: Funding for the IPM program was provided by the Bradford Co-operative Storage Ltd., growers participating in the program, FS Partners, Bayer Crop Science, BASF, Corteva, FMC and Syngenta Crop Protection.

Exploring causal relationships to improve the development of production and management scenarios

Paul Esker¹, Spyros Mourtzinis², Shawn Conley³, and Denis Shah⁴

¹Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, University Park, PA, USA.

²AgStat Consulting, Athens Greece

³Department of Plant and Agroecosystem Sciences, University of Wisconsin-Madison, Madison, WI, USA.

⁴Department of Plant Pathology, Kansas State University, Manhattan, KS, USA

E-mail: pde6@psu.edu

As the volume of available data in the agricultural sciences increases, it is crucial to consider the best approaches for modeling relationships between potential explanatory variables and the measure of interest. The gold standard in these situations has often been randomized controlled trials (RCTs). Still, these are often limited in spatial distribution and in the number of factor combinations that can be examined in any one trial. An alternative approach we are exploring is the use of multi-state observational data derived directly from grower-reported practices at the field or farm level. We hypothesize that observational data contains complex relationships integrating agricultural production and management practices with measures such as yield or disease beyond that afforded by traditional RCTs. Moving past statistical correlative (associative) structures into causal questions of direct interest to agricultural production is a critical challenge and may be better afforded by observational data. In this talk, we will illustrate the causal approach by making use of a large multi-state benchmarking study on soybean production practices and yield. Data from individual fields were collated across 10 states ($n = 3,614$) over three years (2014-2016). Our question was whether the use of a fungicide seed treatment (FST) in soybean is responsible for a yield increase, compared to an FST having *not been used in the same field*, and to estimate the magnitude of that effect, should it exist. We used different estimators proposed in the causal literature, starting with a very simple difference-in-means estimator and working towards more complex estimators that reduce bias and variance in the estimates of causal effect. Results from our analyses suggest that the causal effect of FST was similar to estimates from published RCTs. Our approach illustrates the power of using causality but also shows that it is important to carefully consider the estimation methods and inference when comparing results from causal modeling with the literature.

Financial support: North Central Soybean Research Program and the USDA National Institute of Food and Agriculture and Hatch Appropriations under Project #PEN04836 and Accession #7005075.

Epidemiology-based management strategies for citrus Huanglongbing

Renato B. Bassanezi¹

¹ Department of Research and Development, Fundecitrus, Araraquara SP Brazil.

E-mail: renato.bassanezi@fundecitrus.com.br

The rapid spread, difficulty in control, and severe fruit yield and quality loss make Huanglongbing (HLB), caused by the phloem-restricted bacterium '*Candidatus Liberibacter asiaticus*', the main citrus disease in the world. Due to the absence of resistant varieties and curative measures the disease control is based on exclusion, eradication, and protection measures. However, aspects of HLB epidemiology make its control very difficult. Citrus is a perennial crop exposed for many years to infections. The disease latent period (~14 days) much shorter than the incubation period (≥ 4 months) allows infected trees to serve as an inoculum source before they are detected what makes the disease eradication almost impossible. Inoculum sources outside commercial orchards and the long-distance dispersal of the vector, the Asian citrus psyllid *Diaphorina citri*, makes the disease primary spread as or more important than the secondary spread for the epidemic progress, resulting in almost no effect of removing diseased trees only within commercial orchards on reducing the disease incidence. In addition, diseased adult trees maintain residual production for a few years, leads growers to not immediately remove them and keep potential inoculum sources inside the orchard. Psyllids prefer new shoots to feed on, which requires a greater frequency of insecticide sprays to keep a protective barrier to prevent the bacteria transmission during the development of new leaf tissues. Secondary infections are almost fully controlled with fortnightly insecticide sprays that break the development of psyllid life cycle on infected trees and kill adult psyllids that acquired the bacteria on diseased trees before the latency period of the bacteria in the vector was concluded. In turn, primary infections by infective psyllids that developed in diseased trees and moved to commercial orchards are partially controlled even with weekly insecticide sprays during the vegetative flushing period (poor coverage, rain-wash, growth of unprotected new tissues). The decreasing gradient of the psyllid and diseased trees populations from the orchard edge to the center has been directed the inspections for the vector and diseased trees, as well as the application of measures that reduce the primary dispersion to the interior of the property, such as: planting density and direction, planting of varieties with different vigor, trap-crop, more intensive applications of insecticides and repellent kaolin. The seasonality of the psyllid population and the period of greater disease symptom expression have directed the periods of highest frequency of insecticide application and actions to detect symptomatic trees, respectively. However, all mentioned measures partially control the primary infections, and their efficacy is dependent on the amount of primary inoculum. Thus, for the effective HLB control, citrus growers must control the vector and reduce inoculum sources both inside and outside the orchards in a coordinated and joint way, which is still difficult to achieve in practice due to their diverse profile. Good disease control was achieved where regional and integrated management was carried out, and this is the way until more effective and sustainable measures, such as resistant citrus cultivars, are available.

Financial Support: FAPESP (Project #17/21460-0) and CNPq (Project 304253/2020-0).

INDEX OF ORAL TALKS			
Number	Presenter	Title	Page
O1	Zhanhong Ma	The application of remote sensing in plant disease monitoring	29
O2	Joaquin Guillermo Ramirez-Gil	Development of digital platforms for data management and analysis for evidence-based decision-making of plant epidemics	30
O3	Paul Melloy	Utilising an application programming interface (API) for delivering spatial risk of blackspot to growers through commercial third-party farm management platforms	31
O4	Berea A. Etherton	Disaster plant pathology: smart solutions for natural and human-driven cataclysms threatening global plant health	32
O5	Matt Combes	Examining the effect of ash dieback disease on the spread and detection of Emerald ash borer beetle in the UK	33
O6	Matheus Borba	<i>Colletotrichum</i> species infecting apples in Mid-Atlantic United States: identification, infection sources, geographical distribution, ecology and spore trapping with qPCR	34
O7	Andreas von Tiedemann	Role of seed infection for the near and far distance spread of wheat blast caused by <i>Magnaporthe oryzae</i> pathotype Triticum	35
O8	Alice K. Inoue-Nagata	Enhancing geminivirus detection in plants: unveiling hidden threats with a cost-efficient RCA-RFLP method	36
O9	Lisa Rothmann	Sorghum disease surveillance to understand South African producer perceptions and inform disease management and industry needs	37
O10	Silvio A. Lopes	Variation in the potential of diseased citrus trees in backyard as sources of <i>Candidatus Liberibacter asiaticus</i> to commercial groves	38
O11	Aaron I. Plex Sulá	Global host-pathogen infection networks in major terrestrial agroecosystems	39
O12	Maria Cristina Canale	Natural infectivity of the corn leafhopper, <i>Dalbulus maidis</i> , with the Corn Stunting Complex pathogens in Santa Catarina, Brazil	40
O13	Zvezdomir Jelev	A model to predict spore maturation of <i>Blumeriella jaapii</i> in cherry	41
O14	Vinicius C. Garnica	Novel weather variables associated with epidemics of <i>Stagonospora nodorum</i> blotch of winter wheat	42
O15	Damon L. Smith	Predicting tar spot of corn in the U.S. – Developing the infrastructure for corn disease modeling	43
O16	José F. González-Acuña	Using environmental variables for the development of logistic regressions to predict frogeye leaf spot in soybean in the United States	44
O17	Vinicius A. Cerbaro	Influence of the El Niño Southern Oscillation on the risk of <i>Botrytis</i> fruit rot occurrence in Florida	45
O18	Elin K. Falla	A mathematical model centred on aphid vector feeding behaviour has implications for plant host manipulation by non-persistently transmitted viruses	46
O19	José M. C. Fernandes	Mitigating the impact of drought and wheat blast on rainfed wheat production in the Brazilian Cerrado based on the selection of sowing dates and varieties	47
O20	Maria Chiara Rosace	Spatial modelling of hotspots for plant pests introductions in the EU using regionalized data	48
O21	Israël Tankam Chedjou	Combining masculinizing resistance, rotation and biocontrol to achieve durable suppression of the potato pale cyst nematode:	49

		a model	
O22	Carlos C. Gongora-Canul	Comparative epidemiology of tar spot as an endemic and emerging disease in the Americas	50
O23	Belachew Asalf	Effect of cover crops and green manuring on sclerotinia white rot disease development and yield in carrot	51
O24	Ayalsew Zerihun	What happens to durability of disease control in fields of growers who run a resistance management programme when neighbours use only one component of the resistance management?	52
O25	Juan A. Paredes	Analysis of the field-scale spatial pattern of peanut smut in Argentina	53
O26	Sara Thomas-Sharma	One brick at a time: Building on epidemiological insights for improved management of Cercospora leaf blight on soybean in the mid-South	54
O27	Vincent Philion	Combining foliar deposit distribution and dose-response curve data to predict fungicide efficacy against scab in apple orchards, and practical implementation in the AOS43 dosing system	55
O28	David M. Gadoury	A review of pathogen biology, ecology, epidemiology, and the use of germicidal ultraviolet light to suppress plant pathogens	56

The application of remote sensing in plant disease monitoring

Jianmeng Gao, Jie Deng, Ziqian Yang, Zhanhong Ma

Department of Plant Pathology, China Agricultural University 100193 Beijing.

E-mail: mazh@cau.edu.cn

The efficient detection of plant diseases, especially airborne diseases such as wheat rusts and corn rusts, is vital for disease epidemic forecast and disease control. Conventional disease investigation relies on field scouting which is labor intensive and generally shows low efficiency. Disease monitoring based on remote sensing techniques is an alternative to detect diseases in a fast and non-destructive way. Several studies about disease monitoring based on remote sensing data acquired at different levels have been conducted and satisfying results have been obtained. In order to explore the reliability of spectra collected under solar illumination (SCUSI) and evaluate the impact of maize leaf curvature (the smoothness of the leaf surface) on disease severity classification, single-leaf level hyperspectral data obtained under different measuring conditions was analyzed based on analysis of variance (ANOVA) and random forest classifier. The results indicated that the PRI was the optimal index for SCR classification based on the SCUSI, with an overall accuracy of 81.30% for mixed samples. The results lay the foundation for SCR detection in the incubation period. Our other studies mainly focused on RGB and hyperspectral imageries acquired on unmanned aerial vehicle (UAV) platform. Convolutional neural networks (CNNs) and RGB-based high spatial resolution images were explored to detect wheat stripe rust transmission centers (Infected area accounted less than 1.35 %) occurrence in complex fields conditions. CNNs semantic segmentation architecture (deeplabv3+) was applied to per pixel classify the imagery for the detection of healthy wheat and stripe-rust-infected wheat (SRIW) and SRIW was accurately detected (Rust class F1 = 0.81). In terms of the application of UAV hyperspectral imagery, vegetation indices (VIs) and their optimal band combinations for the quantitative inversion of wheat stripe rust were assessed. In addition, we proposed an end-to-end, pixel-level quantitative regression methodology, underpinned by deep learning techniques. The optimal results were achieved using the Laplacian + MSE loss function combined with the HRNet_W18 algorithm model, yielding a test set R² value of 0.875 and a mean squared error (MSE) of 0.0129.

Financial support: the National Key Research and Development Program of China (2021YFD1401000, 2023YFD1400800) and the Key Research and Development Projects of Ningxia Hui Autonomous Region (2016BZ09).

Development of digital platforms for data management and analysis for evidence-based decision-making of plant epidemics

Kevin Steven Quiroga-Benavides¹, Camilo Andrés Borda-Gil², Joaquin Guillermo Ramirez-Gil^{1*}

¹Universidad Nacional de Colombia sede Bogotá, Facultad de Ciencias Agrarias, departamento de Agronomía. Laboratorio de Agrocomputacion y Analisis Epidemiologico

²Universidad Nacional de Colombia sede Bogotá, Facultad de ingeniería.

E-mail: jgramireg@unal.edu.co

The advent of Industry 4.0 has ushered in a new era in agriculture, characterized by digital, intelligent, or 4.0 agriculture. Decision support systems (DSS) and Internet of Things (IoT)-based application development platforms are noteworthy technologies within this paradigm. This study focuses on the development of user-friendly, accessible, and free interfaces to facilitate the management, visualization, and modeling of plant epidemics in tropical agricultural systems. The digital ecosystem, encompassing data capture, transmission, and consumption, provides robust tools for presenting results, statistics, and model projections. End-users can utilize a mobile application, developed in an open multi-platform language (such as Dart) using the Flutter framework, connected to a web application developed in Python through the Flask framework. Communication between platforms is cloud-based, utilizing a database and a virtual server, facilitating file hosting and information exchange between the web and mobile platforms. The study's outcomes successfully demonstrate technological solutions with a high problem-solving capacity in plant epidemics management. This achievement is attributed to the seamless integration and coordination of technological tools, user-driven data capture and transmission, and the validation, consumption, and application of free-access products through Application Programming Interfaces (APIs). The presented approach offers a promising avenue for advancing plant epidemics management practices in tropical agricultural settings.

Financial support: Universidad Nacional de Colombia, sede Bogota and Fedearroz (Project # 51201), and Fedepapa (Project # 44763.)

Utilising an application programming interface (API) for delivering spatial risk of blackspot to growers through commercial third-party farm management platforms

Paul Melloy¹, Art Diggle², Jean Galloway³, Jenny Davidson⁴, Victor Galea¹, Adam H. Sparks^{5,6}

¹ The University of Queensland, School of Agriculture and Food Sustainability, Gatton, Queensland, 4343 Australia

² Department of Primary Industries and Regional Development, 1 Nash St, Perth 6000, Western Australia, Australia

³ Department of Primary Industries and Regional Development, 75 York Road, Northam 6401, Western Australia, Australia

⁴ South Australian Research and Development Institute, GPO Box 397, Adelaide 5001, South Australia, Australia

⁵ University of Southern Queensland, Centre for Crop Health, Toowoomba, Queensland, 4350, Australia

⁶ Curtin University, Centre for Crop and Disease Management, Bentley, Western Australia, 6102, Australia

E-mail: p.melloy@uq.edu.au

While decision support tools (DSTs) can inform farm management strategies and improve the economic return for interventions lowering plant disease impacts, their widespread adoption can remain a challenge. Since 2004, Blackspot Manager has been instrumental in aiding agronomists and growers to mitigate black spot (*Mycosphaerella pinodes*) risks in Australian field peas in Australia. Each week it calculates the residual ascospore inoculum load depending on local weather condition records, advising delayed sowing until the inoculum load on crop residue drops below 40%. The latest version, Blackspot Fieldpea Manager (BlackSpotFPM), integrates a spatiotemporal spore dispersal model by leveraging satellite data to remotely sense previous season field pea paddocks, potential sources for black spot inoculum. Encapsulated within a Docker instance for streamlined cloud deployment, BlackSpotFPM includes an API that provides access to spatial disease risk maps. This API integration allows commercial third-party farm management software to seamlessly incorporate black spot risk assessments into existing crop rotation planning to strategically avoid areas estimated as prone to spore showers. However, crop rotation decisions are generally prepared between 3 – 7 months prior to sowing dates, leading to inflexibility in paddock choice in the sowing window. Due to this fact a spatial spore dispersal model is ineffective in decision support when actual weather records are used. To overcome this issue and provide spatial risk maps we used up to 12 years of weather station data, and epidemiological knowledge of *M. pinodes* ascospore ejection behavior, to determine the likely prevailing weather conditions during spore dispersal events for each day of the year. From this data we stochastically estimate weather data and the associated spore dispersal risk. This approach provides timely disease risk information and significantly lowers adoption barriers, serving as a blueprint for the deployment of future DSTs.

Financial support: The Grains Research Development Corporation DAW2112-002RTX, DAW1810-007RTX

Disaster plant pathology: smart solutions for natural and human-driven cataclysms threatening global plant health

Berea A. Etherton¹, Robin A. Choudhury^{1,2}, Ricardo I. Alcalá Briseño^{1,3}, Romaric A. Mouafo-Tchinda¹, Aaron I. Plex Sulá¹, Disaster Plant Pathology Group, Karen A. Garrett¹

¹ Plant Pathology Department and Global Food Systems Institute, University of Florida, Gainesville, FL, USA,

² School of Earth, Environmental, and Marine Sciences, University of Texas Rio Grande Valley, Edinburg, TX, USA,

³ Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, USA

Email: betherton@ufl.edu and karengarrett@ufl.edu

In our era marked by compounding natural disasters, exacerbated by the influence of climate change and geopolitical conflicts, we need to understand the complex interplay between these cataclysms and plant health. We develop the concept of “disaster plant pathology,” which we define as the study of the effects of disasters on plant health and the design of management solutions. Disaster plant pathology delves into the intricate connections between natural and human-driven disasters and their impacts on the emergence and establishment of plant diseases, posing threats to plant health and global food security. Here we provide examples of a disaster plant pathology perspective on potato health in Cameroon and Ethiopia. We conducted expert knowledge elicitation and analyzed trade and cropland data to generate risk maps for key potato pests and pathogens. For example, bacterial wilt is spreading in Ethiopia and the surrounding region, and efforts to limit spread are challenging, in part due to national and regional conflicts. In Cameroon, locations in the Northwest were identified to be at high risk for the establishment and spread of key potato diseases, and are experiencing mass migrations due to the Anglophone Crisis. As part of the general framework of disaster plant pathology, we describe the effects of pulse disasters, such as flooding, landslides, or insect swarms, which cause plant pests and pathogens to spread and establish in unique ways, distinct from press disasters, such as droughts, armed conflicts, or deforestation. We propose strategic solutions to mitigate the effects of disasters through risk map development and management priority maps. Disaster preparedness and resilient food security can be bolstered by the integration of early warning systems, decision support systems, and digital agriculture.

Financial Support: UF/IFAS, CGIAR, USAID

Examining the effect of ash dieback disease on the spread and detection of Emerald ash borer beetle in the UK

Matt Combes¹, Nathan Brown^{2,3}, Vasthi Alonso Chavez³, Alice Milne³, Stephen Parnell¹

¹ Warwick Crop Centre, School of Life Sciences, University of Warwick, Stratford-upon-Avon, CV35 9EF, United Kingdom.

² Forest Research, Alice Holt Lodge, Farnham, GU10 4LH, United Kingdom.

³ Rothamsted Research, Harpenden, AL5 2JQ, United Kingdom.

Email: matt.combes@warwick.ac.uk

Symptoms of ash dieback disease (ADB), caused by the East Asian fungus *Hymenoscyphus fraxineus*, were first noticed in Poland in the early 1990s. The disease is now present across much of the European continent and results in high mortality of European ash, with estimates reaching around 50% mortality 30 years after pathogen arrival. This has resulted in European ash being listed as an endangered species in Sweden, and the costs of the disease have been estimated to be billions of pounds in the UK alone. Meanwhile, *Agrius planipennis* (emerald ash borer beetle (EAB)), also native to East Asia, has resulted in the death of millions of ash trees across North America since it was first detected in 2002. The beetle was first recorded on the European continent in Moscow in 2003, and has now spread as far west as Kiev. Efforts are currently underway in the UK to prepare effective surveillance and management strategies for the beetle given the potential consequences of pest arrival and spread. However, to optimise surveillance and management of the pest, its interaction with ADB must be considered. Therefore, in this study a compartmental model was developed for the arrival, spread and progression of ADB in the UK, which accounted for both stand and environmental effects on disease progress. This model was then linked to a spread model for EAB in the UK. The impact of likely ADB and EAB interactions on spread and surveillance of the pest were examined. Our results will facilitate optimisation of surveillance and management measures for both the beetle and ADB in the UK.

Financial support: Funded by United Kingdom's Research and Innovation (UKRI) Programme through the Natural Environment Research Council (NERC) (Project: NE/T007729/1).

***Colletotrichum* species infecting apples in Mid-Atlantic United States: identification, infection sources, geographical distribution, ecology and spore trapping with qPCR**

Matheus Borba¹, Nathaniel Boeckman¹, Phillip Martin², Kari Peter³, Srđan Aćimović¹

¹ Plant Pathology Laboratory, School of Plant and Environmental Sciences, Alson H. Smith Jr. Agricultural Research and Extension Center, Virginia Polytechnic Institute and State University, Winchester, VA, United States.

² LABServices, Hamburg, PA, United States

³ Department of Plant Pathology and Environmental Microbiology, Fruit Research and Extension Center, The Pennsylvania State University, Biglerville, PA, United States.

E-mail: matheuscb@vt.edu

In the Mid-Atlantic region of the United States, apple growers face escalating challenges in managing bitter rot, a destructive disease caused by *Colletotrichum* spp. (CS). Various factors, including apple cultivar susceptibility, temperature, rainfall and pathogen biology, contribute to the complexity of the issue. The Mid-Atlantic region is responsible for the production of \$500 million worth of apples, making it a globally important region for production. Understanding CS infection is hindered by knowledge gaps related to primary infection sources, geographical distribution and epidemiological aspects such as infection timing. The *C. gloeosporioides* species complex (CGSC) and the *C. acutatum* species complex (CASC) are the primary causal agents of bitter rot in apples. These fungi can survive in various structures, such as buds, mummies, dead wood and cankers serving as potential sources of infection. We collected 226 apple buds from two locations and six cultivars and found that 10% were infected with the CGSC and 4% with the CASC. We conducted spore trapping in PA orchards and adjacent forested woodlots and quantified rain-splashed conidia by qPCR. Surprisingly, the forests contained the highest conidia quantities, supporting the hypothesis of forest plants as a source of conidia stemming from leaf endophytes. Fruit samples with characteristic bitter rot lesions were collected from 38 orchards across NY, PA, MD, VA, DE, and OH yielding over 600 fungal isolates, with 510 identified as CS. Eight species were identified, with *C. fiorinae*, *C. chrysophilum*, *C. noveboracense* and *C. siamense* constituting 97% of the isolates. The remaining 3% included *C. fructicola*, *C. henanense*, *C. nymphaeae*, or *C. gloeosporioides* sensu stricto. Temperature-dependent growth rates influenced the distribution of these species, with CASC favored at lower temperatures and CGSC at higher temperatures. A latitudinal CS diversity pattern emerged from NY, over PA to VA. These results lay the groundwork for future epidemiological research employing ddPCR to quantify the DNA of CS propagules from infection sources. Furthermore, we aim to pinpoint the timing and morphological distinctions of symptoms for each species and evaluate the precision of current infection prediction models in the context of Mid-Atlantic weather conditions. This knowledge will identify the optimal timing for preventive spray applications, enhancing the effectiveness of existing disease management strategies. Additionally, we delve into the mechanisms of apple skin resistance to infection, contributing to improved disease management strategies.

Financial support: Northeast SARE (Subaward # GNE16-180-32231); USDA NIFA and SHAP (Project #PEN04694); New York ARDP (Projects #83268 #86698); USDA SCBG (Award #89379-P001/SCBG 19 006); NSF GRFP.

Role of seed infection for the near and far distance spread of wheat blast caused by *Magnaporthe oryzae* pathotype *Triticum*

Musrat Zahan Surovy ^{1,2*}, Andreas von Tiedemann ^{1*}

¹ Department of Crop Sciences, Division of Plant Pathology and Crop Protection, Georg-August-Universität Göttingen, Grisebachstraße 6, 37077 Göttingen, Germany

² Institute of Biotechnology and Genetic Engineering (IBGE), Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur - 1706, Bangladesh

E-mail: atiedem@gwdg.de

Magnaporthe oryzae pathotype *Triticum* (MoT) causes wheat blast which may threaten wheat production in warmer climate zones. Effective disease control is hampered by limited knowledge about the life cycle and epidemic spread of MoT. Since MoT mainly infects and colonizes the inflorescences of wheat, seed transmission is a potential major path of far distance dissemination, while not much is known about the near distance spread within a field. In order to explore these aspects, infection, invasion routes and colonization of MoT on wheat ears and in wheat seeds were investigated histologically. MoT was spray inoculated on two wheat cultivars (Sumai 3, susceptible and Milan, resistant) at three spike maturity stages (full ear emergence, growth stage (GS) 59; mid flowering, GS 65; and end of flowering, GS 69). Incidence of MoT on Sumai 3 seeds was 100% and 20-25% on Milan. Accordingly, MoT sporulation rate on Sumai 3 contaminated seeds was more than 15 times higher than on Milan. The colonization of MoT within various seed tissues was followed by light and confocal laser scanning microscopy (CLSM). Invasion of MoT in seeds predominantly occurred in the caryopsis germ region, but entry via other seed parts was also observed, confirming the potential of intense colonization of MoT in wheat grains. Fungal spread in wheat plants growing from MoT infected seeds was monitored through plating, microscopic and molecular techniques. Under greenhouse conditions, no spread of MoT from infected seeds to seedlings later than GS 21 or to ears was detected, neither in Milan nor in Sumai 3. We therefore conclude that MoT may not systemically contaminate inflorescences and seeds in plants grown from infected seeds, in neither susceptible nor resistant cultivars. However, seed-derived initial blast symptoms, only found on seedlings of Sumai 3 but not Milan, resulted in early conidial propagation, which may serve as inoculum source for plant-to-plant dissemination by airborne infection of plant stands in the field (short distance spread). Ultimately, this initial inoculum may infect young inflorescences in the field and contaminate the seeds. Our findings confirm the risk of long-distance dissemination of wheat blast across continents through MoT-contaminated seeds and clarify the mechanisms of dissemination on the field scale. This underlines the importance of using healthy seeds and/or effective chemical seed dressings as strategies to control any further spread of wheat blast.

Enhancing geminivirus detection in plants: unveiling hidden threats with a cost-efficient RCA-RFLP method

Alice K. Inoue-Nagata¹, Roberta R. P. N. Lima, Yanca F. M. Ferreira, Erich Y. T. Nakasu¹

¹ Laboratório de Virologia, Embrapa Hortaliças, Brasília DF Brasil.

E-mail: alice.nagata@embrapa.br

Monitoring diseases is crucial for effective plant health management. Choosing the right analysis method is key to obtaining maximum information with minimal effort and cost. In Virology, traditional diagnostics based on symptom analysis and specific tests might overlook viruses causing mild symptoms or asymptomatic infections, especially in cases of unknown agents or mixed infections. High Throughput Sequencing (HTS) technology has emerged as an efficient tool for detecting unknown or unreported viruses. However, its high per-sample cost limits widespread use. This work describes a highly efficient method for detection of ssDNA viruses, the RCA-RFLP, for universal detection of geminiviruses. RCA, a unique DNA amplification technique, coupled with RFLP, generates species-specific band profiles, allowing preliminary identification of circular ssDNA viruses. Until recently, begomoviruses were the only geminivirus members identified in Brazil. Their detection relied on a widely adopted PCR method using universal primers. Since 2018, however, two other geminivirus members, mastreviruses and topileviruses, were also identified in the country; these viruses cannot be detected by begomovirus universal PCR. An analysis of composite tomato leaf samples exhibiting typical begomovirus infection symptoms over different years, G1 (2003-05), G2 (2009-11), and G3 (2014-16), revealed a decreasing diversity of begomoviruses in the tomato production area of Taquara, in the Federal District. This shift from high diversity and mixed infections to few viruses in simpler infections was identified using PCR, HTS and RCA-RFLP methods (Souza et al., FPS 2020). The study uncovered the presence of a topilevirus in G1 tomato samples, initially undetected by begomovirus-specific PCR, but later confirmed by HTS and RCA. This indicated the limitations of using PCR for detecting a broad range of geminiviruses. Recent visits to Brazilian tomato fields consistently identified two topileviruses, which were spread in the major growing areas. Symptoms induced by topileviruses resembled those caused by begomoviruses, leading to failures in topilevirus detection if using begomovirus-specific PCR. Therefore, our laboratory now adopts RCA-RFLP as the standard test for suspected geminivirus infections. Ongoing research focuses on understanding the importance and distribution of topileviruses in tomatoes and associated plants.

Financial support: Embrapa, FAPDF and FAPESP

Sorghum disease surveillance to understand South African producer perceptions and inform disease management and industry needs

Thabiso V. Masisi¹, Kwanele S. Sabela¹, Nomvula Moloi¹, Sethulego Z. Matebesi², André J. Pelser², [Lisa A. Rothmann](mailto:coetzeeLA@ufs.ac.za)¹

¹Plant Pathology, Department of Plant Sciences, University of the Free State, Bloemfontein, Free State, South Africa, 9300; ²Department of Sociology, University of the Free State, PO Box 339, Bloemfontein 9300, South Africa.

E-mail: coetzeeLA@ufs.ac.za

The establishment of best practices for managing plant diseases are defined by the context and knowledge available at the time of concern. As grain sorghum production is undergoing a 'revival' in South Africa there is a need to revise the context of production and diseases impacting sorghum to support producers. Disease surveys were conducted in 2023 (n = 26 fields) and 2024 (ongoing) to determine the occurrence, distribution and prevalence of foliar and panicle diseases affecting commercial and small-scale production systems. A minimum of 500 plants per field, from late flowering to soft/hard dough stages were visually scored for fungal diseases. Ten fungal diseases (values in brackets indicate prevalence, followed by incidence ranges) were identified from characteristic symptoms, including anthracnose (34%; 0.6 - 100%), covered smut (1%; 0 - 2.5%), grain mold (9%; 0 - 64%), head smut (4%; 0 - 0.2%), leaf blight (70%; 3 - 69%), oval leaf spot (8%; 1.2 - 12.2%), rust (1%; 0 - 23%), sooty stripe (18%; 2.7 - 71.8%), target leaf spot (4%; 13 - 23%), and zonate leaf spot (1%, 0 - 1.2%). Fungal species associated with grain mold were confirmed through sequencing *ITS* and *EF* gene regions. Ten fungal genera were confirmed, although predominant species include mycotoxigenic fungi, *Alternaria*, *Curvularia*, *Fusarium*, and *Phoma/Epicoccum*. Concurrent sociological interviews (n = 24 in 2023; ongoing in 2024) were conducted with producers to provide insight into perceptions of production risks, disease constraints, and management practices to elucidate the context of sorghum production. Sociological interviews with five key sections; 1) demographics, 2) production practices, motivation, and frustrations, 3) awareness of pests, diseases, and mycotoxins, 4) climate change-focused practices and 5) information sources were designed. Farmers perceived bird predation, leaf blight, ergot, and grain mold as the greatest yield-limiting biotic constraint, which aligned with our findings in the field, except for ergot which was recognised as seasonal and sporadic. Six producers were certain they can distinguish between healthy and molded grain, although, 64% of those respondents were unaware of mycotoxins risks and their effects. Integrated management practices implemented include a range of cultivar/landrace selection, crop rotation, tillage, pesticides, and fertilisation. Producer information sessions were held to provide feedback on diseases, share possible management strategies and raise awareness of mycotoxins and mitigation thereof. Collaborations to include nematodes, fungal/bacterial soilborne and viral diseases have been initiated to strengthen and provide a comprehensive assessment of challenges producers face. Next-generation sequencing will be conducted on samples collected in 2024 to explore fungal taxa associated with grain mold under contrasting production systems and climates. This is the first South African sorghum disease survey in 30-years, providing farmers, researchers, funding bodies, and governmental agencies with guidelines for phytosanitary priorities, developing appropriate disease management and assisting the newly established pre-breeding programme.

Financial support: Sorghum Trust; National Research Foundation: Thuthuka Grant (TTK220323450) .

Variation in the potential of diseased citrus trees in backyard as sources of *Candidatus Liberibacter asiaticus* to commercial groves

Silvio A. Lopes, Fernanda A. Q. Benedito, Julio C. S. Vasconcelos, Juan C. Cifuentes-Arenas

Departamento de Pesquisa e Desenvolvimento, Fundo de Defesa da Citricultura, Araraquara SP, Brasil.

E-mail: silvio.lopes@fundecitrus.com.br

Candidatus Liberibacter asiaticus (CLAs), transmitted by the Asian citrus psyllid (ACP) *Diaphorina citri*, causes Huanglongbing (HLB), the most destructive disease of citrus. Success in the management of HLB requires regional control of ACP and removal of symptomatic trees in commercial and abandoned groves, and in backyards near commercial groves. Although mandatory in São Paulo state (SPS), diseased trees in backyards usually are not eliminated and hardly submitted to any measure to reduce vector establishment and reproduction. Since in diseased trees the presence of new shoots (NS) is frequent, conditions exist for ACP to reproduce in backyards making the trees potential sources of CLAs-carrying ACP that migrate to commercial groves. The processes involved in CLAs dissemination are complex with the bacterium titer in NS of diseased trees an important part. It will dictate the probability that the pathogen will be acquired by ACP and further transmitted to healthy trees. The higher the titer, the higher the acquisition probability. The titer of CLAs in NS of the diseased trees is, in turn, associated with the environmental conditions at which the trees had been exposed to. Since the climate varies considerably across the main citrus belt of Brazil, which includes several municipalities in SPS and Minas Gerais state, we evaluated the potential of HLB-symptomatic trees in backyards of different regions as sources of infective ACPs. From June 2018 to September 2023, CLAs-negative adult ACPs were caged for one week to lay eggs on NS of diseased trees growing in the regions of Triângulo Mineiro (municipalities of Frutal-Campo Florido, located in the upper north of citrus belt), Bebedouro (municipality of Barretos, north), Votuporanga (northwest), Matão (São Lourenço do Turvo, center), and Itapetininga (south). The adult offsprings that resulted from the confinement were transported to an acclimatized room located at Fundecitrus and confined individually for another week on NS of healthy plants or plantlets. Air temperature of the acclimatized room was $26\pm 2^{\circ}\text{C}$ and the NS on the healthy plants or plantlets were at the v2-v3 stages, both conditions highly favorable to CLAs infection. As a control, insects were confined on potted symptomatic plants kept at the same acclimatized room, and their offspring treated as those from the field. After the inoculation access period, the adults were removed and kept in the freezer and the plants/plantlets transferred to a greenhouse. Eight months later, plants and frozen insects were evaluated through qPCR for the presence of CLAs. Percentage of CLAs-carrying ACP positively correlated with CLAs titers in NS where the psyllids developed ($R^2 = 26.59\%$). Percentage of successful CLAs transmission positively correlated with CLAs titer in ACP ($R^2 = 48.83\%$). The average percentage of CLAs-carrying ACPs reared on the diseased plants in the acclimatized room was $74.8\pm 8.1\%$, ca. 2.3 times higher than the average percentage of ACPs reared on the diseased trees in backyards (min. $23.6\pm 11.6\%$ in São Lourenço do Turvo; max. $39.7\pm 9.7\%$ in Itapetininga). However, of the CLAs-carrying ACP, only ca. one half of insects reared in the acclimatized room, and one third of those reared in backyards, were able to transmit CLAs. All these variations in abilities to acquire and/or inoculate CLAs by ACP, between regions and seasons or between field and acclimatized room, might be the result of variations in the environment where the diseased trees and ACP had been exposed, and should be considered during the development of epidemiological models aimed to estimate favorability indexes of CLAs dissemination based on climate data.

Financial support: FAPESP (Project # 2017/21460-0).

Global host-pathogen infection networks in major terrestrial agroecosystems

Aaron I. Plex Sulá^{1,2,3}, Karen A. Garrett^{1,2,3}

¹Plant Pathology Department, University of Florida, Gainesville, FL USA

²Global Food Systems Institute, University of Florida, Gainesville, FL USA

³Emerging Pathogens Institute, University of Florida, Gainesville, FL USA

Email: plexaaron@ufl.edu and karengarrett@ufl.edu

Cross-species transmission of plant pathogens has multifaceted impacts on natural and agricultural ecosystem sustainability. The structure of host-pathogen infection networks is important for anticipating cross-species transmission dynamics, yet remains largely unquantified. We aggregated species-specific infection reports into a new reference data inventory to build global bipartite host-pathogen networks based on experimentally tested or naturally sampled compatible interactions between 1,000 economically important pathogens and ~10,000 plant species. In these bipartite networks, pathogen species are linked to host species if the pathogen is known to infect the host. The number of pathogens reported per crop species varies widely. For example, almost twice as many tomato pathogens have been reported compared to wheat pathogens. We also found that a single crop's pathogens can infect at least 1,273 plant species, from which a minimum of 1,700 host-switching events can be inferred. Although most host species that share a pathogen with a crop belong to the same plant family, the plant species most closely related to a crop often share fewer pathogens than plant species in other genera. In the global infection network, *Hordeum vulgare*, *Secale cereale*, and *Avena sativa* have an exceptionally high pathogen-sharing potential for wheat pathogens, indicating strong epidemiological similarities between these widely cultivated (perhaps highly exposed) species. Close relatives of modern bread wheat, such as *Triticum dicoccum*, *Triticum monococcum*, or *Triticum durum*, which are morphologically or phylogenetically similar, share fewer reported wheat pathogens and have a medium pathogen-sharing potential. These findings contrast with the hypothesis that closely related plants would share more pathogens. Whether differences in reported pathogen sharing may be due to unevenly distributed research efforts remains to be assessed. There is a strong positive correlation between host sharing and host range, where pathogens with high average host sharing potential had a large host species range, a pattern that is consistent with expectations. Understanding geographic multi-host and multi-pathogen assemblages can boost epidemic surveillance planning with epidemiologically intelligent strategies. Host-pathogen infection networks can serve as a data-driven foundation for future quantitative assessments, for example, to identify relationships among pathogen host ranges, lifestyles (e.g., necrotrophy), life cycles (monocyclic versus polycyclic), and pathogen taxonomic groups, expected from traditional knowledge.

Financial support: USDA.

Natural infectivity of the corn leafhopper, *Dalbulus maidis*, with the Corn Stunting Complex pathogens in Santa Catarina, Brazil

Maria Cristina Canale¹, Marcos Vinícius Silva de Andrade¹, Eduardo S. Gorayeb², Lilian Katiany Castello Rabello Zinger², Monalisa Cristina De Cól³, Emerson Medeiros Del Ponte³ and Fábio Nascimento da Silva²

¹ Centro de Pesquisa para Agricultura Familiar (Cepaf), Empresa Brasileira de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (Epagri), Chapecó SC Brasil.

² Centro de Ciências Agroveterinárias (CAV), Universidade do Estado de Santa Catarina (UDESC), Lages SC Brasil.

³ Departamento de Fitopatologia, Universidade Federal de Viçosa (UFV), Viçosa MG Brasil.

E-mail: cristinacanale@epagri.sc.gov.br

The Corn Stunting Complex is a growing concern in Brazil, marked by numerous outbreaks since 2015, particularly impacting Santa Catarina state. In the 2020/21 season alone, the state experienced a significant drop in productivity from the usual 7.7 t/ha to 5.5 t/ha, resulting in a 38% decrease in yield production. This complex involves the Maize bushy stunt phytoplasma ('*Candidatus* Phytoplasma asteris'), Corn stunt spiroplasma (*Spiroplasma kunkelii*), and Maize rayado fino virus (MRFV), all persistently transmitted by the corn leafhopper, *Dalbulus maidis* (Hemiptera: Cicadellidae). We intended to verify the natural infectivity of *D. maidis* with both mollicutes and the virus during the 2021/22 and 2022/23 maize crop years in Santa Catarina State. Yellow sticky traps were installed in 23 maize crops in different municipalities. The traps were weekly replaced and addressed to the laboratory during 40 weeks, from July to April, which comprehended interseason (before maize sowing), main season (first planting period, in August or September, depending on the location), second season (second sowing season, generally in January) and postharvest. *D. maidis* specimens were removed from the traps and up to 7 samples were set using insects in triplicates for each location and week, and submitted to molecular diagnosis. Both mollicutes and the virus were found infecting the leafhoppers. Comparable prevalence with an average count of 11.96 insects positive to spiroplasma and 7.51 to phytoplasma occurred in the 2021/22 maize crop year, with the second season exhibiting the highest incidence of mollicute-infected insects. In the subsequent maize crop year (2022/23), MRFV emerged as the dominant pathogen with an average count of 25.5, followed by spiroplasma (11.1), while phytoplasma exhibited a lower prevalence at 5.9. The seasonal analysis revealed heightened prevalence of viruses and phytoplasma during the second season, contrasting with spiroplasma, which exhibited higher prevalence during the main season and interseason. This exploratory analysis showed that *D. maidis* infectivity with the corn stunting complex diseases pathogens associated with corn stunting disease complex diseases was distinct between both assessed maize crop years. This suggests that natural infectivity of this leafhopper vector may be associated with singular aspects of each year, such as climate, which perhaps influence the epidemiology of this pathosystem. These results are derived from Monitora Milho SC Program, an advisory system that aims to support the maize productive sector of Santa Catarina state regarding the Corn Stunting Complex. This information can be used in the future to design an accurate risk analysis to this pathosystem.

Financial support: FAPESC (Grant N° 2021TR1246).

A model to predict spore maturation of *Blumeriella jaapii* in cherry

Martin Marinov¹, Arne Stensvand², Anne-Grete R. Hjelkrem², and Zvezdomir Jelev¹

¹ Department of Phytopathology, Agricultural University-Plovdiv, Plovdiv, Bulgaria.

² Norwegian Institute of Bioeconomy Research (NIBIO), Ås, Norway

E-mail: z_zhelev@au-plovdiv.bg

Cherry leaf spot, caused by the ascomycete *Blumeriella jaapii* (anamorph: *Phloeosporrella padi*), is a major disease in sweet and sour cherry worldwide. The disease can cause early defoliation followed by higher risk of winter damage and reduced fruit set in the next one or even two seasons. The main objective of this research was to develop a model to predict maturation of the primary inoculum of the fungus, which consists of both ascospores and conidia (the latter named “winter conidia”) produced in overwintered leaf litter on the ground. Seven-day Burkard volumetric spore traps were installed in sweet and sour cherry orchards in five locations in Bulgaria during the growing seasons of 2017 to 2020. The spore traps were placed on top of a 3 - 4 m² layer of heavily infected overwintered cherry leaves. Continuous seasonal data were achieved in 10 site-year combinations. Spore numbers were recorded with a light microscope. Locally installed automatic weather stations provided hourly records of precipitation, temperature, and duration of leaf wetness. The seasonal spore patterns confirmed ascospores as a main source of primary inoculum for a temperate climate zone country like Bulgaria; however, in certain years winter conidia also had a considerable share of the inoculum. The proportion of matured ascospores and winter conidia was modelled as functions of degree-days. The sigmoid Gompertz growth function was used as base function in all proposed models. Eleven different adjustments for the degree-day accumulation were suggested based on daily air temperature, alone or in combination with precipitation and leaf wetness. Generally, a better goodness-of-fit was detected when validating the model for the ascospores compared to the winter conidia. Among all models, the model with a degree-day accumulation with a base temperature of 0 °C combined with a downscaling of the temperature according to the amount of precipitation was selected. The downscaling was a linear function up to 4 mm of rain. The same model was selected with the best goodness-of-fit for both ascospores and conidia, but with separate parameterization. The proposed forecasting model will be a contribution to improved control of cherry leaf spot.

Novel weather variables associated with epidemics of *Stagonospora nodorum* blotch of winter wheat

Vinicius C. Garnica¹, Peter S. Ojiambo¹

¹ Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, NC, 27695, USA

E-mail: pojiambo@ncsu.edu

Meteorological conditions exert a substantial influence on the dynamics of plant disease epidemics. However, identifying disease-conducive weather factors is challenging due to the complex interplay between weather elements. Window-pane analysis is a popular method for systematically exploring time series for the influence of weather factors on a biological phenomenon, but it can lead to multiplicity issues and inflated type I error rates. In addition, many window-pane studies have relied on disease observations from susceptible cultivars. However, susceptible cultivars may still exhibit some level of resistance, making their response a flawed surrogate for environmental characterization in disease-weather linkage studies. Therefore, this study explored: 1) the use of stability selection algorithm to identify the most stable weather predictors for window-pane applications, and 2) the use of environmental loadings (λ), outputs from factor analytic linear mixed models, as response variables in disease-weather linkage studies. The latter provides a representation of environmental effects across all cultivars in multi-environment field trials. This framework was used to investigate meteorological conditions associated with *Stagonospora nodorum* blotch (SNB; caused by *Parastagonospora nodorum*) epidemics in winter wheat, using data from cultivar performance trials in North Carolina in 2021–2023. A total of 18eighteen commercial wheat cultivars were evaluated for SNB severity and incidence across 12twelve environments in field plots artificially infested with *P. nodorum* straw. Disease metrics examined included the final percent diseased leaf area (λ_{FPDLA}), the relative area under disease progress stairs (λ_{rAUDPS}), Julian day to 50% disease incidence ($\lambda_{T_{50}}$), and the weighted mean absolute rate of increase for disease incidence (λ_{ω}). Hourly meteorological data, including dewpoint (D), precipitation (R), relative humidity (RH), and air temperature (T) were aggregated based on various intra-day periods (daytime, nighttime, dawn, and dusk) and window-pane lengths (5, 10, 15, 20, 25, and 30 days; w_5 , w_{10} , w_{15} , w_{20} , w_{25} , w_{30} , respectively), with the final disease assessment date ($LAG = 0$) used as the delineation point. This combination resulted in >3000 weather-engineered features that were submitted to stability selection. A total of 1,149 stably selected variables were found to be associated with SNB risk across disease metrics and windows examined, with bootstrap Spearman mean correlation ($\hat{\rho}^*$) values ranging from -0.96 to 0.94. Notably, the weather element most consistently associated with λ_{FPDLA} was *RH8.peak3.nighttime* across all windows, except w_5 . Conversely, *TRH.20T25nRH.L35* at w_{10} was negatively associated with λ_{FPDLA} . These associations persisted for nearly 10 consecutive days and occurred as early as 60 to 40 days before the date of disease assessment, underscoring their predictive value in assessing early-season SNB risk. Many other temperature and rainfall-based predictors were associated with λ_{rAUDPS} , $\lambda_{T_{50}}$, and λ_{ω} during the season. Collectively, this study leads to a more comprehensive characterization of weather factors associated with the temporal dynamics of SNB in wheat, which can potentially improve prediction accuracy of disease risk at regional and field levels.

Financial support: Funds appropriated to the Entomology and Plant Pathology Department at North Carolina State University, and the National Institute of Food and Agriculture, United States Department of Agriculture (USDA).

Predicting tar spot of corn in the U.S. – Developing the infrastructure for corn disease modeling

Damon L. Smith¹, Richard W. Webster², Camila Nicolli³, Tom W. Allen⁴, Mandy Bish⁵, Kaitlyn Bissonnette⁵, Jill C. Check⁶, Martin I. Chilvers⁶, Maíra R. Duffeck⁷, Nathan Kleczewski⁸, Jane Marian Luis⁷, Brian D. Mueller¹, Pierce A. Paul⁷, Paul P. Price⁹, Alison E. Robertson¹⁰, Tiffanna J. Ross¹¹, Clarice Schmidt¹⁰, Roger Schmidt¹², Teryl Schmidt¹, Sujong Shim¹¹, Darcy E.P. Telenko¹¹, Kiersten Wise¹³

¹ Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI U.S.A.

² Department of Plant Pathology, North Dakota State University, Fargo, ND U.S.A.

³ Rice Research and Extension Center, University of Arkansas, Stuttgart, AR U.S.A.

⁴ Delta Research and Extension Center, Mississippi State University, Stoneville, MS U.S.A.

⁵ Division of Plant Science and Technology, University of Missouri, Columbia, MO U.S.A.

⁶ Department of Plant, Soil, and Microbial Sciences, Michigan State University, East Lansing, MI U.S.A.

⁷ Department of Plant Pathology, The Ohio State University, Wooster, OH U.S.A.

⁸ Department of Crop Sciences, University of Illinois, Urbana, IL U.S.A.

⁹ Macon Ridge Research Station, LSU AgCenter, Winnsboro, LA U.S.A.

¹⁰ Department of Plant Pathology, Entomology, and Microbiology, Iowa State University, Ames, IA U.S.A.

¹¹ Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN U.S.A.

¹² Nutrient and Pest Management Program, University of Wisconsin-Madison, Madison, WI U.S.A.

¹³ Department of Plant Pathology, University of Kentucky, Princeton, KY U.S.A.

E-mail: damon.smith@wisc.edu

Phyllachora maydis is a relatively new fungal pathogen of corn in the U.S. and is considered a sub-tropical pathogen of corn. However, due to changing climate, *P. maydis* has established itself as the primary pathogen of concern in the Midwest Corn Belt. Efforts of the National Predictive Modeling Tool Initiative (NPMTI) Corn Research Area Committee (RAC) led to coordinated field and on-farm trials that resulted in 588 observations of tar spot severity from both small-plot trials and commercial fields between 2018 and 2023. These data were combined with gridded, site-specific weather data. The blended dataset was then used in correlation analyses, 'windowpane' analyses, logistic regression analysis, and machine learning modeling to develop new tools appropriate for tar spot prediction in the U.S. Corn Belt. The resulting models were used to develop the decision support system (DSS) called Tarspotter, which is now deployed freely as a smartphone application (app) across the U.S. The infrastructure established to develop the models and DSS for tar spot will be used to develop models and DSSs for northern corn leaf blight, gray leaf spot, and other important diseases of corn in the U.S. In addition, models will be augmented with spore trapping information and subsequent modeling to improve accuracy.

Financial support: National Predictive Modeling Tool Initiative

Using environmental variables for the development of logistic regressions to predict frogeye leaf spot in soybean in the United States

José F. González-Acuña¹, Mandy D. Bish², Carl A. Bradley³, Travis R. Faske⁴, Jessica M. Scherer⁵, Heather M. Y. Kelly⁶, Dean K. Malvick⁷, Dylan Mangel⁸, Samuel G. Markell⁵, Daren S. Mueller¹, Paul P. Price III⁹, Damon L. Smith¹⁰, Darcy E. P. Telenko¹¹, Richard W. Webster⁵

¹ Department of Plant Pathology and Microbiology, Iowa State University;

² Division of Plant Science and Technology, University of Missouri,

³ Department of Plant Pathology, University of Kentucky;

⁴ Department of Entomology and Plant Pathology, University of Arkansas;

⁵ Department of Plant Pathology, North Dakota State University;

⁶ Department of Entomology and Plant Pathology, University of Tennessee;

⁷ Department of Plant Pathology, University of Minnesota;

⁸ Department of Plant Pathology, University of Nebraska-Lincoln;

⁹ Department of Plant Pathology and Crop Physiology, Louisiana State University;

¹⁰ Department of Plant Pathology, University of Wisconsin-Madison;

¹¹ Department of Botany and Plant Pathology, Purdue University

Email: richard.webster@ndsu.edu

Soybean production worldwide faces challenges from pathogens, particularly *Cercospora sojina*, the cause of frogeye leaf spot (FLS). This polycyclic disease can complete its life cycle in just three weeks. To combat FLS, farmers have turned to chemical fungicides. Since 2005, US farmers have increased fungicide use, driven by rising soybean prices and the threat of FLS and other foliar diseases. This intensive use has led to *C. sojina* populations in the US developing resistance to quinone outside inhibitor (QoI) fungicides. However, there are no reports of resistance to other fungicide classes yet. As a method of ensuring these fungicide options remain effective, the use of predictive models can aid in reducing the frequency of fungicide applications. Between 2015 and 2022, 158 site-years of fungicide trials and field observations were compiled from across 7 US states. From these site-years, 188 total disease observations were used as response variables for developing logistic regression models. This dataset was then separated using a 70:30 split to create training and testing datasets. These data included a binary response if FLS developed between the first and second rating dates or not. To explain the progression of FLS at each site-year, hourly site-specific weather data was extracted, aggregated, and used to create 30-, 21-, 14-, and 10-day moving averages. From correlation analyses, the total number of hours with relative humidity greater than 75% was highly correlated with FLS development, and the highest correlation coefficient was 0.43 ($p < 0.001$) using the 21-day moving averages. Furthermore, both 21-day and 10-day moving averages of daily minimum temperature were significantly correlated with FLS development with the same Pearson correlation coefficients of 0.33 ($p < 0.001$). Multiple logistic regression models were created with these weather variables as predictors and the FLS development as the binary response. These models were evaluated against our testing dataset, and five models were identified as having the highest accuracy. The best-performing model was then integrated into a decision support system called FrogSpotter, currently being evaluated across US soybean-growing regions. In 2023, three risk thresholds were evaluated across eight states. Overall, FLS incidence and severity were low, and analyses are being performed to evaluate the model's accuracy to predict and inform applications of fungicides to manage FLS. The FrogSpotter tool is a step toward a more precise approach to managing FLS and fungicide stewardship. It has the potential to help soybean farmers make more informed fungicide use decisions.

Influence of the El Niño Southern Oscillation on the risk of Botrytis fruit rot occurrence in Florida

Vinicius A. Cerbaro¹, Clyde Fraisse¹, Natalia Peres²

¹ Department of Agricultural and Biological Engineering, University of Florida, FL, USA.

² Gulf Coast Research and Educational Center, University of Florida, FL, USA.

E-mail: cerbaro@ufl.edu

Florida, the second-largest producer of strawberries in the United States, accounts for over 15% of the country's total strawberry production (USDA, 2023). Nevertheless, the state's strawberry industry faces economic, regulatory, weather, and disease-related challenges. Fungal diseases, such as Anthracnose and Botrytis fruit rots, pose a significant threat to sustainable production. Traditional control methods, predominantly reliant on intensive fungicide application, incur substantial costs and contribute to the development of pathogen resistance. Additionally, the El Niño-Southern Oscillation (ENSO), a major driver of global climate variability, introduces an extra layer of complexity to Florida's agricultural landscape. Studies have shown that ENSO's influence on temperature and rainfall patterns may promote conducive environments for the proliferation of various plant pathogens. During El Niño seasons, Florida experiences higher amounts of rainfall and below-average temperatures, fostering increased humidity — a prime condition for escalating fungal diseases. To strengthen the understanding of the spatiotemporal relationship between ENSO and the risk of Botrytis occurrence in Florida, we ran a Botrytis infection risk model for all strawberry seasons (October to March) from 1980 to 2022. Weather data from the North American Land Data Assimilation System (NLDAS) dataset was used as input. Since leaf wetness data is not readily available on NLDAS and is a required model parameter, it was estimated using a majority-vote approach with four leaf wetness models. In the event of a tie, the classification conservatively defaults to wet. The selected Botrytis model has been employed in the strawberry advisory system (StAS), a robust tool that alerts users when conditions are favorable for disease occurrence. The StAS has been supporting strawberry producers in Florida for over a decade. The findings revealed discernible spatial and temporal variations in Florida's risk of Botrytis occurrence. Wetter conditions observed during El Niño seasons resulted in higher leaf wetness duration in southern counties and northeastern coastal regions. Despite the expectation of below-average temperatures during El Niño, warmer conditions were observed in the state's peninsula during periods of leaf wetness. In contrast, fewer days (approximately 12 days) conducive for Botrytis occurrence were observed during La Niña in central Florida. Moreover, considering the typical 7 to 10 days window of protection for spraying, the results suggested that, on average, 1 to 3 extra sprayings might be required during El Niño seasons. This study extends the understanding of ENSO influences in the dynamics of Botrytis occurrence in Florida, potentially inspiring further investigations. The insights gained contribute to strategic decision-making, as the results could be used to send proactive notifications to growers before seasons, offering an overview of expected conditions and allowing them to optimize their disease management strategies.

A mathematical model centred on aphid vector feeding behaviour has implications for plant host manipulation by non-persistently transmitted viruses

Elin K. Falla¹, Nik J. Cunniffe¹

¹Department of Plant Sciences, University of Cambridge, United Kingdom

Email: ekf32@cam.ac.uk

Plant viruses threaten global food security and are often horizontally transmitted by arthropod vectors. Non-persistently transmitted (NPT) plant viruses are characterised by a very short virus retention time in the vector and are transmitted almost exclusively by aphids, attached transiently to the aphid's stylet (mouthparts) and acquired and inoculated via brief epidermal probes. Many NPT viruses can alter their host plant's phenotype to change the behaviour of the aphid vectors in a way that often optimises virus transmission. Mechanistic epidemiological models of this phenomenon have historically overlooked a key feature of NPT virus retention within the aphid: probing or feeding on a plant is often what causes an aphid to lose the virus. A recently developed model captures this behaviour, but makes an assumption that an aphid is guaranteed to lose its infectivity after probing on one healthy plant. There are, to our knowledge, no experimental studies exploring the number of plants an aphid can probe before it loses an NPT virus from its stylet, but information gleaned from population bottleneck studies suggests that this assumption is not justified. Our new compartmental mathematical model includes the ability of an aphid to probe (and therefore potentially inoculate) multiple plants within one viruliferous period, while also capturing the aphid feeding behavioural aspect of their NPT virus retention. We use our novel model structure to explore the effect of NPT virus-induced host phenotypes on epidemic outcomes. We find that previous models underestimate the benefit of an "attract-and-deter" phenotype, where the virus induces increased initial aphid attraction to the infected plant but deters them from prolonged feeding. Our results also highlight the importance of characterising NPT virus longevity within the aphid during probing, as allowing for multiple infective probes increases the effectiveness of virus manipulation and hence resulting epidemic size, with implications for NPT virus epidemic prediction and control.

Financial support: University of Cambridge Department of Plant Science and Gonville & Caius College

Mitigating the impact of drought and wheat blast on rainfed wheat production in the Brazilian Cerrado based on the selection of sowing dates and varieties

Thiago Berton Ferreira¹, José Maurício C. Fernandes², Willington Pavan¹, Camilo de Lelis Teixeira de Andrade³, Gerrit Hoogenboom^{1,4}

¹ Department of Agricultural and Biological Engineering, University of Florida, Gainesville, FL, USA.

² Brazilian Agricultural Research Corporation, Embrapa Trigo, Passo Fundo, RS, Brazil.

³ Brazilian Agricultural Research Corporation, Embrapa Milho e Sorgo, Sete Lagoas, MG, Brazil.

⁴ Global Food Systems Institute, University of Florida, Gainesville, FL, USA.

E-mail:mauricio.fernandes@embrapa.br

In Brazil, the Cerrado biome presents a significant opportunity to expand wheat production in tropical zones. However, rainfed wheat production in this region faces challenges due to both biotic and abiotic stresses. Especially wheat blast, caused by *Magnaporthe oryzae* pathotype *Triticum (MoT)*, is a severe threat capable of rendering production nonviable during epidemic years. Sowing is timed to coincide with crop head emergence/flowering with drier periods to mitigate blast risks; however, this increases the risk for water deficiency. In recent decades, new cultivars that show moderate wheat blast resistance and heat tolerance have emerged. The goal of this study was to analyze the effects of drought and wheat blast on rainfed wheat production in the Cerrado. We considered four sowing dates within the rainy season and three cultivars. The wheat crop simulation model CSM-NWheat of DSSAT was coupled with a wheat blast disease model that was parameterized to simulate the life cycle of MoT. The coupled model has been incorporated into the GSSAT2 platform, a Geospatial Crop Modeling and Decision Support Tool designed for precision agriculture. This platform facilitates data-driven decision-making by enabling users to run spatial simulations across various scenarios. Simulations were conducted for the region at $0.25^\circ \times 0.25^\circ$ resolution using several data layers as input including digital elevation (>800 m), land use and coverage and others. Crop management was determined based on EMBRAPA recommendations for agricultural areas within the Cerrado. Thirty years of weather data (1990-2020) was extracted from the Comprehensive Brazilian Meteorological Gridded Dataset (BR-DWGD) for the entire region. For every grid cell, hourly relative humidity (RH), crucial for simulating MoT development, was retrieved from the NASA Power weather reanalysis dataset. Long-term simulations projections suggested that rainfed agro-ecosystems could achieve a grain yield up to 3.8 t ha^{-1} . However, wheat blast impacts can significantly reduce yield, especially in epidemic years. The outcomes of this will provide optimal combinations of cultivar selection and sowing dates as strategic management practices for wheat cultivation in the Cerrado to balance the threats of wheat blast and drought.

Spatial modelling of hotspots for plant pests introductions in the EU using regionalized data

Maria Chiara Rosace¹, Antonio Vicent², David V. Conesa³, Miguel A. Martinez Beneito³, Antonio Lopez³, Vittorio Rossi¹, Martina Cendoya²

¹ Department of Sustainable Crop Production, Università Cattolica del Sacro Cuore, Via Emilia Parmense, 84, 29122 Piacenza, Italy

² Centre de Protecció Vegetal i Biotecnologia, Institut Valencià d'Investigacions Agràries, 46113 Moncada (Valencia), Spain

³ VaBaR. Departament d'Estadística i I.O. Universitat de València c/Dr Moliner 50, 46100 Burjassot (Valencia), Spain

E-mail: mariachiara.rosace@unicatt.it

Plant pests represent a major challenge to global agriculture and biodiversity. The introduction of non-indigenous pests can have devastating ecological and economic consequences. Understanding the factors that contribute to the emergence of hotspots for these introductions is crucial for devising effective prevention and management strategies. This work aims to explore the results of a hotspot analysis using the dataset of plant pest introductions published recently. Data were collected regarding initial reported occurrences of plant pests in the European Union (EU) from 1999 to 2019, sourced from a range of published literature and online databases, including EASIN and EPPO, to determine pests' introduction trend over the years and spatial aggregation among EU regions. The database contains expert-revised data on 278 pests: it is estimated that on average around 15 new pests are detected within the EU territory each year, and in some years, there are as many as 25 introductions of new pests. Our study aims to reveal spatial clusters and hotspots of plant pest introductions, providing insights into the regions most at risk, also unveiling the key variables that are associated with their occurrence. A substantial portion of first pests' introductions in the EU was reported at region level, without indicating specific geographic coordinates, which is a challenging aspect for the spatial statistical analysis. In order to make use of the information associated with these regionalized data, we employed a Bayesian hierarchical spatial model previously used in disease mapping in public health studies for this type of data, to assess areas of higher risk by including covariates and random effects to borrow information from neighboring areas. This model allows accounting for fixed effects such as climatic or environmental variables, as well as complex structures such as spatial dependence. Due to the excess of zeros in most of the northern EU, a portion of the Mediterranean region has been selected, where introductions are mainly concentrated. Among all the human and environmental covariates we included, the best-fitting model comprises average temperature, average precipitation, human population density, and the spatial random effect. The identification of hotspots and vulnerable regions for plant pest introductions is instrumental in directing limited resources towards areas at higher risk, also contributing to the improvement of early warning systems and the development of targeted prevention, surveillance and mitigation strategies. Our model not only identifies higher-risk areas but also provides insights into the complex interplay of factors influencing pest introductions. Moreover, the utilization of a Bayesian hierarchical spatial model in this type of analysis represents a methodological innovation in the area of plant health. This approach contributes to the advancement of methodologies in the field of pest risk analysis, offering a robust framework for future studies using regionalized data in different geographic contexts.

Financial support: HoPPI (Project reference: GP/EFSA/ENCO/2020/02 - 3)

Combining masculinizing resistance, rotation and biocontrol to achieve durable suppression of the potato pale cyst nematode: a model

Israël Tankam Chedjou*, Josselin Montarry, Sylvain Fournet, Frédéric M. Hamelin¹

Institut Agro, Univ Rennes, INRAE, IGEPP, 35000, Rennes, France

E-mail: israel.tankamchedjou@agrocampus-ouest.fr

The pale cyst nematode, *Globodera pallida*, is a pest that poses a significant threat to potato crops worldwide. The most effective chemical nematicides are toxic to non-target organisms and are now banned. Alternative control methods are therefore required. Crop rotation and biological control methods have limitations for effectively managing nematodes. The use of genetically resistant cultivars is a promising alternative, but nematode populations evolve, and virulent mutants can break resistance after just a few years. Masculinizing resistances, preventing avirulent nematodes from producing females, are thought to be more durable than blocking resistances, preventing infection. Our demo-genetic model, tracking both nematode population densities and their genetic frequencies, shows that virulence against masculinizing resistance may not fix in the pest population, under realistic conditions. Avirulence may persist despite the uniform use of resistance. This is because avirulent male nematodes may transmit avirulence to their progeny by mating with virulent females. Additionally, because avirulent nematodes do not produce females themselves, they weaken the reproductive rate of the nematode population, leading to a reduction in its density by at least 20%. This avirulence load can even lead to the collapse of the nematode population in theory. Overall, our model shows that combining masculinizing resistance, rotation, and biocontrol may achieve durable suppression of *G. pallida* in a reasonable time frame. Our work is supported by an online interactive interface allowing users to test their own control combinations.

Financial support: European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No 899546 (Project NEMO) and ANR project BEEP (Behavioral Epidemiology and Evolution of Plant Pathogens)

Comparative epidemiology of tar spot as an endemic and emerging disease in the Americas

^{a,b}Carlos C. Gongora-Canul, ^gCarlos Puerto, ^oFidel Jiménez, ^aDarcy E. P. Telenko, ^dNathan Kleczewski, ^cJuan Carlos Rosas, ^oCarolina Avellaneda, ^oArie Sanders, ^fIveth Y. Rodriguez, ^fStephen B. Goodwin, ^eLenin E. Henriquez-Dole, ^aMariela Fernandez-Campos, ^aDa-Young Lee ^aAndres P. Cruz, and ^aC. D. Cruz¹

^aDepartment of Botany and Plant Pathology, Purdue University, West Lafayette, IN, 47907.

^bTecnológico Nacional de México / IT de Ciudad Valles. Calle Al Ingenio 2, 79033 Ciudad Valles, San Luis Potosí, México.

^cUniversidad Zamorano, San Antonio de Oriente, Fco. Morazán, Honduras

^dUniversity of Illinois Department of Crop Science, Urbana, IL 6180.

^eInterdisciplinary Network for Ecosystem Sustainability (EcoAgsus), Lujan de Cuyo, Mendoza, Argentina.

^fUSDA-Agricultural Research Service, West Lafayette, IN, 47907-2054, USA.

^gDuke University School of Medicine, 203 Research Drive, Durham, NC, 27710, USA.

E-mail address: cruz113@purdue.edu

Tar spot is a yield-reducing disease of corn in the regions where it is established. However, the inherent relationships among the host, the pathogen and environmental factors create conditions for its spread as an endemic or arrival as an emerging disease. Although it is endemic in Mexico, Central America and beyond, it apparently has recently established in regions of the U.S. Understanding and comparing its epidemiology in different regions allows us to assess its local impact and support appropriate management strategies. Thus, this research described and compared the temporal epidemiology of tar spot in Honduras and the U.S. (IL, IN) from multiple field trials focused on different disease management strategies during 2019-2021. We used metadata analysis to integrate and analyze heterogeneous data sources. Our results suggest that the disease moves from the lower to the upper canopy in both regions and the time from disease onset (y_0) to maximum disease severity (y_{max}) was longer in the U.S. (57 days) than in Honduras (41 days). In the U.S., y_0 starts late at VT-R1, while in Honduras it is early at V5-V6. While the y_{max} in the U.S. was up to 80%, in Honduras it reached 100%. The linear and nonlinear logistic temporal models best fit disease curves in the two regions, suggesting a polycyclic-like disease. However, apparent infection rates (r_L), standardized AUDPC, and y_{max} were higher in the U.S. than in Honduras in the upper canopy and higher in Honduras than in the U.S. in the lower canopy. In Honduras, as an endemic disease, it occurs at relatively higher levels of severity, probably because of a long-term co-evolutionary equilibrium among the pathogen, host, and environment. Conversely, as an emerging disease in the U.S., the disease level and spread are substantially increasing. This cascade of local epidemiological features of the disease in both regions should be accounted for in specific and unbiased management strategies.

Effect of cover crops and green manuring on *Sclerotinia* white rot disease development and yield in carrot

Belachew Asalf¹, Vinh Hong Le¹, Matheus Morais², Arne Hermansen¹

¹ Norwegian Institute of Bioeconomy Research (NIBIO), Division of Biotechnology and Plant Health, Aas, Norway ²“Luiz de Queiroz” Superior School of Agriculture (ESALQ), SP, Brazil

E-mail: belachew.asalf.tadesse@nibio.no

Sclerotinia sclerotiorum, causal agent of sclerotinia rot disease, poses a serious problem in carrot production. The fungal pathogen has a wide host range and can infect more than 400 plant species. The fungus can survive for several years in the soil without a host, so it makes white rot management challenging. Cover crops and green manuring are recognized for enhancing soil health and reducing the effect of soil borne diseases, but limited information exists on cover crops specifically effective against *S. sclerotiorum*, while improving carrot yield and quality. Pot experiments were conducted to evaluate: i) the susceptibility of ten cover crops to *S. sclerotiorum*, ii) the effect of green manure from five selected cover crops on carrot germination, growth, and yield, and iii) the effectiveness of selected cover crops on suppressing sclerotinia white rot development on carrots. Based on a literature review and input from the expert group involved in the project, the following nine potential cover crops were chosen for the pot experiments: Italian rye grass (*Lolium perenne*), Rye (*Secale cereale*), Oat (*Avena sativa*), Meadow Fescue (*Festuca pratensis*), Oil Radish (*Raphanus sativus*), Crimson Clover (*Trifolium incarnatum*), Buckwheat (*Fagopyrum esculentum*), Phacelia (*Phacelia tanacetifolia*) and common Vetch (*Vicia sativa*). For the green manuring experiments, five selected cover crops were grown in a greenhouse. Their growth was terminated at flowering stage, and both the foliar and root part were chopped into small pieces. These were then mixed with commercial soil in a one-to-two ratio (one-part green manure and two-parts soil). The experiments had eight treatments: Five cover crops as green manuring (Oat, Italian rye grass, Rye, Meadow Fescue and Oil Radish), fungicide as seed dressing, and two control (with *S. sclerotiorum* inoculated and without). There were four replications and three pots per replication, in total 96 pots per experiment. Each pot had a capacity of 20 liters, and there were about 30 carrots per pot. There was at least one week gap between the mixing of the cover crops with soil and date of carrot seed sowing. All the pots except the control were inoculated by *S. sclerotiorum*. Out of the nine cover crops five were found to be hosts for *S. sclerotiorum*. The susceptibility of these cover crops varied significantly, and the most susceptible were Phacelia (incidence 89%), common Vetch (incidence 84%), Oil radish (incidence 73%), Crimson Clover (incidence 58%) and Buckwheat (incidence 7%). Compared to control, there was a significant reduction in the germination of carrot seeds in the green manure treated pots except Oat. For example, carrot seed germination was reduced by 75% on rRye and by 60% on the oil radish treatments. Unmarketable carrots, primarily due to forking, were more prevalent in green manure treatments compared to control, such as 25% forked carrots on *Festuca pratensis* versus 4% in the control. Both the number and weight of carrots were significantly lower in pots that had Rye green manure, while Oat green manure led to higher yields. This indicates that Rye may not be a suitable cover crop for carrot. There was no significant difference on disease incidence and severity on the leaves of carrot between the green manure treated and control. There were few carrots with white rot symptoms at harvesting time, so it was not possible to draw conclusion on the effect of green manuring on visible infection of carrot by *S. sclerotiorum* at harvesting time. Carrots from the different treatments are stored in a cold room (0 + 1°C) and will be evaluated for postharvest disease development and storage quality after the storage period ends in March or April 2024.

Financial support. The Research Council of Norway (CropDrive project # 336570).

What happens to durability of disease control in fields of growers who run a resistance management programme when neighbours use only one component of the resistance management?

Joe Helps¹, Francisco Lopez-Ruiz², Ayalsew Zerihun², Frank van den Bosch²

¹ Rothamsted Research, Harpenden, AL5 2JQ, United Kingdom

² Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Perth, WA 6845, Australia

Email: a.zerihun@curtin.edu.au

There is expectation that growers do practice resistance management methods such as fungicide alternations or mixtures to slow development of resistance. When considering a broader farming landscape, however, it is likely that while many growers implement such resistance management methods, some do not or may even apply solo components of the resistance management programme. Here, with the aid of a spatially implicit epidemiological model, we explored whether growers who use solo components of resistant management programmes compromise the durability of disease control in fields of growers who implement resistance management, using the barley-*Pyrenophora teres* f. *maculata* pathosystem. The model results suggest that growers who use only component fungicides affect the durability of disease control for growers implementing resistance management programmes. The effect sizes depend on factors such as composition [(a)sexual spore] of initial inoculum, spore movement between fields, and resistance management programme in use, which will be discussed.

Financial Support: Grains Research and Development Corporation – research grant CUR00023 to FLR, AZ and FvdB. UKRI grants: Smart Crop protection (SCP) strategic programme 401 (BBS/OS/CP/000001) and the Growing Health (BB/X010953/1) Institute Strategic Programme to JH.

Analysis of the field-scale spatial pattern of peanut smut in Argentina

Juan A. Paredes^{1,2}, Boris X. Camiletti³, Luis I. Cazón¹, Joaquin H. Monguillot^{1,2}, Florencia Asinari¹, Alejandro M. Rago¹

¹ Instituto de Patología Vegetal (IPAVE). CIAP – INTA. Córdoba, Argentina

² Unidad de Fitopatología y Modelización Agrícola, UFyMA-CONICET. Córdoba, Argentina

³ Department of Crop Sciences. University of Illinois, Urbana-Champaign, Illinois, USA

⁴ Centro de Investigaciones Agropecuarias, INTA. Córdoba, Argentina

E-mail: paredes.juanandres@inta.gob.ar

Peanut smut, caused by the soil-borne pathogen *Thecaphora frezzii*, represents a threat to Argentina's peanut production, causing severe damages, yield losses, and compromising the overall quality. The infection occurs when the peg penetrates the soil (local infection), leading to the transformation of kernels into masses of teliospores. Smutted pods break during harvest, spreading spores across fields, where they can remain latent for many years. Various statistical approaches are used to investigate the spatial distribution of plant diseases. In this study, we aimed to investigate the spatial pattern of smut incidence in both small-scale plots and large-scale in peanut fields. For this purpose, peanut samples were collected at the mature pods stage, and the disease incidence (percentage of diseased pods out of the total of sampled pods) was determined. For the small-scale analysis, three fields were selected. Samples were taken at intervals of 1 meter along a 20-meter row by 12 rows, comprising a regular grid of 12 by 20 (240 samples). Each sampling unit consisted of all pods found in 30 cm², representing approximately all pods produced by a single plant. For large-scale analysis, four commercial fields were sampled using a grid pattern with a uniform spacing of 100 meters, ranging from 25 to 96 samples depending on the field. Samples consisted of all pods found in 1 m² of the windrow. Dispersion index, autocorrelation (Global Moran's I), and SADIE (spatial analysis by distance indices) were used to analyze the spatial pattern of smut incidence. The mean incidence in small-scale plots were 2, 4, 29%; while at large scale were 6, 19, 31, 42%. Distribution fitting revealed significant disease aggregation in both small-scale plots and commercial fields. For the small-scale plots, the dispersion index suggested a non-random distribution, with higher disease levels showing wider dispersion. Global Moran's I test indicated no significant autocorrelation for two fields, suggesting random spatial distribution, while one field showed a significant positive autocorrelation ($P=0.008$), indicating spatial clustering of incidences. The SADIE test indicated that two fields exhibited a spatially random pattern of the disease, whereas one field indicated a significant ($P=0.01$) aggregated pattern. For the large-scale analysis, three fields showed no significant spatial autocorrelation, indicating a random spatial pattern of disease, while one field exhibited a significant positive spatial autocorrelation ($I = 0.1129$, $P = 0.017$), indicating clustered distribution. In the SADIE analysis, the Index of aggregation (I_a) values for three fields did not differ statistically from 1, indicating spatially random distribution, while one field showed a significant ($P = 0.01$) clustered pattern with an I_a of 1.73. Overall, the spatial pattern of peanut smut tends to be random at medium-high disease levels (>20%) but non-random at low levels (<6%). These findings provide valuable insights for designing experiments more efficiently, improving the accuracy of experimental results, and the efficacy of disease sampling and monitoring.

Financial support: INTA (I-090) and Fundación Maní Argentino (Technical Assistance Project)

One brick at a time: Building on epidemiological insights for improved management of *Cercospora* leaf blight on soybean in the mid-South

Sara Thomas-Sharma¹, Stephanie Ramos¹, Nelomie N. Galagedara¹, Vinson P. Doyle¹, Jonathan Amie¹, Trey Price^{1,2}, Boyd Padgett^{1,3}, Tom Allen⁴, Terry Spurlock⁵, Mary York⁶, Lyndon Coghill⁶, Lawson Connor⁷

¹Department of Plant Pathology & Crop Physiology, Louisiana State University Agricultural Center, Baton Rouge, LA; ²Macon Ridge Research Station, LSU AgCenter, Winnsboro, LA; ³Dean Lee Research and Extension Station, LSU AgCenter, Alexandria, LA; ⁴Mississippi State University, Stoneville, MS; ⁵University of Arkansas, Monticello, AR; ⁶University of Missouri, Columbia, MO; ⁷University of Arkansas, Fayetteville, AR

Email: sthomassharma@agcenter.lsu.edu

Cercospora leaf blight (CLB), the primary foliar disease of soybean in mid-Southern U.S., has undergone substantial changes in epidemiological understanding within the last decade. CLB, historically caused by *Cercospora kikuchii*, is now known to be predominantly caused by the species *Cercospora* cf. *flagellaris*, and *Cercospora* cf. *sigesbeckiae* in the U.S. The identification of the latter causal agents changed the relative importance of inoculum sources, and directly impacted CLB management. As a host-specific pathogen, *C. kikuchii*, was considered primarily seedborne. *Cercospora* cf. *flagellaris* and *C. cf. sigesbeckiae*, however, are generalist pathogens known to infect several alternative hosts around soybean fields, potentially contributing to airborne inoculum. We studied the contribution of the CLB pathogens to airborne inoculum and disease outbreak in three sites in Louisiana from 2019-2023. Although conidial peaks in different types of traps and their location in the field were not correlated, conidia of all three CLB pathogen species were observed in every year and location. The timing and intensity of conidial peaks varied between species, with *C. cf. flagellaris* contributing more airborne conidia. One to two conidial peaks of *C. cf. flagellaris* were frequently observed before symptoms on soybean (usually observed in reproductive stages). Fungicide trials were set up to target the conidial peaks and compared with currently recommended crop growth-stage based applications. Overall, the targeted fungicide treatments did not cause significant yield or economic impact compared to control and growth-stage based applications. Some positive trends were observed when fungicide applications coincided with conidial peaks, suggesting a need for better prediction of inoculum/fungicide timing. Similar studies are currently underway in Arkansas and Mississippi and the impact of weather variables on conidial peaks and disease outbreaks are being explored. We aim to use the epidemiological data generated through current and ongoing work to collaboratively improve CLB management across the mid-South.

Combining foliar deposit distribution and dose-response curve data to predict fungicide efficacy against scab in apple orchards, and practical implementation in the AOS43 dosing system

Vincent Phillion¹, Peter Triloff², Arne Stensvand³, Mick Wu¹

¹ Institut de recherche et de développement en agro-environnement,
Saint-Bruno-de-Montarville, Québec.

² Marktgemeinschaft Bodenseeobst eG, Friedrichshafen, Germany.

³ Division of Biotechnology and Plant Health, Norwegian Institute of Bioeconomy Research,
1431 Ås, Norway; Department of Plant Sciences, Norwegian University of Life Sciences,
1433 Ås, Norway

E-mail: vincent.phillion@irda.qc.ca

Dose response curves are used to describe the effect of fungicides on disease incidence and severity in laboratory studies. In controlled experiments, the relation is monotonous and often described as a simple two-parameter logistic or probit curve in which the dose required to inhibit 50% of disease (EC_{50}) and the slope of the curve can be determined. In the field, fungicides sprayed on the crop are not deposited uniformly, resulting in leaves with excessive or insufficient deposits to kill the pathogen. In orchards, the leaf-to-leaf variation in deposits is often described by a Gamma distribution using two parameters (scale and shape), with their product giving the mean deposition. Crop characteristics, sprayer performance and settings all impact the mean deposition and variability, and thus the efficacy against the target organism. The nonlinearity in dose response and nonuniformity of fungicide deposits make it difficult to predict the efficacy of sprays at the field scale. The objective of our work was to better understand the interaction between fungicide potency and field spray deposit data in apple orchards on the effectiveness of sprays against *Venturia inaequalis*, the fungal pathogen causing apple scab. An R Shiny web application was built to simulate and visualize the impact from each and combined effect of parameters on the probability density and cumulative probability of dose per leaf in the field and the resulting field mortality distribution. The effect of non-linearities was made visible by plotting separately the mortality against *V. inaequalis* calculated by the simulation and from the mean dose in the field. This simulation could be used to predict the dose of pesticides required to reach a similar mortality given a different dose response slope or spraying performance. Better spraying uniformity could permit lowering of the applied dose or improve efficacy of organic pesticides while maintaining target mortality. This work can also be used for more efficient orchard spraying. The goal of efficient spraying is to obtain good and constant efficacy across orchard systems while using the least amount of resources. The AOS43 dosing system relies on canopy adapted air flow and modulates travel speed based on orchard row width to optimize efficiency while maintaining efficacy. The deposit distribution from AOS43 adjustments has both a higher mean and variability in wide row orchards while the reverse is true in thin row orchards. The effect of adjustments on the predicted disease control using simulation data is better fungicide efficacy in thin row systems and equivalent efficacy in wider rows. Efficiency is increased in thin row orchards by increased travel speed and reduced fungicide use. Trials were conducted in commercial orchards for three years to test the AOS43 dosing system. Optimized sprayers and settings using lowered applied dose were compared to grower practices. Despite a 50% average reduction of dose rate and increased driving speed using AOS43, scab incidence was similar or lower compared to the grower standard.

Financial support: Ministère de l'agriculture des pêcheries et de l'alimentation du Québec

A review of pathogen biology, ecology, epidemiology, and the use of germicidal ultraviolet light to suppress plant pathogens

David M. Gadoury¹

¹Plant Pathology and Plant-Microbe Biology Section, Cornell University, Geneva, NY USA
14456

E-mail: dmg4@cornell.edu

Germicidal ultraviolet light (UV-C) has been used for over 80 years to suppress pathogenic microbes in human health care and in food processing. Use of UV-C to suppress plant pathogens is a more recent development. The principal mode of action is direct damage to pathogen DNA through production of thymine dimers. A major advance was the discovery that efficacy of UV-C was greatly enhanced when applied during night hours, which bypassed photolyase-mediated DNA repair in target organisms, thereby increasing lethality to plant pathogens at greatly reduced doses. Modern UV-C arrays are powerful, scalable, and adaptable, allowing them to rapidly treat large plantings of crops with diverse canopy architectures. However, this sophisticated technology is highly dependent upon equally sophisticated knowledge of pathogen biology, ecology, and epidemiology to achieve effective disease suppression. In the most common case, the mode of action of UV-C is direct damage to pathogen cells, with no residual or protective effect against subsequent inoculation and infection. In these instances, seasonal impacts can be markedly affected by plot size, edge effects, interplot interference, ingress of airborne inoculum, and rebounding of epiphytic populations that survive initial exposures. Less common is the situation where UV-C exposure causes a transient increase in host resistance to one or more members of a pathogen complex; thereby presenting a different relationship with respect to pathogen recolonization of the host. Diverse examples will be presented and discussed involving the practical use of UV-C to suppress a powdery mildew (*Erysiphe necator* on grapevine), a downy mildew (*Plasmopara viticola* on grapevine), a bacterium (*Erwinia amylovora* on apple), an insect and pathogen complex (sour rot of grapes) and heavily melanized hemibiotrophs (*Venturia inaequalis* on apple and *Cercospora beticola* on beet) in the context of integrating technical knowledge of UV-C production with the relevant epidemiological knowledge to achieve the best result.

INDEX OF POSTER PRESENTATIONS			
Number	Presenter	Title	Page
P01	Andrés Cruz-Sancan	Shaping the attributes of a successful and unified tar spot assessment scheme	60
P02	Aaron I. Plex Sula	R2M toolbox for rapid risk assessment to support mitigation of pathogens and pests: Perspectives on rice health in Nepal	61
P03	Andre Bueno Gama	Spread of <i>Neopestalotiopsis</i> sp. from strawberry under simulated rainfall and wind and from different inoculum sources	62
P04	Kelsey Andersen Onofre	Revisiting the epidemiology and biology of <i>Tilletia</i> spp. infecting wheat in the United States	63
P05	Belachew Asalf	Evaluating TOMCAST model for predicting timing of fungicide applications to control <i>Alternaria</i> diseases in Carrot and Potato	64
P06	Breno C.M. Juliatti	Comparison of genotypes with partial resistance against soybean rust in relation to the binomial temperature and leaf wetness duration	65
P07	Marcelo G. Canteri	Using explainable machine learning for Asian soybean rust severity prediction	66
P08	Luis Ignacio Cazón	Improving the accuracy in visual estimation of peanut late leaf spot severity: online training tools, SAD, or both?	67
P09	Claudio Dias da Silva Junior	Meta-analysis of yield responses to fungicide application timings for the control of wheat stripe rust in the U.S.	68
P10	Claudio Dias da Silva Junior	Risk-based surveillance of wheat stripe rust in the Great Plains region of the United States	69
P11	Maria Cristina Canale	Unravelling the spatial dynamics and incidence of corn stunting disease complex in Brazilian maize fields	70
P12	Mariela Fernández-Campos	Evaluating the potential of multisource data for predicting corn tar spot intensity	71
P13	Daiana Maria Queiroz Azevedo	Influence of plastic cover on raspberry late rust and the dynamics of airborne <i>Aculeastrum americanum</i> urediniospores in the field	72
P14	Dalphy O.C. Harteveld	Metabarcoding and AI as tools in diagnostics, disease epidemiology and modeling	73
P15	Daniel R. Maass Steiner	Asymptomatic grapevine leaves harbor inoculum for <i>Colletotrichum</i> spp.	74
P16	Débora Petermann	The removal of symptomatic leaves on the ground has little impact on the development of Glomerella Leaf Spot in apple orchards with a high inoculum potential	75
P17	Elias Zuchelli	Influencing factors on fungicide response in TN soybean	76
P18	Felipe Dalla Lana	Disease reaction classification considering trial accuracy and phenotype stability: A case study with rice	77
P19	Gabriel Ferreira Paiva	Comparison of quantification methods for assessing <i>Gibberella</i> stalk rot severity on corn	77
P20	Maik Leão	Does leaf position influence maize disease severity estimates by remote sensing?	79
P21	Maiara da Silva Freitas	Severity of foliar diseases in maize: how can estimates be improved?	80
P22	Galvin Alonzo	Network analysis of <i>Neopestalotiopsis</i> sp. spread from nurseries to strawberry farms in Florida, USA.	81

P23	Guillermo A. Enciso-Maldonado	Monitoring <i>Phakopsora pachyrhizi</i> with spore traps in commercial soybean fields in Paraguay in the 2023/2024 season	82
P24	Rene Heim	Remotely sensed leaf area index can improve mechanistic <i>Cercospora beticola</i> epidemiological models for disease predictions	83
P25	Hope Renfroe-Becton	The development of weather-based models for six soybean stem diseases observed across North Dakota	84
P26	William B. Moraes	Probability modeling of coffee rust epidemic in conilon coffee: A focus on sustainable management	85
P27	Jacobo Robledo	<i>Fusarium oxysporum</i> f.sp. <i>cubense</i> Tropical Race 4 threatens Colombian bananas: Translating analyses of host connectivity, trade, and stakeholder movement to inform management and surveillance	86
P28	Jessica Danila Krugel Nunes	Impact of water deficit on the initial development of Asian soybean rust	87
P29	Joaquín Guillermo Ramirez-Gil	Advancing plant epidemic analysis through data science: Tools, techniques, and applications	88
P30	Juan M. López-Vásquez	Quantification of airborne basidiospores of <i>Ganoderma zonatum</i> at different altitudinal gradients and their relationship with environmental conditions in oil palm	89
P31	Brenden Lane	What does “bottom-up” actually mean for tar spot disease development in corn?	90
P32	Leandro José Dallagnol	<i>Fusarium</i> species and mycotoxins in barley grains through different physiographic regions of Rio Grande do Sul, Brazil	91
P33	Lilian Amorim	Temperature increase impacts the temporal progress of myrtle rust and physiological damage on guava	92
P34	Lucas Santos Sales	Drought, high temperature and rust (<i>Neophytophthora tropicalis</i>): a dangerous combination for ‘Niagara Rosada’ grapevine	93
P35	Aaron Isaí Plex Sulá	Mitigating the risk from the cut flower trade to protect global systems from invasive pests and pathogens	94
P36	Matt Combes	Estimating the sensitivity and specificity of visual detection of tree pests and diseases	95
P37	Camila Iavorski Zela	Grapevine leaf spot leads to early defoliation and production loss in <i>V. labrusca</i> (Bordô Cultivar)	96
P38	Eduardo S. G. Mizubuti	Spatiotemporal dynamics of Fusarium wilt of banana caused by subtropical race 4 of <i>Fusarium oxysporum</i> f.sp. <i>cubense</i>	97
P39	Madison Kessler	Predictive modeling of sudden death syndrome of soybean in Kansas	98
P40	Mary Ruth McDonald	Success in forecasting downy mildew of onion with DOWNCAS	99
P41	Mary Ruth McDonald	Attempts to forecast <i>Stemphylium vesicarium</i> on onions when the pathogen is resistant to most fungicides	100
P42	M. R. McDonald	Balancing selection complicates management of clubroot and (possibly) other problem diseases	101
P43	Murillo Lobo Junior	Building a hyperspectral library of common bean diseases	102
P44	Natalia A. Peres	Evaluation of disease infection models to time fungicide applications to manage <i>Neopestalotiopsis</i> sp. on strawberry in Florida	103

P45	Natalia A. Peres	Effect of incubation temperature and wetness duration on <i>Neopestalotiopsis</i> sp. germination and Pestalotia Leaf Spot disease development on strawberry	104
P46	Olanrewaju M. Shittu	Fusarium head blight prediction: Assessing the accuracy of iButton microclimate data against weather station data	105
P47	Paulo Henrique Nascimento de Souza	Criteria for fungicide applications in asian soybean rust control: An analysis of Spore collector, scheduled application, and monitoring	106
P48	Paulo Henrique Nascimento de Souza	Unraveling the soybean anomaly: The revealing risk tree and fungicide management	107
P49	Jacqueline D. Puia	Incubation period, number of lesions and severity of isolates of <i>Corynespora cassiicola</i> in soybean cultivars	108
P50	Ricardo G. Tomá	Profitability assessment of fungicides and resistant varieties in wheat blast control: A simulation-based approach	109
P51	Rachel Russell	Baselining prioritization of epidemic control	110
P52	Aaron I. Plex Sulá	Global surveillance and mitigation strategies for laurel wilt, a major threat to avocado production and forests	111
P53	Robin A. Choudhury	Modeling landscape-level transmission of a shared pathogen in a heterogeneous agroecosystem	112
P54	Santosh Sanjel	Evaluating planting date recommendation effects on soybean yield using causal inference	113
P55	Kwang-Hyung Kim	Model-based prediction of the selection of fungicide resistance in pepper anthracnose pathogen, <i>Colletotrichum scovillei</i> , in Korea	114
P56	Thiago de Aguiar Carraro	Environmental requirements for germination, growth, and infection of <i>Alternaria</i> species in mandarins	115
P57	Valdir Lourenço Jr	Genetic resistance and temporal progress of onion white rot in Brazil	116
P58	Victor Alves	A Bayesian-based quarantine exit strategy	117
P59	Yuri Guerreiro Ramos	Injury-Damage relation for yellow spot, leaf rust and multiple pathosystem in wheat	118
P60	Renato B. Bassanezi	Modeling primary huanglongbing infection to determine the most economical strategy for controlling <i>Diaphorina citri</i> in sweet orange edge blocks	119

Shaping the attributes of a successful and unified tar spot assessment scheme

A Cruz-Sancan¹, CD Cruz¹, Da-Young Lee², C Góngora-Canul¹⁰, C Puerto-Hernández³

¹Department of Plant Pathology, Purdue University

²Department of Electrical Engineering, Pohang University of Science and Technology, South Korea

³Universidad Zamorano, San Antonio de Oriente, Fco. Morazán, Honduras

Email: acruzsan@purdue.edu, cruz113@purdue.edu

Assessing or quantifying disease intensity is crucial for managing disease. Multiple platforms are nowadays available for disease assessment and quantification. The general approaches for quantifying tar spot intensity involve traditional visual assessments or electronic measurements. However, visual disease assessments remain the standard for assessing disease intensity and referencing image-based quantification methods. Multiple methods for visual assessment of tar spot have been used, including direct estimation, direct estimation using standard area diagrams, and estimation using disease scales. According to published manuscripts, different groups across the Americas employ different means for assessing tar spot severity visually, including a continuous variable ranging from 0 to 100%. In addition, it was recently proposed that a discrete random variable in the form of counts can also provide a good source of information for quantifying tar spot stroma using RGB imagery. The measurement level of a random variable is essential as it dictates the quantity of information about the characteristic measured. Conversely, the variable type is crucial as it determines the appropriate statistical and mathematical methodologies for analysis. Given this priority, we aim to standardize a tar spot assessment scheme across collaborators and locations of interest. We recommend a linear relationship scale of the percentage of corn leaf area covered by signs (i.e., stromata), symptoms (i.e., chlorosis, fisheye, necrosis), or both associated with corn tar spot. We also recommend using stromata counts for training algorithms such as the recently proposed SCDA.

Financial support: Cruz Lab

**R2M toolbox for rapid risk assessment to support mitigation of pathogens and pests:
Perspectives on rice health in Nepal**

Ashish Adhikari^{1,2,3}, Aaron I. Plex Sula^{1,2,3}, Berea A. Etherton^{1,2,3}, Katelin Alcock^{1,2,3}, Robert Fontan^{1,2,3}, Theodore J. Stronkowsky^{1,2,3}, Romaric A. Mouafo-Tchinda^{1,2,3},
R2M Group for Rice Health in Nepal, Karen A. Garrett^{1,2,3}

¹Plant Pathology Department, University of Florida, Gainesville, FL, USA

²Global Food Systems Institute, University of Florida, Gainesville, FL USA

³Emerging Pathogens Institute, University of Florida, Gainesville, FL USA

Email: adhikariashish@ufl.edu and karengarett@ufl.edu

The emergence of crop pathogens and pests threatens global food security. The R2M toolbox provides analyses to address the critical challenges of plant health management at a national level, based on current data and knowledge. R2M is part of an open-source ecosystem providing stakeholders and decision makers with tools to understand and mitigate plant pathogen and pest risk. R2M includes tools for (a) expert knowledge elicitation, to synthesize expert understanding of risk, (b) habitat or cropland connectivity analysis using the geohabnet R package, (c) trade network analysis, including via the GeoPathome app, and (d) impact network analysis (INA) for scenario analysis of regional management in the INA R package. We used the R2M toolbox to evaluate rice health risks in Nepal. Rice accounts for approximately 40% of the country's caloric intake (Neupane et al. 2021), contributing 51.6% of the total grain production (MOAD 2017). Protecting rice production depends on limiting the spread of crop pathogens and pests. Our objectives were to evaluate rice cropland connectivity and trade networks to understand the potential spread of pathogens and pests in Nepal and the surrounding region, and to identify key locations in potential invasions. Using measures of cropland connectivity with other risk factors for pathogen buildup can improve methods for detecting and mitigating the spread of current and emerging pathogens. Based on cropland connectivity analysis, we identified high-risk areas that are candidate priorities for risk mitigation procedures. Trade network analysis addresses how the movement of goods can contribute to the spread of pathogens. We evaluated trade networks in terms of the potential movement of multiple pathogens, including *Magnaporthe oryzae* and *Ustilaginoidea virens*, to identify highly connected countries with the potential for pathogen movement if there are not sufficient phytosanitary controls in place. These analyses can help guide prioritization for rice health management, and are a baseline for new analyses to improve rice health management in Nepal. This analysis is also an example of a new research workshop format, global research collaboration workshops, to develop new collaborative approaches engaging junior researchers across countries and institutions.

Spread of *Neopestalotiopsis* sp. From Strawberry Under Simulated Rainfall and Wind and From Different Inoculum Sources

Andre Bueno Gama¹, Galvin Alonzo Ortiz², Juliana S. Baggio³, and Natalia A. Peres².

¹ Department of Plant Pathology and Crop Physiology, Louisiana State University, Baton Rouge, LA United States.

² Department of Plant Pathology, Gulf Coast Research and Education Center, University of Florida, Wimauma, FL, United States.

³ Syngenta Crop Protection, Vero Beach, FL, USA.

E-mail: agama@agcenter.lsu.edu

Since 2017, an aggressive *Neopestalotiopsis* sp. poses a significant threat to strawberry cultivation in Florida. This study aimed to assess the dispersal potential of *Neopestalotiopsis* sp. spores from various inoculum sources - strawberry leaves, strawberry fruit, dried/senescent leaves, and inoculated sandy soil from Florida fields. Experiments were conducted in a tunnel simulating wind speeds of 5 and 7 m/s, with or without simulated rainfall using a micro sprinkler. Petri dishes with semi-selective media for *Neopestalotiopsis* sp. were placed at 0.6, 1, 3, 5, and 7 m downwind from the inoculum sources. Statistical analysis, utilizing negative exponential and power law models, compared dispersal gradients under different wind and rain conditions. The results indicated that rain significantly increased the number of colony-forming units (CFU) retrieved from plates compared to wind alone. Wind speed had no significant effect on CFU, except when combined with rain. Strawberry fruit and dried leaves showed comparable CFU counts on selective media, whereas strawberry leaves and inoculated soil exhibited fewer CFU. Distance significantly influenced CFU for all inoculum sources. Separate analyses revealed distinct patterns for each inoculum source. Models fitting the combined experiments runs of treatments with rain demonstrated good fit, with slight variations between negative exponential and power law models. Data from treatments without simulated rainfall were not well described by the models. The dispersal of *Neopestalotiopsis* sp. conidia varied with wind speed and rain application and was particularly notable for strawberry fruit. Overall, this study provides valuable insights into the dispersal dynamics of *Neopestalotiopsis* sp., emphasizing the importance of rain in facilitating spore movement. The findings contribute to a better understanding of the epidemiology of this emerging strawberry pathogen and will shed light in developing effective management strategies.

Financial support: Florida Strawberry Research and Education Foundation (FSREF)

Revisiting the epidemiology and biology of *Tilletia* spp. infecting wheat in the United States

Kelsey Andersen Onofre¹, Erick De Wolf¹, Raissa Debacker Moura¹, Angel Detrinidad¹

¹Kansas State University, Department of Plant Pathology

E-mail: andersenk@ksu.edu

Common bunt (caused by the pathogens *Tilletia tritici* and *T. laevis*) and dwarf bunt (caused by *T. controversa*) are two important but epidemiologically distinct diseases infecting wheat worldwide. Critically, the pathogen that causes dwarf bunt is regulated in several countries resulting in disruptions to global wheat grain trade. The current diagnostic standards for wheat destined for export rely solely on microscopic measurements of teliospore reticulations. We have detected isolates in the Great Plains that would technically fail export criteria for *T. controversa* based on current diagnostic criteria. However, these appear to be false-positives based on a broader range of diagnostic criteria. Additionally, the epidemiological requirements of this pathogen, 60 days of snow cover, are rarely met in states like Kansas. Here we present ongoing work to not only phenotype and genotype >100 isolates of these pathogens collected in the U.S., but also to pair this with known landscape epidemiological factors necessary for disease establishment. For example, we evaluate frequency of years where favorable conditions are met for *T. controversa* establishment in the US with data obtained from the MODIS/Terra daily snow cover data layer from the NASA Snow and Ice Data Center. These evolving findings are highly relevant for the wheat industry worldwide.

Evaluating TOMCAST model for predicting timing of fungicide applications to control *Alternaria* diseases in Carrot and Potato

Belachew Asalf¹, Håvard Eikemo¹, Lars-Arne Høgetveit², Berit Nordskog¹, Arne Hermansen¹

¹ Norwegian Institute of Bioeconomy Research (NIBIO), Division of Biotechnology and Plant Health, Aas, Norway. ² Norsk Landbruksrådgiving, NLR Viken.

E-mail: belachew.asalf.tadesse@nibio.no

Leaf blight of carrot is caused by fungi such as *Alternaria dauci*, *A. alternata* and *Cercospora carotae*. The disease can reduce carrot yield and affect mechanical harvesting. Similarly, early blight of potatoes, caused by *Alternaria solani* and *A. alternata* is a common disease characterized by irregular, black concentric ring-shaped lesions. Both in carrots and potatoes, disease development depends on temperature, leaf wetness and other factors. A predictive model is useful to determine the timing and interval between fungicide application to secure control of the disease and to reduce unnecessary fungicide applications. The TOMCAST model is a decision support system that was originally developed to predict fungal disease development in tomato, and it has been adapted for use in *Alternaria* management in carrot and potato. The model uses daily air temperature and hourly leaf wetness to accumulate the daily disease severity values (DSV). When application is performed and date of application entered in the model system, accumulation of DSV resets at zero and starts accumulation again. The TOMCAST model is available for use in the Norwegian decision support system VIPS (www.vips-landbruk.no). VIPS is an open-source technology platform for prognosis, monitoring, and decision support in plant pest and disease management. In VIPS, the disease risk levels are indicated by green (DSV 0-15), yellow (DSV 15-20), and red (DSV above 20) alerts. A DSV over 20 indicates high risk of infection and a need for spray. The objectives were to evaluate the applicability of TOMCAST model for the management of *Alternaria* diseases in carrot and potato in Norway. Field trials were conducted in 2022 and 2023 in carrot and in 2023 in potato in areas where *Alternaria* normally is problematic. There were three treatments (i) standard fungicide application every two weeks. ii) treatments based on TOMCAST predictions (DSV =20) and iii) untreated controls) and four replications in carrot. These treatments were also applied in the potato field. Fungicides recommended for use in Norway were applied following the recommended dose and number of applications. We counted on natural inoculum of *Alternaria* and *Cercospora* in the experimental fields and the first application was initiated when the diseases were observed on the plants and then following the TOMCAST (DSV= 20) warning and at two-week intervals. Weather data needed for the model were obtained from three weather stations nearby the experimental carrot field. Fungicide spray for TOMCAST treatment plots were initiated when TOMCAST warns based on data from one or more of the three weather stations. Results from carrot field trials showed no significant difference among treatments in disease incidence and severity in both years. In 2022, *Alternaria* disease incidence for the second assessment (on September 09) were 60% in control, 53% in standard and 50% in TOMCAST, whereas in 2023, the incidence was very low in the trial field and the mean disease incidence ranging from 2-8% for all treatments. Based on data from some weather stations the model predicted 2-4 applications, while the standard application required five or more applications. In the potato field, spraying based on the model resulted in 3 fungicide applications, which was the same as farmers practice. Both sprayed treatments had significantly less disease compared to unsprayed plots. There were no differences in potato yield. TOMCAST seems to be a valuable decision support system, aiding in determining spray intervals, timing of fungicide application, and optimizing fungicide use to control *Alternaria* and *Cercospora* leaf blight in carrots and early blight potato in Norway.

Financial support: Skadeterskler (Project # 8390-18)

Comparison of genotypes with partial resistance against soybean rust in relation to the binomial temperature and leaf wetness duration

B.C.M. Juliatti¹, E.A. Pozza², F.C. Juliatti¹

¹ JuliAgro B, G & P Ltda, Consultoria e Pesquisa, Uberlândia MG Brasil.

² Universidade Federal de Lavras, Programa de Pós-Graduação em Fitopatologia, Lavras, MG Brazil.

E-mail: breno.juliatti@juliagro.com

Climatic conditions, inoculum concentration, and plant susceptibility directly affect the manifestation of Asian rust in soybean. Also, plant resistance is characterized by an alteration in pathogen survival skills and perpetuation process. The development of new resistant cultivars against diseases is a primordial step in the preservation of plant yield since the chemical control is losing efficacy in the field. We analyzed a diversity of parameters, interacting with a commercial cultivar and soybean genotypes with partial resistance in Asian rust management, under different conditions. A focal point at LAGER/UFU, is to study clues and characteristics of partial resistance in soybean genotypes of the soybean breeding and improvement program. The objective of the study was to determine the influence of temperature (18, 21, 24, 27 and 30 °C) and leaf wetness duration (0, 6, 12, 24 and 48 hours) on the penetration and temporal progress of ASR was studied using genotypes/cultivar with different levels of partial resistance. The variables evaluated, made before and after inoculation, consisted of agronomic traits and disease progress, also area under disease progress curve (AUDPC) was measured under the interaction and influence of temperature and leaf wetness duration. The incubation period was measured only by the influence of the temperature. There were significant differences ($P=0.001$) in AUDPC between genotypes under the interaction of the binomial (temperature x leaf wetness duration - LWD) and for incubation period at different temperatures. No signs or symptoms of rust appeared at the temperatures 18 °C and above 30 °C. The relationship between temperature and leaf wetness duration (LWD) affect the AUDPC and temperature affects incubation period. The highest AUDPC values occurred at 24 °C and leaf wetting period of 24 hours, and the lower values were achieved at temperatures higher than 27 °C. Genotype 1 or cultivar Desafio RR 8473 RSF, showed susceptibility to the monocycle parameters of ASR. ASR lesions started to appear in average at least 15 days to 20 DAI in partial resistant genotypes: Genotypes 2 - F8 BRSGO Luziânia X Potenza, 3 - F8 BRSGO Caiapônia X Potenza and Genotype 4 - F8 BRSGO Caiapônia X IAC100 who also had lower AUDPC and severity values, during the monocycle experiment.

Financial support: CNPQ and JuliAgro

Using explainable machine learning for Asian soybean rust severity prediction

Christofer Daniel¹, Guilherme Maturana¹, Eduardo H. M Pena¹, Daniel S. Kaster², Marcelo G. Canteri²

¹ Departamento de Computação – Universidade Tecnológica Federal do Paraná, Campo Mourão PR Brasil.

² Departamento de Agronomia, Universidade Estadual de Londrina, Londrina PR Brasil.

E-mail: canteri@uel.br

Asian soybean rust, caused by *Phakopsora pachyrhizi*, is influenced by environmental variables. This study was developed at Artificial Intelligence Center for Agriculture (CIA Agro) and proposes the application of machine learning models to predict the severity of Asian rust on soybean crops, focusing on explainable models. Machine learning models were employed to forecast the severity of Asian soybean rust based on historical severity data, geographical information, and meteorological data. Asian soybean rust severity data were obtained from cooperative fungicide tests coordinated by the Rust Consortium. Additional data, such as monthly maximum, minimum, and average meteorological values of precipitation, evapotranspiration, minimum temperature, maximum temperature, solar radiation, and relative humidity, were utilized for enrichment. Data underwent preprocessing steps to extract only the necessary information related to the desired locations. The Random Forest, XGBoost, CatBoost, and Neural Network models were tested. The Random Forest model was chosen for its higher explainability, provided by Weak Learners, allowing the use of the SHAP technique to observe the impact of each data attribute on the result. Data preprocessing during model training included duplicate removal, column normalization, and missing value elimination to ensure data quality. Results analysis revealed that the inclusion of data from the brclimr package in the R language significantly improved the model's accuracy. The expanded dataset, combined with the chosen models, resulted in a high accuracy for predicting Asian rust severity in various Brazilian cities.

Financial support: Fundação Araucária.

Improving the accuracy in visual estimation of peanut late leaf spot severity: online training tools, SAD, or both?

Luis Ignacio Cazón¹, Juan Andrés Paredes^{1,2}, Noelia González¹, Lautaro Suarez¹, Emerson M. Del Ponte³

¹ Instituto de Patología Vegetal (IPAVE). CIAP – INTA. Córdoba, Argentina

² Unidad de Fitopatología y Modelización Agrícola, UFYMA-CONICET. Córdoba, Argentina

³ Departamento de Fitopatología, Universidade Federal de Viçosa, Viçosa MG Brasil.

E-mail: cazon.ignacio@inta.gob.ar

Despite being one of the oldest practices in phytopathometry, visual estimation remains widely used for quantifying plant disease severity in field and laboratory tasks. The precision of estimation largely depends on the evaluators' characteristics, and various tools can be employed to enhance their assessment capabilities. Online training systems and Standard Area Diagrams (SADs) stand out among these tools. The former has gained popularity alongside recent advancements in computer technology, while SADs persist as a reliable tool over the years. In this study, we aimed to quantify the impact of the online tool TraineR2 (<https://delponte.shinyapps.io/traineR2/>) on the accuracy of a group of raters and compare it with those obtained using a SAD specifically designed and validated in this work. To achieve this, we selected peanut late leaf spot (*Nothopassalora personata* Berk. & M.A. Curtis) (LLS), the primary foliar disease affecting peanut cultivation in Argentina, as our case study. Our results revealed that both the TraineR2 software and our SAD significantly enhanced the precision and accuracy of visual estimation for LLS severity. The concordance correlation coefficient (CCC) increased from 0.82 to 0.91, and Pearson's r increased from 0.73 to 0.88 after completing the training process. Similarly, the CCC increased from 0.89 to 0.96, and Pearson's r increased from 0.85 to 0.95 when using the SAD. Other parameters like the bias coefficient (Cb) and standard error (SE) also showed significant improvements after implementing these tools. It is worth noting that trained raters using the SAD showed greater improvements. The increase in CCC was statistically significant in this case (from 0.91 to 0.97), but the increase in Pearson's r did not reach statistical significance (from 0.88 to 0.96). Our findings underscore the effectiveness of the TraineR2 system and the SAD developed in this study as viable options for enhancing the accuracy of visual severity estimation in LLS.

Financial support: INTA (PI-090) and Fundación Maní Argentino (Technical Assistance Project)

Meta-analysis of yield responses to fungicide application timings for the control of wheat stripe rust in the U.S.

Claudio Dias da Silva Junior¹, Nicolas Giordano², Romulo P. Lollato², Erick De Wolf¹, Kelsey Andersen Onofre¹

¹ Department of Plant Pathology, Kansas State University.

² Department of Agronomy, Kansas State University.

E-mail: cdiasda@ksu.edu

Stripe rust (syn. yellow rust), caused by the pathogen *Puccinia striiformis* f. sp. *tritici* is one of the most important threats to wheat production worldwide. In the US, yield losses can be greater than 90% in susceptible winter wheat varieties, resulting in millions of dollars of economic loss in epidemic years. This disease has increased in global importance over the last two decades with the introduction of isolates better adapted to warm climates. Historically, best management practices for stripe rust include a combination of genetic resistance and well-timed fungicide applications. Even so, there remains open questions about optimal timings for applications and the benefits of early (pre Feekes 8) applications. The objectives of our study were to: 1) Compare the efficacy of five fungicide application timings for stripe rust control; 2) Evaluate the effect of different modes of action for stripe rust management; and 3) Evaluate economic break-even scenarios for the treatments assessed here. The application timings evaluated included T1 (between Feekes 4 – 7); T2 (between Feekes 8 – 10); T3 (at or after Feekes 10.1); T4 (T1 + T2); and T5 (T1 + T3). To systematically answer these questions, we conducted a three-level mixed-effects meta-analysis of peer reviewed studies collected from the United States-based Plant Disease Management Report database. The keywords “stripe+rust” resulted in 130 publications spanning year 2002 to year 2023. Publications were removed from the dataset according to predetermined selection criteria, with 64 publications retained for the analysis. The dataset was later enriched with 8 unpublished trials that matched the criteria. We observed a significant difference between the application timings ($F = 3.6$; $p < 0.0001$), with each resulting in significant yield improvements over the non-treated control. The highest yield improvements were observed when a single application was made at flag leaf (T2) and when an early application was followed by a flowering application (T5). The average yield gain across timings was 21% for T1 ($p < 0.0001$), 29% for T2 ($p = 0.0780$), 24% for T3 ($p = 0.6151$), 34% for T4 ($p = 0.0114$), and 40% for T5 ($p = 0.0050$). For the moderators that were tested, year ($F = 2.17$; $p = 0.1412$) and state ($F = 0.68$; $p = 0.7257$) did not have a significant effect on yield. On the other hand, including wheat growth habit (spring vs. winter wheat) as a moderator resulted in a significant difference ($F = 5.33$; $p = 0.0211$) where winter wheat resulted in an overall higher average yield benefit (36%; $p = 0.0211$) vs. spring wheat (17%; $p = 0.0026$). These findings provide critical information that can be used by wheat producers to better time fungicide applications for the management of stripe rust. Additional results will be presented and discussed.

Risk-based surveillance of wheat stripe rust in the Great Plains region of the United States

Claudio Dias da Silva Junior¹, Erick De Wolf¹, Kelsey Andersen Onofre¹

¹ Department of Plant Pathology, Kansas State University.

² Department of Agronomy, Kansas State University.

E-mail: andersenk@ksu.edu

Stripe rust (*Puccinia striiformis* f. sp. *Tritici*, *Pst*), also known as yellow rust, is a disease of major concern in wheat producing regions worldwide. Over the last decade, there have been major epidemics of stripe rust in the great plains resulting in 4.5% annual average yield loss in Kansas alone. This pathogen cannot overwinter in the central and northern great plains region of the US. It is hypothesized that *Pst* overwinters in the Southern Great Plains and disperses northward along the “Puccinia pathway”. Surveillance of this pathogen in states like Kansas is critical for mobilization of management through fungicides. Even so, surveillance is often haphazard and reliant on a small number of Extension personnel and crop consultants. Our objectives were to 1) curate historical observations of *Pst* in the Great Plains, 2) parameterize a network model of *Pst* spread incorporating early detection events, wheat cropping area, environmental suitability, and pathogen dispersal, 3) compare predicted stripe rust detections with historical observations. *Pst* observations were collected from the USDA cereal disease bulletin for states other than Kansas. In Kansas, observations were available from extension reports at a more frequent reporting interval. Cropping data was collected from the USDA Cropland Data Layer. We present counties of highest importance for surveillance early in the season. This preliminary modeling framework will be used to inform scouting and surveillance efforts early in the season, where resources are limited but early detection is critical for farmer decision making.

Unravelling the spatial dynamics and incidence of corn stunting disease complex in Brazilian maize fields

Maria Cristina Canale¹, Rodolfo Vargas Castilhos¹, Marcos Vinícius Silva de Andrade¹, Cristiano Nunes Nesi¹, Mohamed Cassim Mohamed Zakeel²

¹ Centro de Pesquisa para Agricultura Familiar (Cepaf), Empresa Brasileira de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (Epagri), Chapecó SC Brasil.

² CSIRO Agriculture and Food, Black Mountain Science and Innovation Park, Clunies Ross Street, Canberra, ACT 2601, Australia

E-mail: cristinacanale@epagri.sc.gov.br

Corn stunting disease complex poses a severe threat to maize production in Brazil, with persistent outbreaks and substantial crop losses since 2015. This disease complex involves two phloem bacterial pathogens, the maize bushy stunt phytoplasma (*Candidatus Phytoplasma asteris*) and *Spiroplasma kunkelii*, both transmitted by the corn leafhopper *Dalbulus maidis* (Hemiptera: Cicadellidae). Empirical studies to assess the epidemic dynamics of this disease are scarce. This study aimed to comprehensively assess disease incidence and progression in an experimental field in Chapecó, Santa Catarina, Brazil, during the 2018/19 and 2019/20 cropping seasons. A meticulous visual evaluation of a total of 2860 and 6336 maize plants was conducted, mapping binary data representing the presence (1) or absence (0) of symptoms at 80 days after sowing. The observed corn stunting disease incidence was 7.62% and 4.58% for the 2018/19 and 2019/20 seasons, respectively. Statistical analyses revealed that the binomial distribution better described the 2018/19 data (log-likelihood ratio statistics, LRS = 2.24, df = 1, P > 0.05), while the beta-binomial distribution was more suitable for the 2019/20 data (LRS = 7.82, df = 1, P < 0.05). However, the Fisher's indices of dispersion for both data, close to one, indicated a relatively uniform distribution of diseased plants. Semivariogram analysis confirmed the uniform distribution of diseased plants across the study fields. Geostatistical examination of the large-scale distribution of diseased plants unveiled low spatial dependence, with an index of aggregation around 1 and an intracluster correlation coefficient of ≤ 0.03 . The absence of pronounced spatial clustering emphasizes the critical significance of a widespread distribution throughout the field, highlighting the imminent risk of rapid plant infestation and underscoring the necessity for prompt control measures to prevent potential extensive damage. In conclusion, these findings deepen our understanding of the epidemic dynamics of this disease, providing a basis for targeted interventions and effective management strategies in Brazilian maize production.

Evaluating the potential of multisource data for predicting corn tar spot intensity

Mariela Fernández-Campos¹, Abhishek Subedi³, Carlos Góngora^{1,4}, Chongyuan Zhang¹, Andrés Cruz¹, Camila Rocco Da Silva¹, Tiffanna J. Ross¹, Darcy E. P. Telenko¹, Mohammad R. Jahanshahi^{2,3}, and C. D. Cruz.

¹Dept. Botany & Plant Pathology, Purdue University, USA.

²Lyles School of Civil Engineering, Purdue University, USA.

³Elmore Family School of Electrical and Computer Engineering, Purdue University, USA.

⁴Tecnológico Nacional de México/IT de Ciudad Valles. Calle Al Ingenio 2, Ciudad Valles, San Luis Potosí, 79033, México.

E-mail: cruz113@purdue.edu

Tar spot of corn is a disease caused by the fungus *Phyllachora maydis*. It was first reported in the U.S. in 2015, and yield losses have been up to 50% in the Midwest region. The need for effective strategies to mitigate these losses has called for exploring data-driven models to provide alternative tools for detection, quantification, and disease forecasting. Current data-driven prediction models rely on environmental variables to predict tar spot. However, single-source models often fail to capture the full range of variability in the pathosystem, a limitation that can potentially lead to biases and inaccurate predictions. Our study proposes an innovative approach utilizing multisource data (environmental and vegetation indices) to predict 5% of tar spot disease severity at the ear leaf. Experiments were conducted in Indiana in 2021 and 2022 where the pathogen has been established. We investigated neural networks (NNs) and logistic regression (LR) models to predict tar spot intensity and compared their performance. Before training the LR, a correlation analysis was performed in which vegetation indices, such as NDVI, and environmental variables, such as mean leaf wetness of the night was correlated with the disease. Using a stepwise procedure, the logistic regression model was trained with manually selected features, such as the simple ratio, green band, soil-adjusted vegetation index, temperature, and solar radiation. The NNs was trained using all available variables with five layers. The LR model showed an accuracy of 95.8%, sensitivity of 97.7%, and specificity of 86.8% when predicting 5% of tar spot severity. In the other hand, the NNs model predicted tar spot severity with an accuracy of 96.7%, sensitivity of 99.0%, and specificity of 96.0%. The NNs model provided better predictions of tar spot at 5% severity than LR, as evidenced by its superior accuracy, sensitivity, and specificity. Tar spot prediction models will be further validated using micro-plots and field-scale research plots from 2022 and 2023.

Financial support: Indiana Corn Marketing Council, Purdue AgSEED, Tecsoil Inc.-Solinftec, and USDA-ARS [5020-21220-014-016-S].

Influence of plastic cover on raspberry late rust and the dynamics of airborne *Aculeastrum americanum* urediniospores in the field

Daiana Maria Queiroz Azevedo, Gabriel Wildner Cordeschi Leite, Yasmin Vieira da Silva, Sílvia de Afonseca Lourenço, Lilian Amorim

Departamento de Fitopatologia e Nematologia, Escola Superior de Agricultura “Luiz de Queiroz” (ESALQ), Universidade de São Paulo (USP), Piracicaba, SP.

E-mail: daiana.azevedo@usp.br

Brazilian raspberry producers have adhered to the use of plastic covers at the orchards, which minimize climate variations, mitigate the effects of radiation and excessive temperatures on the fruits, leading to higher yield and extended shelf life. However, the occurrence of late rust caused by *Aculeastrum americanum* challenges growers and limits the yield. Urediniospores of this *A. americanum* are easily dispersed by the wind, contributing to the evolution of epidemics in the field. The aim of this study was to evaluate the influence of plastic covering on the dynamics of airborne *A. americanum* urediniospores and on the spatial and temporal progress of the raspberry late rust in the field. The experiment was conducted in a commercial orchard located in the municipality of Piracicaba, Brazil, on raspberry cv. Heritage plots with and without plastic cover. Disease and airborne urediniospores were monitored on a weekly basis throughout two crop cycles: from January to July 2022 and from January to June 2023. On the covered plot, the plastic was installed as a macrotunnel system, with the arch projection of 5.2 m. The number and position of symptomatic plants, as well as the disease severity in the leaflets, were recorded throughout the evaluations. Three passive impactor spore traps, with glass slides covered by double-sided self-adhesive tape, were installed in the plots with plastic cover and another three were installed in plots without plastic cover. The total number of urediniospores, captured by the traps, as well as those germinated on the slides, were quantified under a light microscope. The results revealed that the raspberry late rust spread from the edges towards the center of the plots. The spatial pattern of symptomatic plants was predominantly aggregated in the covered plot and at random in the uncovered plot. The disease incidence has reached 100% of plants in both covered and uncovered plots in 2022. In 2023, the disease incidence was higher ($p > 0.05$) in the uncovered plot (89%) compared to the covered plot (18%). In both crop cycles, the disease severity was significantly lower in the covered plot. The area under the disease progress curves (audpc) calculated for disease severity for covered and uncovered plots were respectively 1.1 and 7.1 in 2022 and 0.1 and 0.8 in 2023. The presence of airborne urediniospores in the traps was detected in the same period that the disease occurred in the field. The highest daily averages of captured *A. americanum* urediniospores was observed in the uncovered plot, where disease severity was also higher. Most captured spores were organized as clusters. Germinated urediniospores were only observed on slides from the uncovered plot. The results suggested that plastic covering reduces the dispersal and germination of *A. americanum* urediniospores, which delays the progress of raspberry late blight.

Financial support: FAPESP (2022/00216-2 and 2019/13191-5)

Metabarcoding and AI as tools in diagnostics, disease epidemiology and modeling

Dalphy O.C. Harteveld

Department of Fungal Plant Pathology in Forestry, Agriculture and Horticulture, Norwegian
Institute of Bioeconomy Research (NIBIO), Norway.

E-mail: dalphy.harteveld@nibio.no

Key challenges in plant pathology and sustainable disease management include the effects of climate change on important and emerging plant diseases as well as the increased push for non-chemical control in food production. Modern tools such as metabarcoding and artificial intelligence (AI), and combinations thereof, can aid the surveillance of pathogen dynamics and acceleration of the development and continuous adaptation for efficient disease management strategies. The aim of this project (2024-2026) is to use metabarcoding as a tool for studies on the biology and epidemiology of culturable and nonculturable plant pathogens, including investigations on effects of control strategies on microbial communities. Case studies will be presented that include existing and emerging pathogens of fruit and greenhouse vegetables to exploit the opportunities of the tools. AI will be used for analysis of data from metabarcoding, adjoining host-pathogen studies and climate data, and applied in disease modeling. These technologies will enable rapid and early detection of new and emerging pathogens and will be important tools in forecasting economically important plant diseases.

Financial support: NIBIO

Asymptomatic grapevine leaves harbor inoculum for *Colletotrichum* spp.

Daniel R. Maass Steiner¹, Camila Iavorski Zela¹, Debora Franco de Oliveira¹, Jhulia Gelain³, Desirê Alexia Lourenço Petters-Vandresen², Guido Schnabel³, Louise Larissa May De Mio¹

¹ Plant Science and Plant Health Department, Federal University of Paraná, Curitiba PR Brasil.

²Department of Genetics, Federal University of Paraná, Curitiba, PR, Brasil.

³ Department of Plant and Environmental Sciences, Clemson University, Clemson, SC, USA

E-mail: danielrmsteiner@gmail.com

Species of the *Colletotrichum* genus cause grape ripe rot (GRR), a disease that has been causing damage in vineyards in southern and more recently northeastern Brazil. The typical symptoms of GRR are circular, reddish-brown lesions that render fruit unsuitable for commercialization. Fruit mummies are considered the most important inoculum source, and it is unclear if asymptomatic plant tissue could also harbor the pathogen. We studied the endophytic presence of *Colletotrichum* spp. in asymptomatic grapevine leaves and its association to GRR development. A total of 71 *Colletotrichum* isolates were collected from asymptomatic grapevine leaves and 60 from symptomatic fruit during the 2022/23 season in five states of Brazil: Rio Grande do Sul, Paraná, Distrito Federal, Pernambuco, and Bahia. They were identified to the species level using *ITS*, *GAPDH*, *Tub2*, and *ACT* gene sequences. For pathogenicity tests, two different grape species, *Vitis vinifera* (cv. Thompson) and *Vitis labrusca* (cv. Niagara branca) were used. Inoculations were conducted with spore suspensions on uninjured and injured fruit. All 131 isolates caused GRR symptoms in both cultivars, regardless of the presence of wounds. Four species were predominant in the population, including 60 *C. nymphaeae* (32 from leaves and 28 from lesions), 28 *C. viniferum* (26 from leaves, 2 from symptoms), 20 *C. fructicola* (11 from leaves and 9 from symptoms), and 18 *C. siamense* (11 from leaves and 7 from symptoms) isolates. Similar pathogenicity on fruit together with similar proportions of endophytic *Colletotrichum nymphaeae*, *C. fructicola*, and *C. siamense* isolates in asymptomatic grapevine leaves and symptomatic fruit suggest all isolates from these species can serve as inoculum for GRR disease.

Financial support: CNPQ – Grant number 403374/2022-7, 306886/2021-9, 403918/2021-9

The removal of symptomatic leaves on the ground has little impact on the development of Glomerella Leaf Spot in apple orchards with a high inoculum potential

Débora Petermann¹, Nicolly Campezi Xavier¹, Isabela Druciak¹, Leonardo Araújo², Louise Larissa May De Mio¹

¹ Department of Crop Protection, Federal University of Parana, Curitiba, PR, Brazil.

²Agricultural Research and Rural Extension Company of Santa Catarina (EPAGRI), São Joaquim, SC, Brazil.

E-mail: debora1@ufpr.br , maydemio@ufpr.br

Several species of *Colletotrichum* spp. cause Glomerella Leaf Spot (GLS), and the pathogen can survive in fallen leaves on the ground and on the plant. The primary inoculum is crucial for the occurrence of the first disease symptoms in warmer regions, and the removal of fallen leaves could delay the onset of epidemics. In this study, it was evaluated whether the reduction of primary inoculum from soil-borne leaves interferes with the onset and progress of the epidemic. Two experiments were conducted in a commercial orchard in Campo Largo/PR, with the cultivar 'Gala' on Marubakaido rootstock, and trained in a central leader system. One was carried out in the 2018/19 growing season (EXP1) on 14-year-old plants with the following treatments: urea 5%; urea 5% with reapplication after 30 days, and a control group without application. The second experiment was conducted in the 2021/22 growing season (EXP2) on 17-year-old plants, comparing plots with and without the removal of symptomatic leaves fallen on the ground during the dormancy period under the canopy projection. For both experiments, the presence of *Colletotrichum* spp. in fallen leaves on the ground was evaluated, as well as the latent infection of *Colletotrichum* spp. in flowers and asymptomatic leaves on the plant. Additionally, the number of conidia in spore traps and the severity of GLS on the plant were assessed. In EXP1, fallen leaves on the ground showed an incidence of 55.4% for *Colletotrichum*. For asymptomatic flowers, the incidence was above 92.5%, with no significant difference between treatments. Regarding leaves, the lowest incidence (16.6%) was observed in the treatment with a single urea application, while in the control group, the incidence was 41.6%. Thirteen conidia were captured in the control plots compared to 2 to 4 conidia in the urea-treated plots, with and without urea reapplication, respectively. The severity of GLS in leaves located 0.3 m above the ground was around 8% in the control group, reduced by 50% with reapplied urea. However, at 1.8 m height, the treatments did not differ. In EXP2, the incidence of *Colletotrichum* spp. in fallen leaves on the ground varied from 5.6% to 60.7% among repetitions, indicating considerable variation among plots. For asymptomatic flowers and leaves, no differences were observed between treatments. The incidence in flowers ranged from 5.3% to 8.3%, and in leaves, it ranged from 61.6% to 69.2% with and without inoculum in leaves, respectively, under the canopy projection. The total number of conidia until the first symptoms of GLS was 238 with and 306 without fallen leaves left on the ground. Similarly, the severity of GLS did not differ between treatments and evaluation heights on the plant. In conclusion, the management of fallen leaves on the ground was not a sufficient practice to reduce the primary inoculum of *Colletotrichum*. The potential of inoculum on the plant, favorable climate conditions, and orchard age should be considered to prevent or delay epidemics.

Financial support: CNPQ (Project #306886/2021-9, 403918/2021-9) and CAPES (Project #001)

Influencing factors on fungicide response in TN soybean

Elias Zuchelli¹, Hairong Qi² and Heather Kelly¹

¹ Entomology and Plant Pathology Department, University of Tennessee, Jackson, TN, USA
Computer Science

² Min H. Kao Department of Electrical Engineering and Computer Science, University of Tennessee, Knoxville, TN, USA

Email: ezuchell@utk.edu

Soybean disease development is dependent on conducive weather conditions, pathogen presence, and a susceptible host. The combination of such factors occurring early enough in the season can result in a disease epidemic. Disease is managed by the combination of cultural practices, resistant varieties, and fungicide applications; however, due to the variability of disease between years the challenge for growers is knowing what are the most effective practices to utilize in a specific year. The objective of this study was to investigate the interaction between varieties and fungicides on disease and yield, to help guide management decisions in soybean production. Evaluating 268 soybean varieties from 2018 through 2020, a randomized complete block split plot design was used with variety as the main plot and fungicide as the sub-plot with 4 replications across 2 locations each year. Main plots were four rows on 76 cm spacing and 7.6 m long. The right two rows of each plot received an application of Azoxystrobin (19.8%) + Difenoconazole (11.4%), (Quadris Top SBS 0.5 L/ha) at beginning pod development (R3 growth stage). Of the 268 soybean varieties evaluated, 42 varieties were evaluated across multiple years, for a total of 226 unique varieties screened. Frogeye leaf spot (FLS) and target spot disease severities were rated in non-fungicide sub-plots based on percent leaf area affected at full seed (R6 growth stage). Based on rating data, varieties were categorized as susceptible, moderately susceptible and resistant. Yield was also recorded from both fungicide treated and non-treated sub-plots. Among the 268 varieties 59% of the varieties fell within low (59%), moderate (27%), and high (14%) disease development categories for FLS, however the application of fungicide protected 262, 235 and 262 kg/ha respectively. The data was used along with a break-even table to determine the proportion of time a fungicide application would result in a profit. Regardless of FLS susceptibility, 70% of the varieties had at least 134 kg/ha greater yield than non-treated; hence, there are other factors influencing fungicide response, such as occurrence of other diseases. Exploratory analysis using models to estimate the likelihood of obtaining a profit from a fungicide application, has an accuracy of 75.3% for a gradient boosted model and 78.4% for neural network. One particular difference in the training of the two models was in the variable's importance, when the gradient boosted considered yield as the major factor followed by the severity of FLS, whereas the neural network considers the FLS disease severity a major factor and yield as a secondary factor. Further analysis models will include the evaluation of a disease index which compiles FLS, SBS, and TS severities and base the variety susceptibility on it, to further provide the output of the profitability of the fungicide application.

Disease reaction classification considering trial accuracy and phenotype stability: A case study with rice

Felipe Dalla Lana^{1,2}, Karina Lima Reis Borges^{1,3}, Roberto Fritsche-Neto^{1,3}

¹ H. Rouse Caffey Rice Research Station, LSU AgCenter, Rayne, LA, USA.

² Department of Plant Pathology and Crop Physiology, LSU, Baton Rouge, LA, USA.

³ School of Plant, Environmental, and Soil Sciences, LSU, Baton Rouge, LA, USA.

E-mail: fdallalana@agcenter.lsu.edu

Classifying new varieties and breeding lines within disease reaction classes, such as susceptible or moderately resistant, is crucial for disease management recommendations and breeding decisions. New genotypes are released or advanced in the breeding pipeline yearly. Although the breeding process can span 5 to 7 years, lines and varieties are often tested for disease only in advanced breeding stages. While control conditions can speed up the classification process, they often employ methods that are too invasive and do not accurately reflect actual field resistance. Therefore, disease reaction classification studies based on more realistic cultivation scenarios should be preferred. However, field studies are subject to the influence of multiple factors, including the risk of escape, which poses a concern for accurate disease classification. To address this, we aimed to develop an analytic pipeline that includes data quality control and determines the necessary duration for accurately classifying rice varieties' disease responses and its stability over the years. We utilized a historical dataset from the LSU AgCenter's Rice Pathology Lab, which includes evaluations of 10 varieties for four diseases over 25 years. We applied two equivalent mixed-model equations, with genotype as a fixed and random effect, for each year and disease combination to estimate heritability (as a surrogate for accuracy) and the adjusted means (to assess line performance). From the accuracy distribution per disease, we identified outliers and thus removed trials with low reliability from the analysis. Next, the genotypes were ordered based on their performance, and a linear regression was used for each line and disease combination across years to estimate stability. Finally, employing a bootstrap approach in conjunction with mixed-model equations, we calculated the minimum number of years necessary to classify a new rice line's reaction to diseases. Our results enabled us to create graphs combining performance and stability, simplifying the recommendation process. Moreover, our findings suggest that five years of evaluation is optimal for accurately classifying a new rice variety's disease resistance.

Financial support: USDA-NIFA-SAS (No. 2023-68012-39002) and Louisiana Rice Research Board (GR-00014435)

Comparison of quantification methods for assessing *Gibberella* stalk rot severity on corn

Gabriel Ferreira Paiva¹, Lara Lorrayne Silvestre de Andrade¹, Maik Leão dos Santos¹,
Maiara da Silva Freitas¹; Franklin Jackson Machado¹

¹ Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa MG Brazil.

E-mail: franklin.machado@ufv.br

Quantification of plant disease intensity is majorly important in plant pathology, especially for epidemiology and disease management. Disease severity can be visually estimated with or without the aid of a set of standard area diagrams (SAD) or measured via image analysis. For diseases such as *Gibberella* stalk rot (GSR) of maize, caused by members of the *Fusarium graminearum* species complex (FGSC), disease severity can be especially difficult. First, it requires additional steps (e.g. splitting the stalks). Then, disease severity is visually estimated, mostly under field conditions. The present study aimed to compare different methods for the quantification of GSR severity on maize. Severity assessment was conducted on symptomatic internodes of three hybrids that were subjected to artificial inoculation. At physiological maturity, stalks were split longitudinally, and symptomatic internodes were photographed. First, image analysis was performed to obtain the actual severity using the software ImageJ and the Pliman package in R. Second, the visual estimation of stalk rot severity and longitudinal length of the lesion was performed by six experienced raters and six raters with no experience in quantifying plant diseases. Two SADs were used for the aided estimates. First, a black-and-white SAD set developed for anthracnose stalk rot and a proposed colored SAD. Lower levels of concordance ($\rho_c = 0.44$) were obtained between ImageJ and the Pliman measures. In contrast, the severity measurements performed by the Pliman package were considerably less time-consuming. There was an improvement in accuracy and precision using the both SADs relative to unaided estimates only for inexperienced raters. No significant difference was observed between the estimates of the two SADs. Overall, there was a significant correlation between the longitudinal length and the actual GSR severity, particularly when measured by experienced raters. Although SADs are very important tools for disease severity quantification, for GSR may only help inexperienced raters as the experienced ones already accurately estimate the disease. Thus, the need to optimize and improve GSR severity estimates may be achieved using indirect measurements or automated image analysis.

Financial support: CAPES PROEX, FAPEMIG (Project number APQ-00027-21).

Does leaf position influence maize disease severity estimates by remote sensing?

Maik Leão¹, Franklin J. Machado¹

¹ Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa MG Brasil.

E-mail: franklin.machado@ufv.br

The quantification of disease severity, especially foliar diseases in maize, is a very difficult task. Usually, researchers evaluate several leaves per plant, several plants per plot and several plots per field to account for the disease progress and distribution in a crop. On top of that, maize leaves are extremely larger than other cereal crops. Thus, disease quantification methods based on remote sensing have been explored as an alternative to visual estimates in the field. This work was carried out to characterize the effect of the vertical position of leaves in the canopy on the reliability of severity estimates by remote sensing. Visual severity estimates of 88 plots were obtained from field trials conducted in 2023 in Viçosa, MG, Brazil. The visual assessments corresponded to the final severity (stage R4) of different leaves on the plants: the leaf below the main ear (LBME), the leaf of the main ear (LME), the leaf above the main ear (LAME), and the mean severity of the whole canopy of the plot. Simultaneously, the plots were imaged with a multispectral sensor embedded in a Unmanned Aerial Vehicle (UAV). The captured images were georeferenced by the Post Processed Kinematic (PPK) method, then radiometrically calibrated and processed to obtain the orthomosaics (Ground Sample Distance = 2.1 cm) of the spectral bands (Blue, Green, Red, Red-Edge and NIR). Thirty vegetation indices (IV) were calculated with the bands. The corresponding mean value for each IV was measured for each plot, disregarding edges and canopy gaps. These gaps were highlighted using a selection mask based on a threshold on the DVI vegetation index (<0.15). All IVs were evaluated as predictor variables in a multiple linear model using a step-wise approach based on the highest coefficient of determination (R^2) and significance of the coefficients in the linear model. The best-performing variables, Transformed Vegetation Index (TVI), were used to adjust models to predict the severity in the different leaves and in the plot. The performance of the model estimates was evaluated by cross-validation, to obtain the correlation (r), normalized Mean Absolute Error ($nMAE$) and normalized Root Mean Square Error ($nRMSE$), as well as the concordance correlation coefficient (ρ_c). In addition, the equivalence between the values estimated by both methods was subjected to a paired t-test. The five models estimated severity values that did not differ by the t-test from the severity estimated visually. With the exception of the LAME ($\rho_c = 0.68$, $r = 0.74$), the overall accuracy and precision of the estimates were higher than 0.78 and 0.81, respectively. The LAME was the only one to obtain values of $nMAE$ and $nRMSE$ higher than 0.42 and 0.57, respectively. The projection area of the leaves varies depending on their position on the plant which can interfere with the reflectance of the surface. The results of this study suggest that remote sensing can be used as a reliable alternative to estimate severity of foliar diseases in maize. Additionally, the position of sampled leaves should be considered during the validation of sensor-based measurements of plant disease severity in the field.

Financial support: CAPES PROEX, FAPEMIG (Project number APQ-00027-21).

Severity of foliar diseases in maize: how can estimates be improved?

Maik Leão dos Santos¹, Maiara da Silva Freitas¹, Franklin Jackson Machado¹

¹ Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa MG Brasil.

E-mail: franklin.machado@ufv.br

Assessing the severity of foliar diseases is an important task in plant pathology. However, it can be difficult, especially for diseases that affect leaves with complex architecture which are often infected by multiple pathogens. In maize, for example, it may affect the complete visualization of disease symptoms and can affect the reliability of disease severity estimation. This study investigated the effect of lesion size and the presence of co-infection on the accuracy and precision of visual estimates made by a group of inexperienced and experienced raters with or without an aid of a standard area diagram set (SAD). Maize leaves with a representative range of disease severity were randomly collected in a field trial conducted in 2023 in Viçosa, Minas Gerais, Brazil. A set of 38 leaves was digitized with a scanner at 300 dpi. The images consisted of leaves from two maize hybrids, susceptible to leaf spots, with symptoms of at least two different diseases (northern corn leaf blight and gray leaf spot). The actual leaf severity was obtained through image analysis using a pixel-by-pixel segmentation approach. Each pixel was classified into three categories: symptomatic, healthy and background, using ImageJ software. Foliar disease severity was visually estimated by eight raters, four with experience and four with no experience in disease severity quantification. Raters visually estimated disease severity with and without the aid of a SAD developed to assess northern corn leaf blight severity. The time spent to estimate the severity of each leaf was obtained during each round of assessment. Overall, raters underestimated disease severity without SAD aid. Accuracy and precision of the estimates improved when aided by the SAD compared to unaided estimates. Inexperienced raters were more accurate when aided ($p < 0.05$; $R^2 = 0.91$), regardless of the size of the prevalent lesions, compared to the experienced group with an aid of the SAD ($p < 0.05$; $R^2 = 0.73$). Smaller lesions interfered with the visual estimates, resulting in an underestimation of the disease severity. Similarly, disease severity was underestimated when there was an occurrence of multiple diseases in the same leaf. However, leaves with co-infections showed deviations in the estimates with the increase of disease severity. There was no correlation between the time spent to estimate disease severity and the improvement of overall accuracy of estimates. SAD is an effective tool to improve the reliability of disease severity estimates of foliar diseases in maize even when there are multiple diseases in the same leaf.

Financial support: CAPES PROEX, FAPEMIG (Project number APQ-00027-21).

Network analysis of *Neopestalotiopsis* sp. spread from nurseries to strawberry farms in Florida, USA.

Galvin Alonzo¹, Marcus V. Marin, Karen A. Garrett, Natalia A. Peres

Plant Pathology Department, Gulf Coast Research and Education Center (GCREC),
University of Florida, Wimauma, Florida 33598, USA.

E-mail: galvin.alonzoort@ufl.edu

Pestalotia leaf spot, fruit rot, and crown rot have been posing a significant threat to Florida's strawberry industry since 2017. Managing these diseases has been challenging because none of the currently grown cultivars is resistant and fungicides have limited efficacy during periods of extended leaf wetness. Quiescently infected transplants coming from nurseries are the primary inoculum source for most strawberry diseases in Florida. Therefore, our objective was to determine the linkage of infected transplants coming from strawberry nurseries with the onset, progression and establishment of diseases caused by *Neopestalotiopsis* sp. in Florida. Based on data collected from 1,078 Florida strawberry samples brought to the GCREC Plant Diagnostic Clinic from 2018 to 2023, we built networks linking nurseries across the USA and Canada to farms in Florida. Several strawberry fields are represented under the same farm name. Over five consecutive strawberry seasons (October to February), we observed monthly progression of diseases caused by *Neopestalotiopsis* sp. In the 2018-19 and 2019-20 seasons, a specific nursery in North Carolina was linked to most infected samples, which reduced its transplant sales to Florida growers in subsequent seasons. Tropical storm Eta in November 2020 led to widespread disease outbreaks caused by *Neopestalotiopsis* sp. in Florida, demonstrating the impacts of windy storms, prolonged leaf wetness, and overcast conditions. During the 2021-22 season, most samples infected with *Neopestalotiopsis* sp. were cases of crown rot detected in the late part of the season (January to February). Positive *Neopestalotiopsis* sp. samples in the 2021-22 and 2022-23 seasons were randomly distributed in Florida, suggesting possible inoculum survival in farms across seasons, with symptoms emerging under conducive environmental conditions. To mitigate disease spread, using clean strawberry transplants, and managing residual *Neopestalotiopsis* sp. inoculum in Florida strawberry fields are recommended.

Monitoring *Phakopsora pachyrhizi* with spore traps in commercial soybean fields in Paraguay in the 2023/2024 season

Guillermo A. Enciso-Maldonado^{1,4}, Marco Maidana-Ojeda², Marcelo E. Medina-Aquino², Marcos A. Britez-Cardozo², Lourdes F. Acevedo-Medina¹, Nahuel N. Schmid-Bernal¹, Andrés D. Sanabria-Velázquez³, Andrea A. Arrua⁴, Marcos J. Mendoza-Duarte⁵

¹ Universidad Católica “Nuestra Señora de la Asunción” Unidad Pedagógica Hohenau, Hohenau, Itapúa, Paraguay

² Smart Soil PY, Encarnación, Itapúa, Paraguay

³ Department of Entomology and Plant Pathology, North Carolina State University (NCSU), Raleigh, NC, USA

⁴ Centro Multidisciplinario de Investigaciones Tecnológicas, Universidad Nacional de Asunción, San Lorenzo, Central, Paraguay

⁵ Centro de Desarrollo e Innovación Tecnológica, Hohenau, Itapúa, Paraguay

E-mail: guillermo.enciso@uc.edu.py

During the 2023/2024 season, this study was conducted to observe the presence of *Phakopsora pachyrhizi* uredospores, the causative agent of Asian soybean rust (ASR), to understand the inoculum dynamics in commercial production fields. Spore traps SIGA-model were used to capture the uredospores of *P. pachyrhizi*. Sampling was carried out weekly. The spore traps were installed five days after planting in two soybean production fields: one in Santa Teresa (Caaguazú, Paraguay), where the M 6410 soybean variety was planted on September 16, 2023, and the other field located in Yguazú (Alto Paraná, Paraguay), where the NEO 590 I2X variety was planted on September 22, 2023. The distance between both production fields is approximately 50 km in a straight line. In both plots, farmers applied fungicides following a schedule, starting around 30 days after emergence with application intervals of 15 to 25 days until reaching five applications; however, farmers preferred not to share information about the fungicide formulations used. Alongside quantifying the number of uredospores cm⁻², the crop's phenological stage and the severity of ASR were recorded using a diagrammatic scale within 50 meters around the spore trap. In Santa Teresa, the first two *P. pachyrhizi* uredospores cm⁻² were observed on November 10, 2023, 55 days after planting (phenological stage R3), and the first symptoms of ASR were observed on November 29, 2023 (phenological stage R4-R5.1), 19 days after the occurrence of uredospores in the spore trap. The severity of ASR in Santa Teresa did not exceed 1%. On the other hand, in Yguazú, the first three rust uredospores cm⁻² were observed on November 21, 2023, 60 days after planting (phenological stage R4-R5.1), and the first symptoms of rust were observed on November 29, 2023, eight days after the appearance of uredospores in the spore trap (phenological stage R5.1). In Yguazú, the maximum severity reached 55%. The difference in observed severity levels between plots could be attributed to the management practices of each farmer, as well as the re-entry times into the plot for new applications; however, this information was not provided for this study. Early detection of *P. pachyrhizi* uredospores could be essential for implementing effective control measures. Therefore, this study could be a foundation for guiding further research on ASR control in Paraguay and developing soybean disease prediction models.

Remotely sensed leaf area index can improve mechanistic *Cercospora beticola* epidemiological models for disease predictions

Rene Heim^{1,3}, Paul Melloy², Nathan Okole³, Facundo Ramón Ispizua Yamati³, and Anne-Katrin Mahlein³,

¹University of Bonn, Photogrammetry and Robotics Lab, Nussallee 15, 53115 Bonn, Germany

²The University of Queensland, School of Agriculture and Food Sciences, Gatton, 4343, Queensland

³Institute of Sugar Beet Research, Holtenser Landstraße 77, 37079 Göttingen, Germany

E-mail: heim@ifz-goettingen.de

Plant disease epidemiological models, empirical and mechanistic, assist with disease management decisions by providing a prediction of plant disease epidemics. Yet, adoption of predictive models in integrated crop protection can be low as available decision support systems require validation, in-field scouting by growers and agronomists and, from time to time, model parameter reviews. Remote sensing technologies and automation strategies can assist in this process and ease adoption. Remote sensing allows the retrieval of spectral data at local, regional, and national scales. By entering this data into radiative transfer models, structural plant traits such as leaf area index (LAI) can be calculated. While LAI is usually not the focus of epidemiological models, it can still indicate critical time points which impact disease epidemic development as it is strongly linked to canopy cover. Canopy cover can indicate the time of row gap closure and is intrinsically associated with crop canopy micro-climates and therefore the onset of disease epidemics. Recognizing this relationship between disease onset and canopy cover, we integrated LAI as a model parameter for model initiation, crucial for disease forecast accuracy. Focusing on cercospora leaf spot (*Cercospora beticola*) in sugar beet (*Beta vulgaris*), we aimed at building on existing forecast models from the literature and expanding them with remote sensing data. We will demonstrate a retrieval process through radiative transfer modelling, using spectral data from uncrewed aerial systems (UAS) and satellites. Additionally, we present the results of optimizing model initiation using different LAI retrieval times, showcasing the potential of our approach for enhancing disease prediction accuracy. We choose to comply with modern standards to render our research findable, accessible, interoperable, and reusable (FAIR) and are therefore presenting it within the scope of an R package which will be openly available.

Financial support: This work has (partially) been funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) under Germany's Excellence Strategy, EXC-2070 - 390732324 - PhenoRob and by funds of the Federal Ministry of Food and Agriculture (BMEL) based on a decision of the parliament of the federal republic of Germany via the federal office for agriculture and food (BLE) under the strategy for digitalization in agriculture FKZ 28DE104A18.

The development of weather-based models for six soybean stem diseases observed across North Dakota

Hope Renfro-Becton¹, Michelle Gilley¹, Dean K. Malvick², Samuel G. Markell¹, and Richard Wade Webster¹

¹North Dakota State University, Fargo, ND, USA

²University of Minnesota, St. Paul, MN, USA

E-mail: hope.becton@ndsu.edu

Soybeans are a commodity rapidly increasing in economic significance for North Dakota agriculture. Disease is estimated to be responsible for up to 25% of soybean yield losses across the Midwest. In 2017 and 2018, disease incidence was recorded for six stem diseases, pod and stem blight (*Diaporthe longicolla* and *D. sojae*), charcoal rot (*Macrophomina phaseolina*), phytophthora stem rot (*Phytophthora sojae*), stem canker (*D. caulivora* and *D. aspalathi*), white mold (*Sclerotinia sclerotium*), and anthracnose (*Colletotrichum* spp.), across the state of North Dakota. There were 406 total fields sampled across 29 counties in 2017 and 24 counties in 2018. In each field, 20 stems (samples) were collected and rated for incidence of the six diseases. The greatest mean incidence recorded for 2017 was for pod stem blight (52%) while phytophthora (57%) had the greatest mean incidence in 2018. Correlation analysis showed several significant relationships ($P < 0.017$, $r > 0.24$) between stem diseases with respect to incidence, but the strongest correlation ($P = 0.003$, $r = 0.51$) was between charcoal rot and anthracnose. For the predictive models, daily average temperature, wind speed, wind direction, and dew point data were extracted from the North Dakota Agricultural Weather Network (NDAWN) system for the 30 days prior to each observation for the nearest weather station. The average estimated relative humidity was calculated using temperature and dew point. Averages for these weather parameters were calculated for 3, 7, 14, 21, and 28 days prior to sample collection and were also included as variables for model development. Lasso regression was used for variable selection and a logistic regression model was developed separately for each of the stem diseases. The accuracy of these models ranged from 73% to 94% with area under the receiver operating characteristic (ROC) curve for the validation dataset ranging from 0.79 to 0.89. Logistic regression, linear mixed models, and machine learning algorithms are being explored and compared for modeling the effects of weather variables on the incidence of these important stem diseases.

Probability modeling of coffee rust epidemic in conilon coffee: A focus on sustainable management

Willian B. Moraes¹, Breno B. dos Anjos¹, Filipe G. B. Celestino¹, Luiz F. S. Barbosa¹, Igor T. Quarto¹, Otávio B. Oliosi¹, Simone P. C. B. Moraes¹, Waldir C Jesus-Junior², Wanderson B. Moraes³, André S. Xavier¹, Fabio R. Alves¹, Samuel A. Silva¹

¹Programa de Pós-graduação em Agronomia, Universidade Federal do Espírito Santo, Alegre ES Brasil.

²Universidade Federal de São Carlos, Campus Lagoa do Sino, Buri SP Brasil

³Department of Plant Pathology, The Ohio State University, Wooster OH United States.

E-mail: willian.moraes@ufes.br

Coffee leaf Rust (*Hemileia vastatrix*) poses one of the primary threats to conilon coffee, standing out as the main disease affecting this crop. This study aimed to assess the probability of rust occurrence and the need for disease control. A logistic model was developed, taking into account meteorological variables, including maximum temperature, minimum temperature, average temperature, and leaf wetness (relative humidity $\geq 80\%$) between 6 p.m. and 6 a.m., the number of hours with temperatures between ≥ 15 °C and <26 °C, the number of hours with precipitation (> 1 mm) between 6 p.m. and 9 a.m., cumulative precipitation, and the number of days with precipitation ≥ 1 mm. We utilized data from three meteorological stations operated by the National Institute of Meteorology (INMET) in the municipalities of Linhares, Marilândia, and Ecoporanga, located in the northern region of Espírito Santo, from January 2022 to December 2023. The analysis of meteorological data, converted to monthly averages, revealed a significant probability of rust epidemic occurrence ($y > 5\%$ incidence) exceeding 70% from May to September. The critical need for control was also observed with a probability above 50% in January and December throughout the two years analyzed. This pattern aligns with studies indicating that the highest rust severities occur between April and September, peaking in July. A preventive management is recommended during these critical periods to reduce the impacts caused by the epidemic and optimize fungicide use compared to the conventional calendar-based system. The logistic model demonstrated efficiency in predicting epidemics during these critical periods, providing an effective estimate of disease occurrence in the field. This study contributes to sustainable rust management strategies, enabling a more precise and efficient approach to damage reduction and resource utilization.

Financial support: CNPq, CAPES, FAPES e UFES.

***Fusarium oxysporum* f.sp. *cupense* Tropical Race 4 threatens Colombian bananas: Translating analyses of host connectivity, trade, and stakeholder movement to inform management and surveillance**

Jacobo Robledo¹²³, Sydney Barker¹²³, Neha Kallamvalli¹²³, David McDermott¹²³,
Monica Betancourt⁴, Karen A. Garrett¹²³

¹Plant Pathology Department, University of Florida, Gainesville, USA

²Global Food Systems Institute, University of Florida, Gainesville, USA

³Emerging Pathogens Institute, University of Florida, Gainesville, USA

⁴Centro de investigación Tibaitatá - AGROSAVIA, Bogotá, Colombia

E-mail: jacoborobledobur@ufl.edu and karengarrett@ufl.edu

In Colombia, the fourth-largest global exporter of bananas and plantains, the agricultural sector is grappling with the critical challenge posed by the invasive pathogen *Fusarium oxysporum* f.sp. *cupense* Tropical Race 4 (*Foc* TR4), first detected in 2019. This pathogen not only threatens the international export market but also jeopardizes domestic food security, given the staple role of bananas and plantains in the Colombian diet. Connectivity among banana and plantain production areas, through mechanisms such as informal trade and movement of farm personnel and equipment, is an important risk factor for pathogen spread. To address these concerns, we used a rapid risk assessment methodology (garrettlab.com/r2m). Our objectives were twofold: to model the potential effects of actions to minimize connectivity among production areas in Colombia and neighboring countries, and to delineate the current trade and stakeholder network connectivity, assessing its implications from an epidemiological and management standpoint. We evaluated the connectivity of banana and plantain cropland in Colombia using the *geohabnet* package in R, and used expert knowledge elicitation to evaluate the structure of informal and formal trade and stakeholder networks. There was significant regional variation in connectivity, with pathogen dispersal potential in the north Pacific coast primarily driven by internal (within Colombia) connectivity, while central, eastern, and northern regions face heightened risk due to international ties. The banana trade, concentrated in just four departments, operates through formal channels, contrasting sharply with the plantain trade's extensive, informal network, which is spread nationwide and poses a considerable risk for *Foc* TR4 dispersal. This informality, coupled with the movement of agricultural personnel and the extensive service networks connecting Antioquia with global regions, underscores the differential impact of international connectivity on disease spread. Our findings highlight the urgent need for targeted international surveillance strategies, particularly in high-risk areas, and call for the formalization and regulation of the plantain trade to mitigate risks. Additionally, implementing stringent biosecurity measures is critical to managing internal personnel movement and leveraging Antioquia's global connections to safeguard Colombia's banana industry against *Foc* TR4.

Financial support: UF/IFAS College of Agriculture and Life Sciences, UF/IFAS Global Food Systems Institute, AGROSAVIA

Impact of water deficit on the initial development of Asian soybean rust

Jessica Danila Krugel Nunes^{1,2}, Manoel Penachio Gonçalves², Lilian Amorim², Armando Bergamin Filho²

¹Instituto Federal de Rondônia, *Campus* Ariquemes, Rondônia, Brasil.

²Departamento de Fitopatologia, Universidade de São Paulo, Piracicaba, SP, Brasil.

E-mail: jessica.krugel@usp.br

Soybean (*Glycine max*) production in Brazil is already being impacted by climate change, marked by more frequent and prolonged periods of drought. However, effects of water limitation on Asian soybean rust (*Phakopsora pachyrhizi*) are currently poorly understood. This study examined the initial development of the disease in soybean plants exposed to moderate water deficit. Soybean plants cv. BRX Lança, grown in pots, were exposed to optimal water availability (80% of available water capacity – AWC) and moderate water limitation (60% of AWC). Then, the plants were inoculated with *P. pachyrhizi* at the V4 stage and kept in a dark humid chamber at $20 \pm 2^\circ\text{C}$ for 12 h. As a control, plants at the same development stage were sprayed with deionized water and kept under the same conditions. After this period, the plants were maintained in a growth chamber at temperatures (day/night) of $25/20^\circ\text{C}$ ($\pm 2^\circ\text{C}$) and a 12-hour photoperiod. The experiment was carried out in a completely randomized design with four treatments and five replicates. The experiment was repeated once. Lesion density (number of lesions per cm^2), rust severity (proportion of lesioned area), and the number of uredinia per lesion were evaluated at 11 days after inoculation. Areas of 2 cm^2 on two central leaflets of the middle third of each plant were photographed for disease quantification using ImageJ software. Two 1-cm^2 leaf discs per plant were sectioned from the central leaflet of the V4 leaf for uredinia counting. The leaf discs were submerged in a trypan blue solution for staining fungal structures and clarified with chloral hydrate solution. Images of the lesions were recorded on a stereo microscope and the number of uredinia was quantified using Zen Blue software. Lesion density and rust severity were higher in plants exposed to water deficit in both experiments. The average lesion density was 50 and 25.6 lesions. cm^2 in plants subjected to water deficit or not, respectively. The average severity observed was 9.92% in plants exposed to water deficit and 4.85% in plants with adequate water availability. There was no significant difference in the number of uredinia per lesion in the initial period of disease development in either experiment. This result suggests that water limitation can reduce the resistance of soybean plants to *P. pachyrhizi* infection. More studies with other soybean cultivars are necessary.

Financial support: FAPESP (Grant number 2019/13191-5), CAPES and IFRO.

Advancing plant epidemic analysis through data science: Tools, techniques, and applications

Laura Alejandra Valbuena-Gaona¹, Yeimy Carolina Tirado-Ospina^{1,2}, Jessika Dayana Ordoñez-Ordoñez^{1,3}, Jeisson Daniel Torres-Quintero¹, Juan Pablo Ruiz-Rugeles¹, Samuel Alejandro Ramírez-Gonzales¹, William Fernando Cárdenas Urrego, Joaquín Guillermo Ramírez-Gil^{1*}

¹Universidad Nacional de Colombia sede Bogotá, Facultad de Ciencias Agrarias, departamento de Agronomía. Laboratorio de Agrocomputación y Análisis Epidemiológico

²Fedearroz

³Sunshine Bouquet Company

E-mail: jgramireg@unal.edu.co

The field of plant epidemiology is witnessing a transformative era with the introduction of data science (DS), offering unprecedented opportunities for enhancing our comprehension and control of plant epidemics. DS, with its core tools, instigates a paradigm shift in our approach to and mitigation of plant diseases. This encompasses the utilization of open-source software, process automation, and proficient handling of extensive datasets, ultimately augmenting the speed and precision of epidemiological analyses. Key steps in the application of DS include i) original data management, ii) incorporation of new data through web scraping, iii) employment of visualization tools, and iv) modeling, featuring a multi-approach encompassing traditional models, machine learning, and deep learning. Within our laboratory, we are actively implementing and validating numerous DS-associated tools for analyzing plant epidemics across diverse agricultural systems, such as flowers, rice, sugar cane, and more. Through these case studies, we emphasize the versatility and applicability of DS in varied agricultural contexts, demonstrating its potential to revolutionize the management of plant epidemics. DS emerges as a potent suite of tools that significantly enhances the management and analysis of epidemiological data in plants. By providing alternatives to conventional methods, data science stands as a robust and indispensable ally in fortifying plant health, thereby charting a course towards a more resilient and sustainable agricultural future.

Financial support: Universidad Nacional de Colombia, sede Bogotá and Fedearroz (Project # 51201), and Fedepapa (Project # 44763.)

Quantification of airborne basidiospores of *Ganoderma zonatum* at different altitudinal gradients and their relationship with environmental conditions in oil palm

Juan M. López-Vásquez¹, Sandra Y. Castillo¹, Franky L. Zuñiga¹, Greicy A. Sarria¹

¹Phytopathology area, Pest and Disease Program, Colombian Oil Palm Research Centre (CENIPALMA)

E-mail: jlopezv@cenipalma.org

Oil palm (*Elaeis guineensis* and interspecific hybrid OxG (*Elaeis oleifera* X *Elaeis guineensis*)) is one of the main agro-industries in Colombia, with a planted area of more than 559,000 hectares and a palm oil production of 1,528,739 tons, ranking fourth as a producer worldwide. Basal stem rot (BSR), caused by *Ganoderma zonatum*, is one of the most important emerging oil palm diseases in Colombia which until now, is restricted to only two oil palm producing areas in the country. However, despite the controls established to prevent spread to new areas, its containment has not been possible. This study was carried out with the objective of providing key evidence on the mechanisms of spread of BSR and the environmental conditions involved. For that, the hourly concentrations of *G. zonatum* basidiospores in the air were quantified using four 7-day Burkard volumetric samplers at different heights (1, 4, 7, and 10 m) installed on a scaffold-type structure located inside an 18-year lot of African palms (*Elaeis guineensis*) highly affected by the disease. Also, were taken hourly records of the main meteorological parameters such as Solar radiation (Mj/day), Temperature (°C), Relative humidity (%), Precipitation (mm) and Wind speed (m/s) measured at 2 and 10 meters high, and a series of statistical correlation analysis were carried out considering the spore concentration variable (basidiospores/m³) as dependent and the meteorological variables as independent. The study was carried out by applying the non-parametric Spearman correlation test (Rho) with a monthly time window (June 2022 to May 2023), as it was verified that the spores do not follow normal distribution models. The degree of significance was calculated for the 95% (*) and 99% (**) confidence intervals. The results obtained indicated that there are no significant differences in the concentration of basidiospores captured at different altitudinal gradients, which suggests a great dispersal capacity of *G. zonatum* when reaching higher altitudes or close to the palm canopy, which varies according to the seasonality of the year. The results obtained according to the statistical correlation analysis did not show significant values of the meteorological variables Solar radiation, Temperature, Relative humidity, Precipitation and Wind speed at 2 meters high in any of the twelve months evaluated. However, it was possible to show a positive and significant correlation with the variable Wind speed at 10 meters high in the months of December 2022, January, and March 2023 with values of 0.43*, 0.38* and 0.39*, respectively. These types of results show the role of wind in the active dissemination of *G. zonatum* basidiospores where quantification was possible even of high concentrations (>100 spores/m³) when the wind speed measured at 10 meters high exceeds 1 m/s. The other meteorological variables such as Temperature, Relative Humidity and Precipitation seem to be more related to the *in-situ* formation and maturation processes of the basidiocarps at the base of the affected palms in the months of September, October, and November, which favors active dispersion of the basidiospores in the months of highest wind speed such as December, January, February, and part of March.

Financial support: Fondo de Ciencia, Tecnología e Innovación (FCTel) del Sistema General de Regalías (SGR) de Colombia y Fondo de Fomento Palmero (FFP).

What does “bottom-up” actually mean for tar spot disease development in corn?

Brenden Lane¹, Joaquín Guillermo Ramírez-Gil², Carlos Góngora-Canul¹, Mariela Fernandez-Campos¹, C.D. Cruz¹

¹Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN

²Departamento de Agronomía, Facultad de Ciencias Agrarias, Universidad Nacional de Colombia, sede Bogotá

E-mail: lane80@purdue.edu

In 2015, the corn-infecting pathogen *Phyllachora maydis* (causal agent of tar spot disease) was reported for the first time in the United States. The disease has since spread across the Midwest corn belt while causing major yield losses. In 2021 alone, 5.88 million metric tons (231.3 million bushels) of US corn yield were lost to this disease with an economic impact of US\$1.25 billion. Though fungicides can help fight against these agro-economic losses, application timing can be difficult to truly optimize since our understanding of tar spot dynamics is still evolving. The current understanding is that tar spot typically develops bottom-up through a polycyclic infection cycle. Since signs and symptoms are typically seen first on the lower leaves then sequentially up the plant, it has been assumed that the lower leaves fuel the middle leaves, and the middle leaves fuel the upper leaves in terms of sign/symptom development. We dove further into this theory by using the stochastic Markov process to uncover a deeper insight into the vertical dynamics of sign/symptom development. We conducted observational studies in corn production fields by recording visual severity data at three leaf levels: the fifth leaf above the ground, the main ear leaf, and three leaves above the main ear leaf. We then applied this data to a Markov chain model with four severity-based states at the three leaf levels. What we find is that the probability of bottom-up, or even top-down, tar spot sign/symptom development is incredibly low. Instead, it appears that multiple epidemics are occurring mostly independently at each leaf level with 99.5% probability. We see that this disease does not appear to develop up the plant canopy in the same way as previously thought, at least in the US. Instead, it seems that the disease re-circulates at each canopy level without a sizable temporal sequence between the strata. Though our investigations do not tell the entire story of tar spot development, our findings give some fundamental insights into a more data-driven, mechanistic view of tar spot epidemiology and what it could mean for its vertical-temporal development.

Financial Support: United States Department of Agriculture, Purdue University, Solinftec Ag robotics.

***Fusarium* species and mycotoxins in barley grains through different physiographic regions of Rio Grande do Sul, Brazil**

Emanuéli Bizarro Furtado¹, Sabrina de Oliveira Martins¹, Eduardo Guatimossin², Carlos Augusto Mallmann³, Luara Medianeira de Lima Schlösser³, Jeronimo Vieira de Araujo Filho¹, Leandro José Dallagnol¹

¹ Departamento de Fitossanidade, Faculdade de Agronomia Eliseu Maciel, Universidade Federal de Pelotas, Pelotas RS Brasil.

² Instituto de Ciências Biológicas, Universidade Federal de Rio Grande, São Lourenço, Rio Grande do Sul, Brasil.

³ Departamento De Medicina Veterinária Preventiva, Centro de Ciências Rurais, Universidade Federal de Santa Maria, Rio Grande do Sul, Brasil.

E-mail: leandro.dallagnol@ufpel.edu.br

Barley (*Hordeum vulgare*) crop is threatened by several biotic stress, being the *Fusarium* head blight, caused by different species of *Fusarium*, one of the main concerns due to the damage on yield and quality of grains as well as the accumulation of the mycotoxins deoxynivalenol (DON) and nivalenol (NIV). The state of Rio Grande do Sul (RS) is the second largest Brazilian barley producer, in which the crop is cultivated in several physiographic regions with distinct climatic conditions. In the 2021 crop season, spike and grain samples were obtained in ten municipalities belonging to four physiographic regions of RS: Alto Uruguai, Campos de Cima da Serra, Encosta do Sudeste and Planalto Médio. From spikes, seventy-five *Fusarium* isolated were obtained, from which the *ITS*, *rpb2* and *tef1* genes were amplified and sequenced. *Fusarium* species were identified by phylogenetic analysis. For this, the genetic evolution model GTR+I+G was selected using MrModeltest v. 2.3, and it was used to Bayesian analysis using the *tef1* and *rpb2* genes in a concatenated form, was carried out at the CIPRES platform using the MrBayes v. 3.2.1. The phylogenetic trees were visualized in the Geneious v. 9. From grains, forty-three samples, comprising experimental areas and commercial fields, were obtained and used to quantify DON and NIV by HPLC-MS/MS analysis. From each sampled area, grain or spike, geographic coordinates were taken and used to determine the effect of bioclimatic variables (BIO1 to BIO19, which consider mainly variation in temperature and rainfall) obtained from the WorldClim database on the concentration of DON and NIV. Seven *Fusarium* species were identified: *F. asiaticum*, *F. avenaceum*, *F. cortaderiae*, *F. gerlachii*, *F. graminearum*, *F. meridionale*, and *F. poae*. The only species present in all municipalities was *F. graminearum*. The species *F. meridionale*, *F. cortaderiae* and *F. poae* occurred mainly in the colder region of Campos de Cima da Serra, while *F. asiaticum* was only found in the Encosta do Sudeste region. In grains, the mycotoxins DON and NIV were detected in 74 and 70% of the samples, respectively, with concentration ranging from 0 to 10,200 µg/Kg for DON and from 0 to 1,630 µg/Kg for NIV. There was variation in the concentration of mycotoxins among different physiographic regions, with a tendency for higher concentrations to occur in warmer regions. This result is partially explained by the influence of bioclimatic variables, where the seasonality of temperature and rainfall positively influenced the concentrations of DON and NIV, respectively. In conclusion, the differences in climatic conditions among physiographic regions of RS influence the *Fusarium* species occurring in barley fields as well as the type and concentration of mycotoxins in grains. However, it is important to highlight that crop management also has a significant influence, especially on mycotoxins concentration.

Financial support: FAPERGS (grant number 19/2551-0001652-2 PQG/19), CNPQ (grant numbers 305247/2021-2 and 317495/2021-6) and CAPES (Financing Code 001).

Temperature increase impacts the temporal progress of myrtle rust and physiological damage on guava

Manoel P. Gonçalves¹, Ana Laura T. Simões¹, Rafael V. Ribeiro², Lilian Amorim¹

¹ Departamento de Fitopatologia e Nematologia, Universidade de São Paulo, Piracicaba SP, Brasil.

² Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas, Campinas SP, Brasil.

E-mail: lilian.amorim@usp.br

Greenhouse gas emissions have unequivocally caused global warming over the 21st century. The myrtle rust risk model predicts that the disease will be limited by climate scenarios of high temperatures, assuming that there is no infection by *Austropuccinia psidii* at temperatures equal to or greater than 30°C. Most simulation models of disease progress, such as the myrtle rust model, do not consider the damage caused by diseases in plants exposed to high temperatures. In this study, we evaluated the effects of high temperatures on monocyclic components and photosynthetic damage caused by myrtle rust in guava leaves. Potted 'Paluma' guava plants were inoculated with *A. psidii* suspension at 10⁴ urediniospores mL⁻¹ and then kept in a dark moist chamber at 23°C for 12 h. After the incubation period, the plants were kept in growth chambers at temperatures of 25, 30, and 35°C (± 2°C) and a 12-h photoperiod. Five replicates were used in each heat treatment and the experiment was carried out twice. As a control, in each treatment, five plants were sprayed with deionized water and kept under the same environmental conditions. Disease latent period, lesion density, lesion sporulation, and disease severity were evaluated over time. Gas exchange and leaf temperature were evaluated at 9-, 12-, and 16-days post-inoculation using an infrared gas analyzer. The relative net photosynthesis of a diseased leaf (P_x/P_o , where P_x is the net photosynthesis of each diseased leaf and P_o is the average of the net photosynthesis of healthy leaves) was related to disease severity (x) by $P_x/P_o = (1 - x)^\beta$. β -value represents the relationship between the virtual lesion (green leaf area adjacent to the lesion where photosynthesis is reduced or null) and the visual lesion. Guava plants kept at 35°C did not show rust symptoms. The disease monocyclic components were reduced in plants kept at 30°C compared to plants at 25°C, except for the latent period. Although disease severity was lower in plants at 30°C, reductions in net photosynthesis caused by rust were similar at 25 and 30°C, 79 and 75%, respectively, at 16 days post-inoculation. β -values were 2.1 and 3.7 in diseased plants at 25 and 30°C, respectively, indicating that the virtual lesion is greater at 30°C. Therefore, rust severity of 20% reduced 37% and 57% of relative net photosynthesis in plants kept at 25 and 30°C, respectively. Decreases in stomatal conductance and transpiration of diseased plants were also intensified at 30°C, increasing the leaf temperature by 1.2°C on these plants. Taken together, our results showed that the photosynthetic damage caused by myrtle rust is more severe in plants exposed to high temperatures, even though there is less disease intensity at these conditions.

Financial support: FAPESP (grant numbers 2019/13191-5 and 2022/02460-8); CNPq (grant number 301689/2022-9).

Drought, high temperature and rust (*Neophytopella tropicalis*): a dangerous combination for 'Niagara Rosada' grapevine

Lucas Santos Sales, Lilian Amorim

Departamento de Fitopatologia e Nematologia, Escola Superior de Agricultura "Luiz de Queiroz" (ESALQ), Universidade de São Paulo (USP), Piracicaba, SP.

E-mail: lucassales@usp.br

Climate change represents a major risk to food security in the world, as it has great potential to change the dynamics of diseases in cultivated plants. Only recently, studies are being carried out to better understand the consequences of the combination of biotic and abiotic stresses, simultaneously, on plant physiology. Although the individual effects of drought and heat stress on the occurrence of Asian grapevine leaf rust (*Neophytopella tropicalis*) are well characterized, their combined effect in grapevine plants has not yet been evaluated. The objective of this work was to assess the development and impact of rust on grapevines exposed to concurrent water limitations and heat stress. To achieve the objective, 'Niagara Rosada' grapevine plants were kept in chambers with controlled environmental conditions, where they were exposed to both abiotic (water deficit and/or high temperature) and biotic (*N. tropicalis*) stresses. For treatments with and without water deficit, plants were maintained at 40 and 80% of the available water capacity, respectively. Two combinations of day/night temperatures were used: 25/20 °C (no stress) and 30/25 °C (heat stress). Inoculation of grapevine leaves was carried out by spraying a suspension of 5×10^3 *N. tropicalis* urediniospores mL⁻¹ plus Tween 20 (0.05%). For the treatments without biotic stress, leaves were sprayed with deionized water on the abaxial surface. Immediately after spraying, the plants were kept in a humid chamber, in the dark, for a period of 12 h at the respective nighttime temperature of each treatment. The monocyclic components of the disease (latent period, lesion density and disease severity) were evaluated on the abaxial surface of the inoculated leaves. The proportion of necrotic and chlorotic leaf areas was evaluated on the adaxial surface of the leaves. The production of urediniospores per lesion and the remaining leaf area were evaluated by the end of the experiment, 20 days post inoculation. Diseased plants exposed to the combination of abiotic stresses showed slightly higher ($p > 0.05$) lesion density (84 lesions per cm²) compared to the plants without abiotic stresses (77 lesions per cm²) and no difference in disease severity (29% and 26%, respectively). The latent period, 7 ± 1 days, was not affected by abiotic stresses. In plants exposed to the combination 30/25 °C, the number of spores was higher (average of 11,115 urediniospores per lesion) than in plants exposed to 25/20 °C (average of 7,045 urediniospores per lesion), regardless of drought stress. The proportion of necrotic and chlorotic areas was higher in the treatment with combined abiotic and biotic stresses (73%), when compared to the treatment only with the disease (41%). The combination of high temperature, water deficit and the disease also resulted in greater and faster leaf drop, with a remaining leaf area 23.3% smaller compared to plants with only biotic stress. No necrosis or leaf senescence were observed in healthy plants exposed to abiotic stresses. The combination of abiotic and biotic stresses enhances the damage caused by the disease to the leaf tissue. Further studies are necessary to understand the mechanisms that accelerate necrosis and leaf senescence, as well as their consequences on the future vegetative and reproductive development of stressed 'Niagara Rosada' plants.

Financial support: FAPESP (2023/02885-1 and 2019/13191-5)

Mitigating the risk from the cut flower trade to protect global systems from invasive pests and pathogens

Manoj Choudhary^{1,2,3}, Aaron Isai Plex Sulá^{1,2,3}, Cory Penca⁴, Laurent C. Lagos^{1,2,3}, Romaric Armel Mouafo-Tchinda^{1,2,3}, Berea A. Etherton^{1,2,3} and Karen A. Garrett^{1,2,3}

¹Plant Pathology Department, University of Florida, Gainesville, FL, USA; ²Global Food Systems Institute, University of Florida, Gainesville, FL, USA; ³Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; ⁴USDA-APHIS, Miami, FL, USA

Email: m.choudhary@ufl.edu and karengarrett@ufl.edu

International trade in cut flowers reached \$21.3 billion in 2021, growing 28% in the last decade. Most cut flowers are traded fresh with limited sanitation options available, increasing the risk of pest and pathogen introduction and spread to new locations. High rates of invasive pests have been found in inspected cut flowers, and rates are expected to increase with growth in international trade. Species associated with cut flowers also have the potential to spread to other agricultural and wildland species. Strategies for early surveillance and detection for pests and pathogens are needed. Here, we analyzed formal international trade and the geographic distribution of pests and pathogens associated with cut flowers to identify candidate priority locations for surveillance and mitigation. Our analysis highlights the risk that trade networks pose to the USA, the largest importer (20%), and the role of the Netherlands, exporting more than half of global cut flowers, as well as other countries. For example, if adequate phytosanitary measures are not implemented by exporters, France, Germany and Netherlands should monitor carefully for rose rosette disease import. Likewise, in the absence of adequate phytosanitary measures, the role of countries with chrysanthemum white rust, caused by a pathogen which has been subject to quarantine, poses a risk in the chrysanthemum flower trade network. These analyses of trade networks can guide phytosanitary prioritization in the global cut flower trade for effective use of resources to protect agriculture from invasive pathogens and pests.

Financial support: USDA

Estimating the sensitivity and specificity of visual detection of tree pests and diseases

Matt Combes¹, Nathan Brown^{2,3}, Peter Crow³, Robin Thompson⁴, Alexander Mastin⁵,
Stephen Parnell¹

¹ Warwick Crop Centre, School of Life Sciences, University of Warwick, Stratford-upon-Avon, CV35 9EF, United Kingdom.

² Woodland Heritage, Haslemere, GU27 1XQ, United Kingdom.

³ Forest Research, Alice Holt Lodge, Farnham, GU10 4LH, United Kingdom.

⁴ Mathematical Institute, University of Oxford, Oxford, OX2 6GG, United Kingdom.

⁵ Epidemiology & Risk Policy Advice, Animal and Plant Health Agency, SW1P 3JR, United Kingdom.

Email: matt.combes@warwick.ac.uk

The occurrence of invasive tree pests and pathogens has increased exponentially since the 1800s, resulting in large environmental and economic consequences. Recent examples include *Agrilus planipennis*, which has led to the death of millions of ash trees in North America, and *Xylella fastidiosa* which is estimated to cost the EU olive industry billions of euros in losses. Early detection of invasive pests and pathogens maximises the likelihood for eradication and reduces the overall management costs. Currently, detection predominantly relies on visual surveys, yet the sensitivity (probability of correctly identifying a disease positive) and specificity (probability of correctly identifying a disease negative) of surveyors is not known. Quantification of these values enables the estimation of important surveillance metrics such as the probability of pest/ pathogen absence given no detection, and the likely distribution of a pest/ pathogen given a positive case. To obtain an initial estimate of the distributions of surveyor sensitivity and specificity, 23 surveyors examined up to 176 oak trees for three symptoms of acute oak decline (stem bleeds, bark cracks, beetle exit holes) on long-term monitoring sites with known tree status. Datasets were then simulated based on these distributions and used to examine the utility of Bayesian models to estimate the sensitivity and specificity in the absence of 'gold standard' validation dataset. We present a workflow to estimate the distribution of surveyor sensitivity and specificity for a range of tree pests and pathogens in the absence of a 'gold standard' validation dataset that will enable the optimisation of risk-based surveillance strategies in tree health.

Financial support: Funded by United Kingdom's Department for Environment, Food & Rural Affairs through the Future Proofing Plant Health Programme.

Grapevine leaf spot leads to early defoliation and production loss in *V. labrusca* (Bordô cultivar)

Camilla Castellar¹, Camila Javorski Zela¹, José Luiz Marcon Filho¹, Luiz Antonio Biasi¹,
Walmes Marques Zeviani², Louise Larissa May De Mio¹

E-mail: maydemio@ufpr.br

The study addresses Grapevine Leaf Spot (GVLS), caused by *Pseudocercospora vitis*, occurring on *Vitis labrusca*, particularly the Bordô cultivar. GVLS induces leaf lesions, potentially causing defoliation and its impact on productivity remains unexplored. The research investigates whether GVLS damages *V. labrusca* production. Fungicides were applied at varied timings across three growing seasons to establish a disease gradient. Various parameters, including production, fruit number, cluster mass, berry number per cluster, soluble solids content, and pruned shoot mass, were assessed. Disease severity was assessed using a diagrammatic scale on marked leaves throughout the growing season, and the Leaf Area Index (LAI) was determined. Inoculum dynamics were monitored using wind-trap spore traps. Linear regressions combined plant production data and GVLS-related variables within and across seasons. The average production per season was 6.4, 5.7, and 4.0 Kg.plant⁻¹ in 2019/20, 2020/21, and 2021/22, respectively. Disease symptoms emerged in late November, with conidia observed shortly after bud break in September. The conidial count was significantly higher in the 2020/21 season (160 conidia at the 20th week after bud break - wab) compared to the 2021/22 season (50 conidia at 18 wab). The Area Under the Disease Progress Curve (AUDPC) varied from 65.5 to 209.2 (2019/20), 159.2 to 559.5 (2020/21), and 13.0 to 86.7 (2021/22). LAI exhibited a 50% reduction with six fungicide applications compared to no application in both seasons. Plant production in 2021/22 correlated ($p < 0.05$) with early defoliation from the disease in 2019/20, significantly explained ($p < 0.05$) by AUDPC. Higher disease severity consistently explained reduced plant productivity, particularly in fruit number, varying for other variables across seasons. The study underscores the risk of Bordô cultivar production damage after two seasons of elevated GVLS severity and early disease-associated defoliation. Long-term studies are recommended to understand disease damage dynamics considering climate and inoculum variations between seasons.

Financial support: CNPq (Project: 403918/2021-9) and CAPES Financial Code 001.

Spatiotemporal dynamics of *Fusarium* wilt of banana caused by subtropical race 4 of *Fusarium oxysporum* f.sp. *cubense*

Mariela P. González¹, Daniel W. Heck¹, Raphael A. Silva¹, Alessandro Santos¹, Gabriel Alves¹, Emerson M. Del Ponte¹, Eduardo S. G. Mizubuti¹

¹ Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa MG Brasil.

E-mail: mizubuti@ufv.br

Historically, *Fusarium* wilt of banana (FWB) caused by *Fusarium oxysporum* f. sp. *cubense* (Foc) has rendered hectares of banana unusable in Central and South America. To date, Foc subtropical race 4 (SR4) is present in Brazil. However, in 2019, tropical race 4 (TR4), the most virulent race of Foc, was detected in South America and its spread to the main banana-producing regions is a matter of time. In this work, knowledge of the spatio-temporal dynamics of FWB and their relation with environmental features aims at providing background to epidemiologically-based mitigation actions to contain TR4. One banana cv. 'Maçã' (AAB) field was established in 2017 in Minas Gerais, Brazil. Bimonthly assessments of incidence were conducted between 2017 to 2020. Weather variables were also recorded. The spatial pattern was studied using quadrat- and distance-based methods. Temporal analyses were based on epidemiological models fitted to the disease progress curve. Average values of weather variables were estimated for intervals of 2-, 4-, 6-, and 8-weeks before a given assessment date seeking for any correlation with FWB incidence and absolute disease progress rate. The first foci were detected six months after planting and were randomly distributed in the field. FWB incidence increased up to a final value of 43%. As disease incidence increased the pattern of distribution of wilted banana plants in the field changed to aggregation. The FWB progress curve had a sigmoidal-shape and the Gompertz model provided the best description of the temporal dynamics of FWB. Precipitation recorded four weeks before the disease assessment was the weather variable with highest correlation ($r = 0.63$, $P < 0.001$) with progress rate. Mitigation actions based on the spatio-temporal epidemiology of SR4 in highly susceptible cultivars might prevent total crop losses and the expansion of FWB into non-infested regions.

Financial support: CNPq research fellowship grant 310011/2018-3 and Agencia Nacional de Investigación y Desarrollo (ANID) BECAS CHILE en el extranjero/2019 72200127.

Predictive modeling of sudden death syndrome of soybean in Kansas

Madison Kessler¹, Trevor Hefley², Erick DeWolf¹ Rodrigo B. Onofre¹

¹ Department of Plant Pathology, Kansas State University, Manhattan, Kansas

² Department of Statistics, Kansas State University, Manhattan, Kansas

E-mail: mkessler@ksu.edu

Sudden death syndrome (SDS), most commonly caused by the fungal pathogen *Fusarium virguliforme*, poses a significant threat to soybean production. The disease is favored when planting occurs in cool, wet soils, and is exacerbated by post-planting rainfall. Interestingly, there have been years in Kansas with less disease despite seemingly having similar favorable conditions to previous years. While weather remains a significant risk factor, factors such as pathogen population and other environmental conditions also contribute to the overall risk but are less understood. Current research mainly focuses on the impact of weather on in-season disease development, but directing attention to pre-season risk factors and developing an SDS prediction tool could allow growers to adjust management practices proactively. This includes decisions on variety selections and seed treatments, lowering the risk of yield losses due to SDS. Over the past decade, researchers at Kansas State University have compiled data, including weather variables, seed treatment evaluations, evaluation of breeding lines, and evaluation of agronomic practices. This data has resulted in replicated estimates of SDS incidence and severity across different environments, soil types, and soybean varieties. Integrating SDS incidence and severity data with weather information from the Weather Data Library, Kansas Mesonet (Kansas State University), and the National Weather Service will help to identify and estimate pre-season risk factors that influence in-season levels of *F. virguliforme*. Utilizing machine learning and regression model variable selection procedures, the variables and time periods associated with severe disease will be used to create prediction models for SDS. Preliminary data will be presented at the meeting.

Success in forecasting downy mildew of onion with DOWNCAST

Tyler Blauel, Kevin Vander Kooi, Julia Scicluna, Geoff Farintosh, Mary Ruth McDonald

Department of Plant Agriculture, University of Guelph, Guelph, ON Canada

E-mail: mrmcdona@uoguelph.ca

Onion downy mildew, caused by the Oomycete *Peronospora destructor*, is a highly destructive foliar disease of onion. The disease does not occur every year in the Holland Marsh, Ontario, Canada. Symptoms develop 10 – 14 days after infection and downy mildew specific fungicides must be applied prior to infection to be effective. Disease forecasting is used to indicate when no fungicides are needed and to properly time protective fungicide applications when there is disease risk. The integrated pest management (IPM) program at the Ontario Crops Research Centre – Bradford uses the forecasting model DOWNCAST to predict the risk of sporulation and infection, known as sporulation infection periods (SIPs), based on daily air temperature, relative humidity, leaf wetness duration and temperature, plus temperature in the days following potential infection. Fungicide sprays are also recommended if downy mildew lesions are found on onions in the region, or if sporangia of *P. destructor* are found on spore traps. Rotorod spore traps are assessed three times a week throughout the growing season. From 2012 to 2023, the forecasting program was accurate in 10 of the 12 years. This included two years where DOWNCAST was accurate in predicting no disease risk and no downy mildew developed in the Holland Marsh. In 2022, DOWNCAST forecasted SIPs and airborne sporangia were later found, but the disease did not develop in grower fields, likely due to appropriately timed fungicide applications as predicted using DOWNCAST. Weather conditions were very favorable for onion downy mildew development throughout the 2023 growing season. DOWNCAST predicted multiple SIPs and there were high numbers of sporangia found in spore traps. In a fungicide trial, a SIP was identified on 14 July and the first lesions found on 27 July. Disease was assessed on 1, 10 and 15 Aug as lesions per m² of plot. In the 15 Aug assessment, the treatment receiving Ridomil alternated with Orondis Gold (mefenoxam S and oxathiapiprolin plus mandipropamid) had 2 lesions, compared to 79 lesions m² in the nontreated check. In most years, onion downy mildew developed 14 – 17 days after sporangia were found. While the model alone is mostly effective, DOWNCAST can be improved with trapping and rapid microscopy identification of sporangia to confirm disease risk. DOWNCAST continues to be a useful tool for onion growers in the Holland Marsh and other regions in Ontario.

Financial support: This project was funded by the Ontario Agri-Food Innovation Alliance and the California Garlic and Onion Research Advisory Board. Funding for the IPM program was provided by the Bradford Co-operative Storage Ltd., growers participating in the program, FS Partners, Bayer Crop Science, BASF, Corteva, FMC and Syngenta Crop Protection.

Attempts to forecast *Stemphylium vesicarium* on onions when the pathogen is resistant to most fungicides

Mary Ruth McDonald¹, Emily McFaul¹, Julia Scicluna¹, Michael Kooy¹, Kevin Vander Kooi¹, Geoff Farintosh¹, Bruce Gossen²

¹Dept. of Plant Agriculture, University of Guelph, Guelph, ON, Canada and ²Agriculture and Agri-Food Canada, Saskatoon, SK, Canada

E-mail: mrmcdona@uoguelph.ca

Stemphylium leaf blight of onion (SLB), caused by the fungus *Stemphylium vesicarium*, is an important disease of onion in many parts of the world. Infection results in leaf dieback that can reduce yield. Bulb onions in Ontario, Canada, are mostly treated with sprout inhibitor, maleic hydrazide, prior to harvest to prepare for long term cold storage. Approximately five green leaves per plant are needed to effectively take up the sprout inhibitor, so defoliation can reduce the storage life on onions. Forecasting and managing SLB is challenging. Field trials were conducted in Holland Marsh, Ontario in 2022 and 2023 to evaluate fungicides and disease forecasting programs. Biocontrols T-77 (*Trichoderma aroviride*) and Serifel (*Bacillus amyloliquifaciens*) were evaluated and fungicides Merivon (pyraclostrobin and fluxapyroxad), Miravis Duo (pydiflumetofen and difenoconazole), Revysol (mefentrifluconazole), Sercadis (fluxapyroxad) and Dithane (mancozeb). Disease severity was low in 2022 and moderate in 2023. Disease forecasting based on temperature and leaf wetness (TOMcast) in 2022 triggered five fungicides sprays but there were no differences in disease severity at the end of the season (24- 32%) and no differences in yield. There was a similar trend in 2023. Disease forecasting did not reduce SLB compared to the nontreated check, except for a small difference in AUDPC. The small difference (1671 compared to 1833) did not justify six fungicide applications and there were no differences in yield. Spray timing based on regular intervals (6 sprays) had lower cumulative disease severity than the nontreated control, but was not different from fungicides applied based on forecasting programs. Isolates of the fungus from the region are known to have almost complete resistance to strobilurin fungicide, azoxystrobin, and to anilopyrimidine fungicide, fluopyram. Recent assessments also found some resistance to the succinate dehydrogenase inhibitor fungicides penflufen and fluxapyroxad, although there was relatively low resistance to fluxapyroxad when mycelial growth was assessed. A fungicide efficacy trial conducted in 2023 found that the multisite fungicide, fluazinam, reduced SLB severity (51% as compared to 82% in the nontreated control). This product may be useful in resistance management and protecting onions from SLB. Effective management of *Stemphylium* leaf blight requires effective fungicides and disease forecasting programs that indicate when there is low risk of disease development.

Financial support: This project was funded in part by the Ontario Agri-Food Innovation Alliance, the Fresh Vegetable Growers of Ontario and the Bradford Cooperative Storage Ltd.

Balancing selection complicates management of clubroot and (possibly) other problem diseases

Bruce D. Gossen¹, A. Sedaghatkish², M. R. McDonald²

¹Saskatoon Research and Development Centre, Agriculture and Agri-Food Canada, SK

²Department of Plant Agriculture, University of Guelph, Guelph, ON

E-mail: mrmcdona@uoguelph.ca

Balancing selection occurs when multiple alleles are retained over time in a population (usually at very low frequency) and this can result in their preservation over long periods of time. Evidence is accumulating that the Chromist plant pathogen *Plasmodiophora brassicae* Wor., the cause of clubroot in *Brassica* spp., retains many intact genotypes at low levels among the trillions of resting spores that are typically present in an infested patch of soil. For example, two instances of a shift in pathotype at a site were associated with multiple changes in SNPs in about 3000 genes, which is far more than could occur based on a mutation to virulence in the existing population. Similarly, at least six highly distinct genotypes were identified in a relatively small (500 spores) sample of spores from a single clubbed root, using DNA sequencing of single protoplasts. The predominant genotype made up 76% of the spores, while the others were 9% or less. This likely occurs because the dominant genotype suppresses host resistance, facilitating infection and reproduction by less virulent phenotypes. The retention of entire genotypes along with the very high numbers of resting spores in a field or patch, may explain the rapid breakdown of single-gene resistance in this host-pathogen system. Presumably genotypes that can overcome the resistance are already present in the pathogen population. When a new host resistance gene is deployed, this selects for the virulent genotype that is already present in the soil, although probably at low frequency. The pathogen can produce billions of spores per severely infected plant, so disease rapidly increases in only a few generations to form infested patches. Employing single resistance genes to manage clubroot is not durable but stacked resistance genes may provide greater durability. Substantially reducing the total population of spores in soil could slow the breakdown of resistance by reducing the population of the 'new, virulent' pathotype below the threshold for producing large clubs that produce many spores. Rotation of resistant cultivars together with crop rotation, which reduces spore populations by 90–99% over 2–3 years, could substantially reduce the risk of resistance breakdown for producers. The definition of balancing selection could be expanded to include situations where one genotype or even species 'opens the door' to less virulent genotypes, allowing them to infect a host. This may be occurring among AG groups of *Rhizoctonia solani* or among *Pythium* / *Globisporangium* spp.; isolation from infested roots often produce many AG groups or species, but only a few are virulent on healthy roots of the host. It is possible that infection of any host by one group provides an opportunity for related pathogens to colonize dying roots and be maintained in the soil population.

Financial support: Agriculture Development Fund of the Province of Saskatchewan and the Canadian Agriculture Partnership program of Agriculture and AgriFood Canada and the Canola Council of Canada.

Building a hyperspectral library of common bean diseases

William Rafael Ribeiro¹, Andressa de Souza Almeida¹, Amanda Lopes Ferreira¹, Rômulo Moreira Silva², Tavvs Micael Alves², Alaerson Maia Geraldine², José Francisco Arruda e Silva³, Patrícia Valle Pinheiro³, Murillo Lobo Junior³

¹Universidade Federal de Goiás, Goiânia GO, Brasil.

²Instituto Federal Goiano – Polo de Inovação, Rio Verde GO, Brasil.

³Embrapa Arroz e Feijão, Santo Antônio de Goiás GO, Brasil.

E-mail: murillo.lobos@embrapa.br

Sensors attached to unmanned aerial vehicles can detect diseased plants before they become symptomatic, according to differences in their reflectance. Despite the advances in hardware and methods for detecting infections with remote sensing, using these tools to scout common bean diseases is still incipient. The objectives of this study were: 1) to evaluate the effectiveness of a hyperspectral sensor in the diagnosis of common bean diseases; 2) verify differences in the spectral signatures in different genotypes with healthy or infected plants; and 3) to investigate if mulch used in no-tillage can influence the spectral signatures. Since 2022, we have conducted field experiments following randomized block design with factorial arrangement in the Brazilian Center-West region. The experimental factors were soil cover, bean genotypes with different reactions to diseases of epidemiological importance, and inoculation or not of seeds or plants. A multicopter drone DJI M600Pro equipped with a Nano-Hyperspec® VNIR hyperspectral sensor (400 to 1000 nm) for push-broom scanning of 271 spectral bands at 2.2 nm intervals was used to capture images in all experiments. In each one, two flights were carried out at 40m and 80m before and after the onset of visual symptoms. We searched for spectral bands with $R^2 > 0.6$ and the lower AIC. Wavelengths meeting these requisites were submitted to linear regression analysis to investigate relationships between response (previously selected spectral bands) and predictor variables (genotype, inoculation and soil cover) with significance at 5%. Best-quality images were normally obtained with flights at 80m. The results indicate that early detection of root rots is possible, identifying causal agents (*Fusarium* spp. and *Rhizoctonia solani*) and common bean cultivars according to their reaction to the disease. In the case of the *Cowpea mild mottle virus* (CPMMV), early detection can anticipate disease control measures by approximately 14 days, compared to the visual diagnosis after symptom appearance. Mulch is a cause of variation that must be considered when scouting early-cycle diseases such as root rots and CPMMV with hyperspectral sensors. These results demonstrate that hyperspectral image analysis is a promising tool to advise common bean disease management. This approach facilitates better crop health management and the reduction of yield losses.

Financial support: Embrapa (Project 20.19.03.057.00), CNPq (Project 400574/2022-5) and FAPEG (Project 202110267000605)

Evaluation of disease infection models to time fungicide applications to manage *Neopestalotiopsis* sp. on strawberry in FloridaMarcus V. Marin, Adrian I. Zuniga, Natalia A. Peres

Gulf Coast Research and Education Center, Plant Pathology Department, University of Florida, Wimauma, FL 33598, U.S.A.

E-mail: nperes@ufl.edu

A recent outbreak of a new *Neopestalotiopsis* species in Florida has led to significant challenges in the strawberry industry, specifically causing Pestalotia Leaf Spot (PLS) and Fruit Rot (PFR), resulting in substantial yield losses. A previous study developed logistic models based on wetness duration and temperature for conidial germination and leaf infection to understand the pathogen's biology. Different thresholds for predicted disease were selected and evaluated for triggering fungicide applications during the 2022-23 season using strawberry transplants of Sensation® 'Florida127,' and Pearl® 'FL 16.78-109'. The experimental treatments involved the application of fungicides Switch or Thiram based on the thresholds determined by the models. Additionally, a weekly-based treatment approach was used, where Switch was applied during weeks favorable to Botrytis fruit rot development and Thiram in other weeks. The control group included both inoculated and non-inoculated treatments. The effectiveness of these treatments was evaluated based on incidence of PLS and PFR, and severity of PLS based on a scale from 0-6. Remarkably, the model-based treatment strategies had no statistical differences in effectiveness in controlling PLS and PFR on both strawberry cultivars compared to the weekly-based approach. However, a significant advantage of the model-based treatments was their reduced application numbers, as they required only 8 or 9 fungicide applications, in contrast to the 20 applications needed for the weekly-based regimen. It was observed that although the Sensation® 'Florida127' exhibited a higher susceptibility than Pearl® 'FL 16.78-109', both cultivars experienced a significant reduction in the severity of PLS and incidence of PFR (up to 50%) and an 80% decrease in PLS incidence. These results highlight the potential of these models for integration into the Strawberry Advisory System (sas.agroclimate.org) for fungicide application in Florida strawberry production. Following the system could significantly reduce the number of fungicide applications while maintaining effective control of PLS and PFR, compared to traditional calendar-based treatments. Despite these promising results, this study emphasizes the necessity for multi-season trials to validate the effectiveness and reliability of these models over a longer term. This extended research is crucial to ensure the robustness of the models and their ability to provide reliable guidance for fungicide application under various environmental conditions and across different strawberry seasons.

Effect of incubation temperature and wetness duration on *Neopestalotiopsis* sp. germination and Pestalotia Leaf Spot disease development on strawberry

Adrian I. Zuniga¹, Andre B. Gama^{1,2}, Juliana S. Baggio¹, Laurence V. Madden³,
Natalia A. Peres¹

¹ University of Florida, Wimauma, FL, U.S.A.

² Louisiana State University, Baton Rouge, LA, U.S.A.

³ The Ohio State University, OARDC, Wooster, OH, U.S.A.

E-mail: nperes@ufl.edu

In 2017, severe Pestalotia Leaf Spot (PLS) and fruit rot symptoms caused by *Neopestalotiopsis* sp. were reported in commercial strawberry fields in Florida. Symptoms appear irregularly dispersed on infected leaves as necrotic lesions of different sizes with a light to dark brown color and are usually observed soon after consecutive and prolonged rain events. However, there is no information about the effect of weather-related variables on *Neopestalotiopsis* sp. infection on strawberry in Florida. Thus, our objectives were to model *Neopestalotiopsis* sp. conidial germination and PLS development on strawberry leaves based on temperature and wetness duration. Spore suspensions calibrated at 5×10^4 *Neopestalotiopsis* sp. conidia/ml were exposed to 5, 10, 15, 20, 25, 30, 35, and 40°C for 4, 6, 12, 24, 36, and 48 h of continuous wetness in growth chambers. After each interval, 5 μ l of 0.1% lactoglycerol was added to each drop to stop germination and the percentage of spore germination was determined. Strawberry transplants of the Sensation® 'Florida127' cultivar from a Canadian nursery were inoculated with 5×10^4 spores/ml of a mixture of the same isolates and exposed to the same temperatures and wetness durations in growth chambers as mentioned above. PLS incidence was evaluated 14 days after treatments by counting the number of symptomatic leaves per total number of leaves in each plant. The means for the two experiments conducted for germination and incidence of PLS were used to construct two different logistic models, one to estimate conidia germination and the other to estimate leaf spot incidence, both based on wetness duration and temperature. Logistic models fit satisfactorily to our data, describing the effect of temperature and wetness duration in the controlled environment experiments. Germination proportions increased significantly with wetness durations longer than 20 h with optimal temperatures between 20 and 25°C. For leaf infection, disease incidence also increased at longer wetness durations, with about 20°C as the optimal temperature. The logistic models were used to determine thresholds for fungicide applications and tested under field conditions during the 2022-2023 and 2023-2024 seasons. Validation experiments will be repeated with the goal of incorporating fungicide timing recommendations into the Strawberry Advisory System (sas.agroclimate.org).

Financial support: Florida Strawberry Research and Education Foundation (FSREF).

Fusarium head blight prediction: Assessing the accuracy of iButton microclimate data against weather station data

Olanrewaju M. Shittu¹, Tyler McFeaters¹, Mladen Cucak², Paul D. Esker¹.

1 Department of Plant Pathology and Environmental Microbiology, Penn State University, USA.

2. Syngenta Crop Protection, Crop Protection Development, Basel, Switzerland.

E-mail: oms5169@psu.edu

Fusarium head blight (FHB) is a disease that affects wheat, barley, and oat crops, caused primarily by *Fusarium graminearum*. FHB leads to significant yield losses and deoxynivalenol (DON) mycotoxin accumulation, which poses a substantial risk to food safety. Currently, FHB management employs an integrated approach that includes resistant varieties, cultural practices, and fungicide application. This approach is guided by risk assessment tools like the Fusarium Risk Tool, which uses logistic regression models based on National Oceanic and Atmospheric Administration data. This tool predicts FHB risk in specific weather conditions, notably temperatures between 15-30°C and relative humidity of $\geq 90\%$. This comparative study was conducted at the Russell E. Larson Agricultural Research Centre, Rock Springs, Pennsylvania, USA, to evaluate the effect of microclimate data on the predictive accuracy of the Fusarium Risk Tool. We hypothesize that microclimate variations might impact FHB risk assessments and management decisions, particularly at the soil level. To test this hypothesis, soil-level microclimate data were collected using iButtons (DS1923-F5) manufactured by iButtonLink Technology. Hourly temperature (°C) and relative humidity (%) were collected from 05/17/2023 to 06/19/2023. Hourly weather data were also obtained from a weather station located at the research farm (<https://newa.cornell.edu/>). The correlation between the temperature and relative humidity data recorded by the weather station and iButtons was 0.9 and 0.87, respectively. The predicted risk using weather station data was less than 10 % of the FHB index threshold for susceptible, moderately susceptible, and moderately resistant wheat varieties. Though the predicted risk using the iButton data was similar for moderately resistant wheat varieties, the predicted risk was higher than the epidemic threshold for susceptible and moderately susceptible wheat varieties. Meanwhile, the FHB disease recorded from the field showed FHB index below the threshold. This study suggests that soil-level microclimate data may have limitations in predicting FHB disease risk. Future steps involve assessing the predictive capability of canopy-level microclimate data for FHB disease.

Financial support: USDA-NIFA Award Number: 2020-67013-31920

Criteria for fungicide applications in asian soybean rust control: An analysis of Spore collector, scheduled application, and monitoring

Paulo Henrique Nascimento de Souza¹, Lilian Maria Arruda Bacchi², Walber Luiz Gavassoni², Wagner da Paz Andrade²; Anderson dos Santos Dias²

¹Departamento de Data Science, Fundação MT, Rondonópolis MT Brasil.

² Universidade Federal da Grande Dourados, Dourados MS Brasil.

E-mail: paulosouza@fundacaomt.com.br

The control of asian soybean rust typically relies heavily on scheduled fungicide applications. However, this model has the limitation of not considering the epidemiology or the presence of the pathogen in the region at the time of the initial fungicide application. The purpose of this study was to examine criteria for the first fungicide application, aiming at managing Asian soybean rust, taking into account cultivar resistance and sowing time. The experiment adopted a split-split-plot design, 3x2x8, with the main plots defined in three sowing times (October, November, December), subplots for two cultivars (TMG 7063 IPRO [characterized as resistant] and Monsoy 6410 [characterized as susceptible]), and sub-subplots for eight criteria for the initiation of fungicide application during the 2018/19 crop season in the Dourados/MS region (Brazil). The criteria included: I) Control with no application; II) Vegetative stage – V7; III) Reproductive stage R1; IV) Seven days after spore detection (SD) via a collector; V) 14 SD; VI) 21 SD; VII) 10% of leaf area lesioned; VIII) 10% incidence. After the initiation of applications, two more applications were made at 14 and 21 days after reaching the criterion, with the timing of the last application limited to stage R5.4. Evaluated metrics included the area under the progress curve (AUPC) for lesions and uredia, lesioned leaf area at stage R6, first pod insertion height, number of pods per plant, defoliation at R6, thousand grain weight (g), productivity (kg ha⁻¹), and economic yield. Overall, the trial demonstrated that applications starting at 7 or 14 SD were effective in reducing disease severity, with fewer fungicide applications compared to traditional management. For productivity, no difference was observed between application criteria for sowings in October and November, illustrating that there was no gain with the scheduled application strategy, at a time when fewer applications were needed using monitoring criteria, surpassing the actual fungicide needs with fixed calendar applications. Monitoring spores and the incidence of asian soybean rust proved to be a crucial tool to assist in determining the appropriate time to initiate fungicide applications.

Financial support: CNPq (Projeto: 140742/2017-4)

Unraveling the soybean anomaly: The revealing risk tree and fungicide management

Paulo Henrique Nascimento de Souza¹, João Paulo Ascari²

¹Departamento de Data Science, Fundação MT, Rondonópolis MT Brasil.

¹Departamento de Fitopatologia e Biológicos, Fundação MT, Rondonópolis MT Brasil.

E-mail: paulosouza@fundacaomt.com.br

Since the 2019/2020 harvest, a new issue has been troubling soybean producers in Brazil, especially in the mid-north and north regions of Mato Grosso, known as the pod anomaly. This problem is characterized by the partial or complete rotting of grains inside the pod, resulting in losses that can reach up to 40% in the quantity of damaged grains. Since the emergence of the pod anomaly, the Fundação MT has been conducting studies to understand the issue in areas of the Mato Grosso region. In the latest study, a trial was conducted to investigate the effect of the timing of the first fungicide application (15, 25, 35, and 45 days after emergence), carried out in randomized blocks with four replications, in the municipalities of Sorriso and Nova Mutum - MT, in the 2022/23 harvest, using the soybean cultivar BMX Desafio RR. The study also evaluated: 1) site-specific fungicides used in soybean seed treatment; 2) the effect of carboxamide and triazole in isolated applications of the same fungicide; and 3) the effect of site-specific fungicides associated with multisite fungicides. To measure efficacy in controlling rot, the percentage of damaged grains was evaluated. In a complementary study, data from the Foundation MT's anomaly trial were compiled, and an attempt was made to understand the combination of variables through machine learning algorithms. The severity of the anomaly in grains and pods was categorized as: 1) Low: 0 - 12%; 2) Intermediate [average]: 12.1 - 25%; and 3) High: > 25.1% in samples, in 380 records of experimental plots. The variables considered in the model were: A) Application or non-application of fungicide (Fungicide treatments and controls); B) Sowing time (October, November, December); C) Growth habit (Determinate, indeterminate, semi-determinate); D) Flower color of the cultivar; E) Location (Environmental conditions related to Sorriso, Mutum); F) Registered plant stand; G) Maturity group; H) Days to flowering (From emergence). Subsequently, 85% of the database was used for machine training with neural network and naive bayes algorithms, with the remaining used for validation to predict new occurrences of anomaly. In the first study, it was observed that the application of fungicides from different chemical groups mitigated the impacts on the grain concerning the intensity of rot and percentage of damaged grains. No significant differences were observed regarding the initial application time. The Naive Bayes algorithm showed an accuracy rate of 71%, while artificial neural networks achieved 76%, with a confidence interval (95%) between 55% and 84%. This means that the model correctly predicted the anomaly category (low, medium, and high) between 55 and 84 times out of 100 attempts. Preliminary results indicate that, regardless of the real cause of the anomaly, the variables described here are important for expressing the level of damage and, consequently, the reduction in soybean productivity.

Funding entity: Fundação de Apoio à Pesquisa Agropecuária de Mato Grosso (Fundação MT)

Incubation period, number of lesions and severity of isolates of *Corynespora cassiicola* in soybean cultivars

Jacqueline D. Puia¹, Ana M. da S. Moreira¹, Leandro C. Borsato², Sandra C. Vigo², Marcelo G. Canteri¹

¹ Departamento de Agronomia, Universidade Estadual de Londrina, Londrina PR Brasil.

² Departamento de Fitossanidade, Instituto de Desenvolvimento Rural do Paraná, Londrina PR Brasil.

E-mail: puia.agro@gmail.com

Knowledge of epidemiological aspects of target spot is indispensable to manage the disease. This study checked the severity and incubation period of isolates of *Corynespora cassiicola* (C.c) in soybean cultivars, as well verified whether the position of leaflets influences the susceptibility of the plant to target spot. The experiment was conducted in a randomized block with 8 isolates of C.c and 8 soybean cultivars in a factorial scheme, with five repetitions each block. The plants were inoculated with a conidial suspension containing 2×10^4 conidia mL⁻¹. After 12 days of inoculation, the number of lesions per leaf and the incubation period (IP) were quantified by the formula: IP = (number of days for stabilization/2) + 1. The ISO 4S isolate caused greater disease severity in plants, whereas ISO 2A, ISO 2S, and ISO 11S induced the lowest number of lesions. BMX Potência RR, BMX Força RR, and NA 5909 RG had the lowest occurrence of lesions, while the cultivar BMX Elite IPRO showed the highest number of lesions, indicating greater susceptibility to the disease. More lesions were detected in the lower leaf compared to the upper leaf of the plants. The longest IP was observed for ISO 4S in both leaflets, while the lowest IP for ISO 1A, 3A and 2A in the lower leaf, and for ISO 11S and 1S in the median leaf. For cultivars, significant difference in IP was observed only in the lower leaf, with the longest and shortest IP detected for BMX Elite IPRO and BRS 284, respectively. In general, the upper leaf of the plants displayed a shorter IP, while the lower leaf exhibited a longer IP. These findings underscore the intricate interplay between C.c isolates, soybean cultivars, and leaf position, emphasizing the need for tailored management strategies, informed by a more dynamic understanding of the disease.

Financial support: CAPES

Profitability assessment of fungicides and resistant varieties in wheat blast control: A simulation-based approach

Ricardo G. Tomáz¹, Ian M. Trotter², Emerson M. Del Ponte¹

¹ Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa MG Brasil.

² Departamento de Economia Aplicada, Universidade Federal de Viçosa, Viçosa MG Brasil.

E-mail: ricardo.tomaz@ufv.br

Wheat blast is an important disease for food security in the main wheat-producing regions of the world and its economic impact on regions where the disease is established has been mitigated through sequential applications of chemical fungicides and the use of resistant cultivars. However, the profitability of these strategies depends on grain prices, the effectiveness of fungicides and application costs. This study aimed to develop a simulation framework to estimate break-even probabilities between income and costs $Pr(\text{income} \geq \text{cost})$ of chemical fungicides used in wheat blast management programs. Probability distributions were fitted to the intercept, slope, and severity obtained from 42 cooperative networks conducted in Mato Grosso, Goiás, Minas Gerais, Mato Grosso do Sul, and São Paulo between 2012 to 2020 years, and wheat prices reported to the last three harvests. A total of 40,000 Monte Carlo simulations were implemented to estimate the profitability of the chemical control from efficacy ranges (0 to 100%), damage coefficients (low and high) and total costs of 60, 80 and 100 US\$/ha (fungicide + operational costs) to average yield levels (2,000 and 4,000 kg/ha) on susceptible and resistant cultivars. The simulation framework showed that chemical application on resistant cultivars with high yield had the greatest mean yield gain ($1,289 \pm 856,43$ kg/ha), followed by resistant with low yield ($548,23 \pm 424,04$ kg/ha) and susceptible ($361,66 \pm 468,16$ kg/ha) compared to susceptible cultivars without fungicide application. The use of resistant varieties allowed to obtain break-even probabilities above 60% for all total costs and fungicide effectiveness ranges, whereas the chemical application on susceptible cultivars was favorable only when the fungicide showed efficacy above 35% at US\$60/ha, 45% at US\$80/ha and 55% at US\$100/ha costs. Our results showed that the implementation of resistant cultivars provides a wide range of profitability for chemical application against wheat blast, and reinforces the need for its use in an integrated disease management program.

Financial support: FAPEMIG (APQ-03072-18)

Baselining prioritization of epidemic controlRachel Russell¹, Nik J. Cunniffe¹¹ Theoretical and Computational Epidemiology Group, Department of Plant Sciences, University of Cambridge, Cambridge, UK.

E-mail: rjt42@cam.ac.uk

The resources available to stakeholders managing plant disease epidemics are limited by technical and financial constraints. When and where resources should best be allocated to maximize their impact for disease control is not yet understood. An extensive range of approaches for optimizing and improving the prioritization of limited control resources across different subpopulations in epidemics have appeared in the literature. Approaches include heuristic based prioritization (i.e., simple rules of thumb), optimal control, model predictive control and, more recently, reinforcement learning. However, different studies use different disease models, parameterizations, modelling approaches (e.g. stochastic vs deterministic), programming languages, measures of success, assumptions about the information available to the managers, constraints and baselines to evaluate control mechanisms. This diversity has positive aspects as it grounds the work in a particular case study or scenario. However, it makes it difficult to determine the current state of the art for any new given system of interest. In turn, this limits both progress in the field and applicability for managers. As an easy first step towards consistent baselining, we propose that a wider range of simple heuristic controls should be considered as baselines for evaluation of more complex control approaches. The utility of simple baselines is demonstrated with an example evaluating continuous optimal control on a stochastic metapopulation model of geographical spread of a plant disease. The baselines considered were heuristics splitting control evenly per subpopulation and per host and prioritizing allocation of control resources according to simple metrics (e.g. number of infected hosts in a subpopulation or according to a random priority order). We find that although the control generated by optimal control is reliably optimal when the disease spread model is deterministic, it can be outperformed by the simpler heuristics in the more realistic stochastic case. The range of potential outcomes in the stochastic model means that optimizing the continuous case for eradication will not reliably eradicate disease. When stochastic effects are important, effective control requires rates of control that must be higher than the deterministic model would predict. This effect is compounded in the metapopulation model because disease can be reintroduced from other subpopulations. Since the current apparent state of the art can be outperformed by a very simple heuristic, we conclude that considering a wider range of simple baselines should improve how robustly epidemic controls can be evaluated.

Financial support: AgriFoRwArdS CDT, EPSRC, Defra.

Global surveillance and mitigation strategies for laurel wilt, a major threat to avocado production and forests

Romarc Moufa-Tchinda^{1,2,3}, Aaron I. Plex Sulá^{1,2,3}, Berea A. Etherton^{1,2,3}, Robin A. Choudhury^{1,2,3,4}, Romina Gazis^{1,5}, Jonathan Crane⁵, Karen A. Garrett^{1,2,3}

¹Plant Pathology Department, University of Florida, Gainesville, FL, USA

²Global Food Systems Institute, University of Florida, Gainesville, FL, USA

³Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA

⁴University of Texas, Rio Grande Valley, TX, USA

⁵Tropical Research and Education Center, University of Florida, Homestead, FL, USA

Email: rmouafotchinda@ufl.edu and karengarrett@ufl.edu

Laurel wilt is a major threat to many species in the Lauraceae, including avocado. Caused by the fungus *Harringtonia lauricola*, which is dispersed by ambrosia beetles, this disease poses a threat to vital forest services, such as carbon storage and biodiversity support. This disease is not yet present in all laurel-rich regions. We evaluated which locations are candidate priorities for surveillance and mitigation to slow the future spread of this pathogen. Ambrosia beetles carrying the pathogen can be introduced in wood, including wooden packing material. We used a gravity model to analyze the wood trade network and identify countries at higher risk for the introduction or reintroduction of laurel wilt. We also evaluated cropland connectivity to identify candidate priority locations to monitor *H. lauricola* outbreaks. By combining data from Lauraceae host density (GBIF) and avocado host density (Monfreda et al. 2008), we created maps pinpointing networks of critical locations in *H. lauricola* outbreaks based on host availability, geographic proximity, and the relative probability of dispersal between pairs of locations. This analysis used the geohabnet package in R, a component of the R2M toolbox (garrettlab.com/r2m). We subsequently mapped locations with climates likely to be suitable for *H. lauricola* outbreaks using MaxEnt, based on bioclimatic data (WorldClim) and county-level occurrence of laurel wilt (EDDMaps). Analysis of the international wood trade network showed that disease-free countries such as Mexico, Brazil, and Australia have multiple trade links to countries with laurel wilt. Lauraceae host connectivity analysis indicated locations in the Amazon and Western European that are candidate priorities for laurel wilt surveillance. For cultivated avocado, locations in Southern Mexico and Central America are important candidates. Analysis of climate suitability for laurel wilt identified key locations for current and future climate, notably in southern Brazil, southeastern China, and eastern Australia. These results can help inform regional, national, and global strategies for monitoring and mitigating laurel wilt.

Financial support: USDA.

Modeling landscape-level transmission of a shared pathogen in a heterogeneous agroecosystem

Paulina Mata¹, Geovanni Hernandez¹, Robin A. Choudhury¹

¹ School of Earth, Environmental, and Marine Sciences, University of Texas Rio Grande Valley, Edinburg, TX, USA.

E-mail: robin.choudhury@utrgv.edu

The Lower Rio Grande Valley (LRGV) of Texas, USA is a semi-arid to subtropical agricultural area with major production in horticulture, row crops, and an increasing acreage of organic farms. While a few row crops, such as cotton, maize, sorghum, sugarcane, and sunflower, dominate the landscape, smaller farms grow a variety of horticultural crops like okra, squash, watermelon, and peppers. Recent studies of pathogens of sugarcane and sorghum found several *Fusarium* isolates that were able to infect both crops. Surveys of pathogens on frequently used cover crops like sunn hemp also revealed several pathogens capable of infecting sorghum. Furthermore, changes in land-use and water availability have altered the crop choices of many local growers. To understand how crop and land-use changes may have impacted the spread of pathogens across several different crops, we analyzed historic USDA CropScape data for landscape heterogeneity and used the data to model the spread of a pathogen capable of infecting multiple agricultural hosts. We used a gravity model to estimate the spread of the pathogen between adjacent cells in the landscape and simulated spread across multiple iterations. We modeled a range of pathogen infectivity. We found that the overwhelming majority of acreage in the LRGV is devoted to sorghum, cotton, maize, and sugarcane. Year on year monoculture was relatively high, with approximately 23% of cropping area devoted to the same crop as the previous year. We found that large acreages of the LRGV are devoted to single types of crops and that with higher cross-crop pathogen infectivity the pathogen would be able to rapidly spread across the region. Understanding how varietal resistance, pesticides, crop rotation, or other management strategies can impact the overall dynamics of the pathogen infection could help to build a more robust and sustainable agroecosystem.

Evaluating planting date recommendation effects on soybean yield using causal inference

Santosh Sanjel¹, Denis A. Shah², Shawn P. Conley³, Spyridon Mourtzinis³ and Paul Esker¹

¹Department of Plant Pathology and Environmental Microbiology, The Pennsylvania State University, State College, Pennsylvania, USA

²Department of Plant Pathology, Kansas State University, Manhattan, Kansas, USA

³Department of Agronomy, University of Wisconsin–Madison, Madison, Wisconsin, USA

Email: sks7388@psu.edu

Selecting the optimal planting date is a crucial decision for soybean farmers aiming to maximize yield. Planting date recommendations are usually made through several years of field research data and modeling. This study introduces an observational causal inference framework to assess the impact of adhering to early planting recommendation in the North Central United States (NCUS) on soybean yield gains. A grower-derived field survey collected from approximately 5,000 farms in the NCUS over three seasons (2014, 2015 and 2016) was used as the input dataset. A causal graph of the soybean farming system was developed based on agronomic and crop production practices in current use in the NCUS. Based on early planting recommendations made by a group of soybean researchers from 11 different universities in the NCUS, we assigned the observed planting date in the data into optimal or non-optimal planting (a binary categorization, taken as the planting date 'treatment'). Using the backdoor criterion, we identified the minimal sufficient adjustment set of covariates accounting for confounding. Propensity score (PS) full matching was done using a probit regression of the treatment on the covariates; checks indicated that adequate balance was achieved. A weighted (by the full matching weights) linear regression model with yield as outcome, and the binary planting date treatment and covariates as predictors was fitted. Performing g-computation and using cluster-robust variance, we estimated the average treatment effect (ATE) of 270 kg/ha and 95% CI of 185 to 363, for fields adhering to recommended early planting dates. Overall, this study presents a comprehensive observational causal inference framework that is beyond the scope of predictive accuracy with potential applications in decision support systems across various fields. Future research aims to develop causal models interpreting how planting dates may influence soybean disease incidence and severity, as well as management requirements.

Model-based prediction of the selection of fungicide resistance in pepper anthracnose pathogen, *Colletotrichum scovillei*, in Korea

Kwang-Hyung Kim¹, Jeong-Hyeon Byeon¹, Peter Hobbelen², Jin-Yong Jung¹

¹ Department of Agricultural Biotechnology, Seoul National University, Seoul, Korea.

² Epidemiology, Bio-informatics & Animal models, Wageningen Bioveterinary Research, Lelystad, Netherlands.

E-mail: sospicy77@snu.ac.kr

An existing mathematical model for the selection of fungicide resistance in foliar pathogens of cereal crops was adopted to apply for the fungicide resistance of pepper anthracnose pathogen, *Colletotrichum scovillei*, in Korea. Considerable modifications were required as the new model in the study was needed to deal with the conducive environments affecting the development and transmission of anthracnose lesions on pepper fruits. The resulting model was calibrated using one of the four independent data from experimental fields quantifying selection for the G143A mutation conferring resistance to a quinone outside inhibitor fungicide, pyraclostrobin. Similar fungicide treatments, such as applied dose and spray number, were made for all experiments. Right after individual spray, we collected lesions and calculated the observed selection ratio of resistant strain, and compared them with the one before the first spray. The model was successfully calibrated, and then validated against the remaining three independent data from different fields. Although the amount of validation data was not enough to prove the validity of the model at this point, the graphical comparison between the observed selection ratios and the simulated ones showed a good agreement. This indicates that the integration of the weather-based anthracnose infection algorithm into the existing fungicide resistance modeling platform as a module was successful and the pepper fruit growth model represents the field observations. To our knowledge, this is the first fungicide resistance model for plant pathogens developed with field data in Korea. By conducting more and various spray experiments, this model can be validated further, and be used to identify anti-resistance treatment strategies which are likely to be effective in the context of Korean pepper fields.

Environmental requirements for germination, growth, and infection of *Alternaria* species in mandarins

Thiago de Aguiar Carraro¹, Vinícius Charnecki Galvão¹, Walmes Zeviani¹, Geraldo José da Silva Junior², Lilian Amorim³, Louise Larissa May De Mio¹

¹Depto. de Fitotecnia e Fitossanidade, UFPR, Curitiba, PR.

²Fundo de Defesa da Citricultura (Fundecitrus), Araraquara, SP.

³Escola Superior de Agricultura “Luiz de Queiroz”, ESALQ/USP, SP.

E-mail: thiagoacarraro@gmail.com

Alternaria brown spot (ABS), caused by *Alternaria* spp., represents a significant threat to mandarin production, due to intense leaf senescence and fruit drop. There are limited studies of this disease in Brazil, and none of them compared the disease monocyclic components among isolates. The isolates were obtained from two distinct mandarin-producing regions in Paraná, Paranavaí (Northwest region) and Cerro Azul (located North of Curitiba). The objectives of this study were to assess: (i) the effects of temperature on *in vitro* mycelium growth and conidia germination; (ii) the effects of temperature and the wetness period (WP) on the incubation period and disease severity *ex vivo*; and (iii) the effects of the WP on the incubation period and disease severity on potted ‘Murcott’ plants. Three isolates of *A. alternata* (CrAaPR-40 from Paranavaí, PR, Brazil, and CrAaPR-27 and CrAaPR-01 from Cerro Azul, PR, Brazil), and CrAIPR-73 of *A. longipes* from Cerro Azul were used. The range of temperatures for *A. alternata* mycelial growth and conidia germination were 7 to 37 °C. The optimal temperature was 26-29 °C. In contrast, *A. longipes* did not grow above 33 °C, and the optimal temperatures were 24 and 22 °C for mycelial growth and conidia germination, respectively. Infection on detached leaves occurred within the temperature range of 15-33 °C (optimal at 27 °C) for all isolates. Infections of both species were observed 6 h onwards of WP. ABS severity increased as the WP increased. Disease severities caused by isolates CrAaPR-40 (*A. alternata*) and CrAIPR-73 (*A. longipes*) were 10 and 5 times higher, respectively, than the other isolates. The incubation period was variable: 19-23 h for *A. alternata* from Paranavaí, 63-97 h for *A. longipes* from Cerro Azul and 258-305 h for *A. alternata* from Cerro Azul. Our findings highlighted regional/species aggressiveness variations and the importance of environmental requirements on ABS development.

Financial support: CNPQ (Grant number 306886/2021-9, 403918/2021-9) and CAPES (Code 001)

Genetic resistance and temporal progress of onion white rot in Brazil

Débora C. M. Mesquita¹, Valter R. Oliveira², Adalberto Café Filho¹, A. W. Moita², José L. Pereira³, Fernanda M. Inacio⁴, Letícia M. Pinheiro⁴, Everaldo A. Lopes⁴, Gabriela G. Nunes², Valdir Lourenço Jr.²

¹ Departamento de Fitopatologia, Universidade de Brasília, Brasília DF Brasil.

² Embrapa Hortaliças, Brasília DF Brasil.

³ Universidade Pitágoras Unopar Anhanguera, Polo Planaltina, Brasília DF Brasil.

⁴ Universidade Federal de Viçosa, Campus Rio Paranaíba, Rio Paranaíba MG Brasil.

E-mail: valdir.lourenco@embrapa.br

White rot (WR), caused by *Stromatinia cepivora*, is a devastating disease of onion. As there are no reported sources of genetic resistance among onion genotypes, the objective of this study was to assess the temporal progress of WR on cultivars and lineages under field conditions. Two experiments were performed from May to October 2016 and 2017 in the COOPADAP research station, naturally infested with *S. cepivora*, at Rio Paranaíba, MG. Thirty cultivars from genetically distinct groups were evaluated in a randomized complete block design with five repetitions. Sclerotia numbers were assessed in each experimental unit. The monomolecular and the Gompertz models were the most appropriate to describe the temporal progress curves of onion WR in 2016 and 2017, respectively. Differences of susceptibility and disease rate among the genotypes to WR were detected in 2016. The area under the disease progress curve (AUDPC) was higher on BRS Alfa São Francisco (2409). The lowest AUDPC value was observed on Sirius F1 (775). The number of bulbs well-suited to market (BWM) per plot was higher on Sirius F1 (55). Highest BWB weights were obtained on Perfecta (8.5 kg/plot) and Sirius (8.4 kg/plot). Although the incidence and disease rate of WR were higher in 2017, it was possible to detect differences among the cultivars. The highest and lowest AUDPC values were estimated on CNPH 6300 (6010) and Vale Ouro IPA 11 (3901), respectively. Cultivar differences were not detected on the number of BWM. However, the highest BWB weights were found on Sirius F1 (1.4 kg/plot) and Irati S2 (1.4 kg/plot). Soil temperatures lower than 15°C during onion bulbification were more frequent in 2017 than in 2016, which is conducive to infection. No correlation was detected of the number of sclerotia and WR incidence on the onion cultivars. The average number of viable sclerotia was 8 and 9 per 100 cm³ of soil in 2016 and 2017, respectively. Although differences in the susceptibility of onion genotypes to WR were detected, materials with high level of resistance to be used in breeding programs to *S. cepivora* were not identified.

Financial support: FAPDF (Grant n°193.000.995/2015) and CNPq (Grant n° 305.792/2013-0).

A Bayesian-based quarantine exit strategyVictor Alves¹, Neil McRoberts¹¹ Department of Plant Pathology, University of California, Davis CA USAE-mail: vfalves@ucdavis.edu

One of the most problematic aspects of regulatory control of invasive pests and diseases is the open-ended nature of quarantine periods. It is easy to specify the conditions that lead to the need for a quarantine to be imposed, but it is usually far more difficult to specify the conditions under which a quarantine can be lifted in a secure and objective way. Since growers cannot be expected to live indefinitely with the additional costs of the required mitigation(s) and restrictions that quarantines often impose, or rely on regulators' subjectivities, an evidence-based exit methodology seems to be the most appropriate and equitable strategy. We propose a procedure for quarantine exit based on sequential Bayesian probability updating (BPU), focusing on the true, but unknown, incidence of the pathogen in the environment, p . This programmatic method uses a series of well-defined yet flexible steps to first determine an initial, evidence-based probability of disease incidence, and then to combine that estimate with survey sampling data to realistically update the estimate of p over time. Using Bayes' rules to update p provides an objective method for using real-world information to provide a point estimate and credible interval for pathogen incidence. Based on the form of the assumed prior and the structure of the collected data the procedure will define the probability distribution for incidence. Features of this distribution will allow a growing area to exit from quarantine when combined with a formal decision-making process. Since no feasible amount of sampling can prove absence conclusively, the criterion for leaving quarantine must be based on a "beyond reasonable doubt" basis. Typically, this will mean that the updated p , must be lower than a pre-agreed upper threshold to suggest quarantine exit. Negative samples move the initial (or "prior") probability towards a pre-agreed exit criterion, positive samples do the opposite. Sampling occurs until: (a) the accumulation of negative-only samples causes the exit criterion to be reached, (b) the recurrence of both positive and negative samples over a pre-agreed period leads to the conclusion that the area has become endemically infected, or (c) failure to reach the exit criterion results in a re-evaluation of the strategy, but without reaching a conclusion about endemic colonization. The criteria under which a regulatory program might reach conclusions (b) or (c) under BPU can also be agreed in advance to prevent an open-ended regulatory action from occurring. This quarantine exit strategy could be useful for many national or sub-national plant protection organizations as an objective, transparent approach to determining when to suspend regulatory actions. Additionally, it might allow growers and regulators jointly to create surveillance programs that have a defined endpoint, based on growers' own sampling efforts, allowing regulatory programs to combine top-down and bottom-up attributes.

Financial support: USDA-NIFA Hatch project CA-D-PPA-2726

Injury-Damage relation for yellow spot, leaf rust and multiple pathosystem in wheat

Yuri Guerreiro Ramos¹; Marcelo Giovanetti Canteri¹

¹ Departamento de Agronomia, Universidade Estadual de Londrina, Londrina PR Brasil.

E-mail: yuri.guerreiro@uel.br

Establishing the damage function aims to determine the damage caused by a pathogen. This work aimed to relate the damage to the injury caused by yellow spot and leaf rust in wheat, as well as the multiple pathosystem, generating equations of damage functions, subsidizing the calculation of the Economic Damage Threshold (EDT). Three experiments were conducted in the years 2021, 2022 and 2023 containing treatments with different times and number of applications. Severity and productivity assessments were carried out, and the AUDPC, EDT, Action Threshold (AT) and damage equations were subsequently calculated. The experimental design was randomized blocks with eight treatments and four replications. For yellow spot, wheat leaf rust and multiple pathosystems, three or four applications started early provided the lowest severities. The best equations generated to estimate the damage obtained $R^2 = 0,7444$ for yellow spot in 2021, $R^2 = 0,6706$ for wheat leaf rust in 2022 and $R^2 = 0,8345$ for the multiple pathosystem in 2023. The EDT referring to the stages with the highest coefficients of damage were 5,2 % for 4.5 Zadoks in 2021, 11,4 % for 4.1 in 2022 and 5,8 % and 1,7 % for 4.5 in 2023. For every day of delay in starting control, there is a productivity loss of 9,5 kg/ha/day for yellow spot, 15,22 kg/ha/day for wheat leaf rust and 22,131 kg/ha/day for multiple pathosystem.

Modeling primary huanglongbing infection to determine the most economical strategy for controlling *Diaphorina citri* in sweet orange edge blocks

Isabela V. Primiano¹, Eduardo C. Monteferrante^{1,2}, Leonardo Ferreira², Andreia C. de O. Adami², Sílvia H. G. de Miranda², Franklin Behlau¹, Renato B. Bassanezi¹

¹ Research and Development Department, Fundecitrus, Araraquara SP Brasil.

² University of São Paulo, USP/ESALQ/CEPEA, Piracicaba SP Brasil.

E-mail: renato.bassanezi@fundecitrus.com.br

Huanglongbing (HLB) is a destructive citrus disease, vectored by the Asian citrus psyllid (ACP) *Diaphorina citri*, and associated with the bacteria ‘*Candidatus Liberibacter asiaticus*’ (CLAs). HLB control is based on preventive measures, such as (i) planting healthy nursery trees, (ii) removal of symptomatic trees, and (iii) vector control by insecticide application. Ongoing primary infections are a major factor in HLB epidemics and most of them occur at the orchard edge in a decreasing gradient. To protect growing shoots and avoid primary infections, more frequent spraying is necessary. Thus, a question has been raised by growers: “What should be the orchard edge strip sprayed weekly that brings an efficient economic outperformance in comparison to fortnightly spray?”. Therefore, a modeling approach based on epidemiological and economic analysis was used to estimate the width of block edge strip to be weekly sprayed (ESWS) that provided the maximum Net Present Value (NPV) of controlling HLB. The present work considered different combinations of ESWS plus fortnightly spray in the rest of the block. Four regions of the São Paulo and Triângulo/Southwest Mineiro citrus belt were selected: region 1 was located at Triângulo Mineiro; 2, 3, and 4 were located at north, center, and south of Sao Paulo state, respectively. The ACP population and HLB incidence decreased from region 1 to 4. The epidemiological model was based on the number and gradient of immigrating ACP, percentage of CLAs+ ACP, infection efficiency, and insecticide spray efficacy, to estimate the number of HLB-symptomatic trees. Afterwards, The NPV was based on this total number of HLB-symptomatic trees per year in each scenario of weekly spray range. The economic analysis was also performed by four economic panels, varying or not costs and yield. Accumulated benefit (the revenue received from remaining bearing trees) and costs (the expenses with insecticide spray, removal and reset of diseased trees) were considered in the analysis and were calculated according to tree’s age (accumulated from 3 to 15 years-old). The outcomes of the NPV method were transformed into an index for each spray scenario, and the ESWS with the highest index was chosen. Regardless to the economic panel, the ESWS was the same in each region and higher in region with higher HLB favorability: 1 (first row), 217, 189, and 497 m (entire plot) at regions 1, 2, 3, and 4, respectively, indicating that costs and yields can change the NPV, but cannot change the epidemiological result and the optimal width edge strip. Growers should participate in area-wide control campaigns to reduce ACP density within the region and, consequently, reduce ESWS, reduce the operational costs and increase income with less HLB incidence.

Financial support: FAPESP (Projects #17/21460-0, #19/19481-5, and #22/05359-6) and CNPq (Project #304253/2020-0).

INDEX OF DELEGATES		
Name	Institution	E-mail
AARON ISAI PLEX SULÁ	University of Florida	plexaaron@ufl.edu
ADAM SPARKS	Curtin University	adamhspark@icloud.com
ADRIANO A. DE PAIVA CUSTÓDIO	IAPAR-EMATER (IDR-Paraná)	custodio@idr.pr.gov.br
ALEXEY MIKABERIDZE	University of Reading	a.mikaberidze@reading.ac.uk
ALICE KAZUKO INOUE NAGATA	Embrapa Hortaliças	alice.nagata@embrapa.br
ANDRE BUENO GAMA	Louisiana State University	agama@agcenter.lsu.edu
ANDREAS VON TIEDEMANN	Universität Göttingen	atiedem@gwdg.de
ANDRES CRUZ	Purdue University	acruzsan@purdue.edu
ANDRES SANABRIA-VELAZQUEZ	North Carolina State University	adsanabr@ncsu.edu
ANTONIO VICENT CIVERA	Instituto Valenciano de Investigaciones Agrarias (IVIA)	vicent_antciv@gva.es
ARMANDO BERGAMIN FILHO	Universidade de São Paulo	abergami@usp.br
ARNE STENSVAND	Norwegian Institute of Bioeconomy Research	arne.stensvand@nibio.no
AYALSEW ZERIHUN	Curtin University	a.zerihun@curtin.edu.au
BELACHEW ASALF TADESSE	Norwegian Institute of Bioeconomy Research	belachew.asalf.tadesse@nibio.no
BEREA ABAGAIL ETHELTON	University of Florida	betherton@ufl.edu
BRAZ TAVARES DA HORA JÚNIOR	Bayer	braz.hora@bayer.com
BRENDEN LANE	Purdue University	lane80@purdue.edu
BRENO BENVINDO DOS ANJOS	Universidade Federal do Espírito Santo	bbdanjos@gmail.com
BRENO CEZAR MARINHO JULIATTI	Juliagro	brenojuliatti@hotmail.com
CAMILA IAVORSKI ZELA	Universidade Federal do Paraná	camilaiavorskizela@gmail.com
CARLOS CECILIO GONGORA CANUL	Purdue University	cgongora@purdue.edu
CHRISTIAN D CRUZ SANCAN	Purdue University	cruz113@purdue.edu
CLAUDIO DIAS DA SILVA JUNIOR	Kansas State University	claudiodsjr@hotmail.com
DAIANA MARIA QUEIROZ AZEVEDO	ESALQ - Universidade de São Paulo	daiana.azevedo@usp.br
DALPHY HARTEVELD	Norwegian Institute of Bioeconomy Research	dalphy.harteveld@nibio.no
DAMON SMITH	University of Wisconsin-Madison	damon.smith@wisc.edu
DANIEL RICARDO MAASS STEINER	Universidade Federal do Paraná	danielmsteiner@gmail.com
DAVID GENT	US Department Agriculture	david.gent@oregonstate.edu
DAVID M GADOURY	Cornell University	dmg4@cornell.edu
DÉBORA PETERMANN	Universidade Federal do Paraná	debora_peter@hotmail.com
EDUARDO SEITI GOMIDE MIZUBUTI	Universidade Federal de Viçosa	mizubuti@ufv.br
ELENA PEREZ	INIA	elenaperez@inia.org.uy
ELIAS ZUCHELLI	The University of Tennessee	ezuchell@utk.edu
ELIN FALLA	University of Cambridge	ekf32@cam.ac.uk
EMERSON MEDEIROS DEL PONTE	Universidade Federal de Viçosa	delponte@ufv.br
FELIPE DALLA LANA	Louisiana State University	fdallalana@agcenter.lsu.edu
FERNANDO CEZAR JULIATTI	Juliagro	fernandocezar74@gmail.com
FRANKLIN JACKSON MACHADO	Universidade Federal de Viçosa	franklin.machado@ufv.br
GABRIEL FERREIRA PAIVA	Universidade Federal de Viçosa	gabrielarpaiva2009.gf@gmail.com

GALVIN ALONZO ORTIZ	University of Florida	galvin.alonzoort@ufl.edu
GUILLERMO ANDRÉS ENCISO-MALDONADO	Universidad Católica "Nuestra Señora de la Asunción" Unidad Pedagógica Hohenau	guillermo.enciso@uc.edu.py
GUO QINGYUN	Qinghai Academy of Agriculture & Forestry Sciences	guoqingyunqh@163.com
HENRIQUE DA S. SILVEIRA DUARTE	Universidade Federal do Paraná	henrique.duarte49@gmail.com
HOPE RENFROE BECTON	North Dakota State University	hope.becton@ndsu.edu
HU BINHONG	Swedish University of Agricultural Sciences	binhong.hu@slu.se
IBRAHIM SURAJ ZACHARY	Adofo company limited	famdynamic96@gmail.com
ISRAËL TANKAM CHEDJOU	Institut Agro Rennes-Angers	israeltankam@gmail.com
JACOBO ROBLEDO BURITICA	University of Florida	jacoborobledobur@ufl.edu
JESSICA DANILA KRUGEL NUNES	Universidade de São Paulo	jessica.krugel@usp.br
JIASUI ZHAN	Swedish University of Agricultural Sciences	jasui.zhan@slu.se
JOAQUÍN GUILLERMO RAMÍREZ GIL	Universidad Nacional de Colombia	jgramireg@unal.edu.co
JORGE DAVID SALGADO	FMC Global	jorgedavid23@gmail.com
JOSÉ AIRES VENTURA	Incaper	ventura@incaper.es.gov.br
JOSÉ F GONZÁLEZ-ACUÑA	Iowa State University	jgonzal@iastate.edu
JOSÉ MAURÍCIO CUNHA FERNANDES	Embrapa Trigo	mauricio.fernandes@embrapa.br
JUAN ANDRES PAREDES	INTA	paredes.juanandres@inta.gob.ar
JUAN EDWARDS	Bayer	edwardsmolina@gmail.com
JUAN MANUEL LÓPEZ VÁSQUEZ	Centro Nacional de Investigaciones en Palma de Aceite - Cenipalma	jlopezv@cenipalma.org
JUAN NAVAS-CORTÉS	Institute of Sustainable Agriculture	j.navas@csic.es
JULIANA M. K. CARDOSO PERSEGUINI	Universidade Tecnológica Federal do Paraná - Campus Dois Vizinhos	julianam@utfpr.edu.br
KAIQUE DOS SANTOS ALVES	Bayer	kaique.alves@bayer.com
KAREN GARRETT	University of Florida	karengarrett@ufl.edu
KELSEY ANDERSEN ONOFRE	Kansas State University	andersenk@ksu.edu
KWANG-HYUNG KIM	Seoul National University	sospicy77@snu.ac.kr
LAURENCE MADDEN	Ohio State University	madden.1@osu.edu
LEANDRO JOSÉ DALLAGNOL	Universidade Federal de Pelotas	leandro.dallagnol@ufpel.edu.br
LILIAN AMORIM	Universidade de São Paulo	lilian.amorim@usp.br
LILIAN MARIA ARRUDA BACCHI	Universidade Federal da Grande Dourados	lilianbacchi@ufgd.edu.br
LISA ROTHMANN	University of the Free State	coetzeela@ufs.ac.za
LOUISE LARISSA MAY DE MIO	Universidade Federal do Paraná	maydemio@ufpr.br
LUCAS SANTOS SALES	Universidade de São Paulo	lucassales@usp.br
LUIS IGNACIO CAZÓN	INTA	ignaciocazon88@gmail.com
MADISON KESSLER	Kansas State University	madisonkessler14@gmail.com
MAIARA DA SILVA FREITAS	Universidade Federal de Viçosa	maiara.freitas@ufv.br
MAIK LEÃO DOS SANTOS	Universidade Federal de Viçosa	maik.santos@ufv.br
MARCELO GIOVANETTI CANTERI	Universidade Estadual de Londrina	canteri@uel.br
MARIA CHIARA ROSACE	Università Cattolica del Sacro Cuore	mariachiara.rosace@unicatt.it
MARIA CRISTINA CANALE	Epagri	cristinacanale@epagri.sc.gov.br
MARIA DEL ROCIO C. MADRID	Cornell University	rcalderonmadrid85@gmail.com

MARIELA FERNANDEZ CAMPOS	Purdue University	ferna129@purdue.edu
MARY RUTH MCDONALD	University of Guelph	mrmcdona@uoguelph.ca
MATHEUS CORREA BORBA	Virginia Tech	matheuscb@vt.edu
MATTHEW COMBES	University of Warwick	matt.combes@warwick.ac.uk
MONALISA CRISTINA DE CÓL	Universidade Federal de Viçosa	monalisacdecol@gmail.com
MURILLO LOBO JUNIOR	Embrapa Arroz e Feijão	murillo.lobo@embrapa.br
NATALIA A PERES	University of Florida	nperes@ufl.edu
NEIL MCROBERTS	University of California, Davis	nmcroberts@ucdavis.edu
NICHOLAS JAMES CUNNIFFE	University of Cambridge	njc1001@cam.ac.uk
OLANREWAJU SHITTU	Pennsylvania State University	oms5169@psu.edu
OMAR PAINO PERDOMO	Universidad Autónoma de Santo Domingo	operdomo92@uasd.edu.do
PAUL ESKER	Pennsylvania State University	pde6@psu.edu
PAUL MELLOY	The University of Queensland	p.melloy@uq.edu.au
PAULO HENRIQUE N.DE SOUZA	Fundação MT	paulosouza@fundacaomt.com.br
PETER OJIAMBO	North Carolina State University	pojiamb@ncsu.edu
PIÉRRI SPOLTI	Bayer	pierri.spolti@bayer.com
QIANG YAO	Qinghai Academy of Agriculture & Forestry Sciences	yaoqiang2010@126.com
RACHEL TRIMBLE	University of Cambridge	rjt42@cam.ac.uk
RENATO BEOZZO BASSANEZI	Fundecitrus	renato.bassanezi@fundecitrus.com.br
RICARDO GOMES TOMÁZ	Universidade Federal de Viçosa	ricardogomesagro@gmail.com
RICHARD WADE WEBSTER	North Dakota State University	richard.webster@ndsu.edu
ROBERT M BERESFORD	Plant & Food Research	robert.beresford@plantandfood.co.nz
ROBERTO DE ROSSI	Universidad Católica de Córdoba	robderossi@gmail.com
ROBIN CHOUDHURY	UTRGV	robin.choudhury@utrgv.edu
RODRIGO BORBA ONOFRE	Kansas State University	onofre@ksu.edu
SALOTTI IRENE	Università Cattolica del Sacro Cuore	irene.salotti1@unicatt.it
SANTOSH SANJEL	Pennsylvania State University	sanjelsantosh@gmail.com
SARA THOMAS-SHARMA	Louisiana State University	sarathomas23@gmail.com
SILVIO APARECIDO LOPES	Fundecitrus	silpalopes@gmail.com
SYDNEY EVERHART	University of Connecticut	everhart@uconn.edu
THAÍS RIBEIRO SANTIAGO	Universidade de Brasília	thais.santiago@unb.br
THIAGO DE AGUIAR CARRARO	Universidade Federal do Paraná	thiagoacarraro@gmail.com
VALDIR LOURENÇO JUNIOR	Embrapa Hortaliças	valdir.lourenco@embrapa.br
VICTOR H. FERREIRA ALVES	University of California, Davis	vfalves@ucdavis.edu
VINCENT FASANELLO	Bayer	vincent.fasanello@bayer.com
VINCENT PHILION	IRDA	vincent.philion@irda.qc.ca
VINICIUS ANDREI CERBARO	University of Florida	cerbaro@ufl.edu
VINICIUS GARNICA	North Carolina State University	vcastel@ncsu.edu
WILLIAN BUCKER MORAES	Universidade Federal do Espírito Santo	willian.moraes@ufes.br
YURI GUERREIRO RAMOS	Universidade Estadual de Londrina	yuri.guerreiro@uel.br
ZHANHONG MA	China Agricultural University	mazh@cau.edu.cn
ZHENMEI ZHAO	China Agricultural University	mazhzzm@outlook.com
ZVEZDOMIR JELKOV JELEV	Agricultural University - PLOVDIV	zvezdoss@yahoo.com

