2021 North Central Division Meeting Abstracts

Abstracts presented at the APS North Central Division meeting held virtually, June 15–16, 2021. The recommended format for citing division meeting abstracts, using the first abstract below as an example, is as follows:

DANGAL, N. K., Rekabdarkolaee, H. M., Markell, S. G., Harveson, R. M., Mathew, F. M. 2021. Precipitation days affect presence of endophytic *Diaporthe* in sunflower. (Abstr.) Phytopathology 111:S1.26. https://doi.org/10.1094/PHYTO-111-9-S1.26

The abstracts are published as a supplement to *Phytopathology* for citation purposes. They were not reviewed by the *Phytopathology* Editorial Board and were not edited by the APS editorial staff.

https://doi.org/10.1094/PHYTO-111-9-S1.26

Precipitation days affect presence of endophytic *Diaporthe* in sunflower

N. K. DANGAL (1), H. M. Rekabdarkolaee (1), S. G. Markell (2), R. M. Harveson (3), F. M. Mathew (1), (1) South Dakota State University, Brookings, SD, USA; (2) North Dakota State University, Fargo, ND, USA; (3) University of Nebraska, Scottsbluff, NE, USA

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 m^2). 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

A. MANE, T. A. Jackson-Ziems, S. E. Everhart, University of Nebraska-Lincoln, Lincoln, NE, USA

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

V. Kostyukova, D. Koksharov, A. Taskuzhina, A. Pozharskiy, D. GRITSENKO, Institute of Plant Biology and Biotechnology, Almaty, AL, KAZAKHSTAN

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

A. L. MARTINEZ (1), A. Garayalde (2), F. Quiroz (3,4), A. Carrera (5), (1) North Dakota State University, Fargo, ND, USA; (2) Department of Mathematics, Universidad Nacional del Sur, Bahía Blanca, ARGENTINA; (3) INTA, Balcarce, ARGENTINA; (4) Instituto Nacional de Tecnología Agropecuaria (INTA), Balcarce, ARGENTINA; (5) Universidad Nacional del Sur, Bahía Blanca, Bahía Blanca, ARGENTINA

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

G. M. WILLIAMS (1), M. Ginzel (2), (1) Purdue University, Lafayette, IN, USA; (2) Department of Entomology, Purdue University, West Lafayette, IN, USA

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

S. SINGLA (1), Z. Duray (2), R. Dill-Macky (3), P. O'Neill (2), L. Bernhardson (4), S. Tatineni (5), S. Sattler (4), S. N. Wegulo (6), D. L. Funnell-Harris (4), (1) University of Nebraska Lincoln, Lincoln, NE, USA; (2) USDA ARS, Lincoln, NE, USA; (3) University of Minnesota, St. Paul, MN, USA; (4) USDA-ARS, Lincoln, NE, USA; (5) USDA ARS, University of Nebraska, Lincoln, NE, USA; (6) University of Nebraska, Lincoln, NE, USA