2021 North Central Division Meeting Abstracts

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Precipitation days affect presence of endophytic *Diaporthe* in sunflower

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Phomopsis stem canker, caused by *Diaporthe* species, affects production of sunflower (*Helianthus annuus* L.). Although disease symptoms are observed at crop budding stages, it is unknown if *Diaporthe* species can live as endophytes. The objectives of this study were to determine the presence of endophytic *Diaporthe* and the association of their occurrence with weather variables. Field trials were conducted at one location each in Nebraska, North Dakota, and South Dakota in 2019 and 2020. Commercial hybrids, susceptible to Phomopsis stem canker, were planted in eight plots (46.5 m²). Stems were sampled thrice from each plot at 2- to 3-weeks intervals after planting, cut, surface-sterilized, and incubated on potato dextrose agar. *Diaporthe* species were identified by morphology and molecular assays. A logistic regression model (0 = absence and 1 = presence) was used to estimate the probability of endophytic *Diaporthe* presence with total rainfall, average temperature, average relative humidity, number of precipitation days, and wind speed in 3, 5, 7, 10, 15, or 30 days before sampling as predictors. Results showed that the presence of endophytic *Diaporthe* was best explained by the number of precipitation days at 7 days before sampling ($P = 0.034$). The model exhibited 80.9% accuracy, 93.8% sensitivity, and 40.0% specificity. Our study suggests that number of precipitation days, which favors Phomopsis stem canker development, also influences endophytic *Diaporthe* presence.

Identifying factors impacting disease management decisions in Nebraska soybean production

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Fungicide resistance in foliar pathogen *Cercospora sojina* is a widespread concern across Nebraska, yet little is known about how the decision to apply foliar fungicides is made. To fill this gap, we designed a survey to assess perceived importance of soybean diseases, reasons for foliar fungicide applications, and identify sources of information used. This was a 10-question survey with multiple-choice and short-answer responses. Participants were recruited at row crop meetings. Results of 805 responses from 78 counties showed the most cited crop and disease management strategies were crop rotation (24.4%), herbicides (21.6%), and foliar fungicides (12.9%). More than half (63.8%) of participants used or recommended foliar fungicides for soybean in the last 5 years, contradicting the perception that fungicide use is uncommon. A small percentage (3.2%) mentioned using foliar fungicides for plant health. Factors that influenced these decisions were disease severity (23.2%), fungicide cost (21.6%), and crop market value (18.4%). The most cited source of information used to make disease management decisions was recommendations from the local agricultural co-operative service provider (15.2%). Collectively, these results suggest that Extension programs need to continue to appeal to a broad audience and consider how to better incorporate educational materials targeted towards co-operative service providers if we are to promote more sustainable use of fungicides.

DNA barcoding of *Monilinia fructigena* and *Gymnosporangium sabinae* from Kazakhstan

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Fungal pathogens of fruit crops are widely present in Kazakhstan and cause significant economical losses. Garden areas are expanded annually, but no proper treatment is conducted for old orchards, which accumulate pathogens. The most common fungal disease in the Almaty region is brown rot caused by *Monilinia laxa* and *M. fructigena*. The common disease of pear is rust caused by *Gymnosporangium sabinae*. In the present work genetic analysis of *M. fructigena* and *G. sabinae* was conducted. Isolates were obtained from fruits of pear and apple cultivars and pear leaves. Samples were collected from two gardens in the Almaty region, four isolates of *M. fructigena* and *G. sabinae* from each orchard. *M. fructigena* isolates were obtained by extraction of spores from damaged apple and pear fruits. *G. sabinae* isolates were obtained by isolation of spores from pear leaves. DNA barcoding for isolates from Kazakhstan was conducted for the first time, as the previous studies were based solely on classical methods of microbiology. Every isolate was characterized using markers ITS (ITS5, ITS4) and LSU (LR0R-LR5). Results of phylogenetic analysis of *M. fructigena* and *G. sabinae* isolates revealed the closest proximity to European isolates. Twenty ITS sequences and seventeen LSU sequences of *M. fructigena*, one hundred nineteen ITS sequences, and sixteen LSU sequences of *G. sabinae* were selected (all available data in NCBI). ITS and LSU sequences of isolates of each fungus from Kazakhstan had homology 99% or higher.

Genetic characterization of *Plasmopara halstedii* populations in Argentina using simple sequence repeats (SSR) and effector-based markers

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Argentina is the fourth leading producing country of sunflower worldwide. Sunflower downy mildew, caused by the pathogen *Plasmopara halstedii*, is an economically important disease of sunflower. Since 2012, *P. halstedii* epiphytotics were identified in several production regions of Argentina. However, the genetic diversity of the pathogen in Argentina remains largely unknown. Forty-two field isolates from Argentina were analyzed using eight loci SSR. The number of alleles per locus (APL), the expected (HE) and observed heterozygosity (HO) were determined. SSR data were analyzed with regions (two), collection years (four) and races (six) as variation sources (AMOVA), and the population structure was defined (Bayesian method). DNA sequences of two effector genes were obtained from two isolates per race and the polymorphisms were analyzed (ClustalW). The mean APL was 2.6, varying from 1 to 4 (total 21). The highest number of alleles and races were found in 2017. Average HO and HE were 0 and 0.369, respectively. Genetic variation was observed among regions (7%) and years (32%), but not between races. Based on effectors, local races were similar to a group of French races, without variation within the ARG races. Increased genetic variability observed in recent years seems to parallel with the emergence of novel races reducing fungicides and/or R genes efficacy. The effector study suggests that the races evolution depends on country specific factors.

Wood moisture content predicts the survival of *Geosmithia morbida* and fate of *Juglans nigra* threatened by thousand cankers disease

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The success of mutualisms between fungi and bark beetles is likely to be limited by competition with other fungi that are better adapted to the physicochemical conditions of their substrate. These conditions are in turn subject to climatic variation. In particular, wood moisture content is an important factor in fungal competition and, therefore, could help determine environmental suitability for thousand cankers disease (TCD) caused by *Geosmithia morbida* and its vector *Pityophthorus juglandis*. We conducted competition experiments in *J. nigra* wood that was naturally or artificially colonized by *G. morbida* and other fungi over a range of wood moisture content expected across prevailing U.S. climatic conditions. *G. morbida* outcompeted antagonistic fungi *Clonostachys* and *Trichoderma* spp. at <5% equilibrium moisture content. *Aspergillus* spp. outcompeted *G. morbida* at low moisture in wood from Indiana. We fit a logistic regression model to results of the competition experiments to predict survival of *G. morbida* across the U.S. Expected survival of *G. morbida* was highest in historical TCD epicenters and partly explained the low incidence and severity of TCD in the eastern U.S. Our results also predict that under future climate scenarios, the area impacted by TCD will expand into the native range of *J. nigra*. Given its influence on emergent forest health threats, climate change should be a key consideration in the assessment of risks to hardwood resources.

Investigating phenylpropanoid-based Fusarium head blight (FHB) resistance in wheat

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Fusarium head blight (FHB) is a devastating disease of wheat caused by *Fusarium graminearum*. Modification of the phenylpropanoid cell wall components may provide resistance to *F. graminearum*. Spring wheat cv. CB037 was transformed with constitutive expression constructs of sorghum genes involved in monolignol biosynthesis: *SbMyb60*, encodes a transcriptional factor, while *SbC3H*, *Sb4CL* and *SbCCoAOMT*, encode enzymes in the pathway. In a field study (2018 and 2019), lines constitutively expressing each gene were screened for Type-I resistance (initial infection) by assessing Fusarium damaged kernels (FDK), disease index, and levels of the mycotoxin, deoxynivalenol (DON). In a greenhouse study, lines constitutively expressing *SbC3H* and *SbCCoAOMT* were screened for Type-I and Type-II (infection spread) resistance by assessing the area under the disease progress curve (AUDPC) and FDK. In the field, constitutive expression of *SbMyb60* resulted in significantly less FDK than CB037 (recipient check) and DON level similar to that of Sumai 3 (moderately resistant check); the other constitutive expression lines were susceptible. In the greenhouse, Type-I resistance did not increase, but constitutive expression of *SbC3H* and *SbCCoAOMT* each increased Type-II resistance as the lines had significantly less FDK and AUDPC than CB037. Global gene expression analysis of Type-I and Type-II resistant lines will be conducted to identify novel genes and pathways that enhance resistance to FHB.

Investigating brown mustard and winter camelina cover crops after wheat and prior to soybean for soybean cyst nematode (SCN) management

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A recent arrival to the Red River Valley of Minnesota (MN) and North Dakota (ND), SCN can cause substantial soybean yield loss. Accelerated population density (PD) growth of SCN, limited sources of resistance in adapted soybeans, and fewer years of non-host crops in the rotation increase the need for SCN management options. To determine if brown mustard (*Brassica juncea* L., cv. Kodiak) and winter camelina (*Camelina sativa* (L.) Crantz, cv. Joelle) sown as cover crops after wheat and before SCN resistant (R) and susceptible (S) soybean varieties influence SCN PD and soybean yield, trials were established in SCN-infested fields in ND and MN. Data collected included SCN PD before cover crop establishment in fall 2018 and in the spring and fall of 2019 before and after soybean, respectively, and soybean yield. When compared with an R variety, yield of an S variety was numerically or significantly lower in MN and ND, respectively. SCN PD also increased after planting S soybean. When compared to plot without cover, plots planted to S varieties in MN had significantly lower SCN PDs in plots planted to brown mustard, while the same trend was observed in plots planted to winter camelina in ND. In plots planted to SCN R varieties, SCN PDs trended lower in plots planted to either cover crop than in plots with no cover crops. Combining SCN R soybean varieties and a winter camelina or brown mustard cover shows more promise for managing SCN than either practice alone.

Sensitivity of *Diaporthe helianthi* and *D. gulyae* infecting sunflower to fluxapyroxad

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Foliar application of succinate dehydrogenase inhibitor (SDHI) fungicides may serve as a management tool for Phomopsis stem canker in sunflower (*Helianthus annuus* L.). However, the fungal population causing Phomopsis stem canker may develop resistance to SDHI fungicides, reducing their efficacy. The objective of this study is to examine the sensitivity of isolates of two fungi causing Phomopsis stem canker, *Diaporthe gulyae* and *D. helianthi*, to the SDHI fungicide, fluxapyroxad. In this study, 104 isolates were collected from commercial fields affected by Phomopsis stem canker in Minnesota, Nebraska, North Dakota, and South Dakota between 2013 and 2020. A stock solution was prepared by dissolving pure technical grade of fluxapyroxad in acetone. Water-agar media amended with fluxapyroxad at 0.001, 0.01, 0.1, 1, 10, and 100 µg a.i./ml were inoculated by inverting 0.5-cm mycelial plugs on the center of each 9-cm petri dish. The fluxapyroxad concentration of 0 µg/ml served as the control. After 5 days and 7 days of incubation for *D. gulyae* and *D. helianthi*, respectively, in the dark at 22 ± 2°C, the fungal colony diameter was measured and the effective concentration resulting in 50% mycelial growth inhibition (EC₅₀) was determined. Mean EC₅₀ values for *D. gulyae* and *D. helianthi* were 2.67 and 1.47 µg/ml, respectively. This research will be used for future monitoring of sensitivity shifts in populations of *D. gulyae* and *D. helianthi* associated with the fluxapyroxad fungicide.

Student-led computational workshops fill skill gaps for plant pathologists

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Computational skills are increasingly important for conducting research in the agricultural sciences, particularly plant pathology. However, barriers to training availability and accessibility have left many life scientists underprepared. To address these challenges, we developed a workshop series led by plant pathology graduate students to cover topics relevant to research needs. These workshops included introduction to Python, R, and command line alongside general data management and data visualization topics. Further, in response to changes mandated by the COVID-19 pandemic, the workshop series was converted to a virtual series on eXtension Campus and extended to life science researchers outside of our home institution. Currently, we have over 275 enrolled participants from over 22 different institutions, located nationally and internationally. Survey data show our workshops reached a highly diverse group of scientists, with 62.1% of participants coming from an agricultural field of study and 38.1% coming from plant pathology specifically. Further, we demonstrate an increase in self-reported confidence in student abilities to apply concepts to their own research following

content delivery in both virtual and in-person environments. The success of this workshop series shows the importance of hands-on, guided practice in developing computational skills to fill gaps in training in agricultural science and plant pathology.

Corn-soybean-winter wheat rotation reduces corn yields and improves soil health in Ohio

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Crop rotation is a cultural practice that provides benefits such as increased yields, weed and disease suppression. This study explored the differences in corn production and soil health between a corn-soybean (CS) and a corn-soybean-winter wheat rotation (CSWw) in Ohio. Our objective was to measure impacts on corn production by assessing seedling establishment, biomass and yield, and soil health indicators such as organic matter (SOM), total carbon (TC), nitrogen (TN), and active carbon. Long-term crop rotations were started in 2013 at two sites. The experiment was a randomized complete block design with four replicate plots/treatment. Early-season stand counts and biomass were collected in each site year, and yield was collected at harvest. Soil samples were taken during the growing season, and TN, TC, and SOM were measured in 2018, 2019, and 2020. In the CSWw rotation, corn saw lower stands (27%), root (30%), and shoot biomass (34-36%) in at least 1 site year, compared to CS. We also saw 9–12% lower corn yields in the CSWw 5 out of 8 site years. Soil health data, however, shows greater SOM (7–12%) under CSWw, in 2 site years. Our results indicate that the CSWw negatively impacts corn in some soil types or environmental conditions, contrasting other studies that have shown increased corn yields in CSWw in other regions. We hypothesize that an increase in pathogenic fungal communities that attack wheat and corn may play a role in the reduced yields.

Effect of fungicide seed treatment on hard red spring wheat plant stands and yield

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A fungicide seed treatment (FST) is an effective tool for managing seedborne diseases of hard red spring wheat, such as loose smut and common bunt. They are also labeled to suppress early-season root rots and seedling blights and reported to positively influence plant stand and yield. Given the diversity of fungicide seed treatment options for hard red spring wheat producers, it is important to have updated information summarizing the response of a FST on plant stand and yield. Therefore, our goal was to combine and summarize plant stand and yield data from FST experiments conducted during 2003–2020. Experiments were conducted at North Dakota State University and at Research and Extension Centers across the state. The treatment list varied at each location year (environment) and used a certified hard red spring wheat variety. The data set included means from 229 replicated treatments across 46 environments. To help standardize data across environments, percent responses in plant stand and yield (compared to the non-treated check) were determined. The data set was organized and sorted to analyze responses due to geography (eastern and western North Dakota), fungicide modes of action, addition of an insecticide, soil temperatures, and rainfall. Preliminary results suggest that FSTs resulted in favorable stand and yield responses. The results from this analysis will directly influence seed treatment decisions for hard red spring wheat producers.

Understanding the cyclic-di-GMP-mediated regulation of the type III secretion system in *Erwinia amylovora*

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Erwinia amylovora is a gram-negative bacterium that causes fire blight, which affects apple and pear production globally. The type III secretion system (T3SS) is a virulence factor that *E. amylovora* utilizes to infect host cells by secreting effectors that suppress the host immune response and promote pathogenesis. HrpL is an alternate sigma factor that regulates the expression of critical T3SS genes. Cyclic-di-GMP (c-di-GMP) is a ubiquitous bacterial second messenger that negatively regulates *hrpL* expression through a process that is not completely understood in *E. amylovora*. Our findings suggest that a LysR-family transcriptional regulator, Hlr (*hrp*-gene regulator *LysR* protein) along with a YajQ homolog (YajQ_{EA}) positively regulates *hrpL* transcription. The deletion of *hlr* and *yajQ_{EA}* in WT Ea1189 caused a significant decrease in *hrpL* expression in vitro. We evaluated the DNA binding affinity of the Hlr/YajQ_{EA} complex at a potential LysR binding box, characterized by a disrupted palindromic sequencing within the *hrpL* promoter region. We also examined the impact of varying concentrations of c-di-GMP on the stability of the Hlr/YajQ_{EA} complex, as well as its ability to interact with the *hrpL* promoter. Further, we explored the impact of divalent metallic cations on c-di-GMP-mediated regulation of *hrpL*. This study provides a greater understanding of how *E. amylovora* can effectively regulate the expression of T3SS-mediated virulence to successfully infect a host.

Characterization of Kansas wheat virus population using nanopore sequencing

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Wheat streak mosaic complex is one of the most economically significant wheat diseases in the Great Plains. Wheat streak mosaic complex comprises three viruses, including *Wheat streak mosaic virus* (WSMV), *Triticum mosaic virus*, and *High Plains wheat mosaic virus*. The synergistic impact of several concurrent infecting wheat viruses is responsible for millions of dollars lost in wheat production. Wheat growers experience frequent epidemics of the wheat viral diseases in Kansas. Therefore, characterization of wheat virus isolates are essential to determine the population structure in the field. A statewide survey was conducted from 2019 to 2021 in Kansas wheat fields to collect virus-infected wheat samples. Samples were initially subjected to ELISA. Sequencing libraries were made from total RNA of WSMV positive samples using the PCR-cDNA barcoding (SQK-PCB109) kit and loaded onto Oxford Nanopore minion flow cells. Sequencing reads were aligned to virus references. The preliminary results indicated presence of all three viruses of the complex were detected, with TriMV at a higher titer. Other viruses were at high titers in some of the samples. *Brome mosaic virus*, *Barley yellow dwarf virus*, *Barley stripe virus*, and *Foxtail mosaic virus* were also recorded. Characterization of the virus population will enable us to better manage the wheat viruses through genetic resistance more efficiently by knowing the complexity of host-virus interaction.

Elucidating the role of *Sr2* in bacterial leaf blight development through QTL analysis

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Bacterial leaf blight (BLB) of wheat occurs sporadically under wheat production field conditions in the north central great plains. The phenotype requires high humidity and cool temperatures during the boot stage. This phenotype has historically been attributed to the pathogen *Pseudomonas syringae* pv. *syringae* (Pss). The phenotype presents quickly after a high-humidity event as large gray-green blotches on the upper leaves. These blotches quickly become necrotic and desiccate to a bleached gray or white lesion. A correlation between the BLB phenotype and the *Sr2*-linked phenotypes stem melanism and pseudo-black chaff was recently observed, which suggests that *Sr2* may play a role in BLB development. To better understand bacterial leaf blight disease development and management, the role of *Sr2* in pathogenesis must be determined. Three recombinant inbred line populations, containing three unique *Sr2* parents ('Kingbird', 'Thunder CL', and 'KS84HW196'), were genotyped and rated for the disease phenotype. All three populations segregated for severity of BLB. Preliminary QTL analysis with the cv. 'Kingbird'-derived population have identified three QTLs related to the BLB phenotype. QTLs associated with increased disease severity were centered on *Sr2* (3BS) and *Lr34* (7DS). This evidence confirms the correlation of *Sr2* and the BLB phenotype. Isolation studies to date have not shown a clear and constant association of Pss with the BLB phenotype.

Isolation and preliminary characterization of *Fusarium* isolates from celery in Michigan

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Michigan celery growers have observed a disorder, including crown rot, stunting, and vascular discoloration, resulting in yield and quality losses. Symptomatic plants were sampled from fields in four Michigan counties over 2 years. *Fusarium* spp. were the most commonly isolated organism; 209 and 219 isolates were collected in 2018 and 2019, respectively. Sequencing across 2018–2019 showed that *Fusarium* spp. were 45% *F. oxysporum* species complex (FOSC) and 51% *F. solani* species complex (FSSC). Plant symptoms did not differ among samples where FOSC, FSSC, or both were isolated. Fusarium yellows caused by *F. oxysporum* f. sp. *apii* (FOA) race 2 was a production-limiting issue for Michigan celery growers until development of resistant varieties. FOSC isolates were screened using diagnostic primers used for identification of FOA race 2 and race 4. Of 105 FOSC isolates, 21 had a positive band using the race 2 primers and 0 had positive band using the race 4 primers. A pathogenicity testing protocol was implemented and revealed virulence differences among FOSC isolates. Further research is needed to determine if the Michigan crown rot disorder is caused by FOSC.

Are two better than one? Tank-mixing DMI fungicides for managing *Cercospora* leaf spot of sugar beet

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Cercospora leaf spot (CLS) of sugar beet caused by *Cercospora beticola* can cause 40% or more yield loss in certain fields under warm and humid conditions. Effective CLS management relies on the use of fungicides due to the polycyclic nature of *C. beticola* and partial host resistance of sugar beet cultivars. Currently, demethylation inhibitor (DMI) fungicides are the most important class for effective CLS management. It is highly recommended to combine DMI fungicides with a broad-spectrum tank-mix partner. In 2020, a field trial was conducted to evaluate the efficacy of DMI fungicides with and without tank-mix partners for controlling CLS. A five-by-seven split-plot design with four replications was used. Treatments included four DMI fungicides (prothioconazole, tetraconazole, difenoconazole, and mefentrufluanazole) and five tank-mix partners (mancozeb, copper oxychloride plus copper hydroxide, sodium bicarbonate, sulfur, foliar phosphite, and *Bacillus subtilis*). Disease severity was quantified using APS Assess 2.0 software. Differences were observed for the DMI fungicides for root yield and recoverable sucrose per acre but lacked statistical significance. For tank-mix partners, mancozeb resulted in the highest root yield followed by copper hydroxide and foliar phosphite, and lower for other treatments. This study will be repeated in 2021, and results will be used to develop effective fungicide-based recommendations for managing CLS.

Diversity of *Phyllachora* species infecting maize and other grasses in North America

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Phyllachora maydis is a fungal pathogen of maize endemic to the Americas and the Caribbean that has recently established itself within the major corn production regions of North America (NA). The origin and diversity of the NA population is still uncertain. In order to understand the putative origin and diversity of *P. maydis* populations within in NA, we conducted a multi-gene phylogenetic analysis of 189 single-stroma isolates from contemporary and herbarium samples, including maize and non-maize hosts from the Americas and the Caribbean. We identified five distinct genetic groups of *Phyllachora* present in NA representing at least two putative new species and three genetically distinct populations of *P. maydis*. The two putative new species infected grasses, but not maize. The most abundant (101 isolates) of the three maize-infecting populations was widely distributed on both maize and non-maize hosts throughout the Americas based on contemporary and herbarium samples. The other two populations, found only on maize, were rare among herbarium samples (three isolates), and had more restricted geographic distributions; however, this could have been the result of sampling bias. In summary, our data indicate the presence of three genetically distinct populations of *P. maydis* infecting maize in NA, with one of these populations being present throughout the Americas for the last century on both maize and non-maize hosts.

Interactions of plant, pathogens, and beneficial microorganisms in Martian regolith simulant

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Growing plants on space missions provides numerous benefits to the crew members. However, we need to better understand how plants interact with microbes in space conditions. The objective of this experiment was to determine how microbial and fungicide seed treatments affect root health and plant growth in low-quality soil under controlled environment with and without a pathogen. Experiments were conducted on soybean in growth chambers at the ISU Enviratron facility in March 2021. Four seed treatments were evaluated: untreated check, beneficial bacterium (*Bacillus methylotrophicus*), a fungicide (fluopyram), and a combination of fungicide and insecticide (metalaxyl + pyraclostrobin + clothianidin). Soybeans grown in standard sand/soil mix (2:1 v/v) and fine-grade Martian regolith (Mojave Mars Simulant, MMS-1) were infested with *Fusarium virguliforme* and *F. oxysporum*. Data were collected after 34 days of planting. Greater root rot and foliar disease symptoms were observed in *F. virguliforme*-inoculated plants. Plants survived in Martian regolith even though nutrient deficiency symptoms were obvious. Plants grown in Martian regolith were taller, but plant and root biomass were less than plants grown in standard sand/soil mix. Root rot and foliar symptoms were observed in both soil types on inoculated plants. Fresh plant and root weight were greater for *B. methylotrophicus*-treated plants, although not statistically significant. The experiment will be repeated.

In vitro efficacy of nanoparticles against *Xanthomonas translucens* pv. *undulosa*

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Wheat (*Triticum aestivum*) is one of the most important cereal crops in the United States; however, most wheat varieties are susceptible to bacterial leaf streak (BLS), a major disease caused by *Xanthomonas translucens* pv. *undulosa* (*Xtpvu*). BLS is challenging to manage since common chemicals do not provide adequate control. Nanoparticles present a novel eco-friendly approach for plant disease management because of their high surface area and antibacterial properties. However, no data are available on the efficacy of nanoparticles controlling BLS in wheat. The objective of this study was to evaluate the antibacterial activity of nanoparticles against *Xtpvu*. An in vitro study was conducted with five treatments; nano-ZnO, nano-MgO, and nano-CuO amended with polyvinylpyrrolidone surfactant were prepared at 2,000 ppm, with sterile water and Agri-mycin as control checks. Two milliliters of each treatment were applied to 18 mL of 0.01M MgSO₄ solution inoculated with 200 µL of *Xtpvu* suspension and incubated at 25°C on an orbital shaker. A 100-µL aliquot of each treatment was collected at 12, 24, 48, and 72 h and plated on King's B agar medium and CFU/mL were determined after 3 days to quantify *Xtpvu* growth. The experiment was laid out in a complete randomized design with four replicates and was repeated once. Nano-CuO had the lowest CFU, followed by nano-ZnO and nano-MgO at all time intervals. Nano-CuO has potential to control *Xtpvu* and further testing on wheat plants is in progress.

Effects of fungicides and timings on incidence of *Fusarium* head blight, *Fusarium* damaged kernels, and yield in Illinois wheat

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Miravis Ace (MA), a new SDHI + DMI fungicide for *Fusarium* head blight (FHB) management, is currently marketed as having a wider window of application compared to previous industry standards for FHB suppression: Caramba and Prosaro. Marketing claims that MA is as effective as industry standards when applied at head emergence (Feeke's growth stage [FGS] 10.5). However, most data do not include industry standards applied at FGS 10.5 for comparison. We conducted eight trials assessing the impacts of Caramba, Prosaro, and Miravis Ace applied at FGS 10.5, 10.5.1, and 10.5.5+5d on *Fusarium* head blight (FHB) incidence (INC), *Fusarium* damaged kernels (FDK), and yield were conducted across Illinois from 2018–2020. Data showed that MA did reduce INC, FDK, and improve yield over non-treated controls at FGS 10.5, whereas Prosaro and Caramba did not. However, the greatest reduction in FHB and increase in yield for all products was achieved when applied between FGS 10.5.1 and FGS 10.5.1. Our data indicate that although some reduction in FHB can occur with MA applied at FGS 10.5, optimal suppression of FHB with MA occurs when applied at standard, FGS 10.5.1 timings.

Genomic prediction of resistance to *Sclerotinia* stem rot disease in *Brassica napus*

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Genomic selection (GS) is becoming an essential tool for breeders to accelerate the development of improved varieties. In this study, two *Brassica napus* doubled haploid populations, T54DH and T63DH, were used to evaluate the potential of genomic prediction in the selection of resistance to *Sclerotinia* stem rot caused by *Sclerotinia sclerotiorum*. Plants were inoculated using the agar plug method and were incubated in greenhouse rooms. Lesion length (LL) at 9 days post-inoculation and relative area under the disease progress curve (rAUDPC) were used as phenotyping datasets. Three models, Bayesian ridge regression (BRR), BayesB (BB), and reproducing kernel Hilbert space (RKHS), were evaluated. In both populations, five-fold cross-validation was used for training the prediction models. In T54DH, BB had an average accuracy of 52%, while BRR and RKHS showed 44 and 40% accuracy. Prediction accuracy of these models ranged between 37 to 41% in T63DH. The average prediction accuracy of all models was higher for T54DH (45%) compared to T63DH (40%). In terms of phenotyping scoring systems, rAUDPC resulted in higher accuracy, 40%, compared to LL, with an accuracy of 37%. This discrepancy could be due to the variation in the number of data points used in phenotyping scoring systems. Application of GS could decrease the time and cost of breeding programs, including phenotyping for diseases compared to conventional breeding methods such as phenotypic selection.

***Gemmamyces piceae* in Alaska causing bud blight disease of spruce is different from European populations**

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Gemmamyces piceae has been found in Alaska since 2016, although its status as a native or invasive pathogen has not been elucidated. European and Alaskan populations of *G. piceae* were analyzed using phylogenetics of single and concatenated ITS, RPB2, and TEF1 genes but could not be differentiated since no important differences in nucleotides were observed. In order to understand the population structure of *G. piceae* present in Alaska and the relationship with *G. piceae* from Europe a population genetics approach was used. Short sequence repeats (SSR) were used to determine differences between populations. Primers for 24 SSR loci were designed with msatcommander-1.0.8-beta from one de novo assembly from a European isolate and used to genotype several isolates of *G. piceae* collected in Alaska in 2020 and European isolates. Although, only 10 primers had consistent amplification in all isolates evaluated and fragment analyses showed important differences between these populations. Polymorphisms were detected only in the European isolates where seven haplotypes were observed from seven isolates. In Alaskan isolates, ignoring null alleles, only one locus was polymorphic and from 18 isolates evaluated only three haplotypes were observed. Several tests are still required to further conclude these findings and are currently being developed including determining mating types present in Alaska and a diagnostic assay to differentiate European from Alaskan populations.

Understanding the effects of phenolic compounds and competing microbes on the growth of *Fusarium graminearum* in the malting of barley

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Fusarium graminearum is the predominant cause of *Fusarium* head blight (FHB) in barley. Globally, FHB has led to devastating impacts on the grain industry due to lowering of grain quality and yield loss. Further, mycotoxins such as deoxynivalenol (DON) may also be produced. In malting, the conditions encourage fungal growth and its production of DON. Two relevant aspects of *Fusarium* growth on barley during malting are defensive plant compounds such as phenolic acids, and the presence of other microbial colonizers. The functional modifications that occur in malting influence the composition of both the phenolic compounds and the microbes in barley. The antifungal activity of four phenolic compounds (ferulic acid, caffeic acid, p-coumaric acid, and catechin) were examined against *F. graminearum* HSW-15-63. In vitro analysis showed the most significant fungal growth reduction in the presence of ferulic acid. Laboratory-scale malting procedures were conducted to analyze the antagonistic effects of *G. candidum* against *F. graminearum*, where the addition of *G. candidum* in steeping significantly decreased *F. graminearum* density (P value < 0.05). Future work should examine the integrated effects of phenolic compounds and existing microbes in the malting of barley against *F. graminearum*. Understanding the effects of natural compounds in the presence of competing microbes will provide insights that may form the basis for practical approaches to the mitigation of *F. graminearum*.

The *Pseudomonas syringae* pv. *glycinea* effector HopAW1 is an active cysteine protease that suppresses immunity

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Pathogens of soybean (*Glycine max*) are responsible in the United States for an estimated 11% annual soybean yield loss. Soybean immunity is a key natural defense against pathogens, which in response secrete effectors to suppress immunity. However, the mechanisms or soybean pathogen effectors remain mostly unexplored. The genome of the soybean bacterial pathogen *Pseudomonas syringae* pv. *glycinea* (Pgy) strain LN10 was annotated for type III secreted effectors. HopAW1, a cysteine protease in the AvrPphB family, was identified from a screen of putative effectors on the basis of suppression of HopAV1-induced hypersensitive response on tobacco (*N. benthamiana*). Pathogenicity assays were performed in soybean to determine HopAW1's contribution to virulence. HopAW1 was expressed in yeast and transiently expressed in tobacco to evaluate cleavage and localization activity. Deletion of HopAW1 reduces Pgy pathogenicity on soybean. In yeast and in planta, HopAW1 cleaves itself near the N-terminus, a process that is necessary for localization to the plasma membrane. This research provides insights into the virulence mechanisms of a bacterial pathogen of soybean.

Strategies for collaboratively investigating scientific literature and engaging students in a virtual environment

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Reading scientific literature is a challenging task for early-stage or novice learners, especially in interdisciplinary fields such as plant pathology. Unfamiliar vocabulary and lack of content experience can give rise to cognitive overload, which is further intensified through lack of formal training on how to read, interpret, or synthesize primary literature. Beyond content, the organization and communication strategies used in primary literature highlight fundamental processes that train students to "think like scientists." This is a core skill gap, as critical evaluation and analysis are essential skills of the scientific process. To address this need, we developed a virtual journal club that incorporated active learning techniques to promote student engagement and collaboration. Our focus was on undergraduate and graduate students across plant and microbiology disciplines. We highlight three techniques, which can be used virtually or in-person, that facilitate student-driven evaluation and discussion of research activities and outcomes. We further show that meaningful collaborative activities can ensure student buy-in, even in the absence of grades. These types of structured learning activities are crucial for improving student confidence, enhancing critical analysis, and strengthening presentation of science research. Further, guided practice and feedback makes cognitively intensive tasks more manageable, thereby supporting skill gains among students.

Re-envisioning host-microbe interactions through a modified continuum of symbiosis approach

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Current course curricula in plant pathology frequently uses the disease triangle paradigm to characterize host-microbe relationships, wherein disease is taught as a discrete, measurable outcome when three factors (host, microbe, environment) converge. This conceptualization fails to account for beneficial or commensal relationships and ignores the plasticity in host and microbe expression that give rise to a spectrum of phenotypes. While many instructors have adopted more dynamic teaching examples, most examples in introductory and intermediate courses are centered on the relationship between one pathogen and one host. As such, teaching approaches do not adequately address the roles of plant-mediated factors, habitat constraints, co-evolutionary relationships, and the genetic capabilities of microbial organisms. To address these shortcomings, we propose an alternative framework that builds on a continuum of symbiosis approach to reconceptualize host-microbe interactions as a myriad of complex-interacting factors that contribute to organismal ranges. This framework is centered in eco-evolutionary theory and aims to enhance communication among researchers, as well as prioritize holistic consideration of the dynamic factors shaping microbial life strategies. Recognizing how multipartite interactions shape ecosystem-level processes that inform plant-microbe symbiosis outcomes will better prepare students to apply their knowledge to real-world research scenarios.

Characterization and management of oomycete species causing soybean diseases in Illinois

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Oomycetes cause some of the most destructive soybean diseases. Among these are Phytophthora root and stem rot (PRR) and seedling diseases caused by *Pythium*. Seed treatments in combination with resistance are some of the recommended management strategies. However, the effectiveness of seed treatments for disease management can vary by pathogen species and environmental conditions. The objective of this study was to develop precision management techniques for soybean diseases caused by oomycetes. A survey was conducted to obtain a collection of oomycete isolates from Illinois soil samples and symptomatic plants. A total of 96 isolates from 13 species were identified. *Pythium ultimum* var. *ultimum* was the most abundant species, followed by *Phytophthora sojae* and *Phytophthora sansomeana*. *Phytophthora sojae* was more aggressive than *Phytophthora sansomeana* in greenhouse assays. *Pythium*

ultimum var. *ultimum* was the most aggressive *Pythium* species in seed plate assays. All isolates were sensitive to metalaxyl and mefenoxam, but there were insensitive isolates to azoxystrobin and ethaboxam. In addition, multilocation field experiments showed that an ethaboxam and metalaxyl seed treatment effectively protected seedling stand in all environments, but yield protection was significant only in two high disease pressure environments. The disease levels of soybean lines with Rps genes changed by location, but lines with high partial resistance had higher yields than lines with low partial resistance across locations.

Is there fungicide resistance of *Alternaria* leaf blight and head rot of broccoli among other cruciferous crops in the eastern USA?

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Cruciferous vegetables are widely consumed in the USA and represent a national economic value over \$1 billion/year. *Alternaria* leaf blight and head rot is one of the most common and destructive diseases in broccoli and other crucifers crops and is caused by *Alternaria brassicicola*. While fungicide applications are integral to reduce yield loss, resistance is suspected to have led to a loss of QoI fungicide efficacy in multiple locations. However, a competing hypothesis for this loss of efficacy may be due to the emergence of a novel species or sub-species that is less sensitive to QoI fungicides. As such, the goal of this preliminary investigation was to determine whether there is resistance to QoI fungicides and determine the genetic relationships among populations from different geographic regions. A selection of 15 isolates from broccoli and other cruciferous hosts from NY, VA, and GA were used. Fungicide sensitivity will be determined using a conidial germination assay on a series of azoxystrobin (QoI) concentrations to estimate the EC₅₀. The least sensitive isolates will be used for cytochrome *b* gene sequencing and aligned to the *A. solani* reference genome to determine whether mutations conferring fungicide resistance are present (F129L, G137R, and G143A/S). Results will be used to guide subsequent studies to investigate the population genetics and fungicide resistance profiles across the Eastern USA and develop diagnostic tools to detect fungicide resistance.

Efficacy of new foliar fungicide application methods in corn

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Fungicide efficacy for foliar diseases of corn is directly influenced by fungicide coverage. Ground-applied fungicide applications have been promoted to increase fungicide coverage within the corn canopy, resulting in increased disease control and yield. Field trials were conducted at the University of Kentucky Research and Education Center in Princeton, KY in 2020 to determine if using in-canopy drop nozzles (TeeJet XR 80015) and/or 360 Undercover nozzle bodies (TeeJet XR 8001) reduced gray leaf spot (*Cercospora zeae-maydis*) or Diplodia ear rot (*Stenocarpella maydis*), and improved yield and fungicide coverage compared to overhead nozzles (TeeJet XR 8002) alone. A non-fungicide treated control was included. Fungicide nozzle did not affect disease severity or yield in any trials. Fungicide timing did affect disease severity. In one trial, fungicide applications at the 12-leaf collar stage (V12), tasseling (VT), and V12 + VT significantly reduced gray leaf spot compared to the non-treated control. In all trials, fungicide coverage on the ear leaf was the same among all nozzle types. In one trial, the 360 Undercover nozzles resulted in an 388% increase in fungicide coverage on the ear compared to overhead nozzles alone. These results indicate that new nozzle technologies may not influence foliar disease severity, but can increase fungicide coverage on the ear. However, more research is needed to assess the effectiveness of these nozzles on ear rot management.