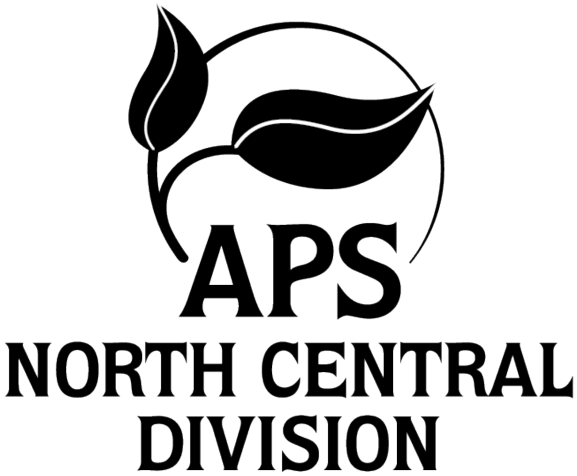

2025 North Central APS Meeting

ABSTRACT SUPPLEMENT

Graduate Student Oral Presentation Abstracts (in order of presentation, presenting author is highlighted in bold)

8:20 – 8:32 AM

Reaction of a clubroot resistant *Brassica napus* Plant Introduction (PI) set to a putative new clubroot pathotype

Neeraja Narra, Venkata Chapara, Luis del Rio Mendoza; *North Dakota State University*

North Dakota is the leading producer of canola (*Brassica napus*) in the United States, with a record production of 3.92 billion pounds in 2024. However, canola production is increasingly threatened by clubroot, a soil-borne disease caused by *Plasmodiophora brassicae*. First detected in Cavalier County in 2013, clubroot has since continued to spread. Genetic resistance is one of the most effective and environmentally sustainable management strategies for clubroot. However, the durability of resistance is under pressure due to the rapid evolution of virulent *P. brassicae* pathotypes capable of overcoming deployed resistance genes. In 2024, severe clubroot symptoms were observed in a field planted with resistant canola cultivars, raising concerns about the possible emergence of a new virulent pathotype. To investigate this, a greenhouse study was conducted using soil from the affected field and seven elite clubroot resistant *B. napus* PIs, along with the susceptible control, Topas. Preliminary results revealed that five PIs were resistant, while two were susceptible. This result, although preliminary, suggests a new pathotype may be involved. To confirm this results, the study is being repeated. In addition, the Canadian Clubroot Differential (CCD) set will be used to characterize the putative new pathotype. These findings highlight the need for continued pathotype surveillance and responsible stewardship of resistance cultivars.

8:32 – 8:44 AM

Pathogenicity Testing of Possible Crown Rot Pathogens in Corn.

Christopher Termunde, Chikoti Mukuma, Tamra Jackson-Ziems, *University of Nebraska – Lincoln*

Crown rot of corn is a disease that has been increasing in importance in the U.S. Corn Belt. Crown rot symptomatic plant samples were collected from nine states from 2022 to 2024. Fungal isolations yielded a diversity of fungi, especially *Fusarium spp.* Representative isolates of *F. graminearum, F. boothii, F. verticillioides* and *F. solani* were selected for pathogenicity testing based on their high isolation frequencies. Five inoculation methods were evaluated with these isolates testing their ability to induce crown rot symptoms. Several isolates by inoculation method combinations caused root rot, but only the toothpick wounding method caused consistent crown rot symptoms. Four greenhouse experiments were conducted with susceptible and resistant corn hybrids to evaluate whether the toothpick method would differentiate isolate aggressiveness. Experiments were arranged in RCBD with five to seven treatments and three to five replications. Inoculation was conducted at V6 or V10. Symptom severity was visually estimated three weeks post inoculation on a scale of 0 to 5 with 5 being most severe. There were differences in the virulence of isolates in the susceptible hybrid (p=0.05). Among the isolates and species tested, *F. boothii* was the most virulent species averaging a severity rating of 2.6. Results suggest that the toothpick method can be used to screen hybrids for susceptibility to crown rot, while also offering a quick method to screen isolate virulence.

8:44 – 8:56 AM

Wheat streak mosaic virus was highly prevalent in a 2024 Michigan winter wheat virus survey.

Martin I. Chilvers, **Keeley Satterfield**, Janette Jacobs, *Michigan State University*

Michigan produces approximately 32 million bushels of soft white and red winter wheat.
Despite wheat viruses impacting production, the only surveys published for wheat viruses in Michigan are from the 1970s. To gain a comprehensive understanding of virus prevalence and incidence, we conducted a survey of commercial wheat fields and tested leaf samples by an ELISA panel of eight common wheat viruses. Four composite samples were collected per field and each sample consisted of 20 symptomatic leaves. The number of fields sampled by county were based on 2023 fall planted acreage estimates, with more samples taken in counties

with higher acreage. In 2024, a total of 135 fields were sampled in 24 counties for a total of 540 samples. Wheat streak mosaic virus (WSMV) was detected in 42% of samples and 68% of fields. Barley yellow dwarf virus (BYDV)-PAV was detected in 39% of samples and 61% of fields. Cereal yellow dwarf virus (CYDV)-RPV was detected in 13% of samples and 33% of fields. Wheat spindle streak mosaic virus (WSSMV), brome mosaic virus (BMV), and High Plains wheat mosaic virus (HPWMoV) were detected in less than 5% of samples and fields. Barley yellow dwarf virus (BYDV)-MAV and soil-borne wheat mosaic virus (SBWMV) were not detected in any samples. Importantly, the survey highlights the prevalence and incidence of eight viruses and will be used to educate growers and inform wheat variety resistance screening. The survey will be repeated in 2025.

8:56 – 9:08 AM

A Survey of Plant-Parasitic Nematodes Associated with Soybean Production in Missouri.

Jefferson Barizon, Alexandria Haafke, Meghan Biggs, Mandy Bish, *University of Missouri*

Plant-parasitic nematodes (PPNs) significantly impact U.S. soybean production, causing annual losses of approximately 10 million bushels or $100 million in Missouri alone. The soybean cyst nematode (SCN) and root-knot nematode (RKN) are particularly damaging, with SCN responsible for 50% of pathogen-related yield losses. This study updates SCN prevalence, population densities, and virulent phenotypes, while expanding knowledge of other PPNs affecting Missouri soybeans. During the 2024 growing season, soil and root samples were collected from 70 fields across 31 counties. Soil samples were composited using a soil probe while root samples were taken from five randomly selected plants per field. SCN cysts were extracted, eggs released, stained, and quantified. Virulent phenotypes are being determined via a Modified HG type test. Other PPNs were extracted using centrifugal-flotation and identified to genus. SCN was detected in 93% of samples, with 92% having ≥200 eggs/100 cm^3 soil. The most common SCN virulent phenotypes to date are HG types 1.2- and 2-, with average female indices of 18% on Peking and 67% on PI 88788. No non-virulent SCN phenotype has been observed. Other PPNs identified include Helicotylenchus, Hoplolaimus, Meloidogyne, Pratylenchus, Tylenchorhynchus, and Xiphinema. Research will continue in 2025 to further assess PPN impacts on Missouri soybean production.

9:08 – 9:20 AM

Bacterial Leaf Streak and *Pantoea spp.* in Northern Great Plains Corn.

Ciera Kotaska, Sophia Enter, Darcy Geerson, Tasneem Fathima, Claire Galvin, Nabina Karki, Tamra Jackson-Ziems, Rodrigo B. Onofre, Madalyn Shires, *South Dakota State University*

A survey of bacterial leaf streak of corn, caused by *Xanthomonas vasicola pv. vasculorum* was conducted in 2023 and 2024 across portions of the northern Great Plains. During the survey, bacterial disease symptoms observed were commonly atypical of bacterial leaf streak, prompting further investigation. In 2023, sample collection was focused in Nebraska due to a lack of disease pressure from the persistent drought conditions in much of South Dakota. Of the 57 bacterial cultures identified, 21 belong to the genus *Pantoea*, while no cultures were identified as *Xanthomonas*. In 2024, sample collection expanded to contain samples from South Dakota, Nebraska, Kansas, and Minnesota in response to the 2023 identification results. One culture out of nearly 300 was identified as *Xanthomonas* in 2024. However, about half of these cultures were identified as a *Pantoea* species. With 172 of 356 total bacterial isolates identified with partial 16S as a *Pantoea sp*., a subset of these *Pantoea* isolates were selected for speciation using multiple bacterial gene regions, including gyrase B and rpl. All sequences were concatenated, and a maximum-likelihood phylogenetic tree was created to visualize the relationship of the samples to the type strains of multiple *Pantoea* species. The results showed large diversity in the northern Great Plains *Pantoea* populations. Further work is ongoing to understand how this diversity may affect pathogenicity and virulence.

9:20 – 9:32 AM

Evaluating the Effectiveness of Peking Soybean for Soybean Cyst Nematode Management in Missouri.

Feyisayo Akande, Alexandria Haafke, Jefferson Barizon, Mandy Bish, *University of Missouri*

Over 95% of commercial soybean varieties rely on SCN resistance from PI 88788, a source used for over 40 years. This overuse has led to increased SCN virulence and reduced PI 88788 effectiveness. Recently, breeding efforts to incorporate resistance from Peking have increased. However, few Peking varieties are available in maturity groups preferred by Missouri farmers. Our objective is to evaluate a commercial Peking variety in Missouri against a comparable PI 88788 variety. Small-plot trials were conducted in 2024 at Columbia and Novelty, MO, comparing Peking, PI 88788 and susceptible soybean, each with one of four seed treatments: 1) non-treated; 2) base (Obvius Plus + Poncho 600 FS + Flo Rite Pro); 3) ILEVO (fluopyram, 0.25 mg ai/seed) + base; or 4) Saltro (pydifluemtofen, 0.15 mg ai/seed) + base. At Columbia, SCN female index values (FI) were 5.5 (Peking) and 95 (PI 88788). Peking had the lowest in-season female counts (0.6 females/g dry root) compared to PI 88788 (2.7) and the susceptible (2.4). At Novelty, FI values were 25 (Peking) and 65 (PI 88788); SCN female counts were 0.2, 0.5, and 0.6 females/g dry root for Peking, PI 88788, and susceptible varieties, respectively. At Columbia, Peking yielded highest (64 bushels per acre). At Novelty, PI 88788 yielded highest (72 bushels per acre). This work will continue in 2025 to support SCN management strategies for Missouri soybean production.

9:32 – 9:44 AM

Genetic Dissection of Bacterial Leaf Streak Resistance in Wheat Reveals Pathogen Complexity and Genomic Targets for Breeding.

Muhammad Ahmad, Jose L. Gonzalez. Hernandez, Guihua Bai, Jeffrey D. Boehm Jr.,
Shyam Solanki, Karl D. Glover, Gazala Ameen, *South Dakota State University*

Bacterial leaf streak (BLS), primarily caused by *Xanthomonas translucens pv. undulosa* (Xtu), is an emerging disease of wheat capable of causing up to 60% yield loss in the Northern Great Plains of the United States. In the absence of effective chemical controls, host genetic resistance offers the most promising avenue for sustainable disease management. This study aimed to (i) identify genetic loci associated with BLS resistance and (ii) characterize the pathogen diversity underlying BLS-like symptoms. Genome-wide association studies (GWAS) were performed on the diverse collection of 412 elite winter wheat panel from different public and private breeding programs across 10 U.S. states. Phenotyping under natural disease pressure and controlled infection assays enabled robust resistance evaluation. GWAS identified nine significant marker–trait associations (MTAs) across nine chromosomes, revealing key genomic regions for resistance breeding. Pathogen isolation and molecular assays indicated that, in addition to Xtu, *Pantoea ananatis*, *P. agglomerans*, and *Xanthomonas prunicola* (Xp) also induce BLS-like symptoms. Preliminary results suggest that resistance to Xtu may not confer protection against *Pantoea spp*. and *X. prunicola*, highlighting the need for broad-spectrum resistance. These findings underscore the complexity of the BLS pathosystem and the importance of understanding host–microbe interactions to develop durable resistance.

9:56 – 10:04 AM

Discovering Resistance to Bacterial leaf streak disease in Global Durum Wheat panel.

Tapish Pawar, Muhammad Ahmad, Chunki Lau, Shyam Solanki, Karl D. Glover, Jeffrey D. Boehm Jr., Filippo Bassi, Gazala Ameen, *South Dakota State University*

Bacterial leaf streak (BLS), caused by *Xanthomonas translucens*, is an emerging threat to small grains, particularly durum wheat (*Triticum turgidum subsp. durum*) and bread wheat (*Triticum aestivum*). Although BLS has been reported in North America for some time, its recent resurgence in the Northern Great Plains has caused significant losses in wheat and barley, with yield reductions up to 40 %, lower protein content, and reduced grain quality. The disease manifests as water-soaked lesions that become large necrotic streaks, reducing photosynthetic and grain yield. With no effective control measures, identifying genetic resistance is crucial. While limited resistance has been identified in bread wheat, little is known about resistance in durum wheat. To address this, we screened 742 tetraploid wheat lines from Global Durum Panel, representing nine *T. turgidum* subspecies at seedling stage under greenhouse conditions. BLS inoculation was performed using an in house spray inoculation method and severity was rated on 1-9 scale. A genome-wide association study was conducted using 16333 SNP makers from Illumina iSelect 90K SNP array. Across four models (GLM, MLM, BLINK and FarmCPU), 48 SNPs were significantly associated with BLS resistance, mapped to chromosomes, 1A, 1B, 2A, 2B, 3A, 3B, 4B, 5A, 5B, 6A, 6B, 7A, 7B. Ongoing field trials and marker validation aim to further confirm these findings and support pre-breeding efforts to develop BLS resistant durum wheat varieties.

10:30 – 10:42 AM

Spatial Transcriptions: A Powerful Tool to Explore Gene Expression Across Tissue Regions During Plant-Pathogen Interaction.

Nikhil Lnu, Karl D. Glover, Nidhi Rawat, Jose L. Gonzalez. Hernandez, Pawel Borowicz, Gazala Ameen, Shyam Solanki, *South Dakota State University*

Spatial transcriptomics enables high-resolution mapping of gene expressions in tissues. This technology offers novel insights into plant-pathogen interactions, where external cues alter expression patterns dynamically. We are applying 10x Genomics Visium technology using the wheat-*Fusarium graminearum* (Fg) pathosystem as a model to study tissue bound localized host responses. Fg causes Fusarium head blight (FHB), a devastating disease in wheat and barley. A key resistance QTL Fhb1, is widely used in wheat breeding, yet its tissue-specific regulation that may involve multiple gene families remains unclear. To capture spatio-temporal immune response (STIR) during resistance segmentation, we used resistant wheat cultivar 'Brick' carrying the Fhb1 QTL and susceptible control 'Boost', inoculated with RFP-tagged Fg (PH-1) to track fungal spread from a single inoculated floret on a spikelet to neighboring spikelets. We collected 10µm cryosections 6, 10 and 15days post inoculation and optimized the tissue permeabilization, RNA release, and spatial probe fluorescence visualization on Visium TO slides. We are currently making gene expression libraries that will be sequenced on Illumina NovaSeqX Plus and data will be analyzed on Space Ranger and Loupe Browser pipeline. This work will generate the first spatially resolved transcriptomic atlas for a cereal crop–fungal pathogen system and serve as a valuable technical resource for the plant–microbe interaction research community.

10:54 – 11:06 AM

Functional characterization of genes involved in rcs5 mediated spot blotch resistance in Barley.

Muhammad Asif Nawaz, Meenu Singh. Sengar, Brian Steffenson, Bob Brueggeman,Shyam Solanki, Gazala Ameen, *South Dakota State University*

Spot blotch disease in barley is caused by a fungal pathogen *Bipolaris sorokiniana* (BS) and is a major disease responsible for yield losses up to 30%. The rcs5 quantitative trait locus (QTL) in barley is the key genetic region providing resistance to this disease. Our previous research revealed that the rcs5 QTL encompasses four WAK genes: HvWak2, Sbs1, Sbs2, and HvWak5. The allele analysis identified phenotype-associated sequence polymorphisms in the coding sequence and promoter regions of Sbs1and Sbs2 genes and gene expression analysis revealed upregulation of Sbs1, Sbs2, and HvWak5 post-infection with BS, suggesting differential transcriptional regulation may contribute to susceptibility against spot blotch disease. We aim to functionally characterize the Sbs1 and Sbs2 via transient overexpression of the functional genes in resistant cultivar Morex and post transcriptional gene silencing in susceptible cultivar Steptoe and Golden Promise. Additionally, we will develop knockdown mutants of Sbs1 and/or Sbs2 gene(s) to further verify their role in spot blotch barley pathosystem. This work will enhance our understanding of WAK-mediated disease resistance mechanisms in crops and address a critical gap in plant immunity research.

11:06 – 11:18 AM

Connecting Stomatal Regulation and Immune Function: Characterizing the Ancestral Progenitor of the Barley NLR Rpg5's Alien Inserted Domain.

Israel Akinlabi, Shyam Solanki, Gazala Ameen, Bob Brueggeman, *South Dakota State University*

The pathogen-targeted host molecules act as susceptible factors, encoded by vulnerable regions of the plant genome. However, dynamic genome reorganization in the host can utilize susceptible targets as inserted domain (ID) fused in immune receptors to bait pathogens. In barley, the NLR receptor Rpg5 contains an inserted serine/threonine protein kinase (STPK) domain required for its function against stem rust pathogen *Puccinia graminis f. sp. tritici* (Pgt). We identified the STPK-ID progenitor in barley, PRK1, an ortholog of the characterized Arabidopsis guard cell kinase AtApk1b. The conservation of PRK1 homologs in stomata-bearing plants suggests its ancestral role in guard cell regulation, potentially explaining why it is targeted by Pgt and subsequently inserted into the NLR. To test our hypothesis, we created HvPRK1::GUS and AtAPK1b::PRK1-RFP constructs to generate stable transformants in the heterologous atapk1a-atapk1b Arabidopsis mutant to validate the PRK1 function by stomata aperture rescue. Additionally, we are testing if the retained PRK1 function allows Pgt penetration through a non-host's stomatal pore, where Pgt naturally cannot go past the epidermal layer. Currently, we are testing our constructs in the tobacco plant via transient assay while a stable transformation pipeline is ongoing. Our work will shed light on plant genome restructuring mechanisms leading to NLR-ID evolution.

11:18 – 11:30 AM

Comparative genome analysis of *Fusarium luffae* causing soybean wilt to characterize effectors associated with evolved pathogenicity.

Sachin Sharma, Gazala Ameen, Jose L. Gonzalez. Hernandez, Shyam Solanki, *South Dakota State University*

We recently published the first report of *Fusarium luffae* (FL) causing disease in soybean fields in the USA. The identified FL isolate SLSDF2 shows aggressive root rot and foliar wilt symptoms compared to established pathogenic Fusarium species on soybean. We hypothesize that SLSDF2's highly virulent nature may be due to uncharacterized virulence effectors that are either newly evolved or capable of evading the soybean's existing resistance mechanisms. To identify the genomic regions of SLSDF2 harboring unique effectors, we assemble a chromosome level genome of *Fusarium luffae* using Oxford Nanopore long-read technology as genome availability announcement, and compared our data to publicly available *Fusarium oxysporum* (Foxy) and *Fusarium oxysporum f. sp. luffae* (FoL) (both nonpathogenic on soybean) genome data. The de novo assembly of SLSDF2 produced 38.14 Mb genome with 8 contigs (N50: 6.89 Mb, BUSCO completeness score: 98.6%), 12,231 predicted genes, and 35 secondary metabolite clusters, significantly improving over existing assemblies. Comparative analysis with FL, Foxy, and FoL revealed enriched repetitive elements, an expanded effector repertoire, and only three highly divergent effector proteins. Our long-term aim is to functionally characterize the putative effectors and to timely identify cognitive resistance loci in soybean germplasm so that we can stay ahead in the host resistance race against this potentially emerging pathogen species.

11:30 – 11:42 AM

Reproduction potential of root-lesion nematode, *Pratylenchus scribneri* under different population densities, with selected corn cultivars.

Rekha Neupane, Guiping Yan, Andrew Friskop, Claire Keene, *North Dakota State University*

Pratylenchus scribneri, a root-lesion nematode, is a migratory endoparasite that infects a wide range of host plants, including corn. This nematode reduces root volume and impairs water and nutrient uptake. Population density of *P. scribneri* is often linked to the severity of damage on corn. However, limited information exists on the reproductive potential of this nematode on corn cultivars in the Northern Great Plains. This study evaluated the reproductive capacity of *P. scribneri* on eleven commercial corn cultivars under controlled greenhouse conditions. Each pot with a plant had an initial inoculum of 1,300 nematodes per 1.5 kg soil, and it was grown for 14 weeks. Then, nematodes were extracted from the soil and roots and a reproductive factor (Rf = final/initial population) was calculated. In the first trial, Rf values ranged from 3.9 to 14.2. A second trial using a higher inoculum (4,700 nematodes/pot) resulted in lower Rf values ranged from 0.6 to 1.3, suggesting possible intraspecific competition. Final population densities ranged from 5,241-18,687 among the cultivars with low inoculum, but 2,646-6,244 with high inoculum. These findings highlight the highly variable and strong reproductive ability of *P. scribneri* and its potential impact on corn cultivars in the Northern Great Plains.

11:42 – 11:54 AM

Response of sunflower to culture filtrates from *Diaporthe gulyae* and *D. helianth*i causing Phomopsis stem canker.

Karthika Mohan, Daniel Back, William Underwood, Melvin Bolton, Robert Harveson, Samuel Markell, Megan McCaghey, Febina Mathew, *North Dakota State University*

Phomopsis stem canker, primarily caused by *Diaporthe gulyae* or/and *D. helianthi*, can reduce sunflower (*Helianthus annuus L.*) yield by up to 40% in the U. S. Previous studies suggest that metabolites in culture filtrates of *D. helianthi*, such as 4, 6 dihydroxymellein—a compound known to cause phytotoxic symptoms—may contribute to disease severity, but this has not been examined for U.S. isolates of D. *gulyae* or *D. helianthi*. This study evaluated the sensitivity of a susceptible sunflower hybrid to six isolates of two fungi and their culture filtrates in two separate experiments. For filtrate treatments, fungi were grown in potato dextrose broth (PDB) for 21 days in dark, then filtered and centrifuged. A 200 µL aliquot of each filtrate was infiltrated into leaves at V3 growth stage (three pairs of true leaves). For fungal treatments, mycelial plugs were placed on leaves. Each treatment was replicated six times, with autoclaved PDB or non-infested plugs as controls. After seven days, leaf area infected (LAI) and leaf area necrotic (LAN) were measured for fungal and filtrate treatments, respectively. A significant correlation ($P< 0.0001$) between LAI and LAN was observed for *D. gulyae* ($r=0.63$) and *D. helianthi* ($r=0.83$), suggesting a potential role of fungal metabolites in symptom development. These results indicate that metabolites in culture filtrates may contribute to disease symptoms; however, further research is needed to confirm their specific role in pathogenicity.

1:30 – 1:42 PM

Comparison of UAV and Airplane for Fungicide Application in Missouri Corn Production.

Jesse Yount, Mandy Bish, Rusty Lee, Wayne Flanary, Mattheus Noguera, Kevin Bradley, *University of Missouri*

Timely fungicide applications in corn (*Zea mays*) production are essential when conditions favor disease development. While fungicides are commonly applied by aircraft, access can be limited in parts of Missouri, where planes may be available only once per season. Unmanned aerial vehicles (UAVs) may offer a more flexible alternative. A 2024 field experiment across three Missouri cornfields evaluated UAV feasibility for fungicide application. Treatments were applied at the R1 or R3 growth stage using a DJI Agras T40 UAV and compared to a standard aircraft. Three treatments were tested: 1) UAV at 19 L ha^{-1}, 2) UAV at 37 L ha^{-1}, and 3) aircraft at 28 L ha^{-1}, each replicated four times. Spray coverage was assessed using water-sensitive cards placed at three points per plot on adaxial and abaxial leaf surfaces of the ear leaf (E), E+2, and E–2 at application. Disease severity was rated at application, R3, and R6. At one of two locations where coverage was measured, aircraft application resulted in lower coverage than either UAV treatment. Gray leaf spot (C*ercospora zeae-maydis*) severity was low (< 5%) and was similar among treatments or reduced following UAV treatments, depending on location. Tar spot (P*hyllachora maydis*) exceeded 5% at one location and severity was reduced in UAV-treated plots. Yield improved with UAV treatments at one location. These initial results suggest UAVs may provide comparable or better coverage and disease control than conventional aircraft.

1:42 – 1:54 PM

Fluopyram Sensitivity in *Fusarium virguliforme* Isolates Associated with Soybean (Glycine max L.) Sudden Death Syndrome.

Nitha Rafi, Ryan Hamilton, Hossein Moradi Rekabdarkolaee, Dilorom Rasuleva, Suzette Baldwin, Alyssa Betts, Martin I. Chilvers, Ahmad Fakhoury, Heather Marie Kelly, Dean Malvick, Daren S. Mueller, Taofeek Mukaila, Damon Smith, Richard Webster, Febina Mathew, *North Dakota State University*

Sudden Death Syndrome (SDS), caused by *Fusarium virguliforme*, is a major disease affecting soybean (Glycine max L.) in the U.S. and Ontario, Canada. A fungicide seed treatment containing fluopyram (BASF) has been registered for managing SDS in the U.S. since 2014. This study aimed to assess fluopyram sensitivity in 28 isolates collected in and after 2014 (referred to as "contemporary" isolates) from North Dakota [n=16], Michigan [n=6], Minnesota [n=3], Wisconsin, Delaware, and Tennessee [n=1 each], as well as eight isolates collected before 2014 (referred to as "historical" isolates) from Michigan [n=6], Minnesota, and Iowa [n=1 each]. The identity of all isolates was confirmed via amplification of the IGS region. Technical grade fluopyram was added to half-strength PDA at concentrations of 0, 1, 5, 10, 25, 50, and 100 µg a.i. mL^{-1}. A 4 mm plug from a 14-day-old culture was placed at the center of each plate, and the plates were incubated in the dark at 21±2 °C for 10 days. Colony diameters were measured and used to calculate percent mycelial inhibition and EC50 values. The experiment was performed twice using a completely randomized design. The results indicated no significant differences in the mean absolute EC50 between historical and contemporary isolates (P=0.55), suggesting no change in fluopyram sensitivity. Future research will focus on broadening the geographic scope of isolate sampling to better understand variations in fluopyram sensitivity.

2:06 – 2:18 PM

Refining the rhizosphere microbial consortia for enhanced biocontrol of corn pathogens.

Pranaya Kaki, Devanshi Khokahni, *University of Minnesota*

Microbial consortia play a vital role in plant protection by suppressing soil-borne pathogens. A root-associated consortium of seven bacterial strains (C7) previously showed biocontrol activity against *Fusarium verticillioides*. To enhance this potential, we introduced a free-living biocontrol strain (S8), forming a modified community (C8). This study evaluated the biocontrol efficacy of S8, C7, and C8 against *Pythium ultimum*, *Fusarium graminearum*, *F. subglutinans*, and *Rhizoctonia solani*. Plate assays showed that S8 and C8 inhibited *P. ultimum* (>65%) but were less effective against Fusarium spp. (25–30%); none suppressed *R. solani*. In growth chambers, S8 alone outperformed C7 and C8, suggesting integration did not improve efficacy. 16S sequencing showed no major shifts in C7 strain abundance after S8 addition, implying a lack of functional integration. Since some individual strains showed stronger suppression than C7, we assembled sub-communities (SC1–SC3) based on highest inhibition. Pot assays revealed that SC1 and SC2 significantly improved plant height and root biomass. These findings suggest that biocontrol activity is driven by specific strain interactions. The current research focuses on identifying and characterizing antimicrobial compounds involved in pathogen suppression, with the goal of developing optimized microbial consortia for sustainable disease management.

2:18 – 2:30 PM

Towards Efficient Harnessing of the Soil Microbial Managers for Nutrient Uptake and Disease Resistance in Cereal Crops.

Riya Jain, Nikhil Lnu, Sachin Sharma, Brian Kontz, Arsalan Quresh, Sukhvir Kaur, Ravi Mural, Jose L. Gonzalez. Hernandez, Volker Brozel, Gazala Ameen, Christopher Graham, Shyam Solanki, *South Dakota State University*

The tiny microbial fraction of soil inhabitants surrounding crop roots manage the biggest role in maintaining the soil's unprecedented giving nature that supports plant health. One of the grand challenges for us is to develop a reliable framework of predicting microbial functional behavior in a designer community that is assembled to reduce our overreliance on synthetic fertilizers and pesticides, which pose environmental risks. Thus, our research focuses on corn and wheat microbiomes as a model to dissect how microbial diversity and functionality modulates in agricultural soils under variable treatments and attempts to recover some of these microbial managers (MM) to test their functional activities for developing predictable behavior models. We have collected soil samples from corn and wheat fields treated with organic biostimulants (2024), as well as from hard winter wheat trials (2022–2024) in South Dakota, where urea fertilizer was applied at rates of 0, 56, 112, and 168 kg/ha. Deploying full-length 16S rRNA gene and ITS region sequencing on Oxford Nanopore and PacBio platforms, alongside N gene function-based qPCR (amoA, UreC) approaches, we have identified taxonomic units that are more responsive to synthetic N application and organic biostimulants and associated with each treatment type (β-diversity, PERMANOVA S test).

Currently, we are cultivating bacterial OTUs in the lab with an ultimate aim of harnessing them in a predictable fashion.

2:30 – 2:42 PM

Evaluating a Saponin Biological Seed Treatment on Soybean Disease and Yield in Michigan and the Challenges in Biological Seed Treatment Efficacy.

Ryan Hamilton, Eric Anderson, Hyunkyu Sang, Dechun Wang, Martin I. Chilvers, *Michigan State University*

Soybean sudden death syndrome (SDS; *Fusarium virguliforme*) and white mold (*Sclerotinia sclerotiorum*) are major threats to soybean production in Michigan and all major soybean producing regions of North America. White mold and SDS management strategies mainly rely on host resistance and fungicides: typically, demethylation inhibitors (DMI – FRAC 3), succinate dehydrogenase inhibitors (SDHI – FRAC 7), or quinone outside inhibitors (QoI - FRAC 11). Fungicide resistance in pathogen populations is a continual concern and there is interest among soybean stakeholders around integrating biologicals into disease management programs. This study examined the efficacy of a *Chenopodium quinoa* saponin seed treatment in managing SDS and white mold in soybeans, as well as its yield impacts across Michigan in 2022-2024, by applying two treatments: a standard commercial base seed treatment (base) and base + Heads Up (61.3% a.i.; 15 mL·cwt-1), to 7 commercial soybean cultivars across 20 site-years of randomized small plot trials. Treatments were also applied to 7 additional cultivars across 8 site-years of on-farm split plot trials. No differences in soybean yield ($P = 0.9$), SDS root ($P = 0.7$), SDS foliar ($P = 0.3$), or white mold ($P = 0.5$) disease indices were detected. These findings expose knowledge gaps regarding fungal saponin detoxification mechanisms and potential negative off-target effects and provide practical insights to aid in soybean disease management programs.

2:42 – 2:54 PM

Biocontrol potential of a bacterial strain against *Fusarium spp.* in pulses.

Suruchi Aryal, Danielle Tarver, Malaika K. Ebert, *North Dakota State University*

Root rot is a destructive disease in pulses caused by a complex of soilborne pathogens, including *Fusarium spp., Rhizoctonia spp., Aphanomyces euteiches*, and *Pythium spp*. Among these pathogens, Fusarium is the predominant genus. Our research aims to explore the biocontrol potential of a specific bacterial strain that shows the potential to decrease fungal sporulation and hinder virulence of different *Fusarium spp*. To assess the effect on sporulation, we conducted in vitro assays for which we grew six different *Fusarium spp*. in spore producing conditions either in the presence or absence of the bacterial strain. Since most of the *Fusarium spp*. produce both macro-and microconidia, we counted both spore types after seven days of incubation. Our preliminary data show that overall spore production was significantly reduced ($p \leq 0.0012$) when the fungus was grown in the presence of the bacterial strain compared to Fusarium-only cultures. We are currently sequencing the genome of the bacterial strain. In addition, we will assess the inhibitory effect of the bacterial strain on sporulation and virulence of other *Fusarium spp*. and other fungal pathogens. Furthermore, we are interested in identifying the biochemical compound(s) produced by the bacteria that are interfering with spore production of the fungal pathogen. Ultimately, this research is aimed to advance the identification of an environmentally friendly alternative to manage root rot in pulse crops.

2:54 – 3:06 PM

Evaluating Oregano Essential Oil Seed Treatments for Managing Root Rot Pathogens of Dry Peas in Montana

Rowan Edwards, Carmen Murphey, Monica Brelsford, Uta McKelvy, *Montana State University*

Montana is leading the nation in both conventional and organic pulse crop production. Root disease is a major limitation to the yield and sustainability of Montana dry pea and lentil production. A survey of soil-borne pathogens in Montana dry pea and lentil fields revealed that 70% of fields sampled had *A. euteiches* present and *Fusarium spp.* were ubiquitous in all soil sampled with *F. avenaceum* among the most prevalent species detected. Essential oils present an alternative to conventional seed treatments and are compatible with organic production systems. Previous studies have shown that oregano essential oil (OEO) effectively inhibits *A. euteiches* and *F. avenaceum* growth in vitro. Based on these results, we conducted greenhouse experiments with dry pea to evaluate six OEO seed treatment formulations for their efficacy in suppressing root rot caused by *F. avenaceum* and *A. euteiches*. None of the OEO treatments nor the conventional fungicide Intego®Solo reduced Aphanomyces root rot severity. At a high inoculation rate of *F. avenaceum* (1g of inoculated millet/500g soil), OEO treatments did not significantly reduce root rot severity, while the conventional seed treatment CruiserMaxx®Vibrance®Pulse reduced average root rot severity by 14.6% compared to an untreated control. However, under moderate disease pressure (half inoculation rate), OEO formulation with gum arabic reduced Fusarium root rot severity by 10%, which was comparable to the conventional seed treatment.

Non-Competitive Oral Presentation Abstracts (in order of presentation, presenting author is highlighted in bold)

9:44 – 9:56 AM

*Screening USDA soybean accessions for resistance to *Rhizoctonia solani* AG 2-2 IIIB.

Denis Colombo, Matias Dominguez, Taofeek Mukaila, Athul Manoj, Febina Mathew, *North Dakota State University*

Rhizoctonia solani Kühn causes Rhizoctonia root rot in soybean (*Glycine max L.*). This study aimed to identify USDA soybean accessions with resistance to *R. solani* AG 2-2 IIIB and to identify common quantitative trait loci (QTLs) along with four Fusarium species (*F. proliferatum, F. sporotrichioides, F. subglutinans*, and *F. graminearum*), using a genome-wide association study (GWAS). A total of 203 accessions were evaluated, including 'PI518671' as a susceptible variety. Autoclaved sorghum (*Sorghum bicolor*) seeds were inoculated with a single isolate of *R. solani* and incubated for two weeks. The experiment followed a completely randomized design with six plants as replication per accession and was repeated once. Surface-sterilized seeds were pregerminated and planted in cups with three grams of inoculum using the layer inoculation method. Soil water-holding capacity was maintained at 60%. After 21 days, roots were rated for disease severity and analyzed using non-parametric statistics. Thirty-five accessions showed significantly lower relative treatment effects compared with PI518671 ($P< 0.001$). The GWAS conducted with 35,793 single-nucleotide polymorphism markers identified two QTLs associated with resistance to *R. solani.* However, no common QTLs were found between *R. solani* and the four Fusarium species examined in the study. The USDA accessions and the identified QTLs could serve as valuable resources for soybean breeding programs targeting resistance to *R. solani*.

10:42 – 10:54 AM

*AtNHR2A and AtNHR2B: two players of plant secretory pathways functioning in stress responses against non-adapted pathogens

Thiago Maia, Biwesh Ojha, Sophie Alvarez, Michael Naldrett, Clemencia Rojas, *University of Nebraska-Lincoln*

AtNHR2A and AtNHR2B are essential proteins involved in plant immunity, as shown by the susceptibility of *Arabidopsis thaliana* single mutants (Atnhr2a and Atnhr2b) to *Pseudomonas syringae pv. tabaci* (Pstab), a pathogen that does not naturally infect Arabidopsis plants. Notably, the Atnhr2b Atnhr2a double mutant exhibits even greater susceptibility than either single mutant, indicating that AtNHR2A and AtNHR2B function synergistically in immune defense. Both proteins localize to endomembrane compartments and interact with secreted proteins, suggesting a role in immunity-related secretory pathways. To explore this, we conducted a comparative proteomic analysis of apoplastic fluid from wild-type (Col-0) and Atnhr2b Atnhr2a plants after Pstab inoculation. We identified 52 differentially abundant proteins (DAPs) containing N-terminal signal peptides, with approximately 50% showing reduced abundance in the double mutant, suggesting a disruption in conventional secretion. In parallel, we compared the proteomes of whole leaf and apoplast to identify secreted proteins enriched in the apoplast that lack signal peptides, uncovering 59 DAPs dependent on AtNHR2A and AtNHR2B for their secretion via an unconventional pathway. These findings show that AtNHR2A and AtNHR2B are critical for both conventional and unconventional secretion pathways, highlighting their integral roles in mounting effective immune responses and reinforcing the plant's frontline defense against biotic stress.

1:54 – 2:06 PM

*Beneficial and pathogenic fungi associated with high soybean cyst nematode infestation and their response to plant sugars

Timothy S. Frey, Melanie Medina Lopez, Niah Cohen, Olivia Humbert, Angelica Rebollar Garcia, Horacio Lopez-Nicora, Soledad Benitez Ponce, *The Ohio State University*

Soybean cyst nematode, *Heterodera glycines* (SCN), is the pathogen responsible for the most economic damage to soybean in the United States. Controlling SCN is difficult because cysts can survive in the soil for up to seven years. SCN can also be affected by synergistic infections with other pathogenic fungi and oomycetes, including *Fusarium virgulliforme* (FV), *Macrophomina phaseolina* (MP), and *Phythophthora sojae* (PS). These synergistic infections can be more severe than SCN or the fungal disease alone. Our lab isolated 210 fungal morphotypes from a production field with high SCN abundance. Sixteen strains with protease activity, chitinase activity, and the ability to parasitize SCN eggs, and/or inhibit SCN egg hatching and motility were identified. These beneficial and pathogenic fungi were tested for their response to sucrose, trehalose, myo-inositol, and sorbitol. We are using capillary electrophoresis to identify sugars, including sucrose and myo-inositol, from soybean root exudates. Some sugars increased the growth rate of FV, MP, PS, and at least four beneficial strains. In addition, pathogenic fungi were grown with SCN and sugars to measure their response to changes in sugar concentrations. Sucrose application was found to increase FV infection in the presence of SCN but did not affect MP infections. Understanding these interactions will be critical for future control options as these pathogens continue to spread.

Other submitted posters (Presenting author highlighted in bold)

1) Assessing Winter Pennycress (*Thlaspi arvense*) as a Potential Trap Crop for Soybean Cyst Nematode (*Heterodera glycines*) Management.

Fariba Heydari Soreshjani, Cody Hoerning, Julia X. Zhang, James A. Anderson, Mitch Hunter, Donald Wyse, Senyu Chen; *University of Minnesota*

The soybean cyst nematode (SCN, *Heterodera glycines*) is a major pest of soybean (*Glycine max*) in the U.S., causing significant yield losses in Minnesota and necessitating sustainable management. While chemical nematicides and resistant cultivars offer control, integrated approaches are critical for long-term efficacy. Trap crops, such as Brassicaceae species, allow nematode entry into roots but prevent reproduction, offering a promising alternative. Winter pennycress (*Thlaspi arvense*), a cold-tolerant Brassicaceae and moderate SCN host, may disrupt the SCN life cycle, but its trap crop efficacy is untested. In this study, pennycress plants in cone-tainers were inoculated with SCN second-stage juveniles (J2) and grown for 2, 5, 9, or 14 days to establish nematode developmental stages, then overwintered in the field. J2 survival in soil was also assessed under field conditions. Nematode viability was evaluated via cyst formation and developmental stages in pennycress roots or subsequent soybean crops grown in soil with overwintered J2. Results showed J2 survived winter in soil, but more advanced stages (J2–J4) in pennycress roots did not. Pennycress grown for 14 days failed to survive overwintering, preventing post-J4 survival assessment. These findings suggest fall-planted winter pennycress may act as a trap crop, interrupting the SCN life cycle and supporting integrated nematode management.

2) Comparing mycelia-based infection methodologies for *Aphanomyces* root rot disease in peas.

Francisco G. Bittara Molina, Carmen Murphy, Malaika K. Ebert; *North Dakota State University*

Root rot caused by *Aphanomyces euteiches* is a major disease that affects pea. The pathogen overwinters as resting spores (oospores) and can survive for over ten years in the soil. Early symptoms such as water-soaked appearance, honey-brown discoloration, and loss of turgency can be observed on roots. Due to the hardiness of the overwintering structures produced by *A. euteiches*, the management of the disease can be challenging. Therefore, including host resistance as part of the integrated disease management approach plays a key role. In this study, we compared mycelia-based methodologies for greenhouse infection experiments and for the laboratory-set infection experiments in their efficiency and reliability to cause root rot in peas. When using mycelia as source of inoculum, root rot symptoms developed on the inoculated plants evaluated in both the greenhouse and the laboratory. No root rot symptoms developed in non-inoculated plants. Furthermore, the severity of the root rot of plant inoculated under greenhouse conditions was similar to the degree of disease of plant that were kept on petri dishes. Both assays were brought to completion within 14 and 8 days, respectively, compared to zoospore-based methods that are reported to take 21 days. With this research, we are hoping to develop a reliable, fast and easy screening method for *A. euteiches* that has the potential to substantially reduce screening time and costs for Aphanomyces root rot infection assays.

3) Cyanobacterium *Nostoc* species enhanced soybean against soybean cyst nematode.

Chuntao Yin, Nathan Lahr, Ruanbao zhou; *South Dakota State University/USDA-ARS*

Soybean cyst nematode (SCN, *Heterodera glycines Ichinohe*) is the most devastating and yield-limiting pathogen that threatens soybean production globally. Sustainable SCN disease management strategies are needed. In this study, a cyanobacterial strain was isolated from SCN-infected soybean soil and identified as *Nostoc punctiforme* using the cyanobacterial 16S rRNA gene sequence. When susceptible soybean plants were grown in the SCN-inoculated soil, *N. punctiforme* inoculants significantly reduced the total number of SCN eggs and second-stage juveniles (J2s), compared to the control with SCN inoculation only. Further microbial analysis showed that *N. punctiforme* inoculants changed the bacterial and fungal communities in the soybean rhizospheres and significantly increased the relative abundance of several bacterial and fungal species with potential nematicidal activities, suggesting the changes of soybean rhizosphere microbiota may partially contribute to the activity of *N. punctiforme* inoculants against SCN. However, *N. punctiforme* inoculants did not directly induce soybean defense reactions against SCN. Thus, *N. punctiforme* may be a potential nematicide against SCN invasion in soybean.

4) Efficacy of fungicides on foliar fungal diseases and their impact on cucumber yield in South Dakota.

Janani Perera Waduwarage Dona, Keigo Imai, Sean Toporek; *South Dakota State University*

Cucurbits comprise the largest acreage of vegetable production in SD. An ongoing statewide cucurbit disease survey identified *A. alternata* as the most common pathogen causing foliar fungal disease. Little fungicide efficacy data is available for controlling this pathogen in cucurbits. The objective of this study was to determine if fungicide prevention and control of *A. alternata* had a significant effect on cucumber yield. In 2024, a randomized complete block experimental design field trial with four replications per treatment, eight plants per replication, was conducted using cucumber 'Straight 8' and natural inoculum. The four treatments included: 1) Kocide (copper hydroxide), 2) Fontellis (FRAC 7), Inspire Super (FRAC 3 + FRAC 9), or Quadris (FRAC 11) rotated weekly with Bravo Weatherstik (M5) 3) Fontellis (FRAC 7), Switch (FRAC 9 + FRAC 12), or Cabrio (FRAC 11), rotated weekly with Bravo Weatherstik (M5) and 4) a water control. Whole plots were rated for disease severity each week on a 1-10 scale to calculate AUDPC and yield data was collected. Both *Colletotrichum orbiculare* and *A. alternata* isolates were recovered from plots. Although there was significantly reduced foliar disease development in treatment 3 compared to the water control, no significant differences in total or marketable yield were observed between any treatments. These preliminary results indicate fungicide management of *A. alternata* may not be economically necessary in South Dakota.

5) Evaluating Biologicals for Tar Spot Management in Corn.

Juan David Peña Roncancio, Edward Peña, Morgan Goodnight, Sujoung Shim, Darcy Telenko; *Purdue University*

Tar spot, caused by *Phyllachora maydis*, has significantly reduced yield in corn (*Zea mays*) across the North Central United States and Canada. Biological fungicides are a promising component of sustainable and integrated disease management strategies by reducing environmental impact compared to conventional chemical controls. However, their efficacy under field conditions remains inconsistent. A research trail was conducted at four locations in the United States and Canada (Indiana, Michigan, Iowa, and Ontario, Canada). Treatments included a nontreated control, a standard conventional fungicide (pyraclostrobin + metconazole), Serifel (*Bacillus amyloliquefaciens*), Actinovate (*Streptomyces lydicus*), Badge X2 (copper oxychloride + copper hydroxide), and Oxidate 2.0 (hydrogen peroxide + peroxyacetic acid). All products were applied at tassel/silk (VT/R1) growth stage, and disease severity was assessed at the dent (R5) growth stage. All locations reached moderate to high disease severity (>5%), except Iowa, which had less than 1%. Only Headline Amp (pyraclostrobin + metconazole) significantly reduced tar spot severity compared to the nontreated control. No significant differences between treatments were observed for yield. Further research is needed to continue testing the efficacy of biological fungicides in order to improve management strategies for this disease.

6) Evaluation of USDA Soybean accessions for Resistance to *Globisporangium ultimum*.

Milsha George, Matias Dominguez, Denis Colombo, Taofeek Mukaila, Bijula Sureshbabu, Nitha Rafi, Febina Mathew; *North Dakota State University*

Globisporangium (*Pythium*) *ultimum* Trow is a major oomycete pathogen that causes soybean (*Glycine max L.*) root rot and leads to yield losses in the U. S. The objective of this study was to screen USDA G. max accessions for resistance to *G. ultimum* in the greenhouse using 'Williams' (PI 548631) as susceptible check. Autoclaved sand cornmeal (19:1) was inoculated with a single isolate of *G. ultimum*. Surface sterilized seeds of 100 accessions were planted in plastic cups using the inoculum layer inoculation method with 20 grams of inoculum, and the greenhouse temperature was maintained at 23oC±3°C. The experiment followed a completely randomized design with six plants per accession and conducted twice. Soil water-holding capacity was maintained at 90%. Disease severity was assessed 21 days post-inoculation using 1 to 5 rating scale, and data was analyzed using non-parametric statistics. Thirty-three accessions exhibited significantly lower relative treatment effects compared to Williams (P< 0.0001, ATS=17.86, df=8.6). Genome wide association study conducted with 35,892 single-nucleotide polymorphism markers identified two Quantitative Trait Loci (QTL) significantly associated with resistance to *G. ultimum*. The QTLs were located at chromosomes 18 and 20, explaining 43.8 and 12.8 % of the phenotypic variance respectively. These results may serve as valuable sources of resistance to *G. ultimum* and used as parental materials in breeding programs following field validation.

7) Expanding Free Plant Diagnostic Services for Amish and Mennonite Communities in Missouri.

Dhruba Dhakal, Ramón Arancibia, Peng Tian; *University of Missouri*

Amish and Mennonite communities are historically underserved people in Missouri. They are primarily involved in small-scale commercial horticulture crop production and sell their produces at the weekly auctions or from their farms. Their adherence to traditional methods, which often exclude contemporary technologies, poses significant challenges in developing sustainable disease management plans. This is due to the lack of reliable plant disease diagnosis and the implementation of efficient disease control techniques. Communication barriers further extend the turnaround time for services, limiting the benefits of the diagnostic services provided by the MU Plant Diagnostic Clinic. Thus, the objective of this project is to expand on-site plant diagnostic clinic services throughout the 2024 and 2025 growing seasons, offering in-person consulting services and diagnostic services free of charge, to assist the farmers in resolving plant health issues. In 2024, we processed 60 samples from 39 clients, visited more than 40 greenhouses, high tunnels, gardens and crop fields, attended 6 auction sites, hosted 66 on-site diagnostic sessions and presentations at local produce auctions, meetings and trainings, published and printed three issues of Missouri Produce Grower (MPG) Bulletin. With all of this, we hope to improve services to the local communities, build strong relationship, and assist them in finding long-term solutions to plant health issues.

8) Exploring resistance to Aphanomyces root rot in sugar beet using Genome-wide association studies.

Samantha Rude, Olivia Todd, Kevin Dorn, Cory Hirsch, Ashok Chanda; *University of Minnesota - Twin Cities*

Aphanomyces cochlioides, the causal agent of seedling damping-off and root rot of sugar beet can cause significant yield reduction. These diseases are primarily managed by use of fungicide seed treatments, incorporation of factory waste-lime, and selecting moderately resistant varieties. Breeding efforts have focused on improving adult plant resistance although the mechanisms of disease resistance are unclear. Ninety-six USDA-ARS pre-breeding lines were screened for seedling resistance using a zoospore inoculation method and scored using a standardized 0-3 ARR rating scale. Individual plants within an accession were selected and pooled into equally sized (n=106) highly resistant or highly susceptible pools. Genomic sequencing was conducted on the pools for an extreme phenotype genome-wide association study (XP-GWAS) to identify potential genomic variants associated with ARR resistance which identified 29 statistically significant SNPs. Allele frequency analysis was also used to identify additional novel genomic regions with a high proportion of divergent SNPs.

9) Fungicide Comparison for Foliar Diseases of Corn in Indiana.

Edward S. Peña, Juan D. Peña, Morgan Goodnight, Sujoung Shim, Darcy Telenko; *Purdue University*

Foliar diseases of corn (*Zea mays*) such as tar spot, caused by *Phyllachora maydis*, and gray leaf spot, caused by *Cercospora zeae-maydis* have resulted in a 2.9% average annual estimated yield loss since 2015 in Indiana. The evaluation of new fungicides with the potential to reduce foliar diseases on corn yield is vital. A research trial was conducted at the Southwest Purdue Agricultural Center (SWPAC) in Vincennes, IN and at the Purdue Agronomy Center for Research and Education (ACRE) in West Lafayette, IN during 2023 and 2024. Ten foliar fungicides were applied at tasse/silk growth stage to evaluate their efficacy against corn foliar diseases. Both locations exhibited low disease severity (< 5%) in both years. Tar spot and gray leaf spot were present at both locations in both years, except for tar spot at SWPAC in 2023. Significant differences among treatments compared to the nontreated control were observed only at ACRE for both years and both diseases. At SWPAC, significant differences were observed only for tar spot severity in 2024. No significant differences between treatments were observed for grain moisture and corn yield. Low level of disease development limited the observable efficacy of the fungicides, this is why it is important to continue to evaluate fungicides for efficacy in different environments and years.

10) Fungicide Efficacy Tools for Field Crops from the Crop Protection Network.

Adam Sisson, Ed Zaworski, Kiersten Wise, Albert Tenuta, Daren S. Mueller; *Iowa State University*

The efficacy of fungicide products for managing diseases in field crops can vary widely. Selecting the most effective products for specific diseases is important for minimizing yield loss, reducing the risk of fungicide resistance, and improving on crop protection investments. To support decision-making, members of the Corn Disease Working Group and the North Central Regional Committee on Soybean and Wheat Diseases (NCERA-137 and NCERA-184) annually update fungicide efficacy tables for corn foliar diseases, soybean foliar diseases, soybean seedling diseases, and wheat foliar diseases. These tables are published by the Crop Protection Network (CPN) at https://cropprotectionnetwork.org, and from 2018 to 2024, they were downloaded nearly 70,000 times. To further improve access and usability, CPN developed an online tool that allows users to filter fungicide efficacy data by product or disease, enabling customized inquiries. The accuracy of the fungicide efficacy tables has been validated through field research. A previous survey of CPN contributors revealed that 97% of their extension clients reported increased knowledge of fungicide efficacy, and 60.5% indicated they changed their behavior as a result. These regularly updated fungicide efficacy tables continue to be a valuable resource for farmers and agribusiness employees, supporting the adoption of best practices in disease management.

11) Genetic heterogeneity and pathogenicity gene profiling of soil and tuber-derived *Streptomyces spp*. Isolates.

Sonal Srivastava, Kriti Tyagi, Manish Ranjan, Grace Petzold, Ashish Ranjan; *University of Minnesota*

Potato common scab (PCS) is a major disease caused by soil-borne Streptomyces species, including *S. scabies* and *S. turgidiscabies*, which produce thaxtomin, a phytotoxin that disrupts cell wall integrity, leading to scab-like lesions that reduce tuber marketability. This study examined 40 *Streptomyces* isolates from infected tubers and surrounding soil in Becker, MN, characterizing their genomic heterogeneity using 16S rRNA sequencing and multi-locus sequence analysis (MLSA) with four housekeeping genes (atpD, gyrB, rpoB, and trpB). PCR assays screened three pathogenicity genes (TxtAB, Nec1, and TomA), and pathogenicity tests including radish seedling and potato tuber slice assays were conducted to assess disease induction. Findings revealed greater pathogenic attributes in tuber-derived isolates versus soil-derived ones, with some TxtAB-lacking strains still inducing symptoms, suggesting alternative virulence mechanisms. The genetic variability among isolates highlights its role in disease severity, advancing understanding of Streptomyces-mediated pathogenicity to inform future PCS mitigation strategies.

12) High-Throughput Detection of *Fusarium graminearum* Chemotypes Using a Multiplex High-Resolution Melting assay.

Lovepreet Singh, Milton Drott, Robert Proctor, Hye-Seon Kim, Susan McCormick, J.Mitch Elmore; *University of Minnesota*

Fusarium graminearum is a primary causal agent of Fusarium head blight (FHB) on wheat and barley in North America. The fungus produces trichothecene mycotoxins that render grains unsuitable for human and animal consumption. Isolates of *F. graminearum* can differ in trichothecene production phenotypes (chemotypes), with single isolates producing one of the four toxins: 3-ADON, 15-ADON, NIV, or NX-2. Large-scale field surveys for monitoring chemotype distribution are critical for FHB disease management. However, contemporary molecular diagnostic assays used for chemotype surveillance remain inefficient. This study aimed to develop a single-tube, multiplex molecular assay based on high-resolution melting (HRM) chemistry to predict all four chemotypes. Conserved functional regions of three trichothecene biosynthetic genes (TRI1, TRI8, and TRI13) were targeted to develop the HRM assay. Multiplex HRM analysis produced unique melting profiles for each chemotype. The assay was validated on a panel of 80 diverse Fusarium isolates. The assay was highly sensitive, with a limit of detection (LOD) below 0.02 ng of fungal DNA. We applied machine-learning-based linear discriminant analysis (LDA) to automate the classification of chemotypes from HRM data, achieving a prediction accuracy of 99.7%. Our results demonstrate that this simple, rapid, and accurate assay can be applied to study the dynamics of *F. graminearum* populations in large-scale surveillance programs.

13) Influence of Capsicum species and cultivars on Alternaria internal rot incidence.

Keigo Imai, Janani Perera Waduwarage Dona, Sean Toporek; *South Dakota State University*

Alternaria internal rot is an exteriorly asymptomatic disease of peppers caused by *A. alternata* in eastern South Dakota that presents a dark, internal discoloration after dissection. A South Dakota farmer reported upwards of 50% infection in his *Capsicum chinense* peppers in 2023. In 2024, a randomized complete block design with four reps, five peppers per rep of 10 cultivars representing four *Capsicum spp.*, was established at the SDSU specialty crop research farm in Brookings, SD. Every red-ripe pepper was harvested weekly until the first frost, cut open, and recorded as either infected or non-infected. Damaged peppers were culled from the data. One symptomatic pepper was cultured from every plot of each cultivar per week to confirm the presence of *A. alternata. C. chinense* - Bhut Jolokia 'Red Ghost' (81% infected) and habanero 'Helios' (79%) - had significantly higher disease incidence than any other *Capsicum spp*. or cultivars. More commonly grown *C. annum* cultivars, bell 'Green Machine' (32%) and jalapeno 'Pantera' (11%), had significantly lower, yet intolerably high disease incidence. These preliminary findings suggest varying susceptibility to Alternaria internal rot among *Capsicum spp*.

14) Managing DMI cross resistance in *Cercospora beticola* using tank-mixing and fungicide rotation programs.

Ashok Chanda, James Deleon, Austin Lien; *University of Minnesota*

Cercospora leaf spot (CLS), caused by *Cercospora beticola*, is a foliar disease affecting sugar beet production in major growing areas of the US and worldwide. *C. beticola* has developed resistance to multiple classes of fungicides including cross resistance to select Demethylation inhibitor (DMI) fungicide. In 2023 and 2024, field trials were conducted to evaluate the efficacy of 4-spray programs with two alternating DMI fungicides, beginning with either mefentrifluconazole (MEF) or tetraconazole (TET) in the first application and rotating with either prothioconazole (PRO) or a pre-mix of difenoconazole (DIF) + propiconazole in the third application. Five representative leaves were collected from each plot at the end of the season to assess CLS severity and to obtain multiple single-conidia isolates. EC50 for all DMI fungicides was determined using a microplate-based assay and a qPCR assay was used to determine the potential haplotypes (A to E) of CbCyp51involved in DMI resistance. All fungicide treatments significantly reduced CLS severity compared to the nontreated control. Despite known cross-resistance among PRO and TET, DIF and MEF, these fungicides effectively managed CLS in a spray program that utilized multiple mode-of-action fungicides as tank-mix partners. In 2023, haplotype E was predominant among isolates which is known to be associated with decreased sensitivity to all four DMI fungicides. Tank-mixing DMI fungicides is essential to retain their efficacy.

15) Pivot irrigation affects corn canopy microclimate and diseases in 2024 eastern Nebraska fields.

Talon M. Mues, Saleh Taghvaeian, Dylan Mangel, Lincoln; Tamra Jackson-Ziems; *University of Nebraska – Lincoln*

In 2024, tar spot continued to spread and impact corn fields in Nebraska. Among diseases, tar spot was estimated to cause the most corn yield loss nationwide in the United States during the 2024 growing season. In eastern Nebraska, foliar disease severity was evaluated using a visual assessment to estimate total canopy disease coverage as a percent across three regions of 25 pivot-irrigated fields. These regions, based on center pivot irrigation systems, included the second pivot span, the outermost pivot span, and a rainfed corner. Results, averaged across the 25 fields, show that the irrigated portions of fields developed more severe tar spot and southern rust than the rainfed corners ($p\text{-value} < 0.001$). The second pivot span averaged 3.5% tar spot, while the outermost span and rainfed regions averaged 3.3% and 1.6%, respectively. Similar effects were seen for southern rust with 5.4%, 4.8%, and 1.9% for the second span, outermost span, and rainfed regions. When observing corn canopy microclimates, significant levels of leaf wetness occurred during each irrigation averaging 8.5 hours. Specifically, leaf wetness was recorded under the second span for 105 minutes longer for each irrigation event on average than under the outermost span ($p\text{-value} = 0.065$). Both temperature and relative humidity were impacted during irrigation events when compared to the rainfed environment, but duration of change for each parameter was not significantly affected by the pivot region.

16) Tailgate Diagnostics: Extension Demonstrations of Affordable Microscopes for Expanded Crop Disease Diagnostics.

Claudia L. Barrios, Kyle C. Broderick, Dylan Mangel, Tamra Jackson-Ziems, Amy D. Timmerman, Madilyn K. Shires, Rodrigo B. Onofre, Talon M. Mues; *University of Nebraska – Lincoln*

Plant diseases continue to pose significant threats to global crop production, often requiring rapid and accurate diagnosis and treatment. Effective visual identification of symptoms and pathogens is a critical first step toward implementing timely and appropriate management strategies. However, subtle or overlapping symptoms often complicate diagnoses. This resource and associated training materials introduce users to low-cost, portable microscopes that may help to improve our ability to view, photograph and confirm microscopic pathogen features to identify and differentiate common crop diseases. These tools and improved skills will open conversations with educators. Improve diagnostic capabilities but will not replace the advanced services provided by a plant diagnostic laboratory and experience of a trained diagnostician. This initiative, Tailgate Diagnostics, aims to improve early detection and field-level accuracy by offering practical, hands-on training in real-world settings. During demonstrations, an online survey was provided and results showed 86% of participants will use portable microscopes to examine plant samples, develop their observational skills, and gain confidence in identifying diseases through guided field exercises and expert feedback. These findings demonstrate the value of hands-on training in improving early diagnostic capabilities and promoting greater accuracy in field-based disease assessments.

Student Poster Competition Abstracts (numbered, presenting author is highlighted in bold)

17) A Systematic Analysis of Genome to Phenome Associations in Soybean Frogeye Leaf Spot Pathogen for Fungicide Resistance and Evolving Virulence.

Kyle Reese, Sachin Sharma, Shyam Solanki; *South Dakota State University*

Frogeye Leaf Spot, caused by the fungal pathogen *Cercospora sojina* (Cs), is a notable mid-season concern for soybean growers in the Midwestern US, including South Dakota (SD). Limited resistance against frogeye leaf spot in the commercially available soybean varieties necessitates fungicidal usage as a primary management tool. Fungicides belonging to quinone outside inhibitors (QoI) have been extensively utilized for managing Cs, but indiscriminate use of fungicides also creates selection pressure and favors the evolution of fungicide-resistant populations. Thus, we initiated a systematic approach to survey the prevalence and genetic diversity of Cs in SD for fungicide resistance and virulence. During a 2024 statewide disease survey, all the visited counties had Cs, and more than 70 representative isolates were retrieved. After purification of these isolates and DNA was extracted for PCR based detection using G143A specific primers that help us identify QoI fungicide resistance. However, there could be other novel mutations that have not been reported, so we are using a partial-length marker-based approach using a MinION sequencer to detect novel mutations. Detection of these novel mutations will help to create fungicidal formulations to tackle this disease and reduce losses. Our goal is to develop a logical approach to understanding frogeye leaf spot pathogen diversity and support SD farming communities.

18) Assessment of aerial drones for applying foliar fungicides to soybean in Indiana.

Monica Sayuri Mizuno, Darcy Telenko; *Purdue University*

Soybean diseases cause a significant challenge to agricultural production, presenting a considerable risk to yield. While ground sprayers are widely used to apply fungicides and achieve sufficient coverage in dense soybean canopies, drones offer a new solution to apply where ground equipment cannot reach a field or risk crop damage. The main objective of this research is to evaluate different fungicide application methods by comparing ground sprayers and drone applications for soybean disease management. Trials were conducted in northeast (NE), central (CE), and southeast (SE), Indiana. Trifloxystrobin + fluopyram + prothioconazole at 0.6L/ha was applied at the beginning pod/beginning seed (R3/R5) growth stages. The fungicide was sprayed with a ground rig at 187.3 L/ha and a drone at 18.7 L/ha and 46.9 L/ha and compared to nontreated control. Frogeye leaf spot (*Cercospora sojina*), Septoria brown spot (*Septoria glycines*), and downy mildew (*Peronospora manshurica*) were rated. At NE and SE, there were no significant differences between application type over nontreated control for disease severity (< 1.5% severity). At CE, all application methods reduced frogeye leaf spot over nontreated control, but there was no difference between application types. There was no significant effect of treatment application on yield compared to nontreated control. Overall, drones show potential for managing diseases; however, they may not consistently result in yield protection.

19) Characterizing and monitoring soybean cyst nematode (*Heterodera glycines*) populations in North Dakota.

Addison Plaisance, Dalvir Singh, Dinesh Poudel, Guiping Yan; *North Dakota State University*

Soybean cyst nematode (SCN; *Heterodera glycines*) causes major yield loss in U.S. soybean fields. Although host resistance has been an effective tool for control, SCN populations are overcoming commonly used resistant source, PI 88788. Characterization of virulent populations of SCN helps in selecting resistant varieties. In this study, SCN populations from 15 fields in North Dakota were evaluated for virulent phenotypes (HG types) using seven indicator lines and susceptible check ‘Barnes’ in growth chamber conditions. Thirteen samples with SCN levels at 330-2310 eggs/100 cm^3 of soil were assessed using naturally infested soil. Two samples with higher infestations, SCN eggs were extracted from field soil, and inoculated at 2,000 per cone-tainer with 100 cm^3 autoclaved sand at planting. Pre-germinated seeds were planted in cone-tainers with four replications. Plants were harvested at 30 days, and SCN females were quantified. Female index [FI = (average number of SCN females on test line/average number of SCN females on the susceptible check) × 100] was calculated, and HG types determined based on >10% FI. HG types were 2.5.7 (eight fields), 0 and 7 (two fields each), and 5.7, 2.7, and 5 (one field each). Unlike 2015-2017 survey data, where HG type 0 (36%) dominated, our results showed HG type 2.5.7 as most prevalent (53%), suggesting a shift that may lead to resistance ineffectiveness. Continuous HG type monitoring is critical for guiding resistance selection.

20) Characterizing Fungal Pathogens Associated with Sweetpotato Postharvest Diseases.

Ujjwal Kamboj, Waana Kaluwasha; Lincoln University of Missouri

Fungal pathogens are among the major causes of postharvest diseases in sweetpotato (*Ipomoea batatas*), but there is limited information on the common pathogens causing postharvest decay of sweetpotatoes in Missouri. The aim of the research was therefore to isolate and identify fungal pathogens from sweetpotato storage roots with symptoms of postharvest decay. Sweetpotato roots with symptoms of end rots, soft rots, scurf, or surface rots were either purchased from a local farmers market or collected from stored roots harvested from the University farm in 2024. Following disinfection in 10% sodium hypochlorite and 70% ethanol, root pieces (5mm) were cultured on Potato Dextrose Agar (PDA) amended with antibiotic for 4-5 days. Developing colonies were then transferred to new PDA plates to obtain pure cultures, which are currently being characterized based on morphology and amplification of the internal transcribed spacer (ITS) region. Pathogenicity assays of eight distinct isolates in addition to non-inoculated controls were conducted using storage roots of four sweetpotato cultivars (Covington, Mahon Yam, Murasaki, and White Bonita) and results will be discussed in the poster. This research will provide information on the prevalent fungal pathogens causing diseases during sweetpotato storage in Missouri and will allow for further research evaluating sustainable disease management strategies to reduce storage losses.

21) Comparing the impact of soybean disease management levels on yield components using field evaluation.

Cooper Hicks, Bhanu Dangi, Dylan Mangel; *University of Nebraska – Lincoln*

Soybean (*Glycine max Merr.*) yield is shaped by complex interactions between genetic potential, environmental conditions, and crop management practices. In the North Central U.S., yield loss due to disease remains a prevalent challenge, leading to the widespread adoption of chemical control strategies, especially seed treatments and foliar fungicides. However, the effectiveness of these practices in improving yield and grain quality is highly dependent on environmental conditions. The purpose of this research is to evaluate a spectrum of management intensities, ranging from non-treated plots to integrated strategies, across multiple environments in the U.S. North Central region. Strategies include a seed treatment, single or double foliar fungicide applications, and two different foliar application timing methods. We aim to understand how these disease management intensities impact key yield components, including pod density, seed number per pod, and individual seed weight. Additionally, we seek to understand the individual and combined impact of seed treatment and foliar fungicide use on the incidence of seed-borne diseases in harvested grain. The insights gained from this research will demonstrate the relationship between diverse management practices and yield components.

22) Decoding WAK-Dependent Immune Signaling in Barley Bipolaris sorokiniana Pathosystem.

Meenu Singh Sengar, Brian Steffenson, Bob Brueggeman, Shyam Solanki, Gazala Ameen; *South Dakota State University*

Plant immunity is mediated by specific receptors that detect pathogen signals and trigger defense responses, often involving programmed cell death. Necrotrophic fungal pathogens such as *Bipolaris sorokiniana* (Bs) can exploit this response to promote infection and cause yield losses. In the barley-spot blotch pathosystem. We previously identified two wall-associated kinases (WAKs), Sbs1 and Sbs2 that are manipulated by the Bs to induce cell death. Our study investigates whether Sbs1 and Sbs2 physically interact and if it is essential for susceptibility function. To test our interaction hypothesis, we performed heterologous co-transient expression and Bimolecular Fluorescence Complementation (BiFC) assay of our candidates in *Nicotiana benthamiana* leaves and analyzed five replicated samples and three independent experimental runs on Leica Stellaris5 confocal microscope. BiFC complemented fluorescence was visible at the plasma membrane, suggesting potential interaction of the Sbs1&2. Co-localization further confirmed that both proteins are localized at the plant cell membrane periphery. Our findings provide molecular evidence of WAK-WAK interaction in barley and reveal a possible mechanism exploited by *B. sorokiniana* to induce susceptibility. This work aims to advance our current molecular understanding of WAK-mediated immunity signaling in cereal crops.

23) Developing an environment-based risk-assessment model for Sclerotinia stem rot in Nebraska soybean fields.

Roshani Baral, Bhanu Dangi, Rebecca Higgins, Dylan Mangel; *University of Nebraska – Lincoln*

Apothecia formed from overwintered sclerotia are the primary source of airborne ascospores that initiate Sclerotinia stem rot (SSR) infection in soybean fields. Fungicides are the primary management tool, but application success depends on the timing relative to apothecia formation, ascospore release, and favorable weather during flowering. As these factors must coincide for infection to occur, accurately assessing risk remains a challenge, often resulting in poorly timed or unnecessary fungicide applications. This research aims to identify site-specific, weather-based disease risk factors that can be integrated into a decision-support system to guide economic and environmentally sustainable fungicide applications. Natural sclerotia overwintered from the previous season will be scouted and monitored across five geographically dispersed soybean fields in Nebraska. Each site will be equipped with an on-site, meteorological-grade weather station recording hourly air temperature, precipitation, humidity, and light intensity above and below the canopy, along with soil temperature and soil moisture. Disease ratings will be conducted throughout the season, and time-lapse cameras will document apothecial development and ascospore dispersal. By correlating environmental variables with pathogen activity, we aim to identify risk factors to enhance SSR risk prediction and optimize fungicide timings.

24) Developing a real-time quantitative PCR assay for direct detection and quantification of the root-lesion nematode, *Pratylenchus penetrans*, from potato roots.

Dinesh Poudel, Guiping Yan; *North Dakota State University*

Root-lesion nematodes, *Pratylenchus penetrans*, are migratory endoparasites that attack potato roots, causing necrotic lesions and yield losses up to 70%. Traditional detection methods are labor-intensive, time-consuming, and require prior nematode extraction and taxonomic expertise. This study aimed to develop a SYBR Green-based real-time quantitative PCR (qPCR) assay for detection and quantification of P. penetrans directly from DNA extracts of potato roots. A primer pair previously designed for *P. penetrans* was evaluated for specificity in root tissue with other nematode species. Bovine serum albumin (BSA) was tested to neutralize qPCR inhibitors in root DNA extracts. The assay showed high specificity and sensitivity to P. penetrans detecting 1.56×10-2 of a single nematode in 0.2 g of roots. A standard curve based on artificial nematode inoculations demonstrated a strong linear relationship between Cq values and log-transformed nematode numbers (R2=0.993) with high amplification efficiency. Validation using root samples from two greenhouse experiments involving five potato cultivars with varying resistance levels showed strong correlations (R2=0.814 and 0.787) between qPCR estimates and traditional counting. This qPCR assay is rapid, sensitive, and specific for detecting P. penetrans directly from potato roots, providing a useful tool for monitoring the nematode population in roots to facilitate effective management strategies for control of this nematode pest.

25) Developing and Evaluating Real Time Recombinase Polymerase Amplification Assay for Detecting *Heterodera glycines*.

Nabina Karki, Madalyn Shires, Connie Tande; *South Dakota State University*

Soybean cyst nematode (*Heterodera glycines Ichinohe*; SCN) is the biggest economic constraint to soybean production in South Dakota. Precise and rapid diagnosis of the nematode population in the sample is critical for its effective management. Traditional molecular techniques require a thermocycler to adjust temperature variations for amplification, limiting the use in laboratory conditions. This study focuses on developing a real-time Recombinase Polymerase Amplification (RPA) assay as a rapid and isothermal alternative for the detection of SCN in infested soil samples. Specific primers and probes were tested to target the putative parasitism gene CLE, which plays a crucial role in SCN's ability to parasitize soybean roots. Initial testing of the RPA assay has demonstrated reliable detection of SCN from genomic DNA of a single cyst. Serial dilutions of genomic DNA were performed to assess the assay sensitivity, showing sensitivity of 1/1000 of a single cyst. Background correction and threshold optimization will be performed to ensure precise identification and quantification of the *Heterodera glycines* population. Although the assay is still under development, these preliminary results highlight its potential for providing an accurate and accessible diagnostic tool for SCN detection. This method could improve pest management strategies, particularly in limited-resource settings by facilitating in-field diagnostics.

26) Do Fungicide and Insecticide Applications at the R3 Growth Stage Protect Soybean Yield in Missouri?

Jeova Da Silva, Lennis Rodrigues, Lucas Severo, Alexandria Haafke, Mandy Bish, Ivair Valmorbida; *University of Missouri*

Missouri soybean growers commonly apply preventative fungicides and insecticides. Adoption of this practice increased substantially after soybean rust became a concern in the US in 2004. We evaluated the effect of calendar-based applications of fungicides and insecticides on foliar diseases, insect pests, natural enemies, and soybean yield. Field experiments were conducted at three locations in Missouri during 2024. Fungicides and insecticides were applied in combination or alone at the R3 soybean growth stage. Weekly insect scouting was conducted from V4 to R6 growth stages, while foliar disease and defoliation assessments were performed at R5. Low foliar disease incidence was observed at each location, regardless of treatment. Brown leaf spot (*Septoria glycines*) was the most prevalent. Cercospora leaf blight (*Cercospora spp.*) and frog eye spot (*Cercospora sojina*) were occasionally found. Bean leaf beetle (*Cerotoma trifurcata*), Japanese beetle (*Popillia japonica*), green cloverworm (*Hypena scabra*), and stink bugs (*Euschistus spp.* and *Chinavia hilaris*), were present but did not reach economic threshold levels. Natural enemies were significantly affected by treatments ($P < 0.05$). Yield was not significantly increased regardless of the treatment. These preliminary results suggest that preventative applications were not cost-effective under low insect pest and foliar disease pressure. This research will be repeated in 2025.

27) Effect of Humidity on the Efficacy of Foliar Fungicides for Managing Frogeye Leaf Spot in Soybean.

Victor Olubunmi Ayodele, Nabin K. Dangal, José F. González-Acuna, Daren S. Mueller; *Iowa State University*

Foliar fungicides are typically applied via ground or aerial equipment, but drone use is increasing. Due to their narrower spray swath, some applicators are exploring application windows beyond daytime hours. However, the impact of nighttime fungicide applications remains uncertain. This study examined how high humidity simulating dew affects fungicide performance on disease development under controlled conditions. A two-factorial randomized complete block design with six replications was used. The first factor was humidity (>95% RH vs. 56% RH) before and after spraying; the second was fungicide: (Delaro Complete, 8 fl oz/acre + NIS 0.25% v/v) vs. non-treated control (NTC). Soybean plants (cv. Williams 82) were sprayed at V2, inoculated with *Cercospora sojina* six hours later, and incubated at >89% RH, 26°C, and a 12-hour light/dark cycle for four weeks. Frogeye leaf spot (FELS) severity was assessed every three days from 6 to 24 days after inoculation to calculate the area under the disease progress curve (AUDPC), which was log transformed. Results showed no significant humidity x fungicide application interaction ($P = 0.970$) and no effect of humidity on AUDPC ($P = 0.756$). However, fungicide application significantly reduced AUDPC (94.9%, $P < 0.001$). Thus, under controlled conditions, high humidity before and after fungicide application does not affect fungicide efficacy, and Delaro Complete is effective in reducing FELS severity under varying humidity conditions.

28) Effects of Compost Blend and Poultry Manure on Reproduction of *Pratylenchus penetrans* and Performance of Potato.

Addison Plaisance, **Bonventure Mumia**, Guiping Yan, Marisol Quintanilla; *North Dakota State University*

Root-lesion nematode, *Pratylenchus penetrans* is a damaging pest on potato. Compost blend and poultry manure were compared to an untreated control to determine their effects on nematode reproduction factor (RF), plant growth, and seed tuber weight. Two greenhouse trials were conducted in 2024 and 2025 by applying recommended rates of 18g (1.25 t/acre) of compost blend or poultry manure in 2kg of soil inoculated with 1,030 P. penetrans/kg of soil, and planted with potato cv. Russet Norkotah. Nematodes were quantified at midseason (60 days after planting)

and at trial termination (120 DAP). Results showed significant differences among treatments and untreated control on RF and seed tuber weight, but not on fresh root and shoot weight. At midseason, there were significantly different ($P < 0.05$) RFs for untreated control (1.83), compost blend (0.99) and poultry manure (0.45) in trial 1, but there were no statistical differences between the two applied treatments in trial 2. At harvest, poultry manure resulted in the lowest RFs (1.14 and 1.97) but the highest tuber weight (103.6g and 111.8g) in trials 1 and 2, respectively, compared to compost blend (RFs = 2.3 and 2.5, tuber weight = 96.3 and 101.7g) and untreated control (RFs = 3.8 and 5.7, tuber weight = 62.7g and 79.8g). This study shows a negative correlation between RFs and tuber weight ($r = -0.62$), and the organic manure has the potential to increase potato yield without greatly increasing *P. penetrans* populations.

29) Efficacy of Selected Fungicides for Management of Phytophthora blight (*Phytophthora capsici*) of Cucurbits.

Sahil Redhu, Mohammad Babadoost; *University of Illinois Urbana Champaign*

Fungicides use is essential for managing Phytophthora blight of cucurbits, caused by *Phytophthora capsici*. Laboratory and field studies were conducted to assess the effectiveness of eight fungicides, including cyazofamid (Ranman 400SC), dimethomorph (Forum 4.16SC), dimethomorph + ametoctradin (Zampro 525F), ethaboxam (Elumin 4SC), fluopicolide (Presidio 4SC), mandipropamid (Revus 2.09SC), mandipropamid + oxathiapiprolin (Orondis Ultra), and potassium phosphite (ProPhyt) for managing P. capsici. In the laboratory, the fungicides at the rates of 0.001, 0.01, 0.1, 1, 5, 10, 50, 100, 500, and 1000 µg/ml were evaluated against six P. capsici isolates. Mandipropamid + oxathiapiprolin had the lowest (0.0046 µg/ml) EC50. A trial was conducted in an irrigated commercial field of a processing pumpkin. The field was naturally infested with *P. capsici*. Plants were sprayed seven times from the first sign of the disease to 6 days to harvest. The incidence of infected fruits ranged from 3.49% (in plots sprayed with Forum 4.16SC) to 45.40% (in untreated plots). The highest number of marketable fruits (44.33 fruits/plot) was in the plots sprayed with Orondis Ultra plus ProPhyt, alternated with Ranman plus ProPhyt, alternated with Revus plus ProPhyt. The lowest marketable fruit number (18.00 fruits/plot) was in untreated plots. The percentage of infected vines in treated plots was significantly lower ($P = 0.05$) than that of untreated plots.

30) Evaluating fungicide application programs to manage Cercospora leaf spot (CLS) of sugar beet.

Anu Ranabhat, Eric Branch, Andrew Fuchs; *North Dakota State University*

Cercospora leaf spot (CLS) caused by *Cercospora beticola* severely impacts sugarbeet root yield and sucrose concentration. Along with tolerant varieties, growers rely on fungicide application at or around row closure followed by subsequent applications throughout the season. However, unnecessary application can cause increased production costs thereby reducing profit margins. This project focuses on relationship of spray programs differing in application timing and fungicide selection and CLS infection severity and yield parameters. Fungicide programs were based on recommendations of sugarbeet cooperatives in Minnesota and North Dakota. A field experiment was conducted in a randomized complete block design in 2024 near Foxhome, MN. Ten treatments, including a nontreated control, were tested on a CLS-tolerant (CR+) variety. The timing of treatments differed in initial application (Mid-June, Late June, Early July) and the interval between subsequent fungicide applications. The result illustrated higher CLS rating and significantly greater disease severity in nontreated plots compared to treated plots. Although there were no statistically significant differences among fungicide programs when evaluated for root yield and recoverable sugar, all were numerically improved over the nontreated control, indicating possible economic benefits for sugarbeet growers. These results support current fungicide program recommendations to manage CLS in Minnesota and North Dakota.

31) Evaluating the role of *Xanthomonas translucens pv. translucens* type III effectors in their virulence on barley.

Sefunmi Alaofin, Gongjun Shi, Timothy Friesen, Zhaohui Liu; *North Dakota State University*

Bacterial leaf streak (BLS) of barley caused by *Xanthomonas translucens pv. translucens* is a disease that is becoming increasingly significant in North Dakota and the surrounding areas. Understanding the virulence mechanisms of this bacterium is crucial for developing resistant cultivars. Hence, this study aims to investigate the role of all type III effectors of the bacterial pathogen in the development of BLS through targeted gene disruption. So far, we have created individual bacterial mutants for five transcription activator-like effector (TALE) genes and three Xop genes: XopR, XopF1, and XopAP. We tested all the mutants on a set of barley lines to determine if there were any changes in virulence compared to the wild type strain. Both the mutant strain and the wild type strain were infiltrated into the same leaf area on each side of the midvein, and the development of water-soaked symptoms was monitored daily after infiltration. The preliminary results indicated that no significant changes in virulence were observed for all five TALE mutants and the XopR mutant. However, the mutants for XopF1 and XopAP displayed a significantly reduced amount of water-soaked symptoms. The virulence testing is being repeated to confirm these results and the mutants for other Xop genes are being generated. This work will provide valuable insights into the molecular mechanisms of bacterial virulence and the interactions between the pathogen and its host in this pathosystem.

32) Evaluating the sensitivity of *Phaeocytostroma ambiguum* to fungicides used in commercial seed treatments on corn.

Daniel Kiprop Kimtai, Clarice Schmidt, John Shriver, Alison robertson; *Iowa State University*

Crown rot of corn is an emerging disease in the U.S. Midwest, raising concerns due to its increasing incidence and potential yield impacts. From 2022 to 2024, *Phaeocytostroma ambiguum*, a pathogen previously associated with crown rot in other countries, was consistently isolated from symptomatic corn plants across the region. In the United States, fungicide seed treatments are widely used to protect seedlings from soil-borne pathogens; however, the efficacy of these treatments against *P. ambiguum* remains unclear. This study assessed the fungicide sensitivity of 54 *P. ambiguum* isolates using in vitro poison plate assays. Discriminatory doses for each fungicide were based on EC_{50} values previously determined from a representative subset of isolates. Preliminary results indicate that all isolates were sensitive to fungicides in the succinate dehydrogenase inhibitor (SDHI), demethylation inhibitor (DMI), and phenylpyrrole (PP) classes. However, variation in sensitivity was observed among isolates exposed to fungicides in the quinone outside inhibitor (QoI) class. These data are crucial for refining seed treatment strategies to effectively manage *P. ambiguum*.

33) Evaluation of aggressiveness of *Septoria glycines* isolates using detached leaf methods on soybean cultivars.

Parbati Joshi, Nabin K. Dangal, Edgar H. Nieto-Lopez, Daren S. Mueller; *Iowa State University*

Septoria brown spot, caused by *Septoria glycines*, is a major foliar disease of soybean (Glycine max). This study evaluated the aggressiveness of *S. glycines* isolates using a detached leaf assays under greenhouse and in vitro conditions. The detached leaf method was tested as a practical approach for screening both cultivar susceptibility and pathogen virulence. Two soybean cultivars (William 82 and NK008-PXF) were inoculated with two *S. glycines* isolates (HS02 and S38), both collected in Iowa. Result showed no significant interaction between cultivar and isolate for brown spot symptom development ($P = 0.350$). While the isolates did not differ significantly in aggressiveness, symptom development varied significantly between the two cultivars. NK008-P8XF had significantly less brown spot severity than Williams 82 at at 7 days after inoculation (DAI) (67.3%, $P < 0.001$), 14 DAI (55.3% $P = 0.001$) and 21 DAI (54.0%, $P = 0.008$). These findings suggest that the detached leaf assay has potential as a tool for evaluating soybean response to *S. glycines*, but additional research is needed to validate this method across a wider range of cultivars and isolates.

34) Evaluation of Sulfur Fertilizers on Sudden Death Syndrome of Soybean.

Emily Anne Duncan, Shaun Casteel, Darcy Telenko; *Purdue University*

Fusarium virguliforme infect the roots of soybean resulting in sudden death syndrome (SDS) that causes chlorosis, root rot, and pod abortion. SDS increases with high soil moisture, heavy rain, and cold soil. Growers manage SDS with resistant varieties and seed treatments. In recent years soybean has responded to sulfur application and field observations have raised the question of the potential of sulfur providing disease suppression in soybean. To address this, a research trial was established in two locations in northern and central Indiana. The experimental was split-plot with the main plot planting date (April, May) and sub-plots a factorial arrangement of SDS inoculation (non-inoculated, inoculated) by sulfur treatment (nontreated control, ammonium sulfate, ammonium thiosulfate, calcium sulfate). Sulfur was applied after planting at a rate of 22.4 kg/ha. SDS was present but low. At full seed, SDS Index (DX) was higher at the northern Indiana field in soybean planted in April and lowest in soybean applied with calcium sulfate. Yield was not affected by plant date or treatment at the northern location. In central Indiana, there was no effect of treatment on SDS symptoms. All sulfur treatments increased soybean yield over the nontreated in the inoculated plots. In non-inoculated plots soybean yield was reduced over nontreated with ammonium thiosulfate and calcium sulfate, but was not significantly different from nontreated with the ammonium sulfate treatment.

35) Exploring *Triticum sphaerococcum* germplasm for resistance to wheat stem and leaf rusts.

Gayatri Sharma, Upinder Gill; *North Dakota State University*

Wheat (*Triticum aestivum*) is the second most important food crop, contributing 20% of dietary intake, with an annual production of 796.85 million metric tons cultivated over 217 million hectares. Wheat rusts are historically significant diseases of wheat that threaten global food security. In North Dakota, leaf, stem, and stripe rusts are reported frequently in wheat fields. Although new resistance genes are being introduced in wheat varieties, rusts are continuously emerging to generate new virulence variants, often rendering the resistance genes ineffective after a few years. This highlights the need for new sources of durable resistance. *Triticum sphaerococcum* (6X, $2n = 42$), which is also known as Indian dwarf wheat, has not been explored for resistance to wheat rust races prevalent in North Dakota. In this study, we phenotypically characterized the *T. sphaerococcum* accessions to identify novel resistance sources against multiple races of stem rust (caused by *Puccinia graminis f. sp. tritici*) and leaf rust (caused by *Puccinia triticina*). Preliminary findings suggest that some of the tested accessions show high resistance, which will be further characterized to find potential resistance loci. The new sources of resistance will foster the development of resilient wheat cultivars capable of withstanding future rust epidemics.

36) Fumonisin Contamination in Corn from Nebraska: A multiyear Snapshot.

Ram Kumar Shrestha, Tamra Jackson-Ziems, Jayne Stratton, Heather Hallen-Adams, Andreia Bianchini; *University of Nebraska-Lincoln*

Fumonisins are among the most toxic mycotoxins, primarily produced by *Fusarium proliferatum* and *F. verticillioides*. They are involved in disrupting sphingolipid metabolism and inhibiting ceramide synthase. Exposure to these mycotoxins can cause equine leukoencephalomalacia and porcine pulmonary edema. Fumonisins have also been associated with esophageal cancer and neural tube defects in humans. Notably, corn is known as the most susceptible cereal to fumonisin contamination; fumonisin contamination in corn can pose a significant food safety concern. . In this multi-year study, fumonisin levels in corn were monitored from 2022 to 2024 across the major corn-producing counties in Nebraska. A total of 134 corn samples were analyzed using a fluorometer-based fumonisin test. Results indicated that 70.1% of the corn was positive for fumonisin, with an average of 1.97 ppm. The total fumonisin concentration ranged from 0.25 to 19 ppm, and the average among the positive samples was 2.80 ppm. The percentage of samples exceeding 4.0 ppm fumonisins was 12.7%. Further, crop damage by insects and weather events, including hail and wind, significantly affected fumonisin contamination in corn grain. This dataset suggests a reasonable risk of fumonisins associated with corn produced in Nebraska and indicates the necessity to effectively mitigate affected crops intended for human consumption and animal feed.

37) Fungicide Comparison for Tar Spot on Short Corn.

Emilia Myers, Darcy Telenko; *Purdue University*

Short stature corn hybrids have been developed to decrease the risk of lodging that may result in lower yields or less efficient harvesting. These new hybrids offer a unique advantage to growers, but the impact foliar fungicide application in this new architecture for disease management is still unknown. With a denser canopy and an increased tolerance of higher plant populations, short corn may be more susceptible to foliar diseases. Trials were established at the Purdue Agronomy Center for Research and Education (ACRE) and the Pinney Purdue Agricultural Center (PPAC) to evaluate foliar fungicide efficacy on two short corn hybrids. The experiment was a randomized complete block design with four replications. Hybrids PR111-20SSC and PR108-20SSC were planted in May with Delaro Complete (8.0 fl oz/A) applied at tassel/silk (VT/R1). Disease ratings for tar spot, gray leaf spot (GLS), and northern corn leaf blight (NCLB) were assessed at dent (R5). At ACRE, PR111-20SSC had less NCLB and higher yield than PR108-20SSC. At PPAC, PR111-20SSC showed reduced tar spot severity. Delaro Complete reduced tar spot, GLS, and NCLB severity at both locations and increased yield at PPAC only as compared to nontreated control. These results suggest short corn hybrids differ in disease susceptibility, and fungicide can effectively managing foliar diseases in short corn production.

38) Fungicide Efficacy for Managing Sclerotinia Stem Rot on Soybean Genotypes with Varying Susceptibilities.

Rachel Konshok, Hope Renfroe-Becton, Richard Webster; *North Dakota State University*

Sclerotinia stem rot (SSR), caused by *Sclerotinia sclerotiorum*, is a major threat to soybean production in North Dakota with limited genetic resistance available due to its quantitative nature. Effective management often requires an integrated approach, such as combining fungicide applications with host resistance. In this study our objective was to identify the treatment or combination of treatments that resulted in the least amount of SSR under naturally inoculated field conditions. The treatments studied were fungicides—boscalid (Endura) at a rate of 8 oz/ac and Thiophanate methyl (Topsin) at a rate of 20 floz/ac—and soybean cultivars with differing susceptibilities to SSR. Three genotypes were selected for this trial: W19-2484 (highly resistant), 51-23 (moderately resistant), and MN 1410 (moderately susceptible). The plants were grown under irrigated field conditions with three repetitions per treatment. Disease incidence (%) and severity were assessed at the R6 stage, and additional measurements were recorded at harvest. Partial profitability was later calculated. Results from the first year of this trial indicated that Endura outperformed Topsin in reducing disease severity index ($p = 0.065$) and yield ($p = 0.087$). Additionally, MN 1410, the moderately susceptible genotype, showed superior yield ($p < 0.001$) and partial profitability ($p < 0.001$). However, these results are from a single season with low disease pressure, so greater replications are needed.

39) Fusarium Head Blight (FHB) disease severity in Spring Barley cultivars adapted for South Dakota.

Tapish Pawar, Tasneem Fathima, Joseph Tilstra, Sunish K. Sehgal, Christopher Graham, Jose L. Gonzalez. Hernandez, Shaukat Ali, Shyam Solanki, Gazala Ameen; *South Dakota State University*

Fusarium Head Blight (FHB), primarily caused by *Fusarium graminearum*, poses a major threat to U.S. small grains production by reducing yield and contaminating grains with harmful mycotoxins. Developing host resistance is crucial for disease management. This study assessed 32 spring barley genotypes, sourced from three U.S. barley breeding programs, for FHB resistance using a local *F. graminearum* isolate, Fg1 over three years 2022-2024. Results revealed considerable variation among genotypes in disease severity and mycotoxin accumulation. Analysis of variance (ANOVA) indicated that genotypes had a significant effect on FHB severity, Fusarium-damaged kernels (FDK), and deoxynivalenol (DON) content. Averaging disease severity across the three seasons provided a reliable measure of each genotype’s resistance. Notably, genotypes S2M190 (39.38%), MT17M02507 (42.87%) S2M196 (46.62%), S2M197 (46.88%) displayed lower disease severity, suggesting they carry moderate genetic resistance to FHB. S2M190 (37.50% FDK, 0.68 ppm DON) and MT17M02507 (31.25% FDK, 0.70 ppm DON) also consistently exhibited reduced FDK and DON levels, making them strong candidates for FHB-resistance. In contrast, the genotypes Robust (52.47%) and Tradition (62.33%) were highly susceptible to FHB. These findings highlight the importance of selecting resistance genotypes along with fungicides to effectively manage FHB and reduce mycotoxin contamination in barley production in the state of South Dakota.

40) Host–Pathogen Dynamics in Soybean Under Organic Management: Genomic Insights into Organic Acid–Mediated Suppression of White Mold.

Sachin Sharma, Kyle Reese, Gazala Ameen, Shyam Solanki; *South Dakota State University*

White mold (WM), caused by *Sclerotinia sclerotiorum* (Ss), continues to threaten soybean production in the Midwest U.S., especially under organic cultivation. Organic acids (OAs), such as humic (HA) and fulvic acids (FA), released from organic amendments, may modulate plant-pathogen interactions, yet their role in the soybean–Ss interactions remains unclear. From surveys conducted across South Dakota in 2023–2024, we collected 107 Ss isolates and screened them in vitro with FA and HA (20–150 mg/L). Significant variations ($p< 0.05$) for OA responsiveness across isolates and two isolates showing contrasting FA responses were selected for greenhouse assays on Williams 82 (susceptible) and PI 416805 (resistant) under OA amended soils. Concurrently, we are performing long-read whole-genome and transcriptome sequencing on 25 Ss isolates to identify OA-responsive genes. We also assembled a panel of 350 diverse soybean lines, now being phenotyped under controlled greenhouse conditions for genome-wide association study (GWAS) to identify host loci associated with white mold resistance. This research integrates pathogen genomics and host genetics to support sustainable WM management in soybean production in the US.

41) Identification and Validation of QTL Conferring Race-nonspecific Resistance to Wheat Tan Spot.

Md. Mukul Islam, Jamie Sherman, Jason P. Cook, Zhaohui Liu; *North Dakota State University*

Tan spot, caused by the fungus *Pyrenophora tritici-repentis* (Ptr), is a significant foliar disease affecting wheat globally. The spring wheat cultivar McNeal demonstrates high levels of resistance against multiple Ptr races, indicating race-nonspecific resistance. To characterize and map this resistance in McNeal, we utilized a recombinant inbred line (RIL) population developed from a cross between McNeal and Thatcher for quantitative trait locus (QTL) identification. The entire RIL population, along with the parental lines, was evaluated at the seedling stage for their reaction to tan spot caused by race 1 (Pti2), race 2 (86-124), and race 5 (DW5) isolates. The population had been previously genotyped with 619 markers covering all wheat chromosomes. Preliminary results from the QTL analysis revealed a major QTL on chromosome 3B that confers resistance to all three races, likely corresponding to a previously identified race-nonspecific resistance QTL. Additionally, a specific QTL for race DW5 was identified on chromosome 2B, presumably corresponding to the Tsc2 locus. This study confirms the presence of race-nonspecific resistance in the U.S. spring wheat cultivar McNeal, and the flanking markers identified will be useful for transferring this QTL to local wheat cultivars.

42) Identification of Fungal Pathogens in Heirloom Tomato Production.

Monika Pokharel, Waana Kaluwasha; *Lincoln University of Missouri*

Heirloom tomatoes (*Solanum lycopersicum L*) are desired for their unique flavor, taste and appearance. Heirloom tomatoes are, however, more susceptible to diseases than their hybrid counterparts, with fungal diseases being a limiting factor in their successful cultivation. This study was therefore conducted to identify prevalent naturally occurring fungal pathogens affecting three popular heirloom tomato cultivars (Brandywine, Cherokee Purple and Mortgage Lifter) at two locations in Central Missouri, using a randomized complete block design with four replications. Symptomatic leaf and fruit samples were collected during the 2024 growing season for pathogen isolation and isolate purification. Pure fungal isolates are being identified based on morphological characteristics and sequencing of the ITS region. Pathogenicity assays using three heirloom cultivars arranged in a randomized complete block design are also being conducted simultaneously in a greenhouse, and results will be discussed. It is expected that this research will provide valuable information on the important fungal pathogens in heirloom tomato production, as well as provide initial insights into potential resistance sources among heirloom tomato cultivars.

43) Identification of QTLs Associated with Resistance and Susceptibility to Spot Blotch in Two RIL Mapping Population of Barley.

Abraham Hangamaisho, Thomas Baldwin, Belayneh Yimer; *North Dakota State University*

Spot blotch disease caused by *Cochliobolus sativus* is an important barley foliar disease limiting productivity by affecting yield quantity and quality. Quantitative trait locus (QTL) mapping is an effective approach for studying genetic complexity of plant disease resistance. To identify loci conferring resistance, this approach was used to identify the most important QTLs controlling barley spot blotch resistance in two recombinant inbred line (RIL) biparental mapping populations from the USDA Small Grains and Potato Germplasm Research Unit in Aberdeen, ID, USA. The collection was genotyped using 50 K Illumina-chip and 5817 SNP markers. The two populations of 192 lines each were planted in hill-plots with a completely randomized block design with two replications at NDSU Fargo research station in 2024. The phenotypic assessments were made using a 1-9 scale that captures percentage of infected leaf tissue (1=0–5%;2=5–10%;3=10–20%;4=20–30%;5=30–40%;6=40–50%;7=50–60%;8=60–75% and 9=75–100%) at soft dough growth stage. In this study, QTL with adult resistance were identified, some QTL were mapped on novel genetic regions. Thus, implying new sources of disease resistance. These findings present valuable insights for enhancing barley spot blotch resistance, reinforcing the critical role of marker-assisted barley breeding. The future work will validate the QTLs by more seasons of phenotyping RIL mapping populations to explore their applicability in elite breeding lines.

44) Interspecific interactions and virulence variation among *Fusarium* species infecting pulses.

Anmol Dhaliwal, Rovel E. Austria, Dmitri Fonseka, Malaika K. Ebert; *North Dakota State University*

Pulses are essential for ensuring global food security. However, pulse crops are a common host for root rot pathogens like fungi, oomycetes, and bacteria. In the Northern Great Plains, the genus *Fusarium* is the most prevalent pathogen within the root-rot disease complex. Preliminary data on *Fusarium spp.* infecting lentil have shown that some species can inhibit each other when co-inoculated. To see if similar interactions occur in *Fusarium spp.* infecting other pulse crops we decided to quantify the level of virulence of various combinations of Fusarium species infecting chickpea in greenhouse inoculation tests. To quantify the diversity of *Fusarium spp.* that infects chickpea in North Dakota, we conducted field surveys during 2022 and 2023. We isolated and identified 94 *Fusarium* isolates to the species level. These isolates belonged to six species namely: *Fusarium oxysporum, Fusarium solani, Fusarium acuminatum, Fusarium equiseti, Fusarium redolens*, and *Fusarium avenaceum*. Representative Fusarium strains are being tested in greenhouse co-inoculation studies on chickpeas in pairwise and multi-species combinations. The virulence levels of combinations are compared against single-species inoculations to identify the combinations that either show enhanced or suppressed disease severity. We aim to identify the biological compound(s) responsible for antagonism or synergy among Fusarium species and to characterize the functional mechanism involved in these interactions.

45) Investigating Field Infection in Corn Crown Rot Across Key Growth Stages.

Chikoti Mukuma, Christopher John. Termunde, Tamra Jackson-Ziems; *University of Nebraska - Lincoln*

Corn is the most important cereal crop produced in the U.S. Recently, crown rot disease in corn has emerged as a potential production constraint across the Corn Belt. Several pathogens have been associated with late season crown rot symptoms. Members of the *Fusarium graminearum* species complex were consistently isolated at high frequency from samples collected by Bayer Crop Science during a regional survey between 2022-2024. The growth stage at which the pathogens infect the crown remains unknown. Corn crown rot resistance screening trials were established in 3 western Nebraska field locations Bayer Crop Science in 2024. One hundred plant pairs of symptomatic and neighboring asymptomatic plants were tagged in one half-mile long rows of susceptible and resistant hybrids at vegetative stage V3. Three plant pairs were sampled from the two hybrids at five crop stages V3, V6, VT, R2 and R5. Fungi were isolated from the crowns, identified by molecular and morphological characterization and their isolation frequencies at each stage calculated. *F. graminearum* species complex was isolated from plants as early as V3. However, isolation frequencies varied between the vegetative and reproductive stages. These preliminary results show *F. graminearum* species complex infects plants early and peak in late season. Knowing the onset of infection could help further understanding of crown rot in corn and development of improved management strategies.

46) Mapping and characterization of Wheat Stem Rust Resistance Quantitative Trait Loci.

Sittal Thapa, Jason Fiedler, Upinder Gill; *North Dakota State University*

Stem rust, also known as black rust, is caused by the fungus *Puccinia graminis f.sp. tritici* (Pgt), that threatens the global production of both durum and common wheat. Ug99 race (TTKSK), detected in 1998, has completely devasted the long-term resistance conferred by the Sr31 gene which has remained effective against all the races for over three decades. In addition, stem rust resistance conferred by Sr13 and Sr9e, major resistance genes in North American durum cultivars, has been defeated by JRCQC and TRTTF races, leaving our wheat production vulnerable to possible epidemic. To identify the new sources of resistance 497 NSGC durum wheat lines were evaluated at both seedling and adult stages, against eastern Africa and North America races. Two durum accessions (PI383416 and PI520392) showed resistance to two races of rust (JRCQC and TRTTF). These lines were used for QTL mapping by crossing with susceptible durum line, Rusty. F5 progenies screened at CDL, St. Paul along with genotyping data from iSelect 90k SNP assay were used for mapping. Out of five QTL regions on chromosome 2B, 4A, 5B and 6A, three were potentially novel. A series of backcrossing with Rusty was carried out to develop NILs to narrow down our regions for resistance. BC3F2 families were screened for detection of segregation ratio and progenies were selected based on KASP genotyping. To further fine map the QTL regions, sets of KASP markers were developed and critical recombinants were identified.

47) Mining for new sources of stem rust resistance in the global spring wheat panel.

Md Al Mamun, WooJoo Jung, Giseli Valentini, Harsimardeep S. Gill, Sunish K. Sehgal, Upinder Gill; *North Dakota State University*

Stem rust, caused by *Puccinia graminis f. sp. tritici (Pgt)*, is a devastating disease that threatens wheat production globally. The ability of Pgt to rapidly evolve new virulent races makes it one of the most challenging biotrophic fungal pathogen of wheat. Developing resistant wheat varieties is crucial, as genetic resistance provides a more sustainable approach than chemical control. In this study, we evaluated 361 genetically diverse spring wheat accessions for resistance to four Pgt races, TMLKC, QFCSC, HKHJC, and LBBLC which can overcome many known resistance (R) genes. Seedling responses varied widely, with most genotypes showing susceptibility. However, a subset of the population exhibited strong resistance, with 17.5% resistant to TMLKC, 24% to QFCSC, 11.5% to HKHJC, and 23.5% to LBBLC. To identify genomic loci associated with resistance, we conducted a genome-wide association study (GWAS) using phenotypic data combined with 302,524 high-quality single nucleotide polymorphisms (SNPs). This analysis revealed 34 significant marker-trait associations (MTAs) for stem rust resistance, distributed across 14 wheat chromosomes. Among the significant MTAs, 15 were located near previously reported Sr genes, MTAs, or QTLs for stem rust resistance. The remaining 19 MTAs correspond to genomic regions that may contain novel resistance genes. The candidate gene analysis revealed several genes of interest that could potentially involved in disease resistance.

48) Novel *Streptomyces* strains combat phytopathogens and boost plant growth promotion in soybean.

Mia Copeland, Ashish Ranjan; *University of Minnesota*

Streptomyces is widely studied due to its diverse array of biologically active metabolites. These metabolites often possess antibiotic properties, with applications in both clinical and agricultural settings. As phytopathogens develop resistance to current antibiotics, novel biocontrol solutions are needed. In this study, soil and tuber samples from a potato field in Minnesota were used to isolate two novel Streptomyces strains, designated S10 and T10. Both isolates exhibited broad-spectrum antifungal activity in co-culture: S10 inhibited four fungal phytopathogens *S. sclerotiorum, P. ultimum, R. solani*, and *F. subglutinans* by 40–86%, and T10 by 65–97%. The mechanism of antifungal activity was further investigated using sterile culture supernatant assays, which revealed that S10 supernatant possessed cellulase and protease activities and inhibited mycelial growth of *Sclerotinia sclerotiorum* by 68%. In vivo, both isolates increased germination rates of soybean seedlings infected with Pythium ultimum by 40%

at 14 days post-sowing. Further analyses confirmed that S10 and T10 can fix atmospheric nitrogen, synthesize indole-3-acetic acid, and produce siderophores. Additional experiments supported these findings: soybean germination increased from 77% in controls to 90% with T10 and 100% with S10. Collectively, these results indicate that Streptomyces isolates S10 and T10 are promising candidates for development as both biocontrol agents and plant growth promoters.

49) Optimization of *Agrobacterium*-mediated Transformation in Dodder.

Gopi Chataut, Supral Adhikari, Soyon Park; *University of Missouri-Columbia*

Cuscuta campestris (dodder) is a model plant for studying host and parasitic plant interactions due to its well-annotated genome sequence, broad host range, and identified mobile molecules. To understand molecular functions of parasitism between *C. campestris* and host plants, we developed Agrobacterium-mediated *C. campestris* transformation protocol (Adhikari et al., New Phytologist) with a six-month timeline and 5% transformation efficiency. However, we found that transformation efficiency was significantly reduced due to defective callus growth during the transition from Callus Induction Medium (CIM) to Shoot Induction Medium (SIM). Thus, we investigated a newly modified SIM (mSIM) as an intermediate medium between CIM and SIM, which exhibited enhanced callus development and survival by 80% during media transition. Furthermore, the time required for the growth of calli in each medium was reduced by one month, showing the faster development of the calli with the mSIM. Although additional replicates are necessary for the validation of this intermediate media, this study suggests that optimized transformation could shorten the overall transformation process, improve transformation efficiency.

50) Quantitative Assessment of *Fusarium graminearum* Infection Dynamics in Resistant and Susceptible Barley Genotypes Across Disease Rating Scales.

Abbeah Mae Navasca, Cecelia Castleberry, Brooke Benz, Thomas Baldwin; *North Dakota State University*

Fusarium Head Blight (FHB) is a major cereal disease primarily caused by *Fusarium graminearum*. Apart from discoloration of spikes, *F. graminearum* also produces deoxynivalenol (DON) which contaminate harvested grains. We previously validated a TaqMan multiplex real-time PCR to quantify Fusarium biomass in barley using the Tri5 gene and found a strong positive DON-biomass correlation ($r = 0.77$) but weak correlations between severity and DON ($r = 0.48$) and between severity and biomass ($r = 0.35$). This led us to re-examine disease severity ratings for screening FHB in the field. We collected at least 350 barley spikes of each susceptible (Explorer) and resistant (AAC Synergy) genotypes from *F. graminearum*-inoculated plots and grouped the spikes by severity rating. We measured *F. graminearum* load from outside (Total DNA, Tri5 gene quantity, and mapping rate of short-reads to *F. graminearum* genome) to inside (biomass and colony-forming units, CFU) the barley spikes to identify reliable parameters for consistently measuring fungal infection. Significant Genotype x Rate interactions were noted in Tri5 gene, Fusarium biomass, and CFU, indicating that the effect of one influences the other. Correlation tests found strong positive relationships notably between Biomass and CFU, Biomass and Mapping Rate, Tri5 gene and Mapping Rate. Our findings underscore the importance of integrating these parameters to ensure consistent assessment of *F. graminearum* infection in barley spikes.

51) Rapid detection of Sdh gene mutations in *Alternaria solani* using the Nanopore amplicon sequencin.

Sunil Shrestha, Jatinder Singh, Upinder Gill, Julie Pasche; *North Dakota State University*

Alternaria solani, the causal agent of early blight, is one of the major pathogens of potato. In North American production regions, the management of early blight is primarily achieved through 10 to 12 fungicide applications per season. Extensive use of single-site fungicides such as succinate dehydrogenase inhibitors (SDHI) imposes high selection pressure on pathogen populations, potentially leading to losses in sensitivity. Insensitivity of *A. solani* isolates to SDHI fungicides has been associated with point mutations in the Sdh gene that lead to amino acid substitutions. Existing approaches to detect these mutations are often labor-intensive, limited to known mutations, and lack the capability to identify novel mutations. In this study, we developed a rapid, high-throughput amplicon sequencing method using Oxford Nanopore Technologies (ONT) to detect known and novel mutations in the Sdh gene simultaneously. Multiplex PCR was conducted to amplify the target regions, followed by sequencing using a

Flongle adapter. The Sdh B, C, and D subunits of up to 24 *A. solani* isolates were sequenced in a single assay using Flongle flow cells on a MinION sequencer. With this approach, we reliably identified all previously reported and novel mutations in the Sdh gene. Our new approach offers a rapid and cost-effective tool for monitoring fungicide resistance in *A. solani* and can potentially be used to efficiently detect SNPs in other targets on a multiplexed platform.

52) Screening of soybean lines for resistance to soybean cyst nematode, *Heterodera glycines*.

Addison Plaisance, **Kapil Simkhada**, Dinesh Paudel, Guiping Yan; *North Dakota State University*

Soybean Cyst Nematode (SCN), *Heterodera glycines*, is one of the most significant yield-limiting factors in soybean production across the United States. SCN known to have genetically diverse populations can shift to new virulent forms over time due to continuous planting of cultivars from same source of resistance. Thus, identification of novel genetic source is important for managing SCN. In this study, 26 soybean breeding lines from North Dakota State University were screened in four replicates, with an objective of evaluating host resistance to SCN under controlled growth chamber conditions. Each line was inoculated with 2,000 eggs of HG type 2.5.7, a virulent SCN population. Soybean cultivar "Barnes" was used as the susceptible check. Thirty days post-inoculation, SCN females were extracted from both roots and soil and their numbers were counted to calculate Female Index (FI= average number of SCN females on a test line/ average number of females on susceptible check ×100) for each line. These lines showed a range of resistance responses. One line exhibited resistance (FI< 10%) and five lines exhibited moderate resistance (FI=10-< 30%) indicating promising resistance potential. Conversely, eight lines showed moderately susceptible (FI=30-< 60%) and remaining lines showed susceptible responses (FI≥60%). More breeding lines are being tested for SCN resistance. The findings would provide valuable information for developing new cultivars with improved SCN resistance.

53) Synthetic community approach for investigating microbiome assembly and interactions in barley phyllosphere.

Joan Acaso, Brooke Benz, Eglantina Lopez-Echartea, Thomas Baldwin, Barney Geddes; *North Dakota State University*

The phyllosphere microbiome is essential to plant health, with the potential to enhance host immunity and reduce susceptibility to pathogen invasion. Understanding how microbial communities assemble on above-ground plant surfaces is key to revealing mechanisms that may influence disease resistance in barley. However, few studies have investigated phyllosphere microbiome assembly under controlled conditions. This study employs a bottom-up synthetic community (SynCom) approach to investigate the assembly of barley phyllosphere microbiomes. Core bacterial taxa were isolated from 800 barley heads via high-throughput culturing, and 16 strains were selected to form a defined SynCom. Dwarf, early-heading barley plants were grown in sterile potting medium using Lennard jars under controlled conditions. Inoculation was performed using leaf spraying, seed soaking, or head dipping. Amplicon sequencing of the 16S rRNA gene revealed that the microbial composition was significantly influenced by both plant compartment and inoculum type ($p < 0.05$). The inoculation strategy had minimal effect. SynCom members assembled more effectively in leaves than in heads, with leaf-spraying promoting better assembly in heads. To enable precise tracking, MoBacWISH tags—custom DNA barcodes with a yellow fluorescent protein—were developed. This study establishes a reproducible model for microbiome assembly, providing a foundation for future work on plant-microbe interactions and immunity.

54) The NDSU Plant Diagnostic Lab: A Key Resource for Soybean Disease Diagnosis and Management.

Rachel Yeum, Richard Webster, Suzette Baldwin, Febina Mathew; *North Dakota State University*

The Plant Diagnostic Lab (PDL) provides high-quality, research-based diagnostic services to assist farmers, agronomists, and various stakeholders in identifying and managing plant diseases. As soybean production expands in ND, the incidence of soybean diseases has increased, making accurate and timely diagnosis critical for effective disease management. In the past three years, PDL has diagnosed a range of soybean diseases, including soybean cyst nematode, Fusarium rot, Phytophthora root rot, and abiotic disorders. In 2024, through submitted samples, the presence of sudden death syndrome was confirmed in Cass, Dickey, and Richland counties, marking its spread beyond its initial detection in Richland County in 2018. Due to similar visual symptoms among root diseases, molecular diagnostics are essential for accurate identification. To enhance PDL's diagnostic capabilities, the North Dakota Soybean Council has supported the PDL in developing advanced molecular assays that can simultaneously detect multiple pathogens, including Fusarium, Rhizoctonia, Phytophthora, and Pythium. These multiplex assays save time and resources, providing rapid, accurate results to support informed management decisions during the growing season and long-term crop planning. By leveraging cutting-edge diagnostic technologies, the PDL plays a vital role in disease surveillance, early detection, and management strategies, helping protect soybean yields and enhance farm profitability.

55) Tissue Colonization Flexibility of *Xanthomonas translucens pv. translucens* Confers Competitive Advantage Against Other Bacterial Leaf Streak Pathogen of Barley.

Diel Donne Velasco, Glenrose B. Belen, Joan Acaso, Jeffrey Schachterle, Zhaohui Liu, Barney Geddes, Thomas Baldwin; *North Dakota State University*

The bacterial leaf streak (BLS) disease of barley is caused by three pathovars of *Xanthomonas translucens*, namely *pv. translucens* (Xtt), *pv. undulosa* (Xtu) and *pv. cerealis* (Xtc). Although this may seem to increase the complexity of BLS infections, surveys show that Xtt is the prominent pathogen isolated from barley. Along with Xtt, other genera that are associated with the barley microbiome, such as *Curtobacterium* and *Pantoea*, were also often found. In this study we explored the potential impact of *Curtobacterium flaccumfaciens pv. flaccumfaciens* (Cff) on BLS disease caused by Xtt and Xtu. Using infiltration assays, we assessed if co-inoculating Cff will affect symptom development. Our results show that co-inoculating Cff with Xtu completely inhibited water-soaking and chlorosis. In contrast, co-inoculation of Cff and Xtt exhibited typical, but reduced, symptoms. We hypothesized that Cff could inhibit Xtu growth, but not Xtt. However, our in vitro assays showed that co-cultivation of Cff with either Xtt or Xtu equally inhibited their growth. Since it is known that Xtt can colonize both the mesophyll and the vascular tissues, while Xtu can only colonize the mesophyll tissue, this localization could allow Xtt to escape the inhibitory effects of Cff in the leaf and may explain the dominance of Xtt in causing BLS in barley. To further understand these interactions, we will use confocal microscopy for bacterial localization and RNA-Seq to identify involved genes.

56) Towards cloning the dominant gene Rbs7 conferring resistance to a new pathotype of barley spot blotch pathogen *Bipolaris sorokiniana*.

Olawumi Amusan, Yueqiang Leng, Md Golam Robbani, Abby d'Eustachio, Shengming Yang, Zhaohui Liu, Shaobin Zhong; *North Dakota State University*

Spot blotch caused by *Bipolaris sorokiniana* is an important foliar disease of barley. A few resources of spot blotch resistance had been identified in barley cultivars against the disease. However, a new pathotype (pathotype 7, represented by isolate ND4008) of *B. sorokiniana* had emerged to be highly virulent on barley cultivars with resistance to other pathotypes. Previous study identified a dominant resistant gene (Rbs7) in barley line PI 235186 and mapped within a genomic interval of 304 kb flanked by two DNA markers M13.06 and M13.37 on chromosome 6H. In this study, we aimed to clone and characterize the Rbs7 gene. A total of 2849 F2 individuals derived from the cross between PI 356741 (susceptible) and PI 235186 (resistant) were evaluated for infection response to isolate ND4008, and 685 highly susceptible plants were selected for genotyping with KASP markers M13.06 and M13.37. Fifteen recombinants were identified and further genotyped with nine additional KASP markers, delimiting Rbs7 to a 98 kb genomic region containing 10 predicted genes based on de novo annotation of the resistant line PI 235186. In silico expression analysis identified two genes, HORVU.MOREX.r3.6HG0543600 and HORVU.MOREX.r3.6HG0543610, as the potential candidates. Functional validation of candidate genes via CRISPR-mediated mutagenesis and complementation test is being conducted to confirm the identity of Rbs7.

57) Towards Elucidating the Seed-to-Seed Pathway of *Xanthomonas translucens* on Barley and Wheat.

Glenrose B. Belen, Diel Donne Velasco, Joan Acaso, Zhaohui Liu, Barney Geddes, Thomas Baldwin; *North Dakota State University*

Xanthomonas translucens pv. translucens (Xtt) and *Xanthomonas translucens pv. undulosa* (Xtu) are the two economically important bacterial pathogens that cause bacterial leaf streak (BLS) in cereal crops, particularly wheat and barley. Xtu causes BLS on both wheat and barley, while Xtt causes disease on barley only. Previous studies showed that these pathogens can be detected in seeds, however, there is no report on the exact localization on seeds. Furthermore, transmission rates vary across studies and the mechanisms and extent of seed-to-seed transmission in these pathosystems remain poorly understood. To address these gaps, we developed a technique that will allow us to monitor and detect the presence of Xtt and Xtu on barley and wheat in all stages of the plant. Xtt and Xtu were tagged with green fluorescent protein (GFP) and DNA sequence-based tags. A virulence assay was conducted prior to seed inoculation. Results indicated that the transformed Xtu and Xtt produced water-soaking symptoms comparable to their wild-type counterparts, confirming that tagging did not compromise the virulence. Preliminary results showed that germination of barley seeds inoculated with the tagged Xtt was significantly reduced compared to seeds treated with the heat-killed tagged Xtt. The mechanism underlying the seed-to-seed transmission pathway, as well as the corresponding transmission rate, has yet to be determined.

58) Uncovering Arabidopsis Root Defense: Transcriptomics and Mutant Screening Against Broomrape, *Phelipanche aegyptiaca*.

Supral Adhikari, Sukhmanpreet Kaur, James Westwood, Soyon Park; *University of Missouri-Columbia*

Broomrape, *Phelipanche aegyptiaca*, is an obligatory root parasitic plant that attacks a wide range of crops. This parasitic weed attaches and makes a vascular connection with the host roots and uptakes water and nutrients for its growth, causing severe yield losses. To understand more about host-defense response against this parasite, we performed transcriptomic analysis using RNA sequencing of *Arabidopsis thaliana* and *Lycopersicum esculentum* (tomato) roots infested by *P. aegyptiaca* on different time points after infection (1,2,3,5,7, and 10 days after infection). Strongly upregulated and downregulated genes in response to the infection were sorted out, and potential candidate genes involved in host defense pathways were selected. The Arabidopsis knockout (KO) lines of these potential candidate genes were then ordered and grown on a hydroponic bag system, which was infected with *P. aegyptiaca* seeds. The number and diameter of *P. aegyptiaca* tubercles were measured after two weeks of infection to compare control and KOs. From the screening results of 40 Arabidopsis KO lines, it was found that four lines of Arabidopsis showed a significant difference in the number of tubercles compared to the control, indicating significant genes for host resistance against *P. aegyptiaca*. The future direction for this research project is to conduct the KO screening test in tomatoes that provides valuable insights into the host-defense response against the parasitic plant *P. aegyptiaca*.

59) Using female index to track Soybean Cyst Nematode virulence over time in Nebraska.

Olivia Dooley, Pratibha Karki, Kyle C. Broderick, Dylan Mangel; *University of Nebraska - Lincoln*

Soybean cyst nematode (*Heterodera glycines*, SCN) is the most yield-limiting pathogen affecting soybean production in the United States. Resistance genes differ in effectiveness against diverse SCN populations across the state. Resistance gene effectiveness depends on the SCN populations which change in space and time. To understand changes in virulence over time, the reproduction capability of SCN populations were evaluated. Soil samples submitted by Nebraska farmers between 2008 and 2014 were compared to more recent samples from 2021, 2022, and 2023. These samples are part of a field sampling program that began in 2005. Female Index (FI) values were used to analyze SCN virulence on soybean lines with different sources of SCN resistance. Results show a decrease in the effectiveness of common sources of resistance over time. In SCN populations from 2008-2014, the maximum FI on the PI 88788 resistance line was 60%. It has increased substantially in the last 10 years and is now 87.74%. The percentage of SCN populations considered virulent on PI 88788, the most common source of resistance in commercial seed, has also increased from 46% to 80%. This research provides recent data into SCN population dynamics across Nebraska and shows the need for new management strategies and resistance sources.