2026 American Phytopathological Society North Central Division Meeting

APS NORTH CENTRAL DIVISION

MICHIGAN STATE UNIVERSITY

June 10-12, 2026 | East Lansing, Michigan

Table of Contents

Agenda

WEDNESDAY, JUNE 10 - RESEARCH TOUR AND WORKSHOPS

8:30 a.m.	**Board Bus**
8:45 a.m.	**Agronomy Farm Stop** Precision Planter and Sprayer Potato Breeding and Pathology
9:30 a.m.	**Transition Time**
9:45 a.m.	**Plant Pathology Farm** Fruit Research: Hops, Blueberries, Tree Fruit, Nuts (East Farm) Soybean, Corn, Wheat, Dry Bean and Grapes (West Farm)
11:00 a.m.	**Transition Time**
11:15 a.m.	**MSU Pollinator Center Tour**
11:45 p.m.	**New MSU Dairy Cattle Teaching & Research Center Tour and Lunch**
12:45 p.m.	**Transition Time**
1:00 p.m.	**AI For Plant Health: AI History, Ethics and Data Workflows** *Ron Southwick, MSU*
2:30 p.m.	**Lab Tours or Workshops** Tours of MPS Lab, Growth Chamber Facilities, Greenhouse, and NPDN Hub Diagnostic Lab CV's 101 Workshop - *Maddi Shires, SDSU; Mercedes Diaz, Bayer; and Mikaela Breunig, Bayer*
4:00 p.m.	**Welcome Reception at MPS Atrium (Everyone Welcome)**

THURSDAY, JUNE 11 - PROGRAM PRESENTATIONS (KELLOGG CENTER - BIG TEN A)

7:30 a.m.	**Light Refreshments**
8:00 a.m.	**NC APS Welcome | Announce Plant Disease Competition**
8:05 a.m.	**MSU Plant Pathology: Connections and a Little History** *Dr. Ray Hammerschmidt, MSU (Retired)*
8:30 a.m.	**Changing Weather Patterns** *Dr. Jeff Andresen, MSU*
9:00 a.m.	**Selected Abstracts for Post-Docs** 9:00 a.m. - In vitro and field evaluation of chemical and biological products for chestnut brown rot control (caused by Gnomoniopsis smithogilvyi) in Michigan - Giorgia Bastianelli 9:12 a.m. - Enhancing Fungicide Sensitivity Monitoring of Fusarium graminearum through YOLO-Based Automated Growth Quantification and Media Optimization - Sunkyu Choi 9:24 a.m. - Tracking fungicide use in blueberries across the United States, 1991–2023 - Luisa Parrado Guevara 9:36 a.m. - First detection of Fusarium oxysporum f. sp. apii Race 4 causing celery meltdown in Michigan - Soumya Moonjely 9:48 a.m. - Regional and field-scale population structure and mating strategies of Alternaria brassicicola in cole crops (Brassica spp.) - Roy Davis 10:00 a.m. - Spray-Induced Gene Silencing Suppresses Gene Expression and Growth of the fruit-rot pathogen Colletotrichum fioriniae - Shay Szymanski 10:12 a.m. - Genomic structural variants of Sclerotinia sclerotiorum Lib de Bary isolates contrasting for disease aggressiveness - Ram Neupane

Agenda

10:24 a.m.	**Selected Abstracts for Graduate Students** 10:24 a.m. - Temporal evolution of FRAC 11 fungicide resistance in Colletotrichum fioriniae populations from Michigan highbush blueberry (1999–2024) - Adam Adaskaveg 10:36 a.m. - Population structure, gene prediction, and secondary metabolite diversity of the potato black dot pathogen, Colletotrichum coccodes - Riley Eisenbraun 10:48 a.m. - Optimizing fungicide applications for tar spot and southern rust in Missouri corn production - Hailey Emanuel 11:00 a.m. - Beyond Symptoms: discrete decision windows govern SDHI seed treatment efficacy in soybean sudden death syndrome - Ryan Hamilton 11:12 a.m. - Assessment of fungicide use for managing deoxynivalenol and ear rot on silage corn in Wisconsin using a meta-analytic approach - Lucia Hyzer 11:24 a.m. - Developing and evaluating molecular diagnostic tools, real rime qPCR and recombinase polymerase amplification assay for detecting Heterodera glycines - Nabina Karki 11:36 a.m. - Evaluation of Commercial Biocontrol Products Performance for Managing Soilborne Pathogens in North Dakota Soybean Fields - Madeeha Matloob
11:48 a.m.	**Lunch at Brody Hall** *Located across the street from the hotel - 241 W Brody Rd, East Lansing, MI 48825*
1:12 p.m.	**Selected Abstracts for Graduate Students** 1:00 p.m. - Development and Validation of a PCR Assay for *Xylaria necrophora* from Soybean - *Qiurong Fan* 1:12 p.m. - Prevalence and genetic diversity of Wheat streak mosaic virus-complex and viral like diseases in South Dakota wheat fields - *Anna Lagerhausen* 1:24 p.m. - Soft Winter Wheat Virus Survey and Screening of Germplasm - *Keeley Satterfield* 1:36 p.m. - Assessing the impact of soybean cyst nematode on dry bean yield and growth under field conditions - *Dalvir Singh* 1:48 p.m. - Exploring mobile genetic elements and virulence in the Prunus pathogen *Pseudomonas syringae* pv. *morsprunorum R1 - Sophia Liberto* 2:00 p.m. Theoretical framework and functional characterization of small RNA regulatory networks in *Erwinia amylovora* - *Elise Straub*
2:24 p.m.	**What's that Disease Quiz?**
3:00 p.m.	**Lightning Talks** 3:00 p.m. - Species Associated with Fusarium Head Blight in United States Grain Growing Regions in 2021-2025 - *Gloria Baker* 3:04 p.m. - Diversity of Soilborne Fusarium Associated with Bean Root Rot in Michigan - *Irene Blanco-Casallas* 3:08 p.m. - Can humic acid and chitosan additives control corn diseases as effectively as standard fungicides in central Indiana? - *Mariela Fernández-Campos* 3:12 p.m. - Biosynthetic Gene Clusters Suggest Contrasting Ecological Strategies Among *Clonostachys rosea* and *Fusarium virguliforme* - *Kristen Kater* 3:16 p.m. - Comparison of Soil Infestation Methods for *Phytophthora sojae* - *Keely McQuain* 3:20 p.m. - Evaluating Biological Control Agents for Reducing Survival and Viability of *Sclerotinia sclerotiorum Sclerotia* Across Soil Depths and Time - *Amit Sharma* 3:24 p.m. - First Report of Red Crown Rot Caused by *Calonectria ilicicola* and Its Effects on Soybean Yield Components in Ohio - *Ligia Calderon-Delgado* 3:28 p.m. - Identification and Functional Characterization of *Puccinia graminis* f. sp. *tritici* Effectors Targeting the Rpg5 Integrated Kinase Domain in Barley - *Israel Akinlabi* 3:32 p.m. - Pathogens in an Endophyte World: The Presence of a Phytotoxin Biosynthetic Gene Cluster Reflects Host-Association Strategy in *Xylaria Genera - Annabella Lyndon* *3:36 p.m. - Ralstonia pseudosolanacearum* uses RprR to orchestrate bacterial fitness in response to host-induced stress - *Bridget O'Banion* 3:40 p.m. - Mapping of Bacterial leaf streak (BLS) resistance in barley through Integrative GWAS and Haplotyping - *Thamaraikannan Sivakumar* 3:48 p.m. - Sulfur as a Tool Against Sudden Death Syndrome of Soybean - *Emily Duncan* 3:52 p.m. - Evaluation and Optimization of Crude DNA Extraction Methods for the Molecular Assays of *Calonectria ilicicola - Krishna Raj Pandey* 3:56 p.m. - Diversity, pathogenicity and geographical distribution of root-associated Fusarium spp. in Nebraska soybeans - Kelvin Muchiri
4:00 p.m.	**Break**
4:15 p.m.	**Poster Presentations** *Odd numbers from 4:15-5:15 p.m.; Even numbers from 5:15-6:15 p.m.*
6:00 p.m.	**Strolling Dinner, Poster Presentations Continue and Networking Reception**
7:15 p.m.	**APS Update** *Carolee Bull, APS President*
7:30 p.m.	**Award Presentations**

Agenda

FRIDAY, JUNE 12 - BUSINESS MEETING

7:30 a.m.	Breakfast from Dining Hall
8:00 a.m.	Business Meeting
12:00 p.m.	Business Meeting Adjourns

Meeting Sponsors

PLATINUM PLUS - $12,000

BAYER

GOLD - $3,500

CORTEVA™ agriscience

SILVER - $2,000

ISK Local Insight, Global Impact

COPPER - $1,000

BASF We create chemistry

FMC

MICHIGAN SOYBEAN COMMITTEE

FRIEND PLUS - $600

SUMITOMO BIORATIONAL

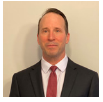
Session Descriptions and Speakers

WEDNESDAY SESSIONS

AI For Plant Health: AI History, Ethics and Data Workflows

Ron Southwick, MSU

A practical introduction to AI and large language models, focused on ethical use, prompt design, and real world applications for research and academic work.



Ronald Southwick serves as the Manager of the Center for Instructional and Research Technology (CIRT) in the College of Agriculture and Natural Resources at Michigan State University (MSU). With over 34 years at MSU, his career has spanned roles as a molecular biologist, researcher, and IT specialist, reflecting a longstanding commitment to supporting science through evolving technologies. His work focuses on research support, bioinformatics, and helping faculty, staff, and students effectively integrate emerging technologies into teaching and research. He is particularly interested in making complex tools accessible and practical within academic environments. In addition to his university work, Ron serves on the Board of Directors for an Olympic National Governing Body. He is also a member of Team USA, representing his country as a world-class athlete. He brings a perspective shaped by both scientific inquiry and disciplined practice to his work and presentations.

CV'S 101 WORKSHOP

Maddi Shires, South Dakota State University; Mercedes Diaz and Mikaela Breunig, Bayer Crop Science

The curriculum vitae (CV) is essential to every job application, but its format and organization can vary significantly depending on the position. Whether you're pursuing a career in academia, industry, or government, a professionally crafted CV is crucial. This workshop provides educators with comprehensive materials to assist students and early career professionals in creating and customizing CVs tailored to different position types. Break-out sessions will offer opportunities for small group discussions and hands-on activities.

https://www.apsnet.org/careers/careersinplantpathology/Careers101/Pages/default.aspx

Dr. Maddi Shires is an Assistant Professor and Extension Plant Pathology Specialist at South Dakota State University. She is also currently serving as the NC-APS Past President. She has been involved with the Careers 101 workshop program as both a student and a professor and part of the APS committee for about a year.

Dr. Mercedes Diaz Arias is the North America Crop Protection Technical Lead at Bayer Crop Science, supporting the development, positioning, and launch of fungicide and insecticide solutions across row crops. She collaborates across research, development, and commercial teams to advance technical strategies and deliver practical disease management insights. With over a decade of experience in plant pathology, she has contributed to fungicides, nematicides, biologicals, and resistance traits. Originally from Costa Rica, she holds degrees in Agronomy and Biotechnology, an M.S. in Crop Protection, and a Ph.D. in Plant Pathology from Iowa State University.

Dr. Mikaela Breunig is a Senior Scientist in Bayer Crop Science's Global Breeding organization, specializing in disease epidemiology, fungal pathology, and disease phenotyping. Mikaela partners with growers, product managers, and plant breeders to define industry needs and accelerate the development of disease tolerant wheat and corn varieties. Mikaela received her her undergraduate degree in plant pathology along with a certificate in agricultural business from the University of Wisconsin–Madison and her Ph.D. in plant pathology from Michigan State University, under the guidance of Dr. Martin Chilvers.

THURSDAY SESSIONS

MSU PLANT PATHOLOGY: CONNECTIONS AND A LITTLE HISTORY

Dr. Ray Hammerschmidt, MSU (Retired)

This session takes a look at the history and impact of plant pathology at Michigan State University, starting with early pioneers like Beal and some of the first fungicide trials on campus. We'll highlight key moments in research, Extension, and diagnostics, along with MSU's role in regional collaborations and leadership within APS and Project GREEEN. The session aims to connect past and present.

Ray Hammerschmidt is Professor Emeritus of Plant Pathology at MSU. He earned a BS in biochemistry and an MS in plant pathology from Purdue University, studying anthracnose resistance in corn, and a PhD from the University of Kentucky on induced resistance in cucumber. He also researched terpenoid accumulation in tobacco. Joining MSU in 1980, he became a full professor in 1991. His work focused on mechanisms of disease and induced resistance across multiple host-pathogen systems, including collaboration with the MSU potato breeding program. He taught undergraduate and graduate courses and mentored 25 graduate students and 10 postdocs. He held leadership roles including department chair, interim director of MSU Extension, and advisor to Project GREEEN. He also led major diagnostic networks and received numerous honors, including APS Fellow and the NPDN Lifetime Achievement Award.

CHANGING WEATHER PATTERNS

Dr. Jeff Andresen, MSU

Weather and climate are among the most influential—and least controllable—factors affecting agricultural production. In this presentation, Michigan State Climatologist Jeff Andresen will explore recent and projected climate trends, including changes in temperature, precipitation patterns, and extreme weather events. Special emphasis will be placed on the implications for plant health and disease management, including how changing environmental conditions may alter pathogen development, disease pressure, and crop risk. Participants will gain insight into the challenges and opportunities facing agriculture in a changing climate and learn how weather-based tools and decision-support systems can help improve resilience and management strategies for the future.

Jeff Andresen is Professor of meteorology/climatology with MSU's Department of Geography, Extension Specialist with MSU Extension, and the State Climatologist for Michigan. He holds a B.S. degree from Northern Illinois University in meteorology and M.S. and Ph.D. degrees from Purdue University in agricultural meteorology/climatology. Previously, he worked with the National Weather Service and with the USDA's World Agricultural Outlook Board. He currently serves as director of Michigan's Enviro-weather information system which supports agricultural pest and production management related decision-making across the state and as an extension specialist maintaining an active outreach program including dissemination of weather and climate data and related information to the general public and continuing education activities. His research has focused on the influence of weather and climate on agriculture, both in the USA and in international production area, including climatological trends and potential impacts, crop simulation modeling, agricultural irrigation, impacts associated with potential future changes in climate, weather and risk management, and the influence of land use changes on regional climate.

Oral Presentations

IN VITRO AND FIELD EVALUATION OF CHEMICAL AND BIOLOGICAL PRODUCTS FOR CHESTNUT BROWN ROT CONTROL (CAUSED BY GNOMONIOPSIS SMITHOGILVYI) IN MICHIGAN

Dr. Giorgia Bastianelli1, Mario Mandujano2, Mr. Cory A. Outwater3, Kerri Neugebauer2 and Dr. Timothy D. Miles2, (1)Michigan State Univ, East Lansing, MI, (2)Michigan State University, East Lansing, MI, (3)Michigan State University, Williamston, MI

The chestnut brown rot (CBR) fungus, *Gnomoniopsis smithogilvyi*, is the main cause responsible for the decay of chestnuts all over the world. The pathogen infects the flowers in the field, with symptoms affecting nut quality at harvest time and during storage. For this reason, orchard management and fungicide applications are crucial factors to prevent infection in flowers and later in kernels. Michigan is the leading producer of commercial chestnuts in the USA. After the first isolation of the pathogen in 2016, CBR was identified in 80% of Michigan orchards. This study aims to compare the efficacy of different fungicides and biofungicides for the inhibition of *G. smithogilvyi.* For the in vitro assay, 15 products in different FRAC groups were tested for fungicide activity against mycelium radial growth and spore germination. In the EC50 evaluation, Inspire Super (Difenoconazole 8%+Cyprodinil 24%) had the highest fungicidal activity, followed by Tilt (Propiconazole 42%) and Cevya (Mefentrifluconazole 35%). For the field trials, fungicide applications with 6 different products were conducted for two consecutive years (2023-2024), with 2 and 4 applications between bloom and harvest. Sysstem Zn (zinc phosphonate 8%) was the most effective treatment based on qPCR assay for the pathogen detection, followed by Inspire Super and Tilt. These results will help the Michigan chestnut industry in preventing pre-harvest CBR spread and will encourage the rotation of fungicides.

ENHANCING FUNGICIDE SENSITIVITY MONITORING OF FUSARIUM GRAMINEARUM THROUGH YOLO-BASED AUTOMATED GROWTH QUANTIFICATION AND MEDIA OPTIMIZATION

Dr. Sunkyu Choi1, Gloria A. Baker2, Dr. Martin Chilvers1, Dr. Alyssa K. Betts3, Dr. Jessica Cooper3, Dr. Rawnaq Chowdhury4, Dr. Briana Whitaker5, Dr. Darcy E. P. Telenko6, Dr. Ruth Dill-Macky7, Dr. Andrew J. Friskop8, Stephen N. Wegulo9, Dr. Madalyn Shires10, Dr. Nidhi Rawat11, Dr. Maira R. Duffeck12, Dr. Alyssa A. Collins13, Prof. Gary C. Bergstrom14, Dr. Mandy Bish15 and Dr. Guy Boyd Padgett16, (1)Michigan State University, East Lansing, MI, (2)Michigan State University, Lansing, MI, (3)University of Delaware, Newark, DE, (4)USDA-ARS, Pocatello, ID, (5)USDA-ARS, Peoria, IL, (6)Purdue University, West Lafayette, IN, (7)University of Minnesota, St Paul, MN, (8)North Dakota State University, Fargo, ND, (9)Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE, (10)South Dakota State University, Brookings, SD, (11)University of Maryland College Park, College Park, MD, (12)Oklahoma State Univ, Stillwater, OK, (13)Penn State University, Manheim, PA, (14)Cornell University, Ithaca, NY, (15)University of Missouri, Columbia, MO, (16)Louisiana State University, Alexandria, LA

Fusarium graminearum, the primary causal agent of Fusarium head blight (FHB), poses significant threats to global cereal production due to yield loss and mycotoxin contamination. Effective management relies on fungicides, necessitating high-throughput monitoring of fungicide sensitivity. In this study, we developed and compared two automated image-analysis pipelines, a zero-shot approach using the Segment Anything Model (SAM) and a supervised approach using YOLOv11-seg, to quantify mycelial growth for half-maximal effective concentration (EC50) determination. Validation against manual measurements showed that while SAM achieved high precision for small colonies, it exhibited recognition instability (< 50%) as mycelia approached the plate edge (> 66 mm). In contrast, the YOLOv11-seg model demonstrated higher robustness, maintaining recognition (> 99%) and linearity (R2 > 0.98) across diverse media (PDA and YBA). Using the optimized YOLO pipeline, we evaluated the sensitivity of more than 500 *F. graminearum* isolates from the United States to tebuconazole, pydiflumetofen, and pyraclostrobin. Results revealed that EC50 values were significantly influenced by the nutritional environment, and positive correlations were observed between tebuconazole and pydiflumetofen sensitivities on both media (P < 0.01). This automated tool allows for faster and more accurate monitoring of fungicide sensitivity, providing valuable biological insights into fungal growth patterns.

TRACKING FUNGICIDE USE IN BLUEBERRIES ACROSS THE UNITED STATES, 1991–2023

Luisa Maria Parrado Guevara1, Kerri Neugebauer1, Ms. Jill C. Check1, Josh VanderWeide2, Dr. Jonathan E. Oliver3, Dr. Chakradhar Mattupalli4, Dr. Peter V. Oudemans5, Virginia O. Stockwell6, Dr. Mengjun Hu7 and Dr. Timothy D. Miles1, (1)Michigan State University, East Lansing, MI, (2) Michigan State University, MI, (3)University of Georgia, Tifton, GA, (4)Washington State University, Mount Vernon, WA, (5)Rutgers University, Chatsworth, NJ, (6)USDA ARS Horticultural Crops Research Unit, Corvallis, OR, (7)University of Maryland, College Park, MD

Blueberry production in the United States spans diverse climates, shaping region-specific disease pressures and fungicide use. We analyzed USDA–NASS chemical-use data (1991–2023) to provide the first long-term comparison between eastern (Georgia, Michigan, New Jersey, North Carolina) and western (Oregon, Washington) regions. Fungicide use metrics were calculated based on years of reported use. Overall, fungicide programs in both regions became more intensive and chemically diverse over time, with state-level practices driving regional differences. Multisite (M), respiration (C), and sterol biosynthesis (G) fungicides comprised >70% of use, with captan (FRAC M04) and DMIs (FRAC 3) dominating. Multisite use diverged between regions, with copper-based fungicides prevalent in the west and ziram in the east, while single-site and plant-defense activator use showed more moderate differences. Fungicide portfolios diversified rapidly in the early 2000s with the adoption of new FRAC groups, increasing reliance on medium- and high-risk chemistries. Despite continued diversification, recent programs remain anchored by a stable chemical core, highlighting the need for regionally informed resistance-management strategies.

FIRST DETECTION OF FUSARIUM OXYSPORUM F. SP. APII RACE 4 CAUSING CELERY MELTDOWN IN MICHIGAN

Dr. Soumya Moonjely, Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, Samuel Sharpe, Depatment of Plant, Soil and Microbial Sciences, Michigan State University, MI and Dr. Mary K. Hausbeck, Michigan State University, East Lansing, MI; Michigan State University, Department of Plant, Soil and Microbial Sciences, East Lansing, MI

Michigan ranks second in the United States for celery production with a value of about $14.2 million in 2023. Recently, the Michigan celery industry has been increasingly negatively affected by celery meltdown, a fungal disease caused by *Fusarium oxysporum* f. sp. *apii* (*Foa*). Infected plants exhibited chlorosis, wilting, and vascular discoloration often leading to plant death. *Foa* is categorized into four distinct pathogenic races. *Foa* Race 4 is recognized as the most virulent and has been previously reported in California (2013) and Florida (2022). We report the first detection of *Foa* Race 4 in Michigan. In 2025, meltdown symptoms were observed in west Michigan (Allegan and Ottawa counties) resulting in severe yield losses. Seventy-two *F. oxysporum* isolates were recovered from multiple celery cultivars exhibiting meltdown symptoms. The colony and spore morphology of the recovered isolates were consistent with *F. oxysporum.* Phylogenetic analysis based on two loci (TEF-1a and IGS rDNA) combined with race-specific primer analysis confirmed that 68% of the recovered *F. oxysporum* isolates were *Foa* Race 4. Pathogenicity assays under greenhouse conditions confirmed the virulence of these isolates using the celery cultivars CR1 and Challenger. The emergence of Race 4 in Michigan highlights the need for continued surveillance, screening of new celery lines and the development of integrated disease management strategies to mitigate its impact on the Michigan celery industry.

Oral Presentations

REGIONAL AND FIELD-SCALE POPULATION STRUCTURE AND MATING STRATEGIES OF ALTERNARIA BRASSICICOLA IN COLE CROPS (BRASSICA SPP.)

Dr. Roy Ladell Davis, University of Connecticut, Storrs, CT and Dr. Sydney E. Everhart, Michigan State University, East Lansing, MI

In the last decade, regional production of broccoli (*Brassica oleracea* var. *italica*) has increased throughout the Easten United States. As a result, diseases associated with broccoli have become more prominent. *Alternaria brassicicola*, the causal agent of Alternaria leaf blight and head rot, is a fungal pathogen of broccoli. Symptoms present as brown-to-black, necrotic lesions on the foliage and heads. During a disease survey in 2022, leaf lesions were collected from nine broccoli leaves in Connecticut, Massachusetts, Virginia, Georgia, and Minnesota, and one cabbage and one brussels sprout field in Minnesota. Five novel microsatellite primers were designed to describe the population structure of 250 *A. brassicicola* isolates within fields and between regions. Mating types, MAT1-1 and MAT1-2, were determined for each isolate. From the 250 isolates genotyped in this study, 158 multilocus genotypes were identified. The mating types were balanced in only 2 of the 11 fields. Discriminant analysis of principle components showed that populations were structured with in the MAT1-2 idiomorph; no such pattern was found in the isolates of the MAT1-1 mating type. Moreover, an analysis of linkage disequilibrium supported the potential of random mating in primarily MAT1-2 populations. This result is consistent with prior studies, which may be a result of either a parasexual cycle or mitotic recombination within the MAT1-2 populations.

SPRAY-INDUCED GENE SILENCING SUPPRESSES GENE EXPRESSION AND GROWTH OF THE FRUIT-ROT PATHOGEN COLLETOTRICHUM FIORINIAE

Shay Szymanski, Michigan State University, Lansing, MI and Dr. Timothy D. Miles, Michigan State University, East Lansing, MI

The fungal pathogen *Colletotrichum fioriniae* causes disease in plant species such as hops, blueberries, and apples. Management of the pathogen is highly reliant on conventional synthetic fungicides, with cultivars having uncharacterized or incomplete resistance. This is increasingly problematic with fungicide-resistant populations of *C. fioriniae* being identified. Spray-induced gene silencing (SIGS) is a developing method of disease control that has recently been investigated in various pathosystems, though it has been reported ineffective in some *Colletotrichum* species. This study investigated the potential of SIGS as a means of inhibiting the growth of *C. fioriniae*. The capacity of *C. fioriniae* to uptake exogenous double-stranded RNA (dsRNA) in-vitro was demonstrated visually by co-incubation with fluorescent dsRNA. Incubation of a green-fluorescent protein (eGFP) expressing transformant of *C. fioriniae* in potato-dextrose broth with 0.5 and 1 ng/ μL of an anti-eGFP dsRNA resulted in reduced expression of eGFP as evaluated by qPCR with the ΔΔCt method. Treating cultures of *C. fioriniae* on potato-dextrose agar (PDA) with 0, 50, and 150 ng/ μL of an anti-translation-elongation-factor-1 (tef1) dsRNA resulted in a dose-dependent reduction in colony diameter. Our results lay the groundwork for future studies to evaluate the potential of SIGS as a biopesticide tool for controlling fruit-rots caused by *C. fioriniae*.

GENOMIC STRUCTURAL VARIANTS OF SCLEROTINIA SCLEROTIORUM LIB DE BARY ISOLATES CONTRASTING FOR DISEASE AGGRESSIVENESS

Dr. Ram Neupane1, Marysia Zaleski-Cox2, Tanya Rose Copley3, Dr. Martin Chilvers2, Mark Derbyshire4, Toby Newman4 and Valerio Hoyos-Villegas2, (1)Michigan State University, East Lansing, MI, (2)Michigan State University, MI, (3)2Centre de recherche sur les grains (CEROM) Inc., Quebec, CANADA, (4)Curtin University, Perth, AUSTRALIA

White mold, caused by *Sclerotinia sclerotiorum* Lib. de Bary (*S. sclerotiorum*) is a devastating pathogen in many staple crops. Understanding this pathogen's genomic variation is crucial for developing effective disease management strategies. This study aimed to generate high-quality genome assemblies, identify and characterize genomic structural variants (SV), and compare their distribution across seven *S. sclerotiorum* disease aggressivity contrasting isolates using Oxford Nanopore long-read sequencing. A total of 2,830 unique SVs were identified across the seven isolates. The majority of these SVs were classified as modifier and low impact SVs (84.2%). However, 446 SVs (15.8%) were high-impact variants affecting 367 genes. The high-impact SVs were predominantly deletions and insertions. Jaccard similarity analysis based on presence/absence of high-impact SVs clustered the seven isolates into three major clusters. The first cluster included isolates with higher disease aggressiveness compared to the second and third clusters. Gene Ontology (GO) enrichment analysis indicated that genes affected by SVs are enriched for transposable element (TE) – related functions. Characterization of structural variants is crucial for understanding the evolutionary processes and adaptation of *S. sclerotiorum*. The SVs reported in this study provide a valuable resource for future studies to understand the role of SVs in virulence of the economically devastating pathogen *S. sclerotiorum*.

TEMPORAL EVOLUTION OF FRAC 11 FUNGICIDE RESISTANCE IN COLLETOTRICHUM FIORINIAE POPULATIONS FROM MICHIGAN HIGHBUSH BLUEBERRY (1999–2024). *

Mr. Adam Jarek Adaskaveg1, Kerri Neugebauer2, Dr. Alejandro Rojas2, Jerri M. Gillett2 and Dr. Timothy D. Miles2, (1)Michigan State Univ, East Lansing, MI, (2)Michigan State University, East Lansing, MI

Fungicide resistance to quinone outside inhibitor (QoI) fungicides poses a significant threat to disease management in Michigan highbush blueberry production. In this study, temporal shifts in resistance to QoI (FRAC 11) fungicides were evaluated using a historical collection of *Colletotrichum fioriniae* isolates from Michigan. Isolates (n = 203) from five sampling years (1999, 2004, 2013, 2019, and 2024) were exposed to phenotypic assays (spiral plate and discriminatory dose methods) using technical-grade azoxystrobin, to quantify sensitivity to FRAC 11 fungicides. Concurrently, molecular analyses were performed by sequencing the cytochrome b (cytB) and β-tubulin (tub2) genes. The cytB locus was used to confirm target-site substitutions associated with QoI resistance (F129L and G143A), while the tub2 locus serve to verify species identity and clade association of *Colletotrichum fioriniae*. The 1999 isolates pre-date the registration and use of QoI fungicides on blueberry in Michigan, which serve as a baseline for assessing the impact of fungicide exposure on pathogen evolution. This work emphasizes the value of long-term monitoring in resistance management and the need to sustain fungicide efficacy. Our results show an increase in the prevalence of both moderate and highly resistant phenotypes (F129L and G143A, respectively) over time, corresponding with increased use of FRAC 11 fungicides in Michigan blueberry production.

Oral Presentations

POPULATION STRUCTURE, GENE PREDICTION, AND SECONDARY METABOLITE DIVERSITY OF THE POTATO BLACK DOT PATHOGEN, COLLETOTRICHUM COCCODES*

Ms. Riley Eisenbraun1, Cheryl Andam2, Michael J. Boehm1 and Dr. Teddy Garcia-Aroca1, (1)Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE, (2)Department of Biological Sciences, University at Albany, Albany, NY

Colletotrichum coccodes, the causal pathogen of potato black dot, has been morphologically and genetically delineated into eight vegetative compatibility groups (VCGs). However, the within-species population structure and secondary metabolite potential remain poorly resolved. Here, we analyzed 61 *C. coccodes* isolates collected from diseased potato across the North Central U.S. and reconstructed their phylogenetic relationships using multilocus sequencing (act, btub, gapdh, & his3). Maximum likelihood analyses with bootstrap support confirmed isolates as *C. coccodes*. Genome-scale analyses of a subset of isolates generated using long-read nanopore sequencing, enabled prediction of biosynthetic gene clusters (BGCs) using antiSMASH. Comparative genomic analyses resolved four distinct populations, consistent with divergent VCGs, with no detectable association between genetic diversity and geographic origin. Most frequent predicted BGCs encoded pathways associated with destruxin A, cercosporin, and squalestatin S1, suggesting potential roles in host infection and competition. This study represents the first regional assessment of *C. coccodes* population diversity in the North Central U.S. and demonstrates that genetically distinct populations are broadly distributed across potato production systems. Further research will focus on the evolutionary processes underlying population differentiation and the ecological role of secondary metabolites produced by *C. coccodes*.

OPTIMIZING FUNGICIDE APPLICATIONS FOR TAR SPOT AND SOUTHERN RUST IN MISSOURI CORN PRODUCTION *

Hailey Emanuel1, Alexandria Haafke2, Nick Wesslak3, Anthony Ohmes4 and Dr. Mandy Bish1, (1)University of Missouri, Columbia, MO, (2) University of Missouri, MO, (3)University of Missouri Employee, MO, (4)Univ of Missouri Ext Serv, Charleston, MO

Early confirmations of tar spot (*Phyllachora maydis*) in June (2022-2025) and the expanding footprint of southern rust (*Puccinia polysora*) have heightened concerns regarding fungicide timing and yield protection in Missouri corn. This research evaluates the benefits of fungicide application timing through small-plot and on-farm trials. Small-plot trials were conducted in 2025 at Columbia, Novelty, and Albany, Missouri and included two fungicides: mefentrifluconazole + pyraclostrobin (Veltyma) or benzovindiflupyr + azoxystrobin + propiconazole (Trivapro). Six application timings were evaluated: V4/V5, a two-pass V4/V5 followed by VT/R1, VT/R1, a two-pass VT/R1 followed by R3 (21 Days Post), R3, and a non-treated control. On-farm trials were conducted in 2024 and 2025 across 13 counties in Missouri to compare a standard VT/R1 application to a 2-pass system using a drone-applied second pass. In low disease environments (<5% disease severity on the ear leaf at R5), disease severity differed in on-farm trials (p=0.007), but yields did not across any trial type. In high disease environments (>5% severity), differences in disease severity occurred among treatments in on-farm trials (p<0.001) and preliminary small-plot analysis indicated differences in yield (p<0.001). Small plot research will be repeated in 2026. This research will provide Missouri farmers with information to optimize return on investment while managing two diseases that prefer distinct weather conditions.

BEYOND SYMPTOMS: DISCRETE DECISION WINDOWS GOVERN SDHI SEED TREATMENT EFFICACY IN SOYBEAN SUDDEN DEATH SYNDROME *

Ryan Hamilton1, Max Ernat2, Dr. Nabin K. Dangal3, Dr. Eric A. Adee4, Dr. Alyssa K. Betts5, Dr. Mandy Bish6, Dr. Kaitlyn Bissonnette7, Dr. Carl A. Bradley8, Dr. Emmanuel Byamukama9, Adam Byrne10, Dr. Travis Faske11, Dr. Tamra A. Jackson-Ziems12, Dr. Yuba R. Kandel13, Dr. Nathan M. Kleczewski14, Dr. Samuel G. Markell15, Dr. Febina Mathew15, Brian Mueller16, Dr. Daren S. Mueller2, Dr. Rodrigo Borba Onofre17, Jessica Scherer15, Damon L. Smith16, Dr. Darcy E. P. Telenko18, Dr. Albert U. Tenuta19, Cheryl Van Herk20, Dr. Dechun Wang1, Stith N. Wiggs3 and Dr. Martin Chilvers1, (1)Michigan State University, East Lansing, MI, (2)Iowa State University, IA, (3)Iowa State University, Ames, IA, (4)Kansas River Valley Exp Field, Topeka, KS, (5)University of Delaware, Newark, DE, (6)University of Missouri, Columbia, MO, (7)Cotton Incorporated, Cary, NC, (8)University of Kentucky, Princeton, KY, (9)USDA-NIFA, Brookings, SD, (10)FMC Corporation, Philadelphia, PA, (11)University of Arkansas, AR, (12)University of Nebraska, Lincoln, NE, (13)5Metis Inc., Durham, NC, (14)Syngenta, Kernersville, NC, (15)North Dakota State University, Fargo, ND, (16)Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, (17)Kansas State University, Manhattan, KS, (18)Purdue University, West Lafayette, IN, (19)Ontario Ministry of Agric & Food, Ridgetown, ON, CANADA, (20)Ontario Ministry of Agriculture, Food & Rural Affairs, CANADA

Soybean sudden death syndrome (SDS), caused by *Fusarium virguliforme*, is a major yield-limiting disease often associated with soybean cyst nematode (SCN). Relationships among *F. virguliforme* and SCN abundance, disease expression, and yield loss remain unclear, in part due to reliance on foliar symptoms. This study evaluated interactions across 102 site-years in 12 U.S. states and Ontario, Canada (2020–2024). Linear modeling showed root disease was strongly associated with pathogen soil DNA and soil pH, whereas foliar disease was associated with soil pH, SCN density, and host resistance. In yield models, foliar disease was the strongest predictor of yield loss, followed by root disease, while pathogen abundance was not significant when disease indices were included. Spearman correlations showed pathogen abundance had the strongest association with yield (ρ = -0.35; $P < 0.0001$), indicating indirect impacts mediated through disease. Multivariate response surface analyses revealed coordinated, nonlinear relationships among pathogen abundance, SCN density, and yield. Targeted seed treatments reduced foliar disease but produced meaningful yield responses only within a discrete risk window defined by moderate pathogen abundance and low SCN density. These results show that SDS outcomes and treatment efficacy are governed by system-level interactions and support integrating molecular diagnostics with predictive modeling for risk stratification and precision management.

Oral Presentations

ASSESSMENT OF FUNGICIDE USE FOR MANAGING DEOXYNIVALENOL AND EAR ROT ON SILAGE CORN IN WISCONSIN USING A META-ANALYTIC APPROACH *

Lucia Ann Hyzer1, Maria Oros2, Rafael Ferreira2, Brian Mueller1 and Damon L. Smith1, (1)Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, (2)Data Science Institute, University of Wisconsin - Madison, Madison, WI

Global livestock production relies heavily on whole plant corn silage, with management practices such as fungicide application deployed to prevent disease and mitigate mycotoxin contamination. Meta-analyses were conducted on a 10-year dataset of 16 trials from Wisconsin to evaluate fungicide program effects on deoxynivalenol (DON) concentration, ear rot severity, and their correlation. A hierarchical random effects model of the standardized mean differences was used to determine if there was an overall effect on DON or ear rot from fungicide application. We found a moderate but highly significant reduction in DON after fungicide use with some between-trial variance (g = -0.35, 95% CI [-0.56, -0.14], p = 0.001, **σ** 2trial = 0.13, k = 179). Amending the model with fungicide product as a moderator revealed Proline (g = -0.49, 95% CI [-0.85, -0.13], p = 0.007, k = 21) and Miravis Neo (g = -0.35, 95% CI [-0.61, -0.09], p = 0.008, k = 51) as the only products to significantly reduce DON. The same model was used to assess overall effect of fungicide use on ear rot severity. No overall (g = -0.023, 95% CI [-0.19, 0.14], p = 0.78, **σ**2trial = 0.051, k = 156) or individual fungicide effect was detected. A hierarchical random effects model of Fisher's z-transformed correlations revealed a significant but weak positive relationship between DON and ear rot (r = 0.19, 95% CI [0.032, 0.34], p = 0.019, **σ**2trial = 0.022, k = 180).

DEVELOPING AND EVALUATING MOLECULAR DIAGNOSTIC TOOLS, REAL RIME QPCR AND RECOMBINASE POLYMERASE AMPLIFICATION ASSAY FOR DETECTING HETERODERA GLYCINES*

Nabina Karki1, Mrs. Connie Tande2 and Dr. Madalyn Shires2, (1)South Dakota State Univ, Brookings, SD, (2)South Dakota State University, Brookings, SD

Soybean cyst nematode (*Heterodera glycines* Ichinohe; SCN) is one of the major yield limiting pathogens of soybean in South Dakota. The nematode often goes undiagnosed in the absence of visual symptoms making precise and rapid diagnosis a crucial step for its management. The study focused on designing and validating molecular diagnostic tools, Quantitative Polymerase Chain Reaction (qPCR) and Recombinase Polymerase Amplification (RPA) for assessing SCN populations in the field. Specific primers and probes were designed targeting the putative parasitism gene, CLAVATA/ embryo surrounding region-related (CLE) gene and evaluated for the specificity and sensitivity. The optimized qPCR assay provided a validated framework of the target region, which was further adapted to develop RPA assay under isothermal conditions. The RPA assay was carried out at 39°C for 20 minutes using Agdia AmplifyRP XRT kit, showing reliable detection of SCN from genomic DNA of a single cyst. The assay was specific to SCN showing no amplification for non-target nematode species with sensitivity of 1/10 dilution of the individual nematode gDNA. To validate the practical application of the assay, it was evaluated using soil samples artificially infested with SCN cysts. The assay amplified only soil DNA extracts of *H. glycines* infested soil samples. The developed RPA assay is effective for quick and sensitive detection of the nematode at the diagnostic site to improve SCN management strategies.

EVALUATION OF COMMERCIAL BIOCONTROL PRODUCTS PERFORMANCE FOR MANAGING SOILBORNE PATHOGENS IN NORTH DAKOTA SOYBEAN FIELDS *

Madeeha Matloob1,2, Dr. Gabriel Dusek1,3, Dr. Febina Mathew1, Dr. Hope Renfroe-Becton1 and Dr. Richard Webster1, (1)North Dakota State University, Fargo, ND, (2)North Dakota State Univ, Fargo, ND, (3)North Dakota State University, ND

Diseases caused by soilborne pathogens significantly threaten soybean production, requiring effective management strategies. This study evaluated nine commercial biocontrol products across three North Dakota locations in 2024 and 2025. Using a RCBD with four replication of 20' x 10' plots, we evaluated Avodigen (*Bacillus licheniformis* FMCH001), F4034-5 (*Bacillus subtilis* RTI477), RootShield Plus (*Trichoderma harzianum* Rifai T-22), RootShield Plus seed treatment (*Trichoderma virens* G-41), Howler (*Pseudomonas chlororaphis* AFS009), Heads Up (*Chenopodium quinoa* saponins), Rhizotrop (*Bacillus* spp.), and RootShield (*Trichoderma harzianum* (KRL-AG2) non-treated control and fungicide CruiserMaxx APX (Mefenoxam, fludioxonil, sedexane) as a positive control. Stand count (plants/ac), root rot severity (%), and yield (bu/ac) were recorded and data showed potential effects on measured traits, though not significant (P>0.05). In 2024, Avodigen yielded 44.7 bu/ac compared to the controls CruiserMaxx APX (44.3 bu/ac) and non-treated (39.8 bu/ac). CruiserMaxx APX showed highest stand count,91563 plants/ac) and lowest root rot severity, 22.35%, followed by RootShield Plus and Heads Up. In 2025, Rhizotrop and RootShield yielded (53.6 bu/ac). Heads Up showed highest stand count, 95484 plants/ac, while CruiserMaxx APX showed lowest root rot severity. These findings provide valuable insight into the potential for effective disease management in soybean.

DEVELOPMENT AND VALIDATION OF A PCR ASSAY FOR XYLARIA NECROPHORA FROM SOYBEAN *

Qiurong Fan1, Richard Rush2, Laura Miles1, Ms. Rebecca Harkness1, Dr. Timothy D. Miles1, Vinson Doyle2, Dr. Terry N. Spurlock3 and Dr. Alejandro Rojas1, (1)Michigan State University, East Lansing, MI, (2)Department of Plant Pathology & Crop Physiology, Louisiana State University, Baton Rouge, LA, (3)University of Arkansas System Division of Agriculture, Lonoke, AR

Soybean taproot decline (TRD), caused by *Xylaria necrophora*, is a soilborne disease reported in the southern United States that can cause seedling death, foliar chlorosis, and extensive root necrosis. Since the first report in 2017 and the formal description of its causal pathogen in 2021, TRD has drawn increasing attention as a threat to soybean production. In this study, we developed and validated a TaqMan-based qPCR assay targeting the nuclear rDNA internal transcribed spacer (ITS) region of *X. necrophora*. The assay had a limit of detection of 10 fg/ **µ**l of genomic DNA in singleplex format. Sensitivity was maintained in multiplex format with sample-specific internal controls: a soybean target served as internal control for plant samples, whereas an exogenous internal control was used for soil samples. The assay was specific to *X. necrophora* and showed no amplification from other soybean-associated pathogens evaluated. Validation showed consistent assay performance and detection limit across laboratories. To evaluate field applicability, we collected grid-based soybean root and soil samples from a naturally infested field and used inverse distance weighting interpolation to visualize spatial patterns of *X. necrophora* DNA. The assay detected localized hotspots and low-signal zones, supporting its use for quantifying and mapping pathogen DNA in field settings. Early field detection using this assay may improve TRD monitoring and support management decisions.

Oral Presentations

PREVALENCE AND GENETIC DIVERSITY OF WHEAT STREAK MOSAIC VIRUS-COMPLEX AND VIRAL LIKE DISEASES IN SOUTH DAKOTA WHEAT FIELDS *

Anna Lagerhausen1, Mrs. Connie Tande2, Clarence Winter3, Cody Molnar2 and Dr. Madalyn Shires2, (1)South Dakota State Univ, Brookings, SD, (2)South Dakota State University, Brookings, SD, (3)South Dakota State University, Rapid City, SD

South Dakota (SD) farms have had increases in viral diseases, such as Wheat streak mosaic virus-complex, which threatens winter and spring wheat. This complex is transmitted by the wheat curl mite. Prevalence and severity of viral wheat diseases are unknown in SD, as symptomology is similar, and genetic confirmation is lacking. Additionally, interest in aster yellows phytoplasma (AYP) in wheat has developed. AYP mimics viral activity and is a yearly, recurrent issue. To target these viral knowledge gaps, RT-PCR for multiple genes was applied to confirm WSMV-complex incidence and distribution across SD counties. To analyze AYP presence, qPCR for a 16S gene was utilized. 165 wheat and 45 alternate host samples were selected from 21 major wheat growing counties. All counties reported at least 1 positive sample (89.7% positivity rate) for Wheat streak mosaic virus (WSMV), with 5 counties harboring other viral diseases in the complex. Therefore, symptoms suspected to be WSMV were correct. There was a 46.7% positivity rate of WSMV in alternative hosts as well. AYP activity was found in 4 counties. Large amounts of genetic diversity within the WSMV coat protein isolates were identified, and their significance is being explored. Overall, WSMV was the most prevalent virus in SD wheat in 2025, and alternate hosts harbor the disease when wheat isn't present. This stresses the need for management of the green bridge, both at planting and between winter and spring wheat fields.

SOFT WINTER WHEAT VIRUS SURVEY AND SCREENING OF GERMPLASM *

Keeley Satterfield, Janette L. Jacobs, Christina D. Difonzo, Eric Olson and Dr. Martin Chilvers, Michigan State University, East Lansing, MI

Michigan produces high quality soft winter wheat (sww) for the milling industry. Recently, concerns have grown about the incidence of viruses present in Michigan wheat fields. To address these concerns two studies were conducted: a two-year field survey to identify prevalent viruses in Michigan wheat fields and a growth chamber screening to determine sww resistance to the most prevalent virus detected in the survey. During 2024 and 2025, 1040 samples were collected from 260 fields. Samples were tested by enzyme-linked immunosorbent assays for barley yellow dwarf virus-PAV, barley yellow dwarf virus-MAV, cereal yellow dwarf virus-RPV, brome mosaic virus, soil-borne wheat mosaic virus, wheat spindle streak mosaic virus, High Plains wheat mosaic virus, and wheat streak mosaic virus (WSMV). WSMV was detected in 580 samples, making it the most detected virus during the survey. The variety screening assessed the responses of 281 sww lines to WSMV infection. The sww lines were grown at 17.5°C for a total of 28 days. Fifteen-day old wheat plants were mechanically inoculated, then rated for symptoms at 28 days post inoculation. The 28-day ratings were used to conduct a genome-wide association study (GWAS). The GWAS revealed that QTLs on chromosomes 2D and 7B provide additive resistance to WSMV in sww. These two studies have investigated virus abundance in Michigan wheat fields and determined sww resistance to WSMV aiding virus management in the Michigan sww industry.

ASSESSING THE IMPACT OF SOYBEAN CYST NEMATODE ON DRY BEAN YIELD AND GROWTH UNDER FIELD CONDITIONS *

Dalvir Singh Dhami, Kapil Simkhada, Dr. Samuel G. Markell, Juan Osorno and Dr. Guiping Yan, North Dakota State University, Fargo, ND

Soybean cyst nematode (SCN) is an emerging threat to dry bean production in North Dakota and Minnesota, but its field-level impact remains largely unexplored. A field study was conducted in 2025 at Prosper, ND, in two experimental areas, each arranged as a randomized complete block design with five replications. Eight dry bean cultivars from navy (Blizzard; Medalist), black (Blacktails; Zenith), pinto (Lariat; ND Falcon), and kidney bean (ND Whitetail; Pink Panther) market classes, and two soybean checks were evaluated. Initial (Pi) and final (Pf) SCN egg densities were measured per plot, and reproductive factor (RF = Pf/Pi) was calculated. Genotype responses varied under contrasting Pi (lower = 2,880-9,800; higher = 20,720-29,720 eggs/100 cm^3). Under higher Pi, Blizzard (RF =1.6) showed larger reductions in seed yield (59%) and plant height (34%), while ND Whitetail (1.8) showed the greatest height reduction (50%). In contrast, Lariat (1.7) showed the least reduction in plant height (3%) and yield (11%), suggesting potential tolerance. ND Falcon (0.7) with known tolerance to SCN HG type 0, showed low SCN reproduction with relatively lower reductions in yield (16%) and plant height (18%). These preliminary results show reduced growth and yield under high SCN pressure, and to our knowledge, this is the first study showing the negative SCN impacts on dry bean under naturally infested field conditions, providing insights for resistance breeding and SCN management.

EXPLORING MOBILE GENETIC ELEMENTS AND VIRULENCE IN THE PRUNUS PATHOGEN PSEUDOMONAS SYRINGAE PV. MORSPRUNORUM R1 *

Sophia Liberto, Dr. George W. Sundin and Dr. Michelle Hulin, Michigan State University, East Lansing, MI

The *Pseudomonas syringae* species complex is made up of a wide range of plant pathogens. Pathogenic variants (pvs.) within the species complex can cause bacterial canker disease (BCD) on economically important *Prunus* spp., such as cherry and plum trees. A primary causal agent of BCD is *P. syringae* pv. *morsprunorum* Race 1 (PsmR1). PsmR1 uses type III effectors (T3Es) as virulence factors to infect Prunus spp. and promote disease. Although PsmR1 isolates share conserved genomic regions, some show distinct virulence on Prunus spp. Differences among these isolates are found in their repertoire of mobile genetic elements (MGE), such as insertion sequence elements (ISE). MGEs play a key role in bacterial evolution. In host-specific PsmR1 from the UK, variation is seen in ISE and T3E abundance. Our goal is to establish a larger population of PsmR1 from Michigan and further assess these ISE and T3E dynamics. To do this, PsmR1 populations were isolated from *Prunus* spp. in Michigan, and whole genome sequencing was performed. Virulence of novel isolates was determined with a detached leaf virulence assay on *Prunus* spp. Bioinformatics was used for ISE analysis. With this, further investigation into ISE/T3E associations and their role in PsmR1 virulence will be possible. Exploration into the genomic dynamics of PsmR1 in Michigan populations can aid in the development of improved disease treatment and prevention measures.

Oral Presentations

THEORETICAL FRAMEWORK AND FUNCTIONAL CHARACTERIZATION OF SMALL RNA REGULATORY NETWORKS IN ERWINIA AMYLOVORA *

Elise Willa Straub and Dr. George W. Sundin, Michigan State University, East Lansing, MI

Erwinia amylovora, the causal agent of fire blight on Rosaceous hosts, uses a wide array of virulence factors throughout its disease cycle to cause devastating symptoms. The molecular regulation of virulence genes deployed by this pathogen is complex but current methods in computational prediction and functional confirmation allow for elucidation of expression networks. The small RNA ArcZ is a central player in post-transcriptional regulation within *E. amylovora* and has been implicated in motility, the type 3 secretion system, and biofilm formation. We predicted an interaction of ArcZ with the 5'UTR of hofC, a putative type IV pilus gene previously shown to be active during the irreversible attachment stage of biofilm formation. This interaction, and the hofC gene, were characterized further and were shown to have distinct effects on biofilm formation by *E. amylovora*. This study, supported by previous work, aids in the development for a theoretical framework that integrates computational prediction for small molecule regulation of genetic elements, functional characterization for RNA-RNA interactions, and experimental results into a functional pipeline for future work.

Lightning Presentations

SPECIES ASSOCIATED WITH FUSARIUM HEAD BLIGHT IN UNITED STATES GRAIN GROWING REGIONS IN 2021-2025*

Gloria A. Baker1, Dr. Martin Chilvers2, Dr. Sunkyu Choi3, Dr. Alyssa K. Betts4, Dr. Jessica Cooper4, Dr. Rawnaq Chowdhury5, Dr. Briana Whitaker6, Dr. Darcy E. P. Telenko7, Dr. Ruth Dill-Macky8, Dr. Andrew J. Friskop9, Stephen N. Wegulo10, Dr. Madalyn Shires11, Dr. Nidhi Rawat12, Dr. Maira R. Duffeck13, Dr. Alyssa A. Collins14, Prof. Gary C. Bergstrom15, Dr. Mandy Bish16 and Dr. Guy Boyd Padgett17, (1)Michigan State University, Lansing, MI, (2)Michigan State University, East Lansing, MI, (3)Michigan State Univ, East Lansing, MI, (4)University of Delaware, Newark, DE, (5)USDA-ARS, Pocatello, ID, (6)USDA-ARS, Peoria, IL, (7)Purdue University, West Lafayette, IN, (8)University of Minnesota, St Paul, MN, (9)North Dakota State University, Fargo, ND, (10)Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE, (11) South Dakota State University, Brookings, SD, (12)University of Maryland College Park, College Park, MD, (13)Oklahoma State Univ, Stillwater, OK, (14)Penn State University, Manheim, PA, (15)Cornell University, Ithaca, NY, (16)University of Missouri, Columbia, MO, (17)LSU AgCenter Dean Lee Research Station, Alexandria, LA

Fusarium head blight (FHB) is a major threat to agriculture, causing approximately $550 million in losses between 2020-2025. This fungal disease results in shrunken kernels, reduced yield, and mycotoxin contamination of the grain. FHB is a disease complex caused by at least 15 species of *Fusarium* and two species of *Microdochium*. The primary causal agent of FHB in the United States is *F. graminearum*; however, FHB species composition varies between hosts and regions. To investigate the species associated with FHB in the US, 644 single spore cultures were collected from symptomatic cereal hosts from 17 states between 2021-2025. The species of each isolate was identified by sequencing two barcoding loci for Fusarium, translation elongation factor 1-α (TEF1α) and RNA polymerase II (RPB2). Phylogenetic analysis of these loci was employed to identify the species of each isolate in the collection. Overall, this collection contained 18 species, including 10 potential first report species, eight of which may be the first report of the species causing FHB globally. This research updates our understanding of the species associated with FHB in the US. We plan to complete Koch's postulate and mycotoxin profiling of potential new species associated with FHB. We will also assess the sensitivity of each isolate to quinone outside inhibitor (QOI), demethylation inhibitor (DMI), and succinate dehydrogenase inhibitor (SDHI) fungicides.

DIVERSITY OF SOILBORNE FUSARIUM ASSOCIATED WITH BEAN ROOT ROT IN MICHIGAN*

Irene Blanco-Casallas1, Scott Bales2, Evan Wright2, Dr. Martin Chilvers1 and Dr. Alejandro Rojas1, (1)Michigan State University, East Lansing, MI, (2)Michigan State University, MI

Fusarium species are ubiquitous soil fungi, many of which are important soilborne plant pathogens. Among these, the Fusarium solani species complex stands out, particularly clade 2 (FSSC2), which includes causal agents of bean root rot. Despite their importance, the diversity of Fusarium species in agricultural soils is poorly understood. This is due to a lack of implementation of targeted community profiling in complex samples like soil. In addition, species within FSSC2 are cryptic, limiting our understanding of their distribution and diversity. To address this gap, we used a metabarcoding approach to characterize Fusarium communities in dry bean farm soils across Michigan. We targeted TEF1 and RPB2 to evaluate their ability to resolve species diversity within these complex communities. Overall, TEF1 provided greater resolution across Fusarium species complexes. The *Fusarium oxysporum* species complex was the most abundant in all samples, but FSSC2 was also highly detected. Within FSSC2, we recovered species previously reported in Michigan along with a subset of unclassified taxa, indicating uncharacterized diversity. These results show that Fusarium diversity associated with bean root rot may be greater than previously recognized. By improving our knowledge of Fusarium communities in soil, this work provides a foundation for accurate disease monitoring and supports the development of targeted management and early detection strategies in dry bean production.

CAN HUMIC ACID AND CHITOSAN ADDITIVES CONTROL CORN DISEASES AS EFFECTIVELY AS STANDARD FUNGICIDES IN CENTRAL INDIANA?

Mariela Fernández-Campos, Sujoung Shim, Jordan Schwab and Dr. Darcy E. P. Telenko, Purdue University, West Lafayette, IN

Effective management of corn diseases is crucial to protect yield as agriculture moves towards more resilient production systems. Alternative products that can be integrated into disease management systems need to be evaluated. In Indiana, tar spot, gray leaf spot, northern corn leaf blight, Curvularia leaf spot, southern rust, and Physoderma brown spot can reduce corn yield. In 2025, a field trial evaluated humic acid (1.17 L/ha) and chitosan (1.17 L/ha), a generic fungicide (azoxystrobin + propiconazole; 769 ml/ha), were compared to a nontreated control. These were applied at five/sixth-leaf collar (V5/V6) and tassel/silk (VT/R1) growth stages. Disease severity, incidence, lodging, and yield were assessed and analyzed using mixed model ANOVA and Fisher's LSD. In the trial disease pressure was low and no significant differences were observed among treatments for tar spot, gray leaf spot, Curvularia leaf spot, or southern rust and yield. All treatments significantly reduced northern corn leaf blight and Physoderma brown spot and decreased lodging. The findings support the potential of humic acid and chitosan as possible components of integrated disease management programs.

BIOSYNTHETIC GENE CLUSTERS SUGGEST CONTRASTING ECOLOGICAL STRATEGIES AMONG CLONOSTACHYS ROSEA AND FUSARIUM VIRGULIFORME*

Kristen Kater1, Michael J. Boehm2, Troy Anderson3, Dr. Dylan Mangel4, Dr. Richard Webster5, Dr. Teddy Garcia-Aroca2 and Dr. Febina Mathew5, (1)University of Nebraska, Lincoln, NE, (2)Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE, (3)University of Nebraska - Lincoln, NE, Lincoln, NE, (4)University of Nebraska-Lincoln, Lincoln, NE, (5)North Dakota State University, Fargo, ND

Clonostachys rosea, an endophytic ascomycete used in biological control, and *Fusarium virguliforme,* a well-characterized soybean pathogen, often co-occur in agroecosystems with different ecological strategies for infection and interspecific competition. Because secondary metabolites mediate fungal competition, plant-microbe interactions, and disease outcomes, comparative analysis of biosynthetic gene clusters (BCGs) provide deeper insights into the ecological strategies distinguishing these species. Here, we assessed the biosynthetic potential of fifteen *C. rosea* and nine *F. virguliforme* genomes through genome mining of publicly available assemblies. Gene prediction for BGCs, followed by similarity-based secondary metabolite profiling, was performed on AntiSMASH to characterize BGC diversity, frequency, and composition across both species. The genomes of both taxa were dominated by Type I polyketide synthase (T1PKS) and non ribosomal peptide synthetase (NRPS) BCGs. *C. rosea* genomes are more likely to produce squalestatin S1, neurosporin A, and clavaric acid, all of which aid in competition against other fungi. Whereas *F. virguliforme* produces phyllosticitine A, fusarin, and oxyjavanicin more frequently, which aid in pathogenicity (phytotoxic effects on the plant). Further research will address how these metabolites influence the ecological fitness of these fungi.

COMPARISON OF SOIL INFESTATION METHODS FOR PHYTOPHTHORA SOJAE*

Keely McQuain, Mr. Timothy I. Ralston, Molly McGuire, Dr. Mesfin Bogale and Dr. Horacio D. Lopez-Nicora, The Ohio State University, Columbus, OH

Phytophthora sojae is a soilborne oomycete pathogen that causes significant yield losses in soybean. Management relies on Rps (Resistance to *Phytophthora sojae*) genes, however repeated deployment can drive pathogen adaptation and reduce effectiveness, highlighting the need to monitor pathogen virulence and new sources of resistance. Greenhouse assays use a mycelial slurry inoculation, which is not practical for field-scale infestation. The objective of this study was to compare different substrates and inoculum rates suitable for field-scale infestation. A 3x4 factorial randomized complete block design was conducted with three substrates (millet, rice, sand-cornmeal) and four rates (0, 1, 5, 10 CFU g-1 soil) applied to a susceptible soybean cultivar under greenhouse conditions. Inoculum was prepared with *P. sojae* pathotype Rps1a, 1b, 1c, 1k, 7. Disease development was assessed using emergence and disease severity. Substrate primarily drove disease development. Sand-cornmeal resulted in minimal disease expression, rice produced moderate severity, and millet consistently resulted in the greatest disease severity and reduced emergence across all rates. Increasing inoculum rate beyond the low threshold did not significantly increase disease severity. These results identify millet as a reliable and scalable substrate and support a standardized soil infestation method to establish disease nurseries for monitoring *P. sojae* virulence shifts under repeated Rps deployment.

EVALUATING BIOLOGICAL CONTROL AGENTS FOR REDUCING SURVIVAL AND VIABILITY OF SCLEROTINIA SCLEROTIORUM SCLEROTIA ACROSS SOIL DEPTHS AND TIME*

Amit Sharma1, Brian Mueller2, Dr. Carol L. Groves2, K. Morgan Goodnight3, Dr. Darcy E. P. Telenko3, Dr. Dylan Mangel4, Dr. Daren S. Mueller5, Dr. Horacio D. Lopez-Nicora6, Dr. Martin Chilvers7, Mr. Alex Michael Bray7, Karandeep Chahal7, Dr. Gabriel Dusek8, Dr. Hope Renfroe-Becton9, Dr. Richard Webster8 and Damon L. Smith2, (1)Department of Plant Pathology, Univeristy of Wisconsin-Madison, Madison, WI, (2) Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, (3)Purdue University, West Lafayette, IN, (4)University of Nebraska-Lincoln, Lincoln, NE, (5)Iowa State University, IA, (6)The Ohio State University, Columbus, OH, (7)Michigan State University, East Lansing, MI, (8)North Dakota State University, Fargo, ND, (9)North Dakota State Univ, Fargo, ND

Sclerotinia stem rot (SSR) is a destructive disease of soybean caused by the soilborne fungus *Sclerotinia sclerotiorum*.The pathogen produces sclerotia, compact aggregates of fungal mycelia that serve as long-term survival structures in soil. Although chemical fungicides are commonly used for in-season SSR management, their efficacy is often inconsistent. An alternative approach is to target the sclerotia through the application of biological control agents (BCA). The objective of this study was to evaluate the efficacy of multiple BCA, including *Coniothyrium minitans* (Contans), *Trichoderma harzianum* strain T-22 (RootShield), and *Pseudomonas chlororaphis* strain AFS009 (Howler EVO), in reducing the survival and viability of *S. sclerotiorum* sclerotia left on the soil surface or buried within the soil over time. In 2025, trials were conducted across Indiana, Iowa, Michigan, Nebraska, North Dakota, Ohio, and Wisconsin. Results indicated no significant differences among these BCA in reducing sclerotial survival or viability compared to the non-treated control ($P>0.05$). In contrast, burial depth and sampling time significantly affected both sclerotial survival and viability, and their interaction was also significant ($P<0.05$). At approximately 270 days after application, buried sclerotia exhibited the lowest mean recovery (37.1%) and viability (24%), regardless of the treatment. These studies are ongoing, and the results will be used to refine SSR management strategies.

FIRST REPORT OF RED CROWN ROT CAUSED BY CALONECTRIA ILICICOLA AND ITS EFFECTS ON SOYBEAN YIELD COMPONENTS IN OHIO*

Ligia Patricia Calderon-Delgado1, Alaina Bell2, Mr. Vinicius Garnica1, Dr. Mesfin Bogale1, Mr. Timothy I. Ralston1, Dr. Francesca Rotondo3, Robert Leeds2, Jacci Smith2 and Dr. Horacio D. Lopez-Nicora1, (1)The Ohio State University, Columbus, OH, (2)The Ohio State University, OH, (3)The Ohio State University, Wooster, OH

Red crown rot (RCR), caused by *Calonectria ilicicola*, was confirmed in soybean fields in Ohio during the 2025 growing season. The pathogen was identified based on morphological characteristics, multigene phylogenetic analysis (ITS, Actin, Histone3, Tef1, BT, cmdA), and pathogenicity assays fulfilling Koch's postulates. Field evaluations conducted at two locations between growth stages R6 (full seed) and R7 (beginning maturity) demonstrated that RCR negatively affected multiple yield components. On average, symptomatic plants had 35.3% lower yield, 25.4% fewer total seeds, 25.5% fewer pods per plant, and 22.3% more undeveloped pods compared to adjacent asymptomatic plants. Disease incidence exhibited aggregated spatial patterns consistent with soilborne pathogens. This study documents the first report of RCR in soybean in Ohio and quantifies associated yield and yield component losses. These findings highlight the need for statewide surveys to determine pathogen distribution and for research to develop effective management strategies.

Lightning Presentations

IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF PUCCINIA GRAMINIS F. SP. TRITICI EFFECTORS TARGETING THE RPG5 INTEGRATED KINASE DOMAIN IN BARLEY*

Israel Akinlabi, South Dakota State University - Brookings, SD, Brookings, SD, Gazala Ameen, Agronomy, Horticulture & Plant Sciences, South Dakota State University, Brookings, SD, Dr. Robert Brueggeman, Department of Crop and Soil Sciences, Washington State University, Pullman, WA and Shyam Solanki, South Dakota State University, Brookings, SD

The stem rust pathogen *Puccinia graminis* f. sp. *tritici* (Pgt) threatens global barley production, yet the effectors that target barley nucleotide-binding leucine-rich repeat immune receptors remain poorly understood. We investigated whether Pgt candidate effectors interact with Rpg5, an unusual barley NLR containing an integrated serine/threonine protein kinase domain. We hypothesized that QCCJB race-specific Pgt effectors directly bind the Rpg5 kinase integrated domain to trigger immune recognition. Through effector prediction and motif analysis, we identified two candidate effectors from the QCCJB race: PGTG_12544 and PGTG_13831. EffectorP analysis predicted both effectors to be cytoplasmic effector while motif analysis showed both proteins contained Ser/Thr-rich phosphorylation-associated motifs, including SP/TP patterns, suggesting potential host-signaling interfaces that require experimental validation. We used AlphaFold3 to predict Rpg5 kinase-ID and effector interactions, with PGTG_12544 and PGTG_13831 showing pTM+ipTM scores of 0.59 and 0.62, respectively. We are validating these predictions through recombinant protein expression in *Pichia pastoris* and co-immunoprecipitation assays. This approach provides a framework for identifying pathogen effectors recognized by NLR-integrated domains and may inform strategies to improve durable resistance against barley stem rust.

PATHOGENS IN AN ENDOPHYTE WORLD: THE PRESENCE OF A PHYTOTOXIN BIOSYNTHETIC GENE CLUSTER REFLECTS HOST-ASSOCIATION STRATEGY IN XYLARIA GENERA*

Annabella Lyndon1, Qiurong Fan1 and Dr. Alejandro Rojas1, (1)Michigan State Univ, East Lansing, MI

The plant-fungal symbiotic continuum ranges from mutualism to parasitism, yet the genomic factors driving transitions between these lifestyles remain poorly understood. While *Xylaria* genera are recognized for their prolific biosynthetic capabilities and prevalence as asymptomatic endophytes, the emergence of *X. necrophora* as the causal agent of soybean taproot decline (TRD) highlights a rare shift towards pathogenesis. Cytochalasin metabolites have been implicated in TRD virulence, however, the specific genomic elements enabling this transition within the predominantly non-pathogenic clade are unexplored. To address this, we performed de novo genome assembly using long-read sequencing for multiple TRD-isolated X. *necrophora* and a soybean endophyte *X. multiplex* 22-34, yielding near telomere-to-telomere, chromosome-level assemblies. While total biosynthetic gene cluster, CAZyme, and putative effector counts were similar across assemblies, we identified a putative cytochalasin gene cluster (Xylachalasin) located on Chromosome 1 of the TRD genomes that was absent in *X. multiplex* 22-34. Further investigation revealed Xylachalasin cluster presence throughout the *Xylaria*; notably, the cluster was present in all reported pathogens whilst absent in most endophytes. Based on additional orthogroup and Xylachalasin phylogenetic reconstruction, we hypothesize that Xylachalasin cluster loss and gain has shaped lifestyle associations in *Xylaria* genera.

RALSTONIA PSEUDOSOLANACEARUM USES RPRR TO ORCHESTRATE BACTERIAL FITNESS IN RESPONSE TO HOST-INDUCED STRESS

Bridget O'Banion1, Hanlei Li1, Jose Sanchez-Gallego2, Prof. Caitilyn Allen3 and Dr. Corri Hamilton4, (1)University of Missouri-Columbia, MO, (2) University of Minnesota, MN, (3)University of Wisconsin-Madison, WI, (4)University of Missouri, Columbia, MO

Ralstonia pseudosolanacearum (Rps), a soil-borne plant pathogen that causes bacterial wilt, encodes a conserved sensory protein termed RprR (Ralstonia plant-responsive regulator). Initial results revealed that some in vitro phenotypes, such as biofilm formation, were only triggered in the presence of ex vivo xylem sap, suggesting RprR requires a plant-derived signal(s) for full cellular functionality. Based on preliminary data from our lab and others, we tested the hypothesis that RprR, which contains multiple sensory and signaling domains, shapes Rps biology in response to plant-induced stress. We performed comparative transcriptomics and metabolomics of the model strain Rps GMI1000 (wild-type and ΔrprR) during infection of a susceptible and quantitatively resistant host. This dual host approach uniquely leverages a natural spectrum of host-induced stress to better understand the biological function of Rps RprR. Specifically, the quantitatively resistant tomato line Hawaii 7996 is known to produce more reactive oxygen species (ROS) and antimicrobial compounds in response to infection. We used these systems-level 'omics datasets to develop a suite of targeted experiments that define several physiological roles for Rps RprR. These include modulating tolerance to ROS, susceptibility to host phenolic compounds, and membrane stability. Altogether, our work establishes RprR as one of the many sensors that enable Rps to cause disease in the dynamic host environment.

MAPPING OF BACTERIAL LEAF STREAK (BLS) RESISTANCE IN BARLEY THROUGH INTEGRATIVE GWAS AND HAPLOTYPING*

Mr. Thamaraikannan Sivakumar1, Muhammad Ahmad2, Joseph Tilstra3, Mr. Tapish Pawar4, Avital Beery5, Schewach Bodenheimer5,6, Dr. Shengming Yang7, Shyam Solanki2, Eyal Fridman5 and Gazala Ameen2, (1)SOUTH DAKOTA STATE UNIVERSITY, Brookings, SD, (2)South Dakota State University, Brookings, SD, (3)South Dakota State Univ, Rock Rapids, IA, (4)Departement of Agronomy, Horticulture & Plant Science, Brookings, SD, (5)Plant Sciences Institute, Volcani Agricultural Research Organization (ARO), Bet Dagan, Central District, ISRAEL, (6)Robert H. Smith Institute of Plant Sciences and Genetics in Agriculture, Rehovot, Central District, ISRAEL, (7)Northern Crop Science Laboratory,Edward T. Schafer Agricultural Research Center, Fargo, ND

Bacterial leaf streak (BLS), caused by *Xanthomonas translucens* pv. *translucens*, is an emerging constraint on barley production across the Great Plains and Canadian Prairies, where resistant germplasm is unknown. With no effective chemical or biological control, improving host resistance in elite cultivars is essential. We investigated the genetic basis of BLS resistance using an integrated genome-wide association study (GWAS) and haplotype analysis in a doubled-haploid subset of an interspecific Cytonuclear Multi-Parent Population (CMPP). Genotyping with the Illumina Infinium 50K iSelect SNP array yielded 13,209 high-quality markers after filtering. Phenotyping over 2 years under controlled conditions, using a 1 (resistant) to 9 (susceptible) scale, revealed substantial variation, with 14 resistant lines identified. Multi-model GWAS detected 28 significant marker–trait associations (MTAs), including 13 high-confidence loci. Linkage disequilibrium–based clustering identified two additive QTL hotspots: QHvBLS_1H_GAT (2.18 Mb) on chromosome 1H and QHvBLS_2H_GAT (1.72 Mb) on chromosome 2H. Favorable allele stacking showed cumulative effects, supporting polygenic resistance. Haplotype analysis further differentiated resistant and susceptible groups within each QTL. These findings define the genomic architecture of BLS resistance and provide functional haplotypes for genomics-assisted breeding of durable resistant barley cultivars.

Lightning Presentations

SULFUR AS A TOOL AGAINST SUDDEN DEATH SYNDROME OF SOYBEAN*

Emily Anne Duncan1, Shaun Casteel1 and Dr. Darcy E. P. Telenko2, (1)Purdue University, West Lafayette, IN, (2)Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN

Sudden death syndrome (SDS), caused by *Fusarium virguliforme*, led to an estimated 0.82% soybean yield loss across the United States and Ontario in 2024. This soilborne pathogen infects roots and produces toxins causing foliar chlorosis and necrosis, reduced root growth, pod abortion, and plant death. Although resistant cultivars and seed treatments are used, additional tools are needed. Soybeans have shown strong responses to sulfur, raising the question of whether sulfur fertilization suppresses SDS. Field studies were conducted in West Lafayette and Wanatah, IN, in 2024 and 2025. Trials used a split-plot design with planting date (April, May) and a factorial of inoculation (non-inoculated, inoculated) and sulfur treatments (control, ammonium sulfate, ammonium thiosulfate, calcium sulfate). Sulfur was applied at 22.4 kg S/ha. SDS developed at both sites, though severity was low. April planting generally had the highest SDS incidence, except at West Lafayette in 2025. In 2024 at West Lafayette, sulfur increased yield in inoculated plots; in non-inoculated plots, some treatments reduced yield. In 2025, April plantings with sulfur yielded more than the control and May plantings. No effects were detected at Wanatah in 2024; in 2025, April had the highest yields. Results suggest sulfur may protect yield under early planting.

EVALUATION AND OPTIMIZATION OF CRUDE DNA EXTRACTION METHODS FOR THE MOLECULAR ASSAYS OF CALONECTRIA ILICICOLA*

Krishna Raj Pandey1, Dr. Boris Xavier Camiletti2, Nancy McCoppin3, Dr. Steven J. Clough2,3, Nathan E. Schroeder2 and Hari Karki2,3, (1) Department of Crop Sciences, University of Illinois, Urbana-Champaign, Urbana, IL, (2)Department of Crop Sciences, University of Illinois Urbana-Champaign, Urbana, IL, (3)Soybean/Maize Germplasm, Pathology, and Genetics Research Unit, USDA, ARS, Urbana, IL

Red crown rot (RCR), caused by *Calonectria ilicicola*, has recently emerged in the Midwestern United States and poses a significant threat to soybean production. This disease produces foliar symptoms similar to other soybean diseases, making visual diagnosis difficult. Reliable molecular assays for *C. ilicicola* depend on the availability of a rapid, cost-effective, and efficient DNA extraction method suitable for downstream applications. To address this need, five published crude DNA extraction methods were standardized for use with *C. ilicicola* mycelia and evaluated: Rapid One-Step Extraction (ROSE), Chelex 100, Proteinase K, NaOH, and sonication. DNA quality and performance were assessed using conventional PCR, Sanger sequencing, and high-resolution melting (HRM) curve analysis. Proteinase K, ROSE, and NaOH methods produced DNA suitable for PCR amplification, sequencing, and genotyping assays. However, Proteinase K and ROSE required multiple reagents and additional incubation steps, whereas the NaOH method used a single reagent with no incubation, making it faster and more practical for high-throughput applications. The NaOH-based method was further evaluated using infected soybean tissue from both greenhouse and field samples and produced DNA suitable for downstream molecular assays. This method provides a cost-effective approach for obtaining working-quality DNA for molecular assays of *C. ilicicola*, with potential for large-scale diagnostic applications.

DIVERSITY, PATHOGENICITY AND GEOGRAPHICAL DISTRIBUTION OF ROOT-ASSOCIATED FUSARIUM SPP. IN NEBRASKA SOYBEANS*

Mr. Kelvin Kagondu Muchiri1, Dr. Dylan Mangel1, Mr. Kyle C. Broderick1 and Dr. Teddy Garcia-Aroca1,2, (1)University of Nebraska-Lincoln, Lincoln, NE, (2)Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE

Fusarium spp. contains many economically important soil-borne pathogens of soybean. Despite their known presence, the diversity, distribution and virulence in root-rot associated *Fusarium* spp. remains poorly documented. We characterized the diversity and distribution of *Fusarium* spp. associated with soybean roots across Nebraska and evaluated in vitro pathogenicity. 96 isolates from 23 counties were sequenced for tef1-**α** and rpb2. In phylogenetic analyses, we resolved seven species complexes (SC): *F. incarnatum-equiseti* SC (FIESC), *F. oxysporum* SC (FOSC), *F. graminearum* SC (FGSC), *F. fujikuroi* SC (FFSC), *F. solani* SC (FSSC), *F. tricinctum* SC (FTSC), and *F. nisikadoi* SC (FNSC). The most abundantly found SCs were FIESC and FOSC. Richness was highest within the eastern and mid-southern regions. FIESC was widespread across all regions, whereas FOSC dominated the mid-southern region. Pathogenicity assays with 36 isolates on two soybean cultivars (AG27xF3 and NK28P6xF1) showed significant variation among treatments ($P = 0.00041$) and between cultivars ($P = 1.92 \times 10^{-6}$). Disease severity from isolates in FGSC (*F. graminearum, F. sporotrichioides*), FSSC (*F. vanettenii and F. virguliforme*), FOSC (*F. liriopes*), FNSC (*F. commune*), FIESC (*F. clavum, F. luffae and F. compactum*) and FTSC (*F. meitneriae*) was higher compared to the non-treated control. Overall, soybean root rot in Nebraska is caused by a diverse and spatially distributed *Fusarium* community belonging to multiple SCs.

Poster Presentations

1. THE IMPACT OF APPLYING FOLIAR FUNGICIDES AND THE TIMING OF SEED HARVESTING ON SEED QUALITY AND INFECTION RATES*

Colette Ackley-Hernandez1, Mariana Araujo Alves Gomes de Souza2, William Widdicombe3, Dr. Martin Chilvers2 and Dr. Alejandro Rojas2, (1)Michigan State University, East Lansing, MI, MI, (2)Michigan State University, East Lansing, MI, (3)Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI

Soybeans, a major Midwest crop, are harvested on over 2 million acres in Michigan. Seed quality is crucial for stand establishment and suitability for oil and protein use. Seedborne diseases caused by *Diaporthe* (Diaporthe Seed Decay – DSD) and *Cercospora* (Purple Seed Stain - PSS) species reduce seed quality. Management of seed quality relies on agronomic practices and fungicide use, yet control is often inconsistent, with severe outbreaks persisting. This study evaluated the combined effects of foliar fungicides and harvest timing on visual seed quality and fungal colonization. Field trials in Michigan in 2024 and 2025 were conducted using a randomized split-plot design. Plots were inoculated with *Cercospora* spp. and treated with six fungicides applied at the R3 or R5 growth stages, plus an untreated control. Harvests were conducted at early and late intervals. Symptoms were grouped into three categories: chalky (DSD), purple (PSS), and brown (multiple stressors). Overall, symptomatic seed incidence was low. Late harvest increased PSS by 0.13% in 2024 and brown seed incidence by 0.42% in 2025. Effects of fungicide and harvest timing on colonization varied by year. In 2024, specific R5 applications reduced total and *Diaporthe* colonization compared to certain R3 applications, but low pathogen pressure in 2025 limited treatment differentiation. Overall, seasonal environment influences seedborne pathogen dynamics, and management may modify impacts on seed quality.

2. AGRICULTURAL BIOECONOMY CO-PRODUCTS INFLUENCE EARLY SOYBEAN HEALTH AND SUDDEN DEATH SYNDROME OUTCOMES

Dr. Leonor F. S. Leandro and Brady James Clausen, Iowa State University, Ames, IA

Agricultural bioeconomy co-products, including biochar and anaerobic digestate, are increasingly promoted as soil amendments that recycle carbon and nutrients, reduce reliance on conventional inputs, and improve crop productivity. However, their effects on soilborne pathogens such as *Fusarium virguliforme*, the causal agent of soybean sudden death syndrome (SDS), remain poorly understood. This study evaluated how biochar and digestate influence early soybean growth and SDS development. Biochar responses varied by feedstock: yellow pine biochar was generally the least disease-promoting, with effects ranging from neutral to suppressive, whereas corn stover-based biochars more frequently increased disease severity. Digestate improved plant health without pathogen pressure, but responses under SDS pressure were dose-dependent, with 10 g kg^{-1} often improving plant health and 30 g kg^{-1} increasing disease severity. Overall, circular bioeconomy co-products can meaningfully alter soybean health and SDS outcomes; however, their disease-suppressive potential is variable and depends on amendment properties, application rate, soil environment, and pathogen pressure.

3. FUNGICIDE SENSITIVITY MONITORING OF PHYTOPHTHORA CAPSICI POPULATIONS IN MICHIGAN*

Dr. Muhammad USMAN Ali1, John Rocliffe Spafford1 and Dr. Mary K. Hausbeck2, (1)Michigan State University, East Lansing, MI, (2)Michigan State University, Department of Plant, Soil and Microbial Sciences, East Lansing, MI

Phytophthora capsici is a destructive oomycete pathogen that causes severe economic losses for Michigan's vegetable producers. Fungicides are an important management tool, but repeated use of site-specific fungicides increases the risk of pathogen resistance developing. Monitoring shifts in fungicide sensitivity is essential for effective management strategies. In our study, the sensitivity of 305 *P. capsici* isolates collected from diseased cucurbit hosts in 17 commercial fields across southwest, central and eastern Michigan from 2022 to 2025 were evaluated for sensitivity to the fungicides mefenoxam (100 ug/ml), oxathiapiprolin (0.0007 ug/ml), fluopicolide (0.24 ug/ml), mandipropamid (0.04 ug/ml), and cyazofamid (500 ug/ml) by using an in vitro discriminatory dose assay. All isolates were sensitive to oxathiapiprolin and mandipropamid. Three isolates were intermediate to fluopicolide, and all others were fully sensitive to this fungicide. Two isolates were resistant to cyazofamid, and eleven were resistant to mefenoxam. These results can guide fungicide selection for Michigan growers. Regular monitoring can assess resistance development in *P. capsici* populations and preserve effective fungicides efficacy.

4. A NEW BOTRYTIS SPECIES CAUSING BLOSSOM BLIGHT ON BLUEBERRIES IN MICHIGAN

Dr. Timothy D. Miles and Dr. Joel Ayebi Abbey, Michigan State University, East Lansing, MI

Blueberries are an important fruit crop worldwide, with Michigan among the largest producers of highbush blueberries, where Botrytis blossom blight and fruit rot are major diseases.While *Botrytis cinerea* was considered the primary causal agent, a recent survey in Michigan identified a novel species as an additional blossom pathogen. This study aimed to characterize this species using phylogenetic analysis, morpho-cultural traits, fungicide sensitivity, and comparative genomics. Phylogenetic analyses placed the new species (*B. michiganensis*) in a distinct clade related to *B. fabiopsis* and *B. galanthina*. Isolates showed diverse cultural/morphological traits on PDA but did not produce conidia on artificial media; however, they formed *Botrytis*-like conidiophores and conidia on plant tissues. Pathogenicity tests on blueberry tissues, grapes, and rose petals confirmed its disease causing ability, with severity comparable to *B. cinerea*. Fungicide assays showed sensitivity to all tested fungicides except cyprodinil. Comparative genomics indicate that *B. michiganensis* is a distinct lineage retaining core necrotrophic machinery but diverging in developmental and regulatory pathways. Genomic changes correlate with unusual phenotypes, including lack of sporulation on artificial media, and cottony colony morphology. These findings improve understanding of the *Botrytis* complex and highlight management implications and the need for further diversity studies.

Poster Presentations

5. EVALUATION OF PHAGE THERAPY AS A BIOCONTROL FOR BACTERIAL CANKER OF CHERRY IN MICHIGAN*

Ms. Ashlyn Amsden1, Mr. Cory A. Outwater2 and Dr. George W. Sundin1, (1)Michigan State University, East Lansing, MI, (2)Michigan State University, Williamston, MI

Bacterial canker, caused by the *Pseudomonas syringae* species complex, is a major disease affecting cherry and other *Prunus* species. A lack of viable management options has driven interest in bacteriophage (phage) biocontrol. We hypothesized that surfactants could increase phage efficacy by disrupting bacterial aggregates and increasing phage access to cells. In a 2024 orchard cherry flower assay, *P. syringae* pv. *syringae* (Pss) populations were reduced 100-fold following phage/surfactant treatments but rebounded to control levels within 76h. In vitro population assays using Pss BY38 showed that phage treatment (log10 6.3 PFU/mL) halted growth, while phage + Oroboost® (0.125%; Rovena Next, Cary, NC, USA), increased suppression compared to phage alone. In a bean leaf model, phage cocktail treatment (log10 7 PFU/mL; AgriPhage®, OmniLytics, Sandy, UT, USA) combined with Oroboost (0.118%) reduced the BY38 population 100-fold within 6h and held through 48h. Oroboost alone produced a similar reduction, suggesting disruption of epiphytic aggregates. In detached cherry flower assays, two applications (4 and 24 hpi) of phage (log10 6.1 PFU) + Oroboost (0.125%) yielded an initial 100-fold reduction, but populations rebounded to control levels within 72h. A field trial targeting overwintering bud populations showed no significant effect. These results signal short term efficacy of phage treatments but demonstrate the need to improve sustained population suppression.

6. IMPACT OF VARIETY MIXTURES ON CERCOSPORA LEAF SPOT OF SUGAR BEET

Dr. Austin Kyle Lien1, Dr. Nathan Andrew Wyatt2, Dr. Melvin D. Bolton3 and Dr. Ashok K. Chanda1, (1)University of Minnesota, Crookston, MN, (2)USDA-ARS, Fargo, ND, (3)Edward T. Shafer Agricultural Research Center, USDA-ARS, Fargo, ND

Cercospora beticola, the causal agent of Cercospora leaf spot (CLS), is a major foliar pathogen of sugar beet. Current CLS management relies primarily on the use of fungicides and cultivars carrying the BvCR4 resistance gene. Populations of *C. beticola* have demonstrated adaptation to BvCR4 primarily through the loss of the effector AvrCR4. The effect of variety mixtures and fungicide programs on CLS severity and *C. beticola* population structure was evaluated in field trials in 2024 and 2025. A split-plot design with four replications was used, with a BvCR4-resistant (CR+) and a moderately susceptible (MS) variety planted in pure stands or mixtures (25:75, 50:50, 75:25), and subplots assigned to no fungicide, a 3-spray or a 4-spray program. Disease severity was assessed weekly. Seven hundred isolates were characterized using microsatellite markers, AvrCR4 presence, and CbCyp51 haplotype. In 2024, mixtures containing at least 50% CR+ reduced mid-season CLS severity, and variety-by-fungicide interactions affected final CLS ratings. In 2025, disease severity decreased with increasing CR+ proportion and number of sprays. The population was dominated by a few multilocus genotypes with temporal shifts in frequencies. Loss of AvrCR4 increased from 2024 to 2025. Fungicide programs were associated with shifts in CbCyp51 haplotypes. These results show that variety mixtures can reduce CLS severity, and host resistance and fungicides influence *C. beticola* population composition.

7. REFINING ENVIRONMENTAL PREDICTORS FOR SCLEROTINIA STEM ROT IN NEBRASKA SOYBEAN FIELDS*

Ms. Roshani Baral, University of Nebraska-Lincoln, LINCOLN, NE and Dr. Dylan Mangel, University of Nebraska-Lincoln, Lincoln, NE

Sclerotinia stem rot (SSR) has become an increasing challenge in Nebraska soybean production, with outbreaks in 2021 and 2023, highlighting the need for improved, region-specific management strategies. Fungicides remain the primary management tool, but their success depends on timing with apothecial formation, ascospore release, and favorable weather during flowering. As these factors must coincide for infection, disease risk is difficult to predict, often resulting in mistimed or unnecessary applications. This study aims to identify site-specific, weather-based risk factors for SSR in Nebraska for integration into decision-support systems. Overwintering sclerotia were monitored across five soybean fields, each equipped with a meteorological-grade weather station recording above and below the canopy air temperature, precipitation, humidity, light, and soil conditions. Disease ratings were conducted from August to September, and time-lapse cameras documented apothecial development. Preliminary results indicate that below-canopy environments maintain more stable temperatures and higher relative humidity than above-canopy conditions. Earlier canopy closure increased disease risk, and rainfall or irrigation created favorable conditions for SSR development. These findings are based on first-year data and require further validation. Overall, these findings will improve SSR risk prediction and optimize fungicide timing for more efficient and sustainable disease management.

8. DEVELOPING A MODEL SYSTEM TO INVESTIGATE WOUND HEALING AND RESISTANCE TO ROT PATHOGENS IN POTATO TUBERS USING CELL WALL-DEGRADING ENZYMES

Dr. Pratima Devkota, Christopher Long and Prof. Raymond Hammerschmidt PhD, Michigan State University, East Lansing, MI

Postharvest losses in potato are strongly influenced by the efficiency of wound healing, yet current methods to assess healing are labor-intensive and not suitable for large-scale screening. The objective of this study was to develop a simple and scalable system to quantify wound healing and evaluate its relationship with susceptibility of wounded tissue to infection. We established a tuber disc-based enzymatic digestion assay, in which resistance of the wounded tissue to digestion by commercially sourced cell wall-degrading enzymes (CWDEs) was used as an indicator of progressive closing layer formation and suberization. Healing data were analyzed to evaluate temporal progression, and *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc) and *Fusarium sambucinum* (FS) infection to assess relationships with healing metrics. Results showed that intact healing tissue as determined by resistance to CWDE action increased significantly with time after wounding, demonstrating a strong positive relationship between healing and days after wounding. In addition, wound healing varied among potato cultivars and was negatively associated with both infection incidence by Pcc and infection depth caused by FS. These findings establish a rapid and reproducible model system for quantifying wound healing and highlight its importance as a structural defense mechanism in postharvest pathology, providing a practical framework for screening cultivars for improved storage performance.

Poster Presentations

9. EXPLORING FUNGAL COMPLEXES ASSOCIATED WITH SOYBEAN FOLIAR AND POD DISEASE SYMPTOMS IN IOWA*

Juan Barrientos, Mr. Edgar Humberto Nieto-Lopez and Dr. Daren S. Mueller, Iowa State University, IA

High frequencies of irregular brown and necrotic spots on soybean leaves have been observed in Iowa. These symptoms resemble Septoria brown spot and Phyllosticta leaf spot. To investigate the causal fungi, a 2025 statewide survey was conducted, collecting symptomatic leaf and pod samples from 18 Iowa counties. Lesions were examined stereoscopically, and fungal structures were plated directly onto PDA. Other samples were surface-sterilized and incubated in humidity chambers to induce sporulation before plating lesion borders and fungal structures. Emerging colonies were purified via hyphal tipping and culturally classified by color and shape. Representative isolates were sequenced confirming the identification of *Colletotrichum sojae, Colletotrichum* sp., and *Diaporthe* spp. The genus *Colletotrichum* was frequently recovered from lesions resembling Septoria brown spot and from acervuli on petioles and pods. Additionally, the genus *Diaporthe.* was commonly isolated from necrotic lesions. In vivo pathogenicity assays using non-wounded and carborundum-wounded leaves are currently underway to investigate their roles as primary or secondary pathogens. This survey suggests that foliar symptoms in Iowa are caused by fungi other than those commonly recognized, highlighting the importance of accurate diagnostic identification beyond visual symptoms. Ongoing studies will help clarify previously overlooked disease complexes occurring under field conditions.

10. FIELD VALIDATION OF A WEATHER-BASED PREDICTIVE MODEL FOR IMPROVED MANAGEMENT OF FROGEYE LEAF SPOT OF SOYBEAN IN THE UNITED STATES

Dr. José F. González-Acuña1, Dr. Tom Allen2, Dr. Mandy Bish3, Dr. Carl A. Bradley4, Dr. Boris Xavier Camiletti5, Dr. Martin Chilvers6, Dr. Nabin K. Dangal1, Dr. Maira R. Duffeck7, Dr. Gabriel Dusek8, Dr. Ahmad M. Fakhoury9, Dr. Travis Faske10, Dr. LeAnn Ranae Lux11, Dr. Dylan Mangel12, Dr. Daren S. Mueller13, Dr. Paul Price14, Dr. Hope Renfroe-Becton8, Dr. Madalyn Shires15, Damon L. Smith16, Dr. Darcy E. P. Telenko17 and Dr. Richard Webster8, (1)Iowa State University, Ames, IA, (2)Delta Research and Extension Center, Mississippi State University, Stoneville, MS, (3)University of Missouri, Columbia, MO, (4)University of Kentucky, Princeton, KY, (5)University of Illinois Urbana-Champaign, Urbana, IL, (6)Michigan State University, East Lansing, MI, (7)Oklahoma State Univ, Stillwater, OK, (8)North Dakota State University, Fargo, ND, (9)Southern Illinois University, Carbondale, IL, (10)University of Arkansas, AR, (11)North Carolina State University, Raleigh, NC, (12) University of Nebraska-Lincoln, Lincoln, NE, (13)Iowa State University, IA, (14)LSU AgCenter, Winnsboro, LA, (15)South Dakota State University, Brookings, SD, (16)Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, (17)Purdue University, West Lafayette, IN

Frogeye leaf spot (FLS), caused by *Cercospora sojina*, is a major foliar disease of soybeans (*Glycine max*). While a fungicide application is often recommended at the beginning of the pod fill (R3) growth stage, a weather-based predictive model could improve the farmers' decision-making process. To evaluate three risk-based action thresholds, derived from a model developed in 2024, field trials were performed in 2024 and 2025 across 37 site-years and 15 states. Our objectives were to evaluate the effects of model-based fungicide applications on FLS suppression and yield protection, and to assess the predictive model's performance under field conditions. FLS severity levels were <4% in most site-years, but across environments, spraying at R3, and at the low or moderate risk action threshold, reduced FLS severity compared to the non-treated control (NTC). Yield was improved in the R3 application and low-risk threshold treatments compared to the NTC. At individual site-years, the model performed as well as the standard R3 spray in most sites but overestimated FLS risk in others. Model accuracy at the highest-risk threshold reached 86% and performed better at the lower FLS severity sites than at higher severity sites. Sensitivity improved with the low-risk threshold, while specificity reached 100% at the high-risk threshold. This work is the first attempt to develop and implement a DSS based on predictive models for timing fungicide applications for FLS in the U.S.

11. TIMING IS EVERYTHING: OPTIMIZING FUNGICIDE APPLICATION TIMING FOR SCLEROTINIA STEM ROT MANAGEMENT IN MICHIGAN SOYBEAN*

Mr. Alex Michael Bray, Peyton Phillips, William Widdicombe and Dr. Martin Chilvers, Michigan State University, East Lansing, MI

White mold of soybean, caused by the fungal pathogen *Sclerotinia sclerotiorum*, remains a significant constraint to soybean production in Michigan. Effective management often relies on fungicide applications near flowering. However, disease risk is driven by environmental conditions such as canopy closure and humidity that promote germination of apothecia, the fruiting bodies that produce ascospores. This study evaluates fungicide application timing based on soybean growth stage compared with field scouting for apothecia as a measure of active inoculum. Field trials were established in central Michigan in 2025 and will be repeated at two sites in 2026 to assess applications across growth stages from late vegetative (V6) through mid-reproductive (R5) and relate application timing to disease development and yield. Weekly scouting between rows provided counts of apothecia to relate to disease onset. Preliminary observations indicated that apothecia presence corresponded with early reproductive stages when initial symptoms developed. Disease severity and yield data from 2025 showed the greatest disease suppression and yield when fungicides were applied between R1 and R3, coinciding with increasing apothecia counts during susceptible growth stages. These findings indicate that growth stage–based applications can support effective white mold management, with apothecia scouting serving as a supplementary tool to refine fungicide timing.

12. GREEN MOLD FUNGI ASSOCIATED WITH SWEETPOTATO POSTHARVEST ROOT ROTS IN CENTRAL MISSOURI

Waana Kaluwasha, Lincoln University of Missouri, Jefferson City, MO and Ujjwal Kamboj, Lincoln University of Missouri, MO

Sweetpotato (*Ipomoea batatas*) storage roots are susceptible to rots caused by a wide range of fungi, including certain green molds. The purpose of this study was to isolate, identify and test the pathogenicity of green mold fungi from diseased storage roots collected in Missouri. Surface sterilized tissues of roots with rot symptoms and/or signs were plated on Potato Dextrose Agar (PDA) supplemented with antibiotics and incubated at 25°C. Isolates were identified by amplifying the internal transcribed spacer (ITS) region using ITS1 and ITS2 primers followed by BLAST analysis of ITS sequences. Isolate pathogenicity was tested on sweetpotato root slices by placing mycelial agar plugs on uniform slices, in addition to plain PDA agar plugs for the control. Inoculated slices were incubated at 25oC for 14 days after which lesion diameter was measured. Of sixteen identified isolates, 3 were Trichoderma koningii while 13 represented five species in the genus *Pencillium (P. fimorum, P. griseofulvum, P. speluncae, P. polonicum and P. fuscoglacum*). Most *Trichoderma* and *Penicillium* isolates caused lesions on slices, while the control slices had no lesions. Lesion diameter varied significantly (p<0.0001) among isolates, with *T. koniingi* and *P. fimorum* causing greatest lesions. This study enhances our understanding of potential sweetpotato postharvest pathogens in Central Missouri and provides a foundation for research on whole-root cultivar responses and management strategies.

Poster Presentations

13. EVALUATION OF FUNGICIDE MODES OF ACTION ON SOUTHERN RUST SEVERITY AND CORN YIELD RESPONSE IN KANSAS*

Leticia Camara Vieira, Madison Kessler, Luan Castegnera, Dr. Kelsey Andersen-Onofre and Dr. Rodrigo Borba Onofre, Kansas State University, Manhattan, KS

Southern rust caused by *Puccinia polysora* is a threat to corn production, causing significant yield losses in the US. Growers currently rely on hybrid selection and a well-timed fungicide application for disease management. In this study we evaluated the effect of the fungicide and fungicide mode of action on southern rust suppression. The experiment was conducted in Rossville, Kansas, during the 2025 season. Six treatments were evaluated, including a non-treated control and five fungicide programs with three modes of action and their combinations: a quinone outside inhibitor(QoI) alone (Headline), a demethylation inhibitor (DMI) alone (Proline), a QoI + DMI combination (Headline + Proline), a succinate dehydrogenase inhibitor (SDHI) + QoI combination (SDHI+QoI; Delaro Complete), and an SDHI + DMI combination (MiravisNeo). All fungicide treatments were applied at the green silk stage. Southern rust severity was evaluated as the average percent leaf area affected per plot at the ear leaf and two leaves below. All fungicide treatments significantly reduced disease severity compared to the control, with reductions ranging from 63 to 82%. Although no fungicide resulted in a significant yield increase compared to the control, fungicide products containing single DMI products or SDHI+QoI showed a numerical yield increase of +23 bu/ac. Future research is needed across additional environments to understand the influence of application timing and optimal fungicide program.

14. ANTIFUNGAL VOLATILE FROM BURKHOLDERIA CEPACIA CMML21-68 AGAINST FUSARIUM OXYSPORUM AND CERATOCYSTIS FIMBRIATA

Ju Gyeong Lee1, Narayan Chandra Paul1,2, Soyoon Park1, Dr. Martin Chilvers3 and Hyunkyu Sang1,2, (1)Dept of Integrative Food, Bioscience, Biotechnology, Chonnam National University, Gwangju, SOUTH KOREA, (2)Kumho Life Science Laboratory, Chonnam National University, Gwangju, SOUTH KOREA, (3)Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI

Sweet potato (*Ipomoea batatas)* is an important food source, cultivated globally. However, Fusarium wilt caused by *Fusarium oxysporum* and black rot caused by *Ceratocystis fimbriata* pose serious threats to both field production and postharvest storage. To develop an effective and environmentally friendly control strategy, we isolated 168 bacterial strains from the rhizosphere, storage roots, and fibrous roots of healthy sweet potato plants in Korea in 2021. Based on antifungal activity screening, *Burkholderia cepacia* strain CMML21-68 was selected for characterization as a source of antifungal metabolites. In planta assays demonstrated that treatment with CMML21-68 suppressed Fusarium wilt and black rot. In field trials, CMML21-68 showed control efficacy comparable to or greater than azoxystrobin, with disease control rates of 67.12 ± 1.01% versus 65.92 ± 6.23% against Fusarium wilt, and 80.31 ± 2.66% versus 59.10 ± 11.13% against black rot. To investigate the antifungal basis of CMML21-68, dual-culture, cell-free culture filtrate, and sandwich assays were conducted. The sandwich assay showed that volatile organic compounds (VOCs) emitted by CMML21-68 strongly inhibited *F. oxysporum* and *C. fimbriata*. Headspace SPME-GC/MS analysis detected dimethyl disulfide (DMDS) as the predominant VOC. These result indicate that CMML21-68-derived DMDS may be a candidate cell-free antifungal volatile to manage sweet potato fungal diseases.

15. SOYBEAN CYST NEMATODE VIRULENCE ASSAY AGAINST RESISTANCE SOURCES IN NEBRASKA*

Olivia Dooley1, Mrs. Pratibha Karki2 and Dr. Dylan Mangel2, (1)University of Nebraska-Lincoln, Norborne, MO, (2)University of Nebraska-Lincoln, Lincoln, NE

Soybean cyst nematode (*Heterodera glycines*) is the most yield-limiting pathogen of soybean in the United States. SCN can cause significant yield loss without noticeable aboveground symptoms. It has been detected in 60 Nebraska counties, where management primarily relies on the rotation of resistant soybean varieties and seed applied nematicides. SCN virulence (HG Type) has evolved over time, reducing the effectiveness of overused resistance sources. This study analyzed 150 soil samples collected from Nebraska soybean fields in 2021, 2022, and 2023. Results show that Nebraska SCN populations can overcome the two most used resistance sources at an average rate of 30% of a true susceptible variety. Knowing which SCN HG types are the most common will help understand why resistance declines and how to breed better soybeans in the future. The second objective of this study involves molecular analysis to help assess the genotypic diversity of SCN populations across Nebraska. To date, one-third of this objective has been completed using 50 samples. Molecular analysis identified two haplotype groups among these SCN populations, indicating low genetic diversity within Nebraska SCN populations. This research will enhance understanding of SCN population behavior and support the development of improved management strategies for sustainable soybean production.

16. FUNGICIDE SENSITIVITY STUDY OF CERCOSPORA SPP. ACROSS THE UNITED STATES AND CANADA TO SDHI, QOI, AND DMI FUNGICIDES

Nik Nurulhidayah Binti Nik Zainal Alam1, Dr. Drake Copeland2, Matthew Wiggins2, Dr. Darcy E. P. Telenko3, Dr. Kiersten A. Wise4, Dr. Nathan M. Kleczewski5, Dr. Tamra A. Jackson-Ziems6, Dr. Alison E. Robertson7, Prof. Gary C. Bergstrom8, Dr. Albert U. Tenuta9, Dr. Austin McCoy10, Janette L. Jacobs1, Hyunkyu Sang1,11 and Dr. Martin Chilvers1, (1)Michigan State University, East Lansing, MI, (2)FMC Corporation, Dayton, OH, (3)Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN, (4)Department of Plant Pathology, University of Kentucky, Princeton, KY, (5)University of Illinois, Urbana, IL, (6)University of Nebraska, Lincoln, NE, (7)Iowa State University, Ames, IA, (8) Cornell University, Ithaca, NY, (9)Ontario Ministry of Agric & Food, Ridgetown, ON, CANADA, (10)Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, (11)Chonnam National University, Gwangju, SOUTH KOREA

Gray leaf spot of corn caused by *Cercospora* spp. is a significant threat to corn production. In a previous study, multiple *Cercospora* spp. were identified on corn including species that cause Cercospora leaf blight and purple seed stain of soybean; *C. zeae-maydis, C. cf. flagellaris, C. kikuchii, C.* sp. C *M*,. sp. *Q*, and *C*. sp. *T*. However, only *C. zeae-maydis* is a confirmed pathogen of corn causing disease symptoms, while the pathogenicity of other species remains unclear. A previous study evaluated sensitivity of *Cercospora* spp. to flutriafol, a demethylation inhibitor (DMI) fungicide. In this study, sensitivity of *Cercospora* spp. to pydiflumetofen (SDHI), pyraclostrobin (QoI), and propiconazole (DMI) were assessed. A total of 140 isolates were selected from 2020 and 2021 collections across the United States and Canada to represent different locations and varying sensitivity to flutriafol. Fungicide sensitivity was determined by amending clarified V8 agar with fungicides at concentrations of 0, 0.01, 0.1, 1, 10, and 50 µg/mL. For pyraclostrobin, 50 µg/mL SHAM was also amended into the clarified V8 medium. The half effective concentration values (EC_{50}) were estimated for each isolate, and cross-sensitivity among fungicides was evaluated. These findings will contribute to the monitoring of fungicide efficacy and detection of potential shifts in sensitivity within *Cercospora* spp. populations affecting corn.

Poster Presentations

17. PATHOGENICITY ASSESSMENT OF PYTHIUM-LIKE ISOLATES ASSOCIATED WITH SOYBEAN SEEDLING DISEASE*

Peter Doroff1, Dr. Richard Webster2, Dr. Gabriel Dusek2 and Dr. Hope Renfroe-Becton3, (1)North Dakota State University, ND, (2)North Dakota State University, Fargo, ND, (3)North Dakota State Univ, Fargo, ND

Soybean seedling diseases are a major cause of early-season stand loss and reduced yield potential in soybean production. These diseases are commonly associated with soilborne pathogens including *Fusarium* spp., *Rhizoctonia solani, Phytophthora sojae*, and *Pythium*-like species. Although *Pythium*-like organisms are oomycetes rather than true fungi, they are widely distributed in agricultural soil and are frequently implicated in seed rot and seedling damping-off in soybean. Despite their prevalence, the pathogenic potential of many *Pythium*-like isolates recovered from field soils remains poorly understood. This project aims to evaluate the pathogenicity of *Pythium*-like isolates collected from soybean field soil surveys across North Dakota and determine their ability to infect soybean seeds and cause seed rot or root rot under controlled conditions. Isolates obtained from the culture collection in Dr. Wade Webster's laboratory were cultured on clarified V8 agar plates prior to inoculation experiments. Surface-sterilized soybean seeds were placed onto actively growing cultures and incubated in the dark at room temperature (25–27°C). Experiments were arranged in a randomized complete block design with four replications per isolate. After seven days, seedlings were evaluated for disease incidence and severity based on germination, seed rot, and root tissue damage. Disease incidence was calculated as the percentage of seeds exhibiting symptoms of infection, while severity was estimated based on the proportion of non-germinated seeds and the extent of root rot observed in germinated seedlings. The results of this study will help characterize the pathogenic potential of *Pythium*-like isolates associated with soybean fields in North Dakota and contribute to improved disease management strategies.

18. VOLATILE-MEDIATED INHIBITION OF SWEET POTATO PATHOGENS BY TRICHODERMA ASPERELLUM CMML20-29 *

Soyoon Park1, Ju Gyeong Lee1, Narayan Chandra Paul1, Dr. Martin Chilvers2 and Hyunkyu Sang1, (1)Dept of Integrative Food, Bioscience, Biotechnology, Chonnam National University, Gwangju, SOUTH KOREA, (2)Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI

Sweet potato (*Ipomoea batatas L.*) yield is reduced by surface rot and black rot caused by *Fusarium oxysporum* and *Ceratocystis fimbriata*, respectively. *Trichoderma* spp. have gained attention as biological control agents that suppress pathogens through competition, antifungal metabolites, and volatile organic compounds (VOCs). This study aimed to identify an effective *Trichoderma* isolate against sweet potato pathogens and determine its antifungal mechanism. Among 25 isolates, *Trichoderma asperellum* CMML20-29 showed the strongest inhibition of *F. oxysporum* and *C. fimbriata* in dual-culture and in planta assays. VOC and cell-free culture filtrate assays showed that VOCs had stronger antifungal activity than culture filtrates, indicating that volatile-mediated inhibition is a major mechanism of pathogen suppression. Gas chromatography–mass spectrometry (GC–MS) analysis identified 6-pentyl-2-pyrone as the predominant VOC produced by CMML20-29. A polyketide synthase gene, PKS1, showing high homology to 6-pentyl-2-pyrone-associated PKS genes in related species, was disrupted using a CRISPR–Cas9 system. Functional analysis showed that the ΔPKS1 mutant exhibited reduced inhibitory activity against both pathogens compared with the wild-type strain. These results suggest that PKS1 may be involved in the antifungal activity of *T. asperellum* CMML20-29, although its direct role in 6-pentyl-2-pyrone production remains to be confirmed.

19. IMPROVING TRICHODERMA BIOCONTROL FOR MISSOURI SOLANACEOUS PLANTS: ENDEMIC ISOLATE CHARACTERIZATION, EFFICACY ANALYSIS, AND VOLATILE ORGANIC COMPOUNDS*

Riley France1, Dhruba Dhakal2, Leland Cseke3, Ramon A. Arancibia2, Walter Gassmann1 and Dr. Peng Tian1, (1)University of Missouri, Columbia, MO, (2)University of Missouri Extension, MO, (3)University of Missouri, MO

Soilborne pathogens such as **Fusarium** spp. significantly limit crop productivity in the North Central Region of the US. This study evaluates the efficacy of the beneficial organism *Trichoderma* in suppressing *Fusarium*, investigates the mode of action and seeks improved techniques for growers to better facilitate biological control in the field and maximize benefits from *Trichoderma*. Twenty-one *Fusarium* and two *Trichoderma* isolates were collected from symptomatic plants on partnering farms, then isolated and identified via microscopy and DNA sequencing of the ITS and the genes EF-1**α** and RPB. They were evaluated alongside two isolates from commercial products, in confrontation assays to compare the inhibitory effects of various *Trichoderma* isolates. To determine the mechanisms of fungistasis, we have been examining the VOCs exuded by the solitary and co-cultured organisms using stir bar adsorptive extraction and GC-MS. To provide practical applications, media amendments to encourage growth are being evaluated and in planta assays to determine the efficacy of pre-inoculating seedlings with *Trichoderma* are underway. This project offers expanded knowledge of North Central Region fungal populations, insights into the mechanisms of fungistasis, and science-based strategies to Missouri growers to maximize the benefits of biological control in integrated pest management systems.

20. HIGH-THROUGHPUT DISCOVERY OF NATURAL BIOACTIVE COMPOUNDS THAT ENHANCE PLANT RESILIENCE TO FUNGAL PATHOGENS

Katherine Rivera-Zuluaga1, Dr. Erika Lisabeth1, Dr. Linda E. Hanson2, Dr. Nicholas Schlecht3, Dr. Aleksandra Skirycz3, Dr. Martin Chilvers1 and Dr. Seung Yon Rhee1,4, (1)Michigan State University, East Lansing, MI, (2)USDA ARS, East Lansing, MI, (3)Michigan State University, MI, (4) Plant Resilience Institute, East Lansing, MI

Plants are exposed to a multitude of diseases that threaten crop yield and global food security. Species within the genus *Fusarium* are exceptionally successful plant pathogens, causing disease in over 300 plant species, including economically important crops such as soybean, corn, tomatoes, and cereals. The Center for Sustainable Plant Innovation and Resilience Through International Teamwork (C-SPIRIT) aims to identify bioactive compounds from natural sources that enhance plant defense responses and inhibit pathogen virulence. We have assembled libraries of natural compounds for microplate testing. To evaluate candidate compounds, we developed and optimized a high-throughput assay based on spectrophotometric quantification of macroconidia growth in liquid culture. To demonstrate the efficiency of the assay, isolates from different *Fusarium* species were screened against the chemical libraries, and metconazole was used as a positive control for growth inhibition. Compounds demonstrating promising activity will be advanced for in plantacharacterization under controlled environmental conditions. The identification of novel bioactive metabolites from natural sources will provide new opportunities to develop sustainable strategies for crop protection and to improve plant resilience.

Poster Presentations

21. EFFICACY OF FUNGICIDES ON REDUCING LODGING IN CORN IN NORTH DAKOTA*

Kevin Gladitsch, Bryan Hansen, Jessica Scherer and Dr. Andrew J. Friskop, North Dakota State University, Fargo, ND

Stalk rot incidence and lodging of corn has increased in North Dakota. In an effort to manage lodging occurrence, questions pertaining to the use of fungicides applied either in-furrow or at VT/R1 (tasseling/silking) have increased. To address these questions, field experiments were established in 2025 to evaluate fungicide efficacy on reducing lodging in northern corn hybrids. Research sites were established in North Dakota near Arthur and Leonard using two corn hybrids with below average corn stalk strength scores (NK9021-D – RM 90; DKC36-48RIB – RM 86). Four independent experiments (randomized complete block design; two for each hybrid) were conducted at research sites and evaluated the efficacy of an in-furrow fungicide flutriafol (XyWay LFR ®) and VT/R1 applications of either mefentrifluconazole + pyraclostrobin (Veltyma ®), benzovindiflupyr + azoxystrobin + propiconazole (Trivapro ®), or azoxystrobin + fluindapyr + flutriafol (Adastrio ®) on stalk lodging. Data assessments included percent lodging (push test), yield, and test weight. Data was summarized by combining and analyzing across all four experiments. Significant differences (α=0.1) occurred among treatments for percent lodging, yield and test weight. Research trials will be conducted again in 2026 to build on trends that were observed in 2025.

22. EVALUATION OF COMPOST AMENDMENTS FOR PLANT-PARASITIC NEMATODE SUPPRESSION AND SOIL HEALTH IN POTATO FIELDS

Esmaeil Saberi, Michigan State University, East Lansing, MI; Michigan State University, MI

Michigan ranks eighth in U.S. potato production with substantial economic value. Plant-parasitic nematodes, particularly *Pratylenchus penetrans*, contribute to yield losses through interactions with *Verticillium dahliae,* causing Potato Early Die. Conventional management using fumigants and nematicides can negatively impact soil health and microbial diversity. This study evaluated compost amendments as sustainable alternatives for nematode suppression and soil health improvement. Field trials were conducted in 2024–2025 in southwestern Michigan using a randomized complete block design with six treatments: spring, fall, and combined compost applications, Vapam fumigation, oxamyl (Vydate), and an untreated control. Soil samples were collected throughout the season, and nematode populations were expressed as reproduction factors (RF). Compost treatments increased free-living nematodes (RF = 2.02–3.46), indicating enhanced biological activity, though differences were not significant. Vapam significantly reduced plant-parasitic nematodes (RF = 0.24), including >90% suppression of *Pratylenchus penetrans*. Compost provided moderate, non-significant reductions (RF = 0.48–0.59). Overall, compost supported beneficial nematodes and soil health but was less effective than fumigation for rapid nematode control.

23. EFFECT OF NITROGEN, SULFUR, AND CEREAL RYE LEACHATES AND THEIR COMBINATIONS ON CORN SEEDLING DISEASE*

Luis Esteban Gonzalez and Dr. Alison E. Robertson, Iowa State University, Ames, IA

While cereal rye (CR) cover crop improves nutrient retention by scavenging residual soil nitrogen (N), high C:N CR residues promote microbial immobilization of N, reducing early-season N availability to corn seedlings that may compromise seedling vigor and increase susceptibility to soilborne pathogens. In addition, the roles of sulfur (S) immobilization, allelopathic compounds from CR leachates, and their combined effects on nutrient dynamics remain poorly understood. The objective of this study was to evaluate the effect of N, S, CR leachates and their combinations on corn seedling disease. Corn was grown in pots in a growth chamber. Treatments included N (64 ppm), S (24 ppm), CR leachates, their combinations, and a non-amended control, applied to soils with or without a history of CR. Seedling disease severity (radicle and seminal root rot) was evaluated at the V3 growth stage. Treatments containing leachates had more severe radicle rot in both types of soil ($P<0.05$), and more severe seminal root rot in soil with a CR history ($P<0.05$). Corn seedlings in soil with no CR history showed no significant differences among treatments for seminal root rot severity ($P=0.1059$). These preliminary findings indicate a potential role of CR leachates in increasing root rot severity, particularly in soils with CR history, highlighting the need to further investigate interactions between nutrient dynamics and allelopathic effects in subsequent experiments.

24. LINKING FUNGICIDE INSENSITIVITY TO REDUCED FIELD PERFORMANCE IN EARLY BLIGHT OF POTATO

Sunil Shrestha and Julie Pasche, North Dakota State University, Fargo, ND

Early blight, caused by *Alternaria solani*, continues to be a major constraint to potato growers in the Midwest US, with management often relying on foliar fungicide applications. The use of single-site mode of action (MoA) fungicides, including succinate dehydrogenase inhibitor (SDHI), demethylation inhibitor (DMI), and anilinopyrimidine (AP), has imposed strong selection pressure on the pathogen, leading to widespread insensitivity. Our previous study revealed insensitivity to SDHI fungicides, the presence of novel amino acid substitutions, and double substitutions in the succinate dehydrogenase (Sdh) gene of *A. solani*, resulting in significant reductions in disease control under greenhouse conditions. Field trials were conducted over multiple seasons to determine the efficacy of single-site MoA fungicides. SDHI, DMI, and AP products were tank-mixed with mancozeb at application-5 and -7 in a 10-application program with chlorothalonil at other applications. Despite reduced greenhouse efficacy, field trial results indicated decreased disease severity and economic gain with programs that include single-site MoA fungicides compared to full-season applications of the multisite fungicide chlorothalonil. Overall, the reduction in field efficacy of SDHI fungicides has been observed over the past 12 seasons, linking with previously documented in vitro and in vivo insensitivity of *A. solani* to SDHI and highlighting the need for improved early blight management strategies.

Poster Presentations

25. EVALUATING FUNGICIDE EFFICACY ON ERGOT WEIGHT IN HARD RED SPRING WHEAT*

Rick Hatchett, Bryan Hansen, Jessica Scherer, Gabe Lakoduk and Dr. Andrew J. Friskop, North Dakota State University, Fargo, ND

Ergot (*Claviceps purpurea* (Fr.) Tul.) is a common disease found throughout the Northern Great Plains on a wide range of grass species, including small grain crops. Although often not considered a yield-limiting disease, the ergot fungus produces toxic alkaloids that reduce grain quality, leading to severe dockage and sometimes rejections of hard red spring wheat. The use of spike-applied fungicides to reduce ergot weight in wheat is underexplored and relatively unknown. The objectives of this research were to evaluate the efficacy of metconazole+prothioconazole (Sphaerex®), prothioconazole+tebuconazole+fluopyram (Prosaro Pro®), and pydiflumetofen+propiconazole (Miravis Ace ®) on hard red spring wheat. Three field experiments were established between 2022 to 2024 in Fargo, ND, that evaluated three fungicide treatments applied at two different timings (half-spike emergence or full-spike emergence). A male-sterile hard red spring wheat line was used in all experiments (susceptible to ergot). At harvest, plot samples were obtained and manually sorted for ergot sclerotia to obtain a mean ergot weight per plot. Results from the field experiments suggest only pydiflumetofen+propiconazole when applied at complete full-spike emergence was able to reduce ergot weight (37% reduction). Information from this research study has been used to guide ergot management conversations with growers in the Northern Great Plains.

26. EVALUATING MULTIPRONGED STRATEGIES FOR MANAGING VERTICILLIUM WILT IN A THREE-YEAR POTATO ROTATION.

Lovepreet Singh1, Mrs. Sonal Srivastava2, Dr. Jim Crants1, Seonghyun Seo1, Matt McNearney1, Prof. Carl Rosen1 and Dr. Ashish Ranjan2, (1) University of Minnesota, Saint Paul, MN, (2)University of Minnesota, St Paul, MN

Verticillium wilt, caused primarily by *Verticillium dahliae*, is a major constraint to potato production worldwide, including the U.S. Midwest, necessitating sustainable management strategies. A 2025 field study under the Potato Soil Health Project (initiated 2019) evaluated three management systems: no fumigation, conventional fumigation, and promicrobial (biofumigation + manure), using susceptible (Russet Burbank) and tolerant (Bannock Russet) cultivars in a three-year rotation at the Sand Plain Research Farm (Becker, MN). The cultivar effect was significant for Verticillium wilt severity (AUDPC; $p < 0.001$), with Bannock Russet exhibiting lower disease than Russet Burbank, while treatment effects and interactions were not significant. Promicrobial treatment numerically reduced AUDPC and Verticillium propagules per gram of soil (Vppg), with effects comparable to conventional fumigation. However, conventional fumigation resulted in greater total and marketable yields and higher tuber numbers than either the no-fumigant or the promicrobial systems. Across treatments, Bannock Russet produced higher yields, larger tubers, and lower soil Vppg than Russet Burbank. Overall, this study reinforces the importance of host resistance in managing Verticillium wilt in potatoes and indicates the potential of biofumigation as a management strategy for further exploration for reducing reliance on chemical fumigation.

27. COMPARING THE RETURN ON INVESTMENT OF LOW- AND HIGH-INTENSITY SOYBEAN DISEASE MANAGEMENT*

Cooper Hicks1, Dr. Martin Chilvers2, Bhanu Dangi3, Dr. Horacio D. Lopez-Nicora4, Dr. Daren S. Mueller5, Damon L. Smith6, Dr. Darcy E. P. Telenko7 and Dr. Dylan Mangel1, (1)University of Nebraska-Lincoln, Lincoln, NE, (2)Michigan State University, East Lansing, MI, (3)University of Nebraska Lincoln, Lincoln, NE, (4)The Ohio State University, Columbus, OH, (5)Iowa State University, IA, (6)Department of Plant Pathology, University of Wisconsin-Madison, Madison, WI, (7)Purdue University, West Lafayette, IN

Soybean (*Glycine max* (L.) Merr.) is a high-value crop in the U.S., yet production is threatened by diseases that reduce yield and profitability. In response, farmers have increasingly adopted intensive disease management strategies, including pesticide seed treatments and foliar fungicide applications. However, agronomic and economic benefits vary widely and narrowing margins demand more targeted recommendations. This research evaluated a gradient of disease management intensities, ranging from no management practice to high intensity, across multiple environments in the North Central region. The objectives were to quantify yield and disease responses and identify conditions under which each strategy maximizes economic return. In 2025, field trials were conducted at seven locations. Measurements included plant stand, disease intensity, and yield. Plant stands were significantly higher with seed treatments. Disease pressure was low; frogeye leaf spot (*Cercospora sojina*) was most common and foliar fungicides significantly reduced disease intensity. Yields were highest when seed treatment and fungicide were combined. However, increased management intensity did not improve profitability, and the seed treatment–only strategy was the only strategy to produce a positive return on investment. These results indicate that while intensive management can increase yield, profitability is more variable under low disease pressure. This research will be repeated in 2026 and 2027.

28. THERMAL SENSTIVITY OF HOP CYST NEMATODE AND IMPLICATIONS FOR ROOT DISINFESTATION

Mr. Muhammad Usman1, Elisabeth Darling2 and Dr. Marisol Quintanilla1, (1)Michigan State University, East Lansing, MI, (2)Michigan State Univ, East Lansing, MI

Hop cyst nematode (HCN) *Heterodera humuli* is a major nematode pest of hop, with 40-50% occurrence in hopyards of Michigan. The use of HCN free-planting materials (hops or rhizome), may help to prevent introduction and spread of this pest. To evaluate this approach, greenhouse bioassays were conducted using 1.5-gallon pot filled with HCN infested field soil. Individual baby hop was grown for about 50 days and then gently uprooted and subjected to different hot water treatments: T1 = undisturbed roots, T2 = roots dipped into normal greenhouse water for 10 min, T3-T6 (roots dipped into 48oC, 50oC, 52oC, 54oC) for 5 min, T7-T10 (48oC, 50oC, 52oC, 54oC) for 10 min respectively. Treated plants were put back into their respective pots. Two months of post treatment application, soil samples were collected to quantify HCN populations and plant shoot weight were measured. HCN population differed significantly ($p = 0.048$) with maximum reduction observed from T8 (50oC for 10 min) while highest HCN populations recovered from T2. Significant difference ($p = 0.013$) was observed in plant shoot weight with highest reduction was observed from T10 (54oC for 10 min). These results confirmed that dipping hop roots into water of different temperatures and exposure period can effectively reduce the HCN populations but may have a negative impact on plant growth

Poster Presentations

30. EFFECTS OF IRRIGATION AND MULCHING ON PLANT-PARASITIC AND BENEFICIAL NEMATODES IN APPLE ORCHARDS

Mr. Muhammad Usman1, Dr. Ali Yaghoubi Akbar1, Dr. Younsuk Dong1, Emily Lavely2 and Dr. Marisol Quintanilla1, (1)Michigan State University, East Lansing, MI, (2)Oceana County Extension, Hart, MI

Plant-arasitic nematodes are key soilborne pests in apple (*Malus domestica*) orchards, yet the effects of irrigation and mulching on their populations are not well understood. A 2025 field study in Michigan evaluated four treatments: non-irrigated mulch, irrigated mulch, soil moisture at ~50% field capacity, and a non-irrigated control. Two cultivars, 'Honeycrisp' and 'Gala', were assessed. Soil samples collected in May and September were analyzed for plant-parasitic nematodes—mainly root-lesion (*Pratylenchus* spp.) and American dagger (*Xiphinema americanum*)—and beneficial nematodes. In 'Honeycrisp', root-lesion nematode reproduction was significantly lower under irrigated mulch and 50% moisture compared to non-irrigated mulch, while American dagger nematodes were reduced under non-irrigated mulch and 50% moisture. No significant treatment effects were found in 'Gala', though irrigated mulch tended to reduce root-lesion nematodes. Beneficial nematodes responded less strongly but were highest under irrigated mulch. Overall, irrigation and mulching influenced nematode dynamics, particularly in 'Honeycrisp', suggesting these practices may suppress harmful nematodes while supporting beneficial ones.

31. PARTIAL IDENTIFICATION OF PLASMODIOPHORA BRASSICAE PATHOTYPES FROM NORTH DAKOTA*

Ms. Neeraja Narra1, Dr. Luis E. del Rio Mendoza1 and Dr. Venkataramana Chapara2, (1)North Dakota State University, Fargo, ND, (2)North Dakota State University, Langdon, ND

Plasmodiophora brassicae is a soil-borne protist that causes clubroot disease in *Brassica* species including canola (*Brassica napus L.*). Clubroot was first detected in canola in Cavalier County, North Dakota, in 2013. Outreach activities and the availability of resistant cultivars, have helped limit disease expansion in the region. However, the ability of *P. brassicae* to evolve new pathotypes necessitates the selection of cultivars with appropriate resistance genes critical to manage this disease. This study aimed to identify pathotypes of twelve *P. brassicae* isolates collected from commercial canola fields in Cavalier County. For each isolate, 10 of the 13 Canadian Clubroot Differential hosts were grown in soilless mix and inoculated with 3 ml of a resting spore suspension with 10^7 spores mL^{-1}. The experiment was conducted twice in a completely randomized design with three replications per treatment. Plants were grown for 45 days in the greenhouse at 22 ± 2°C and disease severity was assessed using Kuginuki's 0-3 rating scale. Nine of the twelve isolates were virulent on 'Mendel', the source of resistance used in first-generation clubroot-resistant canola cultivars, suggesting the potential emergence of pathotypes capable of rendering these cultivars susceptible. These findings highlight the need for continued pathotype surveillance and strategic deployment of resistant cultivars.

32. EVALUATION OF COVER CROP CULTIVARS FOR MANAGEMENT OF SUGAR BEET CYST NEMATODE

Dr. Ali Yaghoubi Akbar1, Razieh Yazdani Fazlabadi2 and Dr. Marisol Quintanilla1, (1)Michigan State University, East Lansing, MI, (2)Center for Tree Science, The Morton Arboretum, Lisle, IL, 60532, USA, Lisle, IL

Sugar beet cyst nematode (*Heterodera schachtii*) is a major constraint to sugar beet production in the United States, and cover crops offer a promising management strategy. This study evaluated the host status and management potential of selected cover crop species and cultivars under greenhouse and microplot conditions. Treatments included oilseed radishes ('Concord', 'Control', 'Defender', 'Nitro', 'Image', 'Select', 'Respect'), daikon radishes ('Eco-Till', 'Enricher'), white mustard 'Master', black oat 'Pratex', Wheeler rye, susceptible sugar beet, and a fallow control. Greenhouse experiments were conducted using a randomized complete block design with five replications. Pots were inoculated with 2,000 eggs, and cyst, egg, and juvenile populations were assessed after two months. Oilseed radish 'Concord' and 'Control' and daikon radish 'Eco-Till' showed non-host status, with no cyst or egg production, whereas white mustard 'Master' supported higher reproduction. Although statistical differences were not significant, clear biological trends were observed. Microplot trials over two years showed that in 2023 only 'Eco-Till' reduced egg and juvenile densities (3.7%). In 2024, 'Eco-Till' and 'Master' reduced populations by 65.8% and 67.0%, respectively, although variability limited statistical significance. Overall, host status varied among cultivars, with 'Concord', 'Control', and 'Eco-Till' showing the greatest potential for integration into SBCN management programs.

33. EVALUATION OF BENZOIC AND TOLUIC ACID ISOMERS ON MYCELIAL GROWTH AND SCLEROTIAL DEVELOPMENT OF SCLEROTINIA SCLEROTIORUM*

Maria Luiza Paiva de Oliveira1, Dr. Richard Webster1 and Glenn Dorsam2, (1)North Dakota State University, Fargo, ND, (2)Biochemistry - NDSU, ND

One of the most important soybean (*Glycine max L.*) pathogens in North Dakota is *Sclerotinia sclerotiorum*, a necrotrophic fungus with global distribution. Disease control has traditionally relied on chemical pesticides, but interest in naturally derived alternatives is increasing. This study evaluated benzoic acid and three derivatives (m-, p-, and o-toluic acid) at four concentrations (75, 125, 250, and 500 µg/ml) for inhibition of mycelial growth and sclerotial development of one *S. sclerotiorum* isolate on amended PDA plates, compared to non-amended PDA and solvent controls. The experiment included 18 treatments with four replicates across two independent runs, totaling 144 plates. Mycelial growth and sclerotial production were used to generate dose-response curves using the 'drc' package in R (v. 4.5.2). We hypothesized that toluic acid isomers would require higher concentrations for inhibition than benzoic acid. However, all derivatives showed lower EC50 values than benzoic acid (98.5 µg/ml): m-toluic acid (48.1 µg/ml), p-toluic acid (67.5 µg/ml), and o-toluic acid (87.6 µg/ml). These results indicate that inhibition varies by metabolite and concentration, and that small structural differences can significantly affect biological activity. Overall, toluic acid derivatives showed greater effectiveness than benzoic acid, suggesting potential as alternative compounds for disease management.

34. MANAGEMENT OF PLANT PARASITIC NEMATODES IN CHERRY ORCHARDS USING FLUOPYRAM AND COMPOST

Dr. Ali Yaghoubi Akbar1, Razieh Yazdani Fazlabadi2 and Dr. Marisol Quintanilla1, (1)Michigan State University, East Lansing, MI, (2)Center for Tree Science, The Morton Arboretum, Lisle, IL, 60532, USA, Lisle, IL

Plant-parasitic nematodes, particularly *Pratylenchus penetrans*, limit cherry (*Prunus* spp.) production in the Great Lakes region, and post-plant management options remain limited. This study evaluated fluopyram (Velum® Prime), organic amendments, and their combinations on nematodes, tree growth, and yield in established orchards. Field trials at two Michigan sites used a randomized complete block design with six treatments: (1) Velum® Prime, (2) Dairy Doo® compost + straw mulch, (3) Layer Ash Blend® compost + straw mulch, (4) Dairy Doo® + straw mulch + Velum® Prime, (5) Layer Ash Blend® + straw mulch + Velum® Prime, and (6) an untreated control, with four replications. Nematodes including *P. penetrans, Mesocriconema* spp., *Xiphinema americanum*, and beneficial groups were assessed using reproduction factors, along with trunk growth and yield. In year one, compost and fluopyram reduced *P. penetrans* reproduction, though not always significantly, while *Mesocriconema* spp. declined significantly. No significant effects were observed for *X. americanum*. Fluopyram reduced bacterivore and fungivore nematodes, whereas compost maintained these groups. Growth and yield responses varied by site and year. At the Northwest site, Velum® Prime treatments increased growth in year one, while compost effects were greater in year two. The combination of Layer Ash Blend® + straw mulch + Velum® Prime produced the highest yield.

35. IDENTIFICATION AND PATHOGENICITY OF FUNGAL ISOLATES ASSOCIATED WITH FRUIT ROT OF HEIRLOOM TOMATOES IN CENTRAL MISSOURI*

Monika Pokharel and Waana Kaluwasha, Lincoln University of Missouri, Jefferson City, MO

Heirloom tomatoes are valued for their distinctive flavor and cultural significance, yet their production is threatened by fungal pathogens. This study aimed to identify and evaluate the pathogenicity of fungi isolated from field-grown heirloom tomato fruits with rot symptoms. Small pieces of symptomatic fruits were surface sterilized prior to being plated on Potato Dextrose Agar (PDA) amended with antibiotics. Fifty-five recovered isolates were identified by amplifying the internal transcribed spacer (ITS) region using primers ITS1 and ITS2 and comparing ITS sequences for similarity using BLAST analysis. The isolates comprised *Daldinia korfii* (1), *Ceratobasidium ramicola* (2), *Penicillium oxalicum* (3) and various *Fusarium* species (47). Pathogenicity of the isolates was performed on surface-sterilized detached tomato fruits by inserting mycelial plugs of each isolate in addition to plain PDA plugs into artificially wounded fruits. Inoculated fruits were incubated at 22–25°C for 7 days. All isolates caused fruit rot symptoms on all inoculated fruits while the control fruits remained symptom-free. Both isolate and day post-inoculation (dpi) significantly influenced disease progression ($p<0.001$). Variations were also observed in isolate aggressiveness, with *F. longifundum* isolates being more aggressive. These findings reveal a diverse fungal community, highlighting the need for continued monitoring to determine potential fungal pathogens affecting heirloom tomatoes.

36. EVALUATION OF FUNGICIDES FOR CONTROL OF POWDERY MILDEW ON POTTED DILL IN THE GREENHOUSE

Madeline Anthony and Dr. Mary K. Hausbeck, Michigan State University, East Lansing, MI

The demand for high-quality, culinary herbs has increased over the past decade, but strategies to control diseases on these crops are limited. Powdery mildew on dill caused by *Erysiphe heraclei* causes foliar necrosis and plant death when environmental conditions are favorable. We evaluated eleven products for their efficacy against powdery mildew on greenhouse potted dill. In 2026, two greenhouse trials were conducted and included five organic and six conventional fungicides. Five, single plant replicates per treatment were arranged in a completely randomized block design. Treatments were initiated prior to symptom development and reapplied every 7 or 10 days, based on the label. Disease severity was visually assessed every three days as leaf area (%) with powdery mildew colonies and the area under the disease progress curve (AUDPC) was calculated. Myclobutanil (FRAC 3), flutianil (FRAC U13), and fluopyram + trifloxystrobin (FRAC 7, 11) were among the most effective active ingredients tested in this study. Copper oxychloride + copper hydroxide (FRAC BM02) and azoxystrobin (FRAC 11) performed similarly to the control. Our results provide data on effective organic and conventional products including some that are not currently registered for use on dill but could be considered for future label expansion. Additional tools for managing powdery mildew in greenhouse potted dill production could increase plant quality and reduce the potential for pathogen resistance.

37. SHIFT IN SOYBEAN CYST NEMATODE (SCN) POPULATIONS IN OHIO*

Mr. Timothy I. Ralston, Mr. Gillyade C. Menino and Dr. Horacio D. Lopez-Nicora, The Ohio State University, Columbus, OH

Soybean cyst nematode (SCN), *Heterodera glycines*, remains the most economically damaging pathogen of soybean in North America and is distributed throughout Ohio. Since 2018, more than 2,300 soil samples were collected statewide to monitor SCN presence and distribution. With support from the Ohio Soybean Council, growers and county Extension educators submitted samples to the OSU Soybean Pathology Lab following standard protocols, with more than 60% of samples testing positive across 67 counties. A subset of populations (n=150) was evaluated using a modified HG type assay to assess reproduction on resistance sources, including PI 548402 (Peking), PI 88788, and PI 437654, with susceptible checks to calculate female index (FI). Compared to the last statewide survey (1992-1995), where ~70% of populations showed no reproduction on indicator lines (SCN type 0-) and 24% reproduced on PI 88788 (SCN type 2-), current populations indicate a shift toward increased reproduction on resistance sources. The proportion of SCN type 0 decreased to 22%, while ~70% of populations reproduced on PI 88788. Reproduction on Peking was observed in ~30% of populations, representing an increase relative to earlier reports. These findings indicate reduced effectiveness of PI 88788 under field conditions and highlight the importance of monitoring SCN population density and reproduction on resistance sources to inform management decisions and support long-term stewardship of available resistance.

38. ASSESSMENT OF VARIETY RESISTANCE TO FOUR POSTHARVEST DISEASES OF POTATO IN MICHIGAN

Mio Satoh-Cruz1, Ms. Sarah Ruth2 and Dr. Jaime F. Willbur1, (1)Michigan State University, East Lansing, MI, (2)Ohio State University, Wooster, OH

Postharvest disease management is critical due to the year-round demand for potato seed and products from the Great Lakes region. Cultivars with postharvest disease resistance can provide economical and effective management; however, robust phenotyping of variety responses using relevant local isolates is needed. In this study, commercial chipping potato lines and germplasm were assessed for resistance to four major postharvest diseases: Fusarium dry rot (*Fusarium sambucinum*), bacterial soft rot (*Pectobacterium carotovorum*), pink rot (*Phytophthora erythroseptica*), and Pythium leak (*Pythium ultimum*). Asymptomatic tubers were injected at the apical and basal ends with inoculum suspensions of 2-5 x 104 Fusarium conidia, Phytophthora zoospores, or Pythium sporangia/ml and 1 x 108 Pectobacterium CFU/ml. For each pathogen, 10 µl of inoculum suspension were injected to 1 cm under the skin. After incubation, tubers were sliced longitudinally through inoculation sites and internal symptom width and depth were measured. In 2025-26, significant differences in variety response were observed for all diseases ($P < 0.05$). No relationship was observed between resistance responses to different diseases. However, some varieties possessed at least moderate resistance to two or more diseases. Continued testing is in progress and will help to inform growing operations, management practices, and breeding directions for the Michigan potato industry.

39. EVALUATING THE EFFICACY OF COMMERCIAL BIONEMATICIDES FOR THE MANAGEMENT OF PIN NEMATODE (PARATYLENCHUS NANUS TYPE B) IN FIELD PEA*

Mr. Subash Saud, Dr. Guiping Yan, Malaika Ebert, Mr. Addison Plaisance and Mr. Bonventure Isaya Mumia, North Dakota State University, Fargo, ND

Pin nematode (*Paratylenchus nanus* type B) is a major migratory ectoparasite that limits field pea growth and productivity in North Dakota. Although management strategies such as host resistance, crop rotation, organic amendments, bionematicides, and chemical nematicides exist, their effectiveness remains limited. Increasing concerns over the environmental and human health impacts of chemical nematicides necessitate sustainable alternatives. Bionematicides offer a promising eco-friendly approach; however, their efficacy against *P. nanus* in field pea has not been explored. Therefore, this study aims to evaluate four commercial bionematicides, including a non-treated control, for suppressing *P. nanus* and enhancing field pea performance under greenhouse conditions using naturally infested soil. The nematode species was confirmed through morphological and molecular identification, and the experiment will be conducted in a randomized complete block design with four replications using the susceptible cultivar Arcadia. At harvest, data will be collected on plant height, root length, biomass, seed weight, and nematode suppression assessed using the reproductive factor (RF). Mechanistic assays will also be performed on the best-performing bionematicide to better understand its mode of action. This research will help identify effective bionematicide options to manage pin nematode and improve field pea productivity.

40. FIELD PENNYCRESS (THLASPI ARVENSE) SERVES AS A HOST FOR THE CAUSAL AGENT OF SOYBEAN SUDDEN DEATH SYNDROME, FUSARIUM VIRGULIFORME

Briana Hashim1,2, Thomas Goodwill3, Dr. Linda E. Hanson4,5 and Dr. Seung Yon Rhee2,6,7,8, (1)Department of Biochemistry & Molecular Biology, East Lansing, MI, (2)Plant Resilience Institute, East Lansing, MI, (3)USDA ARS SBRU, East Lansing, MI, (4)USDA ARS, East Lansing, MI, (5)Department of Plant, Soil and Microbial Sciences, East Lansing, MI, (6)Department of Biochemistry & Molecular Biology, East Lasning, MI, (7)Department of Plant Biology, East Lansing, MI, (8)Department of Plant, Soil, and Microbial Sciences, East Lansing, MI

Pennycress (*Thlaspi arvense L.*) is an emerging intermediate oilseed crop with promising environmental and economic benefits. In the Midwest, it contributes to soil conservation, nutrient retention, and renewable biofuel production. As a winter annual requiring minimal fertilizer, pesticide, and water inputs, pennycress can fit into traditional corn–soybean rotations, helping restore soil health during the off-season without displacing food crops. As domestication advances, it is critical to evaluate potential risks, particularly susceptibility to fungal pathogens that could impact pennycress and summer crops. This study examined interactions between pennycress and *Fusarium virguliforme*, the causal agent of soybean sudden death syndrome (SDS). Plants were inoculated under controlled conditions and monitored to assess host susceptibility. Through fungal culturing and PCR, we confirmed that pennycress can host *F. virguliforme*, often with limited symptoms. Unlike infected soybean, which shows reduced shoot biomass, pennycress showed no decrease in shoot or root biomass. Infected pennycress plants had foliar and root disease ratings <2 (scale: 1–5), whereas inoculated soybean consistently had ratings of 4–5. This asymptomatic colonization suggests pennycress could act as a pathogen reservoir. Continued investigation into pennycress–pathogen interactions will be essential to develop management strategies while minimizing agronomic risk.

41. ASSESSMENT OF FUNGICIDES AGAINST PSEUDOPERONOSPORA CUBENSIS IN MICHIGAN*

John Rocliffe Spafford, David Perla and Dr. Mary K. Hausbeck, Michigan State University, East Lansing, MI

Pseudoperonospora cubensis is the causal agent of cucurbit downy mildew (CDM), a highly destructive foliar disease of cucumber that can cause significant yield loss if not controlled. CDM is managed with weekly fungicide sprays, but the pathogen has developed resistance to several products. We evaluated fungicides for efficacy against CDM in replicated field plots. Six (2023), seven (2024), or ten (2025) fungicide treatments were initiated prior to symptom development, reapplied weekly to 'Vlaspik' cucumber plants, and visually assessed weekly (0% = no symptoms, 100% = completely diseased). The non-treated plants (control) developed foliar disease of 56.3% to 85% by the end of the trial. CDM was reduced by the fungicide treatments and ranged from 0% to 17.2% (2023); 0.0% to 5.3% (2024); and 2.0% to 46.3% (2025). In 2023 and 2024, all fungicide treatments resulted in reduced disease severity and relative area under disease progress curve (rAUDPC) values than the control; the premix of oxathiapiprolin + chlorothalonil was consistently a highly effective treatment. Treatments of fluazinam, cyazofamid, ametoctradin + dimethomorph, and ethaboxam provided a similar level of control to oxathiapiprolin + chlorothalonil in 2024 and 2025 but not in 2023. Season-long field monitoring of available CDM fungicides is important to inform recommendations to growers and monitor pathogen resistance.

Poster Presentations

42. DETERMINING THRESHOLD LEVELS FOR ROOT LESION NEMATODES (PRATYLENCHUS PENETRANS AND P. CRENATUS) IN CARROT PRODUCTION

Esmaeil Saberi, Michigan State University, East Lansing, MI

Root-lesion nematodes (*Pratylenchus penetrans* and *Pratylenchus crenatus*) are major pests in carrot production, causing yield loss, root necrosis, and deformation. However, economic thresholds for these species are not well defined. Microplot experiments were conducted at Michigan State University (2023–2025) to determine damage thresholds under controlled inoculation levels. Field soils naturally infested with each species were used as inoculum sources and increased under greenhouse conditions using ‘Cupar’ carrot (*Daucus carota*). Five inoculum levels (0, 10, 50, 100, and 250 nematodes per 100 cm^3 soil) were evaluated in a randomized complete block design with six replicates per species. Total biomass was not significantly affected, but marketable yield decreased with increasing nematode density. For *P. penetrans*, significant yield reductions occurred at $\geq$50 nematodes per 100 cm^3 soil, with losses of 36.4%, 44.9%, and 65.3% at 50, 100, and 250 nematodes, respectively. *P. crenatus* showed similar trends, with reductions of 38.7%, 80.1%, and 83.7% at the same levels. Overall, both species caused economically important damage beginning at 50 nematodes per 100 cm^3 soil, suggesting a preliminary economic threshold for carrot production.

43. FUNGICIDE SENSITIVITY AND SPACIO-TEMPORAL CHARACTERIZATION OF CALONECTRIA ILICICOLA ISOLATES FROM ACROSS THE UNITED STATES*

Nathan Tyler1, Dr. Mandy Bish2, Dr. Carl A. Bradley3, Dr. Sunkyu Choi1, Dr. Austin McCoy1, Hyunkyu Sang4, Dr. Darcy E. P. Telenko5 and Dr. Martin Chilvers1, (1)Michigan State University, East Lansing, MI, (2)University of Missouri, Columbia, MO, (3)University of Kentucky, Princeton, KY, (4)Chonnam National University, Gwangju, SOUTH KOREA, (5)Purdue University, West Lafayette, IN

Calonectria ilicicola is a soilborne pathogen causing red crown rot of soybean and black rot of peanut. With the expansion of red crown rot into and around the American Midwest over the past decade, understanding the fungicide sensitivity profiles of modern populations is essential for effective disease management. This study characterizes a diverse collection of *C. ilicicola* isolates, including modern soybean-derived strains from Illinois, Missouri, Indiana, and Kentucky, and historical isolates from Louisiana (from soybean) and North Carolina (from peanut). To facilitate screening a wide range of fungicides, a high-throughput microplate-based assay was adapted for use with *C. ilicicola. C. ilicicola* produces pigments and microsclerotia on many growth media; however, a medium was identified where the mycelium remainshyaline, allowing for high-throughput optical density screening of biomass. Isolates are being screened against fungicides representing multiple modes of action, including succinate dehydrogenase inhibitors and demethylation inhibitors. This research will establish baseline sensitivity distributions and identify potential shifts in efficacy across time, geography, and host origin. The results from this high-throughput methodology could provide a framework for long-term resistance monitoring and inform regional management strategies for this threat to Midwestern soybean production.

44. COMMON SCAB DISEASE SCREENING IN AN IRRIGATED FIELD DISEASE NURSERY REVEALS HIGHLY TOLERANT POTATO VARIETIES

Mrs. Sonal Srivastava, Department of Plant Pathology, University of Minnesota Twin Cities, St Paul, MN, Mia Copeland, Department of Plant Pathology, University of Minnesota Twin Cities, St. Paul, MN, Laura Shannon, Department of Horticultural Science, Saint Paul, MN and Dr. Ashish Ranjan, Department of Plant Pathology, University of Minnesota, St Paul, MN

Potato (*Solanum tuberosum*) faces significant biotic stresses, with common scab reducing tuber quality and market value. The primary pathogen, *Streptomyces scabies*, is a Gram-positive actinobacterium that persists in soil for many years and is difficult to manage. While crop rotation, soil fumigation, and soil pH management reduce disease incidence, resistant cultivars provide the most effective long-term strategy. Our objective was to identify potato varieties with strong tolerance to common scab among commercial cultivars and new University of Minnesota breeding lines. We established a disease screening nursery in a heavily infested, irrigated field at the Sand Plain Research Farm in Becker, MN. In 2024 and 2025, cultivars and breeding lines were evaluated using a randomized complete block design with four replications of ten hill plots. At harvest, 10–12 tubers per plot were randomly collected and rated for scab severity using standardized scales to calculate disease severity percentage. Results identified seven highly tolerant UMN breeding lines: MN18CO15083-006, MN21ND1845B-030, MN18CO16154-009, MN21ND1835B-059, MN21ND1835B-031, MN21ND1835B-136, and MN21ND1835B-001. Five commercial cultivars also demonstrated high tolerance: Chieftain, Red Norland, Dakota Russet, Goldrush, and Umatilla Russet. These tolerant lines and cultivars provide valuable genetic resources for breeding programs and offer growers effective options for managing common scab.

45. FUNGICIDE SENSITIVITY OF ALTERNARIA ALTERNATA AND CERCOSPORA BETICOLA ISOLATES IMPACTING MICHIGAN SUGARBEET*

Ms. Emily Jordyn Weedon1, Ms. Sarah Ruth2, Dr. Linda E. Hanson1,3, Dr. Jaime F. Willbur1 and Alexandra Gray1, (1)Michigan State University, East Lansing, MI, (2)Ohio State University, Wooster, OH, (3)USDA ARS, East Lansing, MI

Beet derived sugar makes up about 50-60% of the domestic sucrose production in the United States. Of the many diseases and pests that impact this industry, leaf spots are among the most significant foliar diseases of sugarbeet. Reports of leaf spot prevalence paired with decreased fungicide efficacy have raised concerns about current management programs in the affected regions. The aim of the current study was to identify Alternaria alternata, *Cercospora beticola*, and other foliar pathogen populations impacting Michigan and characterize isolate fungicide sensitivities. Using the spiral gradient dilution method, isolate responses were screened to the active ingredients of fungicides registered for use in Michigan including demethylation inhibitors (DMI), benzimidazoles, quinone outside inhibitors (QoI), and organo-tin. Across five years of data collection, *A. alternata* and *C. beticola* isolates from 2025 were significantly more resistant to tetraconazole and mefentrifluconazole than in previous years ($P<0.05$). Based on preliminary data, there were also significant differences in isolate responses based on county of origin to several active ingredients across all years ($P<0.05$). Additional screening for both pathogens is ongoing, but preliminary data indicates potential areas for improving foliar disease management in sugarbeet.

Poster Presentations

46. A SURVEY OF MISSOURI ELDERBERRY VIRUSES REVEALS A NEW VARIANT OF TOBACCO RINGSPOT VIRUS (TRSV) AND A NOVEL GEMINIVIRUS

Dr. Peng Tian, The Division of Plant Sciences and Technology, University of Missouri, Columbia, MO, Dr. Lili Zhang, The Division of Plant Science and Technology, University of Missouri, Columbia, MO, Dr. James E. Schoelz, Division of Plant Science and Technology, University of Missouri, Columbia, MO, Mr. Patrick Byers, University of Missouri Extension, Springfield, MO and Dr. Andrew Thomas, University of Missouri, Columbia, MO

The American elderberry industry in the U.S. continues to experience rapid growth, with Missouri leading this nationwide interest. Elderberry is a native species and easy to grow. However, as concentrated plantings are established, we are finding increased pest and disease pressure including viral diseases. Information on viruses that infect elderberry is lacking. High-throughput sequencing using total RNA from six elderberry cultivars revealed the presence of common viruses such as elderberry virus C (EVC) and D (EVD), as well as two new viruses; one is potentially a novel variant of tobacco ringspot virus (TRSV) showing 85% homology to the reference genome sequence, and the second is a novel geminivirus, which is most closely related to a Euphorbia caput-medusae virus, with a percent nucleotide identity between the two genomes at 62%. Given a species threshold of 78% nucleotide sequence identity for geminiviruses, we propose that this geminivirus is a new species for elderberry. We designed specific PCR primers for detection of the TRSV variant and the novel geminivirus and screened 400 elderberry samples from different regions of Missouri collected in 2023 and 2024. Of the 400 samples, 55 and 65 samples tested positive for the TRSV variant and the geminivirus, respectively. This project allows us to better understand the diversity of viruses in elderberry and to establish a foundation to assist nursery leaders in generating virus-free cuttings for the market.

47. COMPARATIVE TRANSCRIPTOMICS TO IDENTIFY MULTI-CROP AGGRESSIVENESS DETERMINANTS OF SCLEROTINIA SCLEROTIORUM*

Mr. Hsuan Fu Wang, University of Minnesota, Minneapolis, MN, Dr. Cory Hirsch, Department of Plant Pathology, University of Minnesota, St. Paul, MN and Megan McCaghey, University of Minnesota, Saint Paul, MN

Management of *Sclerotinia sclerotiorum* is limited by its wide host range and partial resistance of host crops. This study utilized comparative transcriptomics to identify genetic determinants of pathogen aggressiveness across crops. RNA sequencing was implemented on soybean and sunflower stem tissues infected with six isolates, including highly and low aggressive isolates, at 24, 48, and 96 hours post-inoculation (hpi). Overall pathogen expression showed distinct infection dynamics between soybean and sunflower. Pathogen expression in soybean gradually increased from 24 to 96 hpi, while in sunflower, expression declined after 24 hpi. Comparing highly versus mildly aggressive isolates at 48 hpi, 3,129 differentially expressed genes (DEGs) in soybean (1,653 upregulated) and 817 DEGs in sunflower (269 upregulated) were identified. Gene Ontology analysis indicated aggressive isolates consistently upregulated intracellular functions and protein synthesis across both hosts. Conversely, host-specific strategies were prominent; aggressive isolates on sunflower upregulated cell wall degrading enzymes and lipid metabolism, while upregulating ATP synthesis and proteasome activity on soybean. Understanding candidate genes upregulated by aggressive isolates across crop species can provide insights into *S. sclerotiorum* virulence and potential targets for RNAi.

48. LINKING WEATHER VARIABLES AND QPCR DETECTION TO TARGET SPOT DISEASE FAVORABILITY IN COTTON BELT

Dr. Carolina Mazo Molina1, Dr. Hui-Ching Yang1, Dr. Akhtar Ali2, Dr. Thomas W. Allen3, Dr. Kaitlyn Bissonnette4, Dr. Maira R. Duffeck5, Dr. Chase Floyd6, Dr. Thomas S. Isakeit7, Dr. Heather M. Kelly8, Dr. Robert Kemerait9, Dr. Kathy S. Lawrence10, Dr. Cecilia Monclova-Santana11, Dr. John D. Mueller12, Dr. Paul Price13, Dr. Ian M. Small14, Dr. Amanda L. Strayer-Scherer15, Dr. Bradley Wilson6, Dr. Terry N. Spurlock16 and Dr. Alejandro Rojas1, (1)Michigan State University, East Lansing, MI, (2)University of Tulsa, Tulsa, OK, (3)Mississippi State University, Stoneville, MS, (4)Cotton Incorporated, Cary, NC, (5)Oklahoma State University, Stillwater, OK, (6)University of Missouri, Portageville, MO, (7)Texas A&M University, College Station, TX, (8)University of Tennessee, Jackson, TN, (9)Department of Plant Pathology, Tifton, GA, (10)Entomology and Plant Pathology, Auburn University, Auburn, AL, (11)USDA Agricultural Research Service (ARS), TX, (12)Edisto Research and Education Center, Blackville, SC, (13)Louisiana State University, Winnsboro, LA, (14)University of Florida, Quincy, FL, (15)Auburn University, Auburn, AL, (16) University of Arkansas System Division of Agriculture, Lonoke, AR

Target spot, caused by *Corynespora cassiicola*, is a foliar disease of cotton that results in defoliation and yield losses. Since 2020, the National Predictive Modeling Tool Initiative has deployed spore traps across 11 cotton-producing states to monitor this pathogen. DNA from spore-trap samples was analyzed by quantitative PCR (qPCR) targeting the elongation factor 1-alpha gene. Preliminary qPCR results confirmed the presence of the pathogen in TX, OK, TN, MO, AR, SC, AL, MS, GA, FL, and LA from July to September in both 2020 and 2021, despite disease symptoms not being observed at every location. Using Crop Risk Tool weather database, environmental factors such as air temperature, dew point (DP), and relative humidity (RH) were obtained for each location and associated with pathogen detection. Here, we found that DP and RH % were major determinants of disease favorability. In TX and OK, DP (15°C) and RH (57%) were lowest, correlating with reduced spore counts (Log10 > 2.6). In TN, SC, MO, AR, and AL, DP (19–21°C) was lower than optimal, but RH (76–82%) increased, leading to higher spore counts (Log10 = 3.1–4.2). In MS, GA, FL, and LA, both DP (21–22°C) and RH (80–82%) were highest, but spore counts remained steady (Log10 = 3.1–4.2). Preliminary conclusions indicate that environmental variables alongside qPCR spore-detection data suggest that locations with DP >19ºC and RH ≥80% may offer favorable conditions for target spot spread and potential development.

49. GLOBAL PATTERNS OF FUNGICIDE RESISTANCE SUGGEST WIDESPREAD MUTATIONS IN FUNGAL FAMILIES ACROSS AGRICULTURAL AND CLINICAL SETTINGS*

Kincer Amburgey-Crovetti, Department of Plant Pathology, University of Nebraska, Lincoln, NE, Xin Zhi Khoo, Department of Ecology and Evolutionary Biology, University of California, Irvine, Irvine, CA and Dr. Teddy Garcia-Aroca, Department of Plant Pathology, University of Nebraska-Lincoln, Lincoln, NE

Fungicide resistance has been an increasing threat to plant disease management since the 1980s; yet, studies rarely focus on global patterns, oftentimes failing to document links between agricultural and clinical resistance. We analyzed patterns of antifungal resistance using FungAMR, the largest publicly available database of fungal antimicrobial data, to assess if resistance-associated mutations were shared across countries and between environments. Entries were filtered to include only isolates with a documented origin source, including geographical data. We compared taxonomic distribution and mutation occurrence globally. Agricultural environments were dominated by members of *Glomerellaceae, Mycosphaerellaceae,* and *Didymellaceae,* while *Saccharomycetaceae, Pneumocystidaceae, and Trichocomaceae* dominated clinical environments. *Nectriaceae* was the only family to appear in both environments, indicating limited taxonomic overlap; however, several resistance-conferring mutations identified in agricultural isolates were historically linked to the clinical environment, suggesting potential convergence across environments. These findings highlight that, while resistance is largely distinct, there are notable and concerning overlaps that may contribute to the emergence and spread of resistance, underscoring the importance of integrating multiple environments and geographic locations to better understand and manage fungicide resistance.

50. CLARIFICATION OF GENETIC RELATIONSHIPS AMONG INTRASPECIFIC GROUPS WITHIN RHIZOCTONIA SOLANI AG 2-2

Dr. Douglas H. Minier, Michigan State Universitry, East Lansing, MI, Dr. Frank N. Martin, USDA ARS, Salinas, CA and Dr. Linda E. Hanson, USDA ARS, East Lansing, MI

Rhizoctonia root and crown rot is a major constraint on sugar beet production worldwide. The causal agent, *Rhizoctonia solani* AG 2-2, also affects many of the crops grown in rotation with sugar beet, complicating management. Strains that affect sugar beet have traditionally been separated into the intraspecific groups (ISGs) IIIB and IV based on growth at 35°C. However, the monophyly of these groups has been questionable for nearly two decades. We conducted a multi-gene phylogenetic analysis to clarify relationships within AG 2-2 and to establish a more biologically meaningful framework for describing its diversity. We also analyzed multilocus genotypes from a global collection of isolates using eight microsatellite markers, providing support for phylogenetic groupings and insight into the generation of diversity. Our results clearly demonstrate that the ISGs IIIB and IV are not phylogenetically supported. Therefore, we propose revised ISGs that more accurately reflect evolutionary relationships and may help explain some behavioral differences among isolates previously considered part of the same ISG. Multilocus genotypes show evidence of genetic exchange between these newly defined ISG, resulting in intermediate or hybrid genotypes. This refined understanding of diversity within AG 2-2 provides a foundation for reexamining host responses and other variability and may inform improved management strategies for Rhizoctonia root and crown rot.

51. MANAGING POTATO EARLY DIE: THE ROLE OF SOIL FUMIGATION IN SUPPRESSING COLONIZATION BY VERTICILLIUM DAHLIAE AND COLLETOTRICHUM COCCODES*

Chloé Buissé, Mr. Daniel James Gill, Dr. Marcio Zaccaron and Dr. Julie S. Pasche PhD, North Dakota State University, Fargo, ND

Soil fungi *Verticillium dahliae* and *Colletotrichum coccodes*, and root lesion nematodes (*Pratylenchus* spp.), interact synergistically to cause potato early dying (PED). Symptoms include wilting, chlorosis, necrosis, and early senescence. PED can cause decreased tuber size and yield losses up to 50%. Management includes cultural practices, resistant varieties, and soil fumigation. The effects of cultural practices are limited, and the processing quality of resistant varieties falls below industry standards. Soil fumigation is the most efficacious solution. In addition to management challenges, the roles of the two fungi in ped remain unclear. Our objective is to evaluate the performance of cultivars and soil fumigants in reducing soil infestation and plant colonization by *V. dahliae* and *C. coccodes* PED, and increasing yield. A commercial field fall-fumigated in replicated strips with one rate of metam sodium and three rates of chloropicrin was planted to frozen French-fry processing cultivars Russet Burbank, Dakota Russet, Hamlin Russet, and Bannock Russet. V. dahliae soil levels were significantly reduced by metam sodium and mid- and high-chloropicrin rates. *C. coccodes* soil levels were low and remained low post-fumigation. Significant yield increases resulted from all fumigation treatments. Bannock Russet displayed the lowest wilt and black dot stem incidence. This research advances PED management through better understanding of pathogen roles and soil fumigation.

52. SPATIO-TEMPORAL DYNAMICS OF RED CROWN ROT OF SOYBEAN: SATELLITE-BASED EVIDENCE OF INTER-SEASONAL PERSISTENCE AND EXPANSION

Mr. Bruno Daniel Pugliese, UIUC, Urbana, IL, Dr. Juan Paredes, University of Illinois, Urbana, IL and Dr. Boris Xavier Camiletti, University of Illinois Urbana-Champaign, Urbana, IL

Red crown rot (RCR) of soybean (*Calonectria ilicicola*) is an emerging soilborne disease that survives long-term in soil as microsclerotia. Quantifying disease spatio-temporal dynamics between soybean seasons in typical Illinois corn-soybean rotations is therefore critical. This study quantified RCR inter-seasonal spatial dynamics using high-resolution PlanetScope satellite imagery (3×3m) and a validated Random Forest model to map RCR across six commercial Illinois soybean fields (three evaluated in 2022 and 2024, and three in 2023 and 2025). Classification maps from each consecutive soybean season were overlaid to derive transition matrices, categorizing pixels as recovered (diseased only in season 1), persistent (diseased in both seasons), or expanded (newly diseased in season 2). The proportion of the original diseased area that persisted between seasons was calculated. Results showed that the RCR-affected area consistently increased across all fields, with net expansion ranging from 9% to 205%. On average, 65% (ranging from 55% to 71%) of the originally diseased areas remained affected in the subsequent season. Newly diseased areas (expansion) consistently outweighed recovered zones. These results indicate that *C. ilicicola* maintains its original spatial footprint across rotations while progressively colonizing adjacent field zones. Rising seasonal disease pressure underscores the need for effective management and further research into what is driving expansion.

Poster Presentations

53. TRACING A RE-EMERGENT COTTON PATHOGEN: DETECTION OF RAMULARIOPSIS FROM FUNGARIUM SPECIMENS*

Jazmin Rocio Gomez Cruz1, Dr. Carolina Mazo Molina1, Dr. Hui-Ching Yang1, Dr. Catalina Salgado-Salazar2 and Dr. Alejandro Rojas1, (1) Michigan State University, East Lansing, MI, (2)USDA-ARS, Beltsville, MD

Areolate mildew is a re-emerging cotton disease in the southern U.S. Although widespread in the U.S. since the late 1800s and persistent in tropical regions, recent disease outbreaks have caused significant damage and yield losses. The fungal genus *Ramulariopsis* contains the two species implicated in the current epidemics, yet available tools and biological understanding remain limited. Diseased cotton collections from the late 1800s and 1900s provide a unique opportunity to investigate the historical population of this re-emergent pathogen, however these specimens pose major challenges due to degraded DNA and host-derived sequences. Although a recently developed qPCR assay targeting the EF-1 gene allows pathogen detection in these samples, recovering pathogen-derived sequences through high-throughput sequencing remains uncertain. To address this, we evaluated *Ramulariopsis* detection in cotton herbarium specimens using short-reads and a targeted bioinformatics workflow. Reads were quality-filtered, host sequences removed, and remaining reads were analyzed using taxonomic classification and targeted searches for pathogen-associated genes. Fungal sequences were consistently recovered and aligned with *Ramulariopsis*, supporting ongoing efforts to expand and strengthen DNA-based sourced for these pathogens, complement molecular diagnostics and enable comparisons between historical and contemporary pathogen populations.

54. ADVANCING GENOMIC RESOURCES FOR SPONGOSPORA SUBTERRANEA F. SP. SUBTERRANEA TO SUPPORT COMPARATIVE ANALYSES

Dr. Sujata SINGH Yadav1, Kim Zitnick-Anderson2 and Dr. Julie S. Pasche PhD2, (1)North Dakota State, Fargo, ND, (2)North Dakota State University, Fargo, ND

Potato powdery scab, caused by *Spongospora subterranea* f. sp. *subterranea* (Sss), is a soilborne protist that reduces tuber quality, marketability, and economic value. Genomic study of this obligate protist remains constrained by the difficulty of obtaining pathogen-enriched genomic resources. This study aimed to recover reliable Sss-derived genomic content from diverse powdery scab samples to provide broader insight into the pathogen and its genetic relationships. Whole genome sequencing was performed on 15 infected samples to assess pathogen sequence recovery from complex biological material for downstream analyses. Pathogen recovery varied widely across samples, allowing clear separation of high-confidence datasets. Those high-confidence samples showed strong genome-wide pathogen representation and were prioritized for de novo assembly to separate strongly supported pathogen contigs from host-associated and non-target sequences. Potential samples for variant calling, phylogenetic analysis, and future genome improvement were identified using sequence alignment, assembly quality metrics, and overall completeness measures. The approach improves genomic analysis of an obligate soilborne protist directly from complex diseased plant tissues. In the longer term, these genomic resources can unlock the pathogen genetic information, enable better tracking of pathogen populations, and advance effective control strategies.

55. PHENOTYPIC DIVERSITY WITHIN RHIZOCTONIA SOLANI ANASTOMOSIS GROUP 2-2 (AG 2-2)*

Vikram Kumbala1, Dr. Douglas H. Minier1 and Dr. Linda E. Hanson1,2, (1)Michigan State University, East Lansing, MI, (2)USDA-ARS, East Lansing, MI

Rhizoctonia solani AG 2-2 is a soilborne pathogen of several crops, including sugar beet, soybean, dry bean, and corn. It can cause damping-off- or root rot. *Rhizoctonia solani* is a species complex, divided into at least 13 anastomosis groups (AGs) based on hyphal fusion. AG 2-2 has been divided into several subgroups relating to symptoms, hosts, temperature response, rather than genetic structure. However, molecular studies have shown that the traditional subgroups AG 2-2IIIB and AG 2-2IV, are not monophyletic. A recent multigene phylogenetic analysis placed AG 2-2 strains into two genetic lineages classified here as PR and BR. The current study evaluated whether these genetic groups exhibit cultural traits that might be diagnostic. Representative isolates from PR and BR were assessed for radial growth, colony morphology, and sclerotial traits on malt extract agar and corn meal agar using two replicates per experiment, with each test conducted twice. Results showed that isolates in group PR exhibited significantly faster radial growth compared to isolates in group BR on both media across runs ($p < 0.001$). Colony morphology, including colony texture and sclerotial traits such as distribution and size of sclerotia, also exhibited group-level patterns. Overall, the tested phenotypic variation aligned with genetic structure, providing further support for the classification of AG 2-2 into these genetic lineages.

56. MITIGATING DISEASE DEVELOPMENT IN CALIFORNIA VEGETABLE TRANSPLANTS WITH HACCP APPROACH AND MICROBIOME ANALYSIS

Dr. Hui-Ching Yang1, Andy Salazar2, Johanna M. Del Castillo Munera3 and Dr. Alejandro Rojas1, (1)Michigan State University, East Lansing, MI, (2)UC Davis, Davis, CA, (3)University of California, Davis, Davis, CA

Vegetable transplant industry in California faces increasing disease management challenges. To enhance best management practices and reduce losses, we conducted a site-specific Hazard Analysis of Critical Control Points (HACCP) assessment across five nurseries from 2022 to 2023. Seedlings (tomato, broccoli, and melon) and environmental samples (benches, trays, substrate, and irrigation water) were analyzed using amplicon sequencing targeting fungal ITS1 and bacterial 16S-V4 regions. Results showed that fungal microbiome diversity varied significantly in seedlings and bench/tray samples across nurseries, while no significant differences were observed in substrate or irrigation water. Pathogen OTUs were generally more prevalent in symptomatic than asymptomatic seedlings. Major fungal pathogens shared across crops included *Alternaria, Fusarium, Stemphylium, Curvularia, Mycosphaerella,* and *Sclerotiniaceae* sequences including *Botrytis/Sclerotinia. Pseudomonas* was the dominant bacterial pathogen across crops. While *Alternaria* was linked to trays and benches, *Fusarium* was detected in water and on surfaces. *Botrytis/Sclerotinia* could not be traced back to any sampled sources, suggesting potential seedborne contamination. Moreover, microbial abundance on sanitized surfaces was not consistently lower than in dirty conditions, suggesting gaps in disinfection protocols. This study identifies critical control points to help reduce infection risks and improve transplant health.

Poster Presentations

57. CHARACTERIZATION OF SOIL DIAZOTROPHS FOR TRIPLE-ACTION POTENTIAL AGAINST FUSARIUM GRAMINEARUM, SCLEROTINIA SCLEROTIORUM AND XANTHOMONAS TRANSLUCENS.*

Mr. Nikhil Lnu1, Sachin Sharma2, Riya Jain2, Christopher Graham3, Jose Gonzalez2, Gazala Ameen2, Volker Brozel2 and Shyam Solanki2,4, (1) South Dakota State Univ, Brookings, SD, (2)South Dakota State University, Brookings, SD, (3)Agronomy, Horticulture & Plant Science, South Dakota State University, Brookings, SD, (4)Department of Agronomy, Horticulture, and Plant Sciences South Dakota State Univ, Brookings, SD

Nitrogen is vital for plant growth and metabolism, yet heavy reliance on chemical fertilizers has compromised soil health and environmental integrity. Soil phytopathogens such as *Xanthomonas translucens* (Xt), *Fusarium graminearum* (Fg), and *Sclerotinia sclerotiorum* (Ss) cause significant crop losses. Some soil-associated diazotrophs exhibit N-fixation potential however, their pathogen suppression ability remains largely unexplored. This study aimed to isolate and characterize soil diazotrophs from South Dakota for their triple action potential of nitrogen fixation and bacterial and fungal pathogen suppression as sustainable bioinoculants. A total of 137 bacteria were cultured on nitrogen-free medium; twelve isolates (A–L) were tested for antagonistic activity against Fg, Ss, and Xt, followed by whole genome sequencing (WGS). In dual culture and bVOCs assays, isolates A, D, E, and K suppressed Fg, with A and D showing the strongest inhibition. Isolates A, D, E, F, and K showed antagonism against Ss. Notably, K and J inhibited Xt, indicating a broader antagonistic spectrum. WGS placed these isolates within Beta- and Gamma-proteobacteria, with a few in Alpha-proteobacteria group. Further, Fast-ANI and dDDH identified isolate-B as a novel *Caballeronia* strain, confirmed by 100% genome completeness via CheckM2. Collectively, these BCAs show strong bioinoculant potential, and ongoing sequencing and plant studies will further validate their role in sustainable agriculture.

58. EVALUATION OF WISCONSIN AND MICHIGAN POST-STORAGE S1084 HEMP GRAIN SAMPLES FOR FUNGAL CONTAMINATION

Derrick Grunwald, University of Wisconsin Madison, Madison, WI, Lia Ashkenazi, University of Wisconsin-Madison, Madison, WI and Shelby Ellison, University of Wisconsin, Madison, WI

An emerging threat to hemp production in the midwestern United States is head blight (HB) in grain hemp. Previously, *Fusarium graminearum* had been isolated from grain hemp grown in Wisconsin during the 2024 growing season. Since then, additional Fusarium species have been isolated from hemp exhibiting HB symptoms during the 2025 growing season. The isolation of these pathogens has motivated investigations into whether *Fusarium* infection may also occur in grain threshed from infected hemp grain heads. This is important for two-fold reasons: (1) infected seed may serve as an inoculum source in future field seasons that use these seeds as planting material, and (2) mycotoxigenic *Fusarium* species that actively produce mycotoxins (e.g., DON) at levels exceeding safety thresholds threaten the salability of grain as feed for animals. Using threshed grain samples obtained from the multi-site S1084 trials, we conducted preliminary investigations into the incidence of *Fusarium* infections in grain lots from hemp grown in Michigan and Wisconsin during the 2024 field season. Here, we report that fungal contamination varied by supplier and trial site with infection rates ranging from 0% to a maximum of 27%. These data set the foundation for understanding overall risk of contamination by fungal species toward hemp grain and highlight the need for better understating how both fungal infection and mycotoxin accumulation may be mitigated in post-harvest systems.

59. SEEDLING DISEASE OF SUGAR BEET CAUSED BY FUSARIUM SPP. IN MICHIGAN*

Pranavasri Maddi, Michigan State University, East Lansing,, MI, Dr. Linda E. Hanson, USDA ARS, East Lansing, MI; USDA-ARS, Sugar Beet and Bean Research Unit, Michigan State University, East Lansing, MI and Thomas Goodwill, USDA ARS SBRU, East Lansing, MI

Sugar beet (*Beta vulgaris*) production in Michigan is affected by seedling diseases that can reduce stand establishment. Field surveys starting in 2008 consistently identified *Fusarium* spp. as one of the common isolates from symptomatic seedlings. Limited research exists on Fusarium interactions with sugar beet at the seedling stage. This study aimed to improve understanding of these interactions. A total of 54 *Fusarium* spp. isolates were selected to represent both commonly recovered species and those not previously reported as pathogenic on sugar beet seedlings. A subset of 13 isolates from eight species was evaluated on two breeding lines, C869 (susceptible) and FC309 (resistant to Fusarium wilt, *F. oxysporum* in adults). Greenhouse assays using colonized sterile barley grain inoculum with *F. acuminatum, F. avenaceum, F. circinatum, F. equiseti, F. graminearum, F. oxysporum, F. proliferatum,* and *F. semitectum*, found all tested isolates caused significant ($P < 0.0001$) seedling symptoms compared to a water control. Disease severity was similar across both breeding lines, indicating that resistance to Fusarium wilt does not confer seedling resistance. Notably, *F. circinatum, F. graminearum,* and *F. semitectum* are reported here for the first time as causal agents of sugar beet seedling disease. These findings support the importance of *Fusarium* spp. in Michigan sugar beet production.

60. PHAGE INDUCTION IN PSEUDOMONAS SYRINGAE PV. MORSPRUNORUM RACE 1

Paige Franklin1, Makayla Ritko2, Dr. Daniel Maddock3 and Dr. Michelle Hulin2, (1)Michigan State Univ - East Lansing, MI, East Lansing, MI, (2) Michigan State University, East Lansing, MI, (3)Michigan state university, MI

Bacterial canker is a devastating disease affecting stone fruit trees. This disease is caused by the *Pseudomonas syringae* species complex, including *Pseudomonas syringae* pv. *morsprunorum* race 1 (PsmR1). PsmR1 evolves through horizontal gene transfer (HGT) mediated by bacteriophages. Previous work shows that prophage 1 (pp1) alters bacterial virulence . Understanding the role of these phages in virulence evolution will provide a better understanding of disease emergence .This project investigates the activation of pp1 in PsmR1. As pp1 is temperate, it's DNA remains integrated in the bacterial genome. When the phage is dormant and passively replicating, it is referred to as the lysogenic cycle. Excision and circularization of the phage occurs with induction into the lytic cycle. In this case, phage DNA is replicated to produce phage particles and lyse the host cell. Polymerase chain reaction (PCR) was performed to detect integrated, excised, and circularized phage DNA. Induction of pp1 was achieved by treating PsmR1 with the antibiotic mitomycin C and with UV treatment. Quantitative PCR (qPCR) was used to assess the amount of circularized phage DNA present. The C1-Cro promoter, which regulates the switch between lytic and lysogenic cycle, was cloned with fluorescent reporters and transformed into PsmR1 to visualize phage activation. This work aims to develop tools to study phage activation in PsmR1 to understand how this phage mediates HGT and evolution.

Poster Presentations

61. COMPARISON OF DRONE AND GROUND RIG APPLICATIONS TO CONTROL FOLIAR DISEASES IN CORN IN INDIANA IN 2025*

Monica Sayuri Mizuno and Dr. Darcy E. P. Telenko, Purdue University, West Lafayette, IN

Foliar diseases in corn cause a significant challenge to agricultural production, presenting a considerable risk to yield. Scouting at VT/R1 growth stage is recommended to guide timely fungicide applications and limit disease impact. While traditional sprayers are widely used to apply fungicides, drones offer an alternative when field access is restricted. The main objective was to evaluate different application methods by comparing traditional sprayer application and drone for corn foliar diseases management. Trials were conducted at Purdue farms located in northeast (NE), central (CE), and southeast (SE), Indiana. Mefentrifluconazole + pyraclostrobin at 0.5 L/ha was applied at the tassel/silk (VT/R1) growth stage. Treatments included a ground rig at 187.3 L/ha and drone at 18.7 L/ha and 46.9 L/ha. Foliar diseases such as gray leaf spot (GLS), tar spot, southern rust (SR), and northern corn leaf blight (NCLB) were rated and yield harvested and adjusted to 15.5% moisture. At NE, all application methods reduced tar spot, SR, and NCLB; in CE, all application methods reduced GLS and tar spot; and in SE, all application methods reduced GLS and SR severity compared to nontreated control. Drone application at 46.9 L/ha resulted in higher yield in CE, while no significant yield differences were observed among treatments in NE and SE. Overall, drone applications demonstrate potential as an effective disease management tool, with yield potential varying by region.

62. MICROBIAL COMMUNITY SHIFTS ON SUGAR BEET LEAVES IN RESPONSE TO CERCOSPORA LEAF SPOT INFECTION*

Asmaa Morsi1, Rachel P. Naegele2, Linda E. Hanson2, Sarah Lebeis1 ; 1Michigan State University 2USDA-ARS, East Lansing, MI

Cercospora leaf spot (CLS), caused by the fungus *Cercospora beticola* is a major foliar disease of sugar beet in many parts of the world. Management strategies such as fungicide application and cultural practices have improved disease control. Investigating plant-microbe interactions has the potential to uncover new tools for strengthening disease resistance while under standard management strategies. In this study, we investigate bacterial community shifts in the sugar beet phyllosphere in relation to CLS infection under inoculated or fungicide-treated field conditions. Field experiments were conducted in 2023 and 2025, evaluating a CLS multi-gene resistant and susceptible beet lines grown under non-inoculated with fungicides applied and inoculated no-fungicide treatments. Leaf samples were collected at early, mid, and late disease progression stages, and ectophytic bacterial communities were characterized using 16S rRNA amplicon sequencing. Preliminary results indicate that bacterial community structure changed significantly over time and was strongly associated with disease progression. Characterizing shifts in community structure could highlight beneficial or detrimental microorganisms involved in CLS progression, possibly informing more targeted disease management.

63. SPONGOSPORA SUBTERRANEA F. SP. SUBTERRANEA DIVERSITY AND CONTROLLED INFECTION ASSAYS FOR POWDERY SCAB RESISTANCE SCREENING IN POTATO*

Fatema Akter Nisha1, Sujata Yadav2, Kim Zitnick-Anderson1 and Dr. Julie S. Pasche PhD1, (1)North Dakota State University, Fargo, ND, (2) North Dakota State University, ND

The cercozoan pathogen *Spongospora subterranea* f. sp. *subterranea* (Sss) causes powdery scab on potatoes and is responsible for significant losses in potato production worldwide. Infection causes root galls and tuber pustules, reducing market quality. The pathogen also vectors potato mop-top virus (PMTV), further reducing tuber quality and increasing economic losses. Currently, effective powdery scab control options are unavailable, making the development of resistant potato cultivars a critical management strategy. However, breeding progress has been constrained by the limited availability of germplasm with dual resistance to root and tuber infection, along with insufficient understanding of pathogen population biology and genetic diversity. Characterizing genetic diversity and Sss population structure are essential for identifying representative samples for resistance screening and supporting durable disease management strategies. Preliminary controlled infection assays detected variation in the incidence and severity of root galls and tuber pustules across potato lines. Ongoing evaluations will incorporate diverse Sss samples and a broader range of potato germplasm to improve understanding of host–pathogen interactions. Phylogenomic analyses of populations across major U.S. potato-growing regions will guide the selection of Sss samples. Findings will support the development of resistant cultivars and improve long-term disease management

64. DEEP LEARNING-BASED CLASSIFICATION OF WHEAT FOLIAR DISEASES WITH A FOCUS ON BACTERIAL LEAF STREAK DISEASE*

Mr. Tapish Pawar1, Carolyn Heisel2, Maitiniyazi Maimaitijiang3, Kishore Chittem4, Shyam Solanki1 and Gazala Ameen1, (1)Agronomy, Horticulture & Plant Science, South Dakota State University, Brookings, SD, (2)Department of Biology and Microbiology, Brookings, SD, (3) Department of Geography and Geospatial Sciences, South Dakota State University, Brookings, SD, (4)Agaiomics Technologies LLC, Garfield, MN

Wheat is a major staple crop worldwide, yet its productivity is threatened by plant pathogens. Among foliar diseases, bacterial leaf streak (BLS), caused by *Xanthomonas translucens*, can lead to 60% yield losses under severe outbreaks. Effective disease management and resistance breeding require accurate phenotyping; however, traditional visual disease assessments are time-consuming, subject to inter-rater variability, and error-prone. This study presents an automated classification using convolutional neural networks to identify wheat foliar diseases under field conditions. A hybrid dataset was developed by combining field and greenhouse acquired BLS imagery, with publicly available wheat foliar diseases datasets captured using smartphones and digital cameras. Multiple deep learning architectures, including ResNet50, VGG16, EfficientNetB0, MobileNetV2, MobileNetV3-Small were benchmarked against a Support Vector Machine (SVM) baseline. Transfer learning was implemented by training the classification head with frozen base layers, followed by fine-tuning at a reduced learning rate. The results show that deep learning models consistently outperformed SVM. ResNet50 achieved the highest accuracy (95.4%) with perfect recall for BLS detection, demonstrating the potential of deep learning for accurate, efficient wheat disease phenotyping. Future work will focus on disease classification to quantification, and deployment for in-field, mobile-based diagnosis.

Poster Presentations

65. MONITORING QOI FUNGICIDE RESISTANCE IN DIAPORTHE SPECIES USING CYTOCHROME B GENE SEQUENCING*

Dilorom Rasuleva1, Ms. Karthika Mohan2, Mr. Danillo Leite3, Dr. Ahmad M. Fakhoury3 and Dr. Febina Mathew2, (1)North Dakota State University, ND, (2)North Dakota State University, Fargo, ND, (3)Southern Illinois University, Carbondale, IL

Diaporthe species cause diseases of soybean (*Glycine max* L.), including Diaporthe seed decay, pod and stem blight (PSB), and stem canker. Yield losses attributed to *Diaporthe* species were estimated at approximately 1 million metric tons in 2024 across 28 U.S. soybean-producing states. Quinone outside inhibitor (QoI) fungicides containing azoxystrobin are used to manage PSB; however, a previous study reported increased prevalence of *Diaporthe* spp. in QoI-treated plots. This study aimed to assess QoI resistance in *Diaporthe* populations using the cytochrome b (cyt b) gene-based polymerase chain (PCR) assay. 50 isolates of *D. aspalathi, D. caulivora,* and *D. longicolla* collected from 15 U.S. states were cultured in potato dextrose broth for 14 to 21 days at 23 ± 2°C under a 12 h light/dark cycle. Genomic DNA was extracted, and the cyt b regions were amplified using primers designed using the *D. longicolla* cyt b sequence. Amplicons were sequenced and analyzed for known QoI resistance-associated mutations such as G143A, F129L, or G137R substitutions. Sequence analysis revealed no G143A, F129L, or G137R substitutions in any of the isolates. These results indicate that the tested *Diaporthe* isolates are likely sensitive to QoI fungicides, supporting their use for managing *Diaporthe*-associated diseases in soybean in the regions sampled. However, due to the high risk of resistance development for QoI fungicides, ongoing monitoring of *Diaporthe* populations is recommended.

66. DISSECTING THE GENETIC ARCHITECTURE OF SPOT BLOTCH SUSCEPTIBILITY IN BARLEY THROUGH GENOMICS AND ASSOCIATION MAPPING*

Ms. Meenu Sengar1, Mr. Tapish Pawar2, Mr. Muhammad Asif Nawaz3, Ahmed Alhusays4, Dr. Brian J. Steffenson5, Dr. Robert Brueggeman6, Ravi Mural7, Shyam Solanki8 and Gazala Ameen1, (1)Agronomy, Horticulture & Plant Sciences, South Dakota State University, Brookings, SD, (2)Departement of Agronomy, Horticulture & Plant Science, Brookings, SD, (3)South Dakota State Univ, Brookings, SD, (4)al qassim university, Buraydah, SAUDI ARABIA, (5)Department of Plant Pathology, University of Minnesota, St. Paul, MN, (6)Department of Crop and Soil Sciences, Washington State University, Pullman, WA, (7)South Dakota State University, Brookings, SD, (8)Department of Agronomy, Horticulture, and Plant Sciences South Dakota State Univ, Brookings, SD

Spot blotch, caused by *Bipolaris sorokiniana* leads to 30-40% yield losses in barley worldwide. The rcs5 locus on chromosome 7H encodes dominant wall-associated kinase (WAK) susceptibility genes Sbs1 and Sbs2, hijacked by the pathogen to trigger programmed cell death. We characterized allelic diversity at Sbs1, Sbs2, and HvWak5 across 142 cultivars, evaluated cumulative effects of 66 validated resistance markers across 21 pangenome cultivars, and conducted GWAS in 117 cultivars genotyped with 35,155 SNPs in GAPIT. ANOVA confirmed Sbs1 as primary susceptibility determinant (partial $\eta^2=0.39$; $p=3.52\times10^{-11}$) with three truncated allele classes (202, 253, 289 aa) demonstrating convergent loss-of-susceptibility. Sbs2 contributed a secondary effect (partial $\eta^2=0.04$; $p=0.018$), while HvWak5 showed no independent effect ($p=0.439$) in susceptibility, resolving its functional role. A single rcs5-linked SNP failed to predict resistance globally ($W=26.5$; $p=0.53$), explained by structural independence of Sbs1 truncation classes. Pangenome analysis confirmed additive genetic architecture ($R^2=0.34$; $p=0.0055$). GWAS identified SCRI_RS_153785 on chromosome 1H as Bonferroni-significant in BLINK ($p=3.48\times10^{-7}$) and FarmCPU ($p=2.21\times10^{-7}$), co-localizing with the validated QRcs-1H-P1 resistance interval. These findings advance understanding of WAK-mediated susceptibility and define a multi-locus genomic framework for durable resistance breeding in barley.

67. CYTOCHALASINS IN DIAPORTHE LONGICOLLA ASSOCIATED WITH SOYBEAN (GLYCINE MAX L.) DISEASE*

Sarina Shrestha, Ms. Karthika Mohan and Dr. Febina Mathew, North Dakota State University, Fargo, ND

Diaporthe longicolla causes pod and stem blight and seed decay of soybean (*Glycine max* L.) in the United States. Warm, humid conditions during the late reproductive stages of the crop, along with delayed harvest, favor these diseases and result in yield losses and poor seed quality. Previous studies reported that isolates of *D. longicolla* may produce toxic secondary metabolites, such as cytochalasin compounds, which pose a risk to sheep's health. However, there is limited information on the presence of these compounds in U.S. isolates of *D. longicolla.* The objective of this study was to conduct untargeted metabolomic profiling of two *D. longicolla* isolates recovered from soybean plants exhibiting pod and stem blight symptoms in the U.S. The isolates were grown in potato dextrose broth (PDB) under dark conditions for 21 days, and cell-free culture filtrates were collected by filtration and centrifugation. Metabolomic analysis revealed that a nitro-phenoxy cytochalasin derivative was significantly upregulated ($P < 0.05$) in both isolates among the top 150 metabolites compared with the non-inoculated PDB control. The detection of cytochalasin compounds in the filtrates of *D. longicolla* suggests that infected soybean may contain metabolites of concern for livestock feed safety. Current *Diaporthe*-associated disease management strategies in soybeans do not fully address these risks, emphasizing the need for increased awareness and possible mitigation approaches.

68. IDENTIFICATION OF TIMINGS OF BLUMERIELLA JAAPII INFECTION THAT RESULT IN FRUIT LESIONS ON TART CHERRIES*

Ms. Vera Soucy, Tyre John Proffer, Mr. Cory A. Outwater and Dr. George W. Sundin, Michigan State University, East Lansing, MI

Blumeriella jaapii, the fungal pathogen that causes cherry leaf spot, infects tart and sweet cherry trees in the Great Lakes region. Necrotic lesions are initially produced on leaves in the spring, and secondary cycles of infection occur throughout the season. These infections can result in defoliation that impacts fruit yield and increases susceptibility to winter injury. In 2024, tart cherries from commercial orchards in Michigan displayed lesions on fruit surfaces for the first time in at least 25 years. This observation led to the need to identify infection timings that result in fruit infection. In 2025 and 2026, field trials were conducted in which 'Montmorency' tart cherry trees were spray inoculated with 2.0 x 105 conidia/mL at developmental stages ranging from bud break to shuck split. Inoculated branches were bagged for varying lengths of time to create a favorable environment for infection. Leaves, bract leaves, pedicels, and fruit were visually rated for disease symptoms three weeks after the last inoculation. Environmental conditions were monitored using a weather station located close to the experimental site. Inoculations during full bloom and petal fall resulted in fruit lesions. Inoculations prior to full bloom and after late petal fall resulted in leaf and bract leaf infections, though no fruit infection was observed. Our results have shown that tart cherry fruit is susceptible to *B. jaapii* infections at the full bloom and petal fall timings.

69. OPTIMIZATION AND VISUALIZATION OF THE INDUCTION OF PROPHAGES IN PSEUDOMONAS AMYGDALI PV. MORSPRUNORUM USING TRANSMISSION ELECTRON MICROSCOPY*

Laely Bishop and Dr. Michelle Hulin, Michigan State University, East Lansing, MI

Pseudomonas amygdali pv. *morsprunorum* (Pam) is a plant pathogenic bacterium that causes bacterial canker on cherry trees and is a part of the *Pseudomonas syringae* species complex. Within their genomes, *P. syringae* species contain prophages. Prophages are dormant bacteriophage viruses. They can increase the pathogenicity by encoding virulence factors. In Pam strain S11 there are three prophage sequences which have been shown to be involved in pathogenicity .. Prophages can be induced to produce viral particles and leave the cell. Once induced they can be visualized to determined which phage is present in each strain. The induction and imaging of phages involve inducing with an antibiotic, cell lysis, and precipitating all under various conditions to preserve the phages once induced, then using transmission electron microscopy (TEM) to image the phages. By optimizing this process, the ideal conditions for each step have been identified and shown to be efficient. Having a repeatable and refined protocol can also help visualize other phages in the *P. syringae* complex in the future. Research on phages is important to understand the pathogenicity and evolution of bacteria, and may inform future research and strategies to help the management and prevention of bacterial canker on *Prunus* spp.

70. BIOLOGICAL CONTAMINATION OF C. SATIVA FLOWER SOLD IN WISCONSIN*

Ella Cain1, Derrick Grunwald2 and Shelby Ellison1, (1)University of Wisconsin, Madison, WI, (2)University of Wisconsin Madison, Madison, WI

Hemp-derived cannabinoids have become widely sold in Wisconsin. Regulations may be further behind market production. Hemp is not currently recognized as an agricultural or food commodity, meaning regulations surrounding hemp are not as strict or thorough for product safety. The possibility that hemp-derived products are lacking necessary testing for biological contaminants, such as mold and yeasts, poses a hazard to consumer safety due to the possibility of mycotoxin contamination. In this study, 15 hemp-derived cannabinoid pre-rolled joints from anonymized smoke shops in Madison, WI were tested for the presence of biological contaminants using media selective for mold and yeast growth. Of the 15, 10 were identified as possessing biological contamination. TEF amplicons of select isolates from the samples were sequenced and found to match closely with *Fusarium* spp., namely, *oxysporum* (97.23%) and *foetens* (96.78%). *Fusarium* spp. are capable of producing many agricultural and medically important mycotoxins. The presence of biological contamination has implications for the implementation of regulations; namely, more stringent and specific testing should be performed on hemp-derived products in Wisconsin to ensure the quality and safety of products sold recreationally.

71. DUAL RNA-SEQ REVEALS HOST-PATHOGEN TRANSCRIPTOMIC INTERACTIONS IN FRAGARIA X ANANASSA ‘ANNAPOLIS’ INFECTED WITH PODOSPHAERA SHEPHERDIAE*

Samantha Thompson, Michigan State University, Okemos, MI and Dr. Timothy D. Miles, Michigan State University, East Lansing, MI

North American strawberry powdery mildew, caused by *Podosphaera shepherdiae,* is a destructive foliar disease that reduces the vigor and yield of cultivated strawberries. To investigate host defense responses and pathogen virulence mechanisms, a time-course dual RNA-seq study was conducted on Fragaria × ananassa ‘Annapolis’ inoculated with *P. shepherdiae.* Leaves were sampled at 6 time points, from 12 hpi to 7 dpi, with 3 biological replicates per time point. Illumina paired-end 150-bp libraries were sequenced. Reads were quality-filtered and aligned to the Fragaria × ananassa ‘Camarosa’ genome for host differential expression analyses. Unmapped reads were aligned to a *P. shepherdiae* reference genome. Principal component analysis showed clear temporal clustering, indicating progressive transcriptomic shifts during colonization. Host gene ontology analyses revealed early enrichment of membrane-associated genes, protein kinase activity, transmembrane transport, and oxidation-reduction processes, consistent with pathogen recognition and defense signaling. Pathogen analyses identified candidate secreted proteins and putative effectors, including small cysteine-rich proteins associated with virulence. These findings provide insight into strawberry defense responses and *P. shepherdiae* pathogenicity factors, supporting resistance breeding and improved disease management.

72. TAR SPOT IMPACT ON CORN HYBRID PERFORMANCE: DISEASE PRESSURE, YIELD RESPONSE, AND TILLAGE SYSTEM EFFECTS*

Fidel Jiménez-Beitia, Michigan State University, MI, Andrea Dolezal, Bayer Crop Science, IL, Dr. Mercedes Diaz Arias, Bayer Crop Science, MO, William Widdicombe, Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI, Tim Dietz, Bayer Crop Science, MI and Dr. Martin Chilvers, Michigan State University, East Lansing, MI

Tar spot, caused by *Phyllachora maydis*, threatens corn production across the Americas. Understanding its dynamics under variable conditions is critical to protect grain yield and hybrid performance. This study provides two scenarios of tar spot impact on corn health. First, we assessed seven hybrids, fungicide efficacy, and remote sensing indicators for disease progression and yield loss. Second, we evaluated tillage effects on tar spot onset and severity within corn canopies. Tar spot pressure was higher in 2024 than in 2025, with consistent trends across the Michigan locations: East Lansing had the highest mean severity (10–20%), followed by Mason (1–9%) and Decatur (0–3%). Non-treated plots had greater disease index and AUDPC than fungicide-treated plots ($P < 0.001$). Hybrids 5, 6, and 7 showed the lowest AUDPC across locations and treatments. Yield differed among hybrids but not between fungicide treatments, and NDVI reflected these differences. In the tillage study, tar spot onset occurred at flowering (R1) in 2024 and dough (R4) stages in 2025. Tilled system (fall chisel and spring cultivation) showed a higher AUDPC than no-till system (undisturbed) in 2024 ($P < 0.001$), but differences were not significant in 2025 due to lower disease pressure and later onset. The results of this study highlight the relationship among weather, inoculum pressure, and hybrid selection, suggesting that tilled systems may be less effective for management than previously thought.

Poster Presentations

73. ASSESSMENT OF ATMOSPHERIC INOCULUM CONCENTRATIONS OF STEMPHYLIUM VESICARIUM ASSOCIATED WITH A BARLEY WIND BREAK AND ONION LEAF BLIGHT IN MICHIGAN*

Matthew John and Dr. Mary K. Hausbeck, Michigan State University, East Lansing, MI

Stemphylium leaf blight (SLB), caused by *Stemphylium vesicarium*, is a relatively new constraint to onion production in Michigan (MI) and other production regions and requires frequent fungicide applications to manage. The pathogen has become resistant to strobilurin fungicides. In MI, onions are rotated with celery and the potential inoculum sources each spring are unknown. We quantified the atmospheric ascospore and conidial concentrations of *S. vesicarium* in a commercial onion field and to evaluate the role of barley used as a windbreak in onion production in SLB development. A Burkard 7-day volumetric spore trap was deployed from March to November 2025 in a commercial field in Hamilton, MI, and SLB progression in untreated onion plots was assessed. Ascospores were first detected in mid-March, prior to onion seeding, and declined as the season progressed. Conidia were observed from late June through September, with peak concentrations coinciding with increased SLB severity. *S. vesicarium* conidia were associated with barley samples. Molecular analyses confirmed isolates from onion and barley as *S. vesicarium*. The number of barley samples with *S. vesicarium* conidia peaked in association with high atmospheric conidial concentrations during critical onion growth stages. These findings demonstrate that atmospheric inoculum is present earlier than anticipated in an annual cropping system, and barley may play a role that should be further examined.

74. ASSESSMENT OF COVER CROPS FOR SUSCEPTIBILITY TO ALTERNARIA CAROTIINCULTAE AND COLLETOTRICHUM SIAMENSE*

Mr. Ethan Tippett and Dr. Mary K. Hausbeck, Michigan State University, East Lansing, MI

Black rot, caused by *Alternaria radicina* and *A. carotiincultae*, and a petiole blight, caused by *Colletotrichum siamense*, are newer diseases in Michigan carrot production. While *A. carotiincultae* is known to infect barley, a commonly used windbreak cover crop, other cover crops may also host these pathogens. Our objective was to screen four cover crops, Sorghum sundangrass, winter rye, common oat, and oilseed radish, for susceptibility to *A. carotiincultae* and *C. siamense*. Cover crops were inoculated with either pathogen, using a conidial root dip (*A. carotiincultae*) or conidial foliar spray *(C. siamense* or *A. carotiincultae)*. Symptoms were observed for 28 days and compared to a foliar water spray (control). Sorghum sudangrass and oat were susceptible to *A. carotiincultae* and developed symptoms within 7-14 days. Chlorosis, followed by dark red-brown lesion development, occurred on Sorghum sudangrass foliage using either inoculation method. Brown lesions with chlorotic halos occurred on oat foliage with the foliar spray inoculation. Sorghum sudangrass and oilseed radish were susceptible to *C. siamense* and developed symptoms within 14 days. Reddish-brown, speckled lesions and plant death occurred on Sorghum sudangrass. Reddish-brown lesions also developed on oilseed radish foliage. Both pathogens were isolated from symptomatic tissues. Our results can cover crop recommendations for Michigan's carrot growers.

75. CHARACTERIZATION OF PSEUDOMONAS SYRINGAE FROM BLUEBERRY STEM BLIGHT THROUGH INVESTIGATION OF VIRULENCE FACTORS AND POLYMICROBIAL DISEASE INTERACTIONS*

Ms. Sanju Bijarniya1, Dr. Daniel Maddock2, Laely Bishop2, Dr. Timothy D. Miles3 and Dr. Michelle Hulin3, (1)Michigan State Univ, East Lansing, MI, (2)Michigan state university, MI, (3)Michigan State University, East Lansing, MI

Blueberry bacterial stem blight threatens Michigan's $530 million industry, yet its pathogenicity mechanisms remain poorly understood. We hypothesized that *Pseudomonas syringae* pv. *syringae* (Pss) functions within a polymicrobial complex rather than as a solitary pathogen. Whole-genome sequencing of 60 Michigan Pss isolates revealed that 80% possess phytotoxin (syringomycin/syringopeptin) and ice nucleation (inaZ) genes. Copper susceptibility screening showed moderate resistance, with 70% of isolates growing at 1.4 mM $CuSO_4$. Pathogenicity assays on blueberry cultivars (Legacy, Jersey, Rubel, Blueray) and cherry (Coral Champagne) demonstrated host-dependent virulence. Notably, co-inoculation with *Neopestalotiopsis* fungi resulted in larger lesions than Pss alone, suggesting a synergistic interaction where Pss toxins enhance disease severity in mixed infections. To isolate specific mechanisms, we are generating targeted, scarless deletion mutants of key genes (syrB, sypA, inaZ, and the T3SS hrcC). Phenotypic evaluation via repeated plant inoculations will determine which factors drive progression. This research clarifies whether Pss is a primary pathogen, opportunistic colonizer, or synergistic partner, providing actionable insights for sustainable disease management in Michigan fruit production.

76. TO BEAN OR NOT TO BEAN: EXPLORING THE ROLE OF PLASMIDS IN THE EVOLUTION OF PSEUDOMONAS SYRINGAE PATHOGENICITY ON LEGUMES*

Makayla Ritko and Dr. Michelle Hulin, Michigan State University, East Lansing, MI

Bacterial pathogens are able to evolve rapidly and threaten global food sources. Mobile genetic elements, such as plasmids, enable bacteria to gain new traits which can lead to an increase in virulence. The bacterial pathogen *Pseudomonas syringae* (Ps) can infect over three hundred plant species, though individual Ps strains vary in their plant host range. This project focuses specifically on phylogroup 2b, which contains important pathogens of legumes. Closely related *Pseudomonas syringae* pv. *syringae* (Pss) and *Pseudomonas syringae* pv. *pisi* (Ppi) will be used to explore the role of plasmids in virulence. Pss is shown to have a wide host range including a variety of legumes and few plasmids, while Ppi has many plasmids and is restricted to pea species. Pss and Ppi provide an ideal system to study the role of plasmids in bacterial evolution. This study will utilize pathogenicity assays to assess the virulence strategies of Pss and Ppi on peas and dry beans. Genomics will be utilized to identify the genetic mechanisms controlling plasmid compatibility. Due to the prevalence of plasmids in bacterial pathogens, this work will also provide knowledge that is critical to environmental and public health. This research will explore the role of plasmids in bacterial pathogenicity to better understand pathogen evolution.

Poster Presentations

77. CONVERGENT MOLECULAR PATHWAYS RESOLVED BY SPATIAL TRANSCRIPTOMICS IN BARLEY RPG5-UG99 MODEL UNDER CONCURRENT BIOTIC AND ABIOTIC STRESSES*

Mr. Mrinmoy Sarker1, Israel Akinlabi2, Mr. Arsalan Quresh3, Gazala Ameen1, Dr. Robert Brueggeman4 and Shyam Solanki5, (1)South Dakota State University, Brookings, SD, (2)South Dakota State University - Brookings, SD, Brookings, SD, (3)Agronomy,Horticulture and Plant Sciences, Brookings, SD, (4)Department of Crop and Soil Sciences, Washington State University, Pullman, WA, (5)Agronomy, Horticulture & Plant Science, South Dakota State University, Brookings, SD

Temperature sensitivity has been reported for several plant disease resistance genes. However, very limited data are available on the molecular mechanisms by which plants confer such responses in a tissue-dependent manner. Barley atypical NLR, Rpg5 provides resistance to wheat stem-rust pathogen *Puccinia graminis* f. sp. *tritici* (Pgt) below 24°C but breaks down at an elevated temperature. Using Rpg5 and insights from previously studied functionally similar genes such as wheat Sr6 and Arabidopsis SNC1, we aim to understand the convergence of genes working on biotic response with abiotic stress pathways. Based on our phenotypic assays, we have collected leaf tissues from seedlings for eight different time points with two contrasting temperatures for susceptible (Steptoe: Rpg5-) and resistance (Q21861:Rpg5+) varieties for bulk RNA sequencing. Ug99 surrogate Pgt race QCCJB and soltrol were used to induce immune response. Currently, we are optimizing the preparation of tissue samples from the stem and leaf of the resistant variety for a BMKMANU S3000 spatial transcriptomics study. Using Keyence BZ-X 1000 automated microscope, we are simultaneously visualizing replicates of spatio-temporal Pgt infected tissues stained with Alexa fluor 488-WGA. Consolidating data from these experiments will allow us to better understand host immune signaling upon pathogen exposure under modulating temperature, hence establishing the scope for designing robust synthetic immune receptors.

78. CHARACTERIZING AIRBORNE FUNGAL AND BACTERIAL MICROBIOMES IN ‘CHARDONNAY’ VINEYARDS ACROSS THE UNITED STATES*

Sukhdeep Singh and Dr. Timothy D. Miles, Michigan State University, East Lansing, MI

Airborne microbes move between vineyard plants, act as disease inoculum, and shape the microbial environment. Though vineyard soils and phyllosphere have been studied extensively, we know relatively little about what is present in the air. This project aims to characterize airborne fungal and bacterial communities across major U.S. grape-growing regions using culture-independent amplicon sequencing. Air samples were collected via vacuum-based method from three ‘Chardonnay’ vineyards each from five U.S. states to examine how communities vary across regions. All samples were collected before harvest in year one to build a preliminary dataset. Total DNA was extracted and processed for amplicon sequencing targeting bacterial 16S rRNA and fungal ITS regions. Main goals include identifying dominant taxa, distinguishing core versus region-specific microbiomes, comparing alpha and beta diversity among states, detecting grapevine pathogens and beneficial microbes. *Cladosporium* and *Alternaria* dominated airborne fungal communities across all states, yet community composition differed significantly by state, with geography emerging as the dominant driver of structure. This data will support a follow-up multi-year study tracking microbiome shifts across seasons and growth stages. Understanding these patterns may improve disease forecasting and guide region-specific disease management strategies in viticulture.

79. HIGH-THROUGHPUT PHENOTYPING PIPELINE FOR RED CROWN ROT OF SOYBEAN USING X-RAY CT TECHNOLOGY*

Emilia Meyers1, Mariela Fernández-Campos2, K. Morgan Goodnight1 and Dr. Darcy E. P. Telenko1, (1)Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN, (2)Purdue Univ, West Lafayette, IN

Red crown rot (RCR), caused by the soilborne fungus *Calonectria ilicicola*, is an emerging soybean disease in the Midwest that has resulted in up to 50% yield loss in affected fields. This disease was initially confirmed in Indiana in 2020 in two counties, but as of 2025, it has been reported in fifteen counties across the state. The diagnosis of RCR can be challenging because infections develop belowground during early growth stages, where root damage cannot be seen without destructive sampling. This project aims to establish a high-throughput phenotyping pipeline using X-ray computed tomography (X-ray CT) scanning technology as a nondestructive approach to monitor root development and disease progression. Research objectives include testing the feasibility of promoting red crown rot infection in soybeans and evaluating the effect of disease infection under X-ray CT imaging. Plants will be grown under controlled greenhouse conditions, and root imaging data will be collected at Purdue University’s Ag Alumni Seed Phenotyping Facility. We expect to successfully infect soybean plants with *C. ilicicola* by testing different inoculation methods and establishing a baseline for investigating the spatial and temporal dynamics of *C. ilicicola* using X-ray CT imaging. This work seeks to generate foundational data and assess novel approaches for improving belowground disease detection and management of red crown rot.

80. BROAD-SPECTRUM RESISTANCE TO BACTERIAL BLIGHT IN RICE USING MULTIPLEXED PRIME EDITING

Dr. Ajay Gupta, University of Missouri-Columbia, Columbia, MO

Prime editing (PE) has the potential to create novel germplasm against *Xanthomonas oryzae* pv. *oryzae* (Xoo). In this study, we developed an improved multiplexed PE system to implement new strategies for broad-spectrum rice bacterial blight (BB) resistance.

We achieved knock-in of Transcription Activator-Like (TAL) effector binding elements (EBEs) into the promoter of executor R gene, xa23, with an editing efficiency of 73.5% in the T0 generation. Additionally, we edited the transcription factor TFIIA gamma subunit gene, TFIIAµ5, which is required for TAL effector-dependent BB susceptibility. This recapitulated the resistance of xa5 at an editing efficiency of 88.5% in the T0 generation. Both the edits provided strong broad spectrum resistance against BB.

Furthermore, we developed a modularly assembled multiplexed platform to enable efficient editing of multiple genes. Using this platform, we achieved simultaneous editing of four agronomically important rice genes with a high efficiency of 42.5% in the T0 generation. This conferred broad spectrum resistance against bacterial blight. In conclusion, we believe that the development of this high-efficiency multiplexed prime editing system in rice can significantly benefit the scientific community for crop improvement and gene functional analysis.

Poster Presentations

81. INFLUENCE OF PLANTING DATE, MATURITY GROUP, AND FUNGICIDE ON FUNGAL SEED INFECTION AND YIELD IN SOYBEAN

Mr. Edgar Yanclot Vargas Moales1, Dr. Nabin K. Dangal1, Dr. José F. González-Acuña1, Mark A. Licht1 and Dr. Daren S. Mueller2, (1)Iowa State University, Ames, IA, (2)Iowa State University, IA

Protecting soybean yield and seed health can be achieved through understanding the effects of management decisions. This study evaluated two planting dates (early vs. late), maturity groups (MG; short vs. long), and foliar fungicide use (non-treated vs. Delaro Complete at R3) across three Iowa environments (central, northwest, southeast). Yield and fungal seed infection incidence were closely linked. A significant interaction between MG and planting date (P = 0.014) indicated a yield penalty for early planted, short-MG varieties compared to long-MG cultivars, regardless of planting date. In northwest Iowa, seed infection reached 11.1% in non-treated, early planted, short-MG cultivars, despite low August precipitation (48.5 mm). The lowest seed infection incidence was observed in southeast Iowa (1.7%), where rainfall was even lower (34.5 mm). Incidence of *Diaporthe* was highest in the non-treated, early planted, short-MG treatment (4.8%), compared with the fungicide-treated, late-planted, long-MG cultivars (1.3%, P = 0.026). In contrast, the incidence of *Cladosporium* in northwest Iowa was greater in long-MG cultivars (6.5%) than in short-MG cultivars (2.9%; P = 0.0030), consistent with delayed senescence. These results demonstrate that soybean yield and seed health are shaped by interactions among planting date, maturity group, and fungicide use, varying across environments and pathogens, underscoring the need for integrated, context-specific management strategies.

Xersperro volupist, quunt laut que non pro dolore eum endaestio. Udis as ium qui at deleniet laborerovit endam, am, tota simo molupta tempos dolendi gnimosam, solori dolorpos imagnihil explab inctem voluptiora nectia quam ut odi ad que everita ssequo doluptam ut lam dolorro enit hil et est, cus, ommolor sitae aut parci re ipidiciis isquam nem escia quam nimos es net hillupta volupta cor re ni sit litinctem ipsa doluptatur audis expliquos sant invendis earum autem autem nosae nobit aborehe nimodip istest verum fugiasi tatur? Otae omnitat quament lam experioribus es eatent quis sedi ipit modis evendist estion nobitia nobis experum corera quiatur? Quia vendign ihiliberi doluptas vendescid quae alibus.

Ecte nosseru ptatur autem ut magnat et evelitaqui derro maximpo reiciissit este nissus, con cus duciendebis nos maionsequi reheniscius es delis dellaborum quat.

Aquibus rempore rationseque voluptatur architium in re, as minci omniend itiatque nobit ommodi ipsam volum accuptu ribusam eium non con ratiasp eriam, undiasp itatumqui apis enes cus aribus magniet destorro blaut ullorum, cumqui cone nus quam rescia num abo. Loriati aectur sinus eum re venia sume omnitas eatur maximet eos volorro voloriam, cullam, ad ma aut est, cone magnimi ntiore moluptam nobis aut ullandamus