2020 Potomac Division Meeting Abstracts

Abstracts presented at the APS Potomac Division meeting held virtually, March 12–13, 2020. The recommended format for citing division meeting abstracts, using the first abstract below as an example, is as follows:

Rogers, L., Koehler, A., and Shew, D. 2020. Recovery of *Macrophomina phaseolina* from stevia roots following fumigation and foliar fungicide treatments. (Abstr.) *Phytopathology* 110:S1.34. <https://doi.org/10.1094/PHYTO-110-7-S1.34>

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-110-7-S1.34>

© 2020 The American Phytopathological Society

Recovery of *Macrophomina phaseolina* from stevia roots following fumigation and foliar fungicide treatments

L. ROGERS (1), A. Koehler (2), D. Shew (1), (1) North Carolina State University, Raleigh, NC, USA; (2) University of Delaware, Georgetown, DE, USA

Stevia (*Stevia rebaudiana*) is a perennial crop harvested for leaves that contain glycosides used as noncaloric sweetening agents. The charcoal rot pathogen, *Macrophomina phaseolina*, was first isolated from stevia roots in NC in 2016 and has been isolated from multiple field sites in subsequent studies in NC. Previous studies also demonstrated an enhanced overwintering survival of stevia roots and crowns following application of some foliar fungicides. To better understand the interaction between fungicide application and root colonization by *M. phaseolina*, stevia roots from various treatments were sampled monthly from October to May for two years (2018–2020) to determine the proportion of *M. phaseolina* recovered from non-treated and fungicide/fumigation-treated plants. In the 2018–2019 sampling period, recovery of *M. phaseolina* from fumigated treatments (5.79%) was significantly lower than non-fumigated treatments (12.73%, $p = 0.0028$). Recovery of *M. phaseolina* from plants treated with foliar fungicides was not significantly different from non-fungicide treated plants. In the 2019–2020 sampling period, no significant differences in recovery of *M. phaseolina* have been observed between fungicide treated and non-fungicide treated plants to date. These observations suggest that foliar fungicide application is not impacting the frequency of root colonization by *M. phaseolina* in stevia and enhanced survival may not be due to suppressing root colonization by *M. phaseolina*.

Septoria leaf spot resistance in accessions of *Solanum habrochaites*, *S. peruvianum*, and *S. cornellimulleri*: Progress in breeding for resistance

M. E. GALLEGLY JR., E. Flores, V. Benedito, M. Rahman, West Virginia University, Morgantown, WV, USA

Tomato genotypes belonging to *habrochaites* and *peruvianum* were screened in the greenhouse for high level of Septoria leaf spot (SLS) resistance to use in tomato breeding program. Resistance to SLS was found in *Solanum habrochaites* accessions LA1721, LA1779, LA1927, LA1978 and LA2329. LA2329 was crossed with Mountaineer Delight (WV '17B) and the F₁ planted at the WVU Organic Farm in 2018. The resistant F₁ was crossed in the greenhouse with WV '63, WV '17A (Mountaineer Pride) and WV '17B. The resulting backcross progeny was planted at the organic farm in 2019. Resistant selections from the 2019 planting were backcrossed again in the greenhouse to the above 3 home garden varieties, and the resulting progeny will be planted on the farm in 2020 for selection for SLS resistance and acceptable horticultural traits. Resistance in LA2329 was assessed, which is likely due to a single dominant gene. Search for possible physiologic (pathogenic) races is in progress; preliminary data with five isolates, two from New York state and three from West Virginia, show no difference among the 5 isolates. Our team has been successful in obtaining F₁ plants by embryo culture from Septoria resistant *S. peruvianum* accessions LA1984 and LA2744, and *S. cornellimulleri* accession LA1910, crossed with WV '63 and WV '17B. The F₂ of these latter crosses will be screened for resistance to *Septoria lycopersici* and this resistance eventually will be integrated into the breeding program.

Discovery of the Tepovirus *Prunus virus T* in pear trees using high-throughput sequencing

L. CARVALHO COSTA, M. M. Malapi-Wight, X. Hu, J. A. Foster, O. P. Hurtado-Gonzales, USDA-APHIS Plant Germplasm Quarantine Program, Beltsville, MD, USA

High-throughput sequencing (HTS) technologies have been successful in the detection of well-known viruses as well as in the discovery of a wide range of novel plant viruses. The Plant Germplasm Quarantine Program imported ten different Bukharan pear trees (*Pyrus korshinskyi* Litv.) from Kyrgyzstan in 2019. All trees were subjected to HTS via the Illumina NextSeq 500 using the TruSeq ribodepletion kit, resulting in ~30M 75bp single-end reads per sample. Bioinformatic analyses identified two pear trees carrying a virus most closely related to *Prunus virus T* (PrVT) of the genus *Tepovirus* reported in *Prunus domestica* (KF700263.1, Marais et al 2015). The gaps in the draft genomes from HTS were filled using Sanger sequencing, resulting in genomes of ~6,847bp in length with an identity percent to PrVT of around 75% and 95% at the nucleotide and amino acid levels respectively. Our findings indicate that these viruses present in Bukharan pears are divergent isolates of PrVT and this is the first report of a *Tepovirus* infecting pears. Primers were designed on the RNA-dependent RNA polymerase region for RT-PCR screening of 116 pear and apple accessions held under quarantine from 26 different countries. Only one other Bukharan pear accession from a different locality in Kyrgyzstan tested positive for this virus. Further transmissibility and symptomatology studies on indicator plants are ongoing to better characterize this virus.

Variable sensitivity of *Ophiosphaerella* spp. to fungicides *in vitro*

W. J. HUTCHENS (1), Y. Nagaoka (2), J. P. Kerns (2), M. Goatley (3), M. Nita (4), D. S. McCall (1), (1) Virginia Tech, Blacksburg, VA, USA; (2) North Carolina State University, Raleigh, NC, USA; (3) Virginia Polytechnic Institute & State University, Blacksburg, VA, USA; (4) Virginia Polytechnic Institute and State University, Winchester, VA, USA

Spring dead spot, caused predominantly by *Ophiosphaerella herpotricha* and *O. korrae* in the United States, is a devastating disease on bermudagrass [*Cynodon* spp.] in areas where winter dormancy occurs. Fungicide efficacy against the disease has been inconsistent with many active ingredients, and potential differences in species susceptibility to fungicides may be a cause of the inconsistency. An *in vitro* laboratory experiment was conducted with four isolates of each *O. herpotricha* and *O. korrae*. The objective was to determine the EC₅₀ values of the four representative *Ophiosphaerella* isolates of each species to 13 different fungicides (DMIs: fenarimol, mefentrifluconazole, myclobutanil, propiconazole, tebuconazole; QoIs: azoxystrobin, fluoxastrobin, pyraclostrobin; SDHIs: fluopyram, fluxapyroxad, isofetamid, penhiopyrad, and pydiflumetofen). Potato dextrose agar was amended with each fungicide at either 0, 0.001, 0.01, 0.1, 1, or 10 mg L⁻¹. Pydiflumetofen was the most efficacious of all fungicides screened, regardless of species, with an average EC₅₀ value of 0.023 mg L⁻¹. *O. herpotricha* was significantly ($P < 0.1$) more sensitive to myclobutanil, propiconazole, azoxystrobin, pyraclostrobin, fluxapyroxad, and penhiopyrad than *O. korrae* while *O. korrae* was more sensitive to fenarimol. All other fungicides suppressed each species equally. Our data suggests inconsistent fungicide efficacy is partly due to variability in sensitivity of species to certain fungicides.

Fulbright Fellowship and Food Security in Africa

D. HADZIABDIC, Entomology & Plant Pathology, University of Tennessee, Knoxville, TN, USA

Starvation and malnutrition are persistent worldwide challenges. For 795 million people globally, including 780 million in developing countries, hunger remains a daily challenge despite the efforts to eradicate food shortages. Africa possesses numerous indigenous crops with high nutritional value, which may play a role in ensuring food security and maintaining economic growth. Yet, food security is often dependent upon success of only a few, widely cultivated crops. These regionally adapted plants may provide better ability to tolerate drought stress and poor quality soils that may be rich in micronutrients. The time to act is now because 75% of the world's agricultural plant genetic diversity has been nearly lost. Contemporary agriculture remains focused on production of high-yielding, genetically uniform plants that have replaced local knowledge and reliance upon native crop alternatives. This talk highlights my recent Fulbright Program funded work in Ghana that addresses food security and conservation indigenous crop species.

Evaluating niche clearing as a practice to improve biological control efficacy against *Rhizoctonia solani* in home lawn turf

J. DOHERTY, J. A. Roberts, University of Maryland, College Park, MD, USA

Increased restrictions on synthetic pesticides are creating significant hurdles to effective turfgrass pest control, leaving biological controls (BCs) as one of a few remaining options. While BCs can be effective for pest control, inconsistencies are often cited with field use, potentially emanating from competition against existing microbiota. A greenhouse research project was initiated to determine if niche clearing practices can be used to improve BC establishment and efficacy against *Rhizoctonia solani* Kühn on perennial ryegrass (*Lolium perenne* L. cv. "Express II"). A split plot experimental design with a factorial treatment arrangement was used to assess niche clearing [hydrogen peroxide and none] in combination with BCs (*Bacillus subtilis* QST-713, *Pseudomonas chlororaphis* AFS009, a *Bacillus* sp. isolate, and none). Treatments were applied on a 14 d interval, with foliage samples collected at 0, 2, 4, 7, 10, and 13 days post-application. Samples were evaluated for disease and selective media were used to enumerate *Bacillus*, *Pseudomonas*, and bacterial populations from leaf washings. Regardless of BC application, treatments including hydrogen peroxide survived under extreme disease pressure 2 days longer than none. Pots treated with hydrogen peroxide and *P. chlororaphis* had higher recoverable *Bacillus* populations than pots treated with *P. chlororaphis* alone. Future research will evaluate these treatments under field conditions with more moderate disease pressure.

Genome-based circumscription of cool-virulent *Ralstonia solanacearum* strains in an attempt to improve their regulation

P. SHARMA (1,2), R. Mazloom (3), C. Allen (4), M. J. Stulberg (5), G. A. Beattie (6), M. Arif (7), L. Heath (8), K. A. Eversole (9), B. A. Vinatzer (2), (1) Genetics, Bioinformatics, and Computational Biology program, Virginia Tech, Blacksburg, VA, USA; (2) School of Plant and Environmental Sciences, Virginia Tech, Blacksburg, VA, USA; (3) Department of Computer Science, Virginia Tech, Blacksburg, VA, USA; (4) University of Wisconsin-Madison, Madison, WI, USA; (5) USDA-APHIS-PPQ-S&T-CPHST, Beltsville, MD, USA; (6) Dept of Plant Pathology & Microbiology, Iowa State University, Ames, IA, USA; (7) University of Hawaii at Manoa, Honolulu, HI, USA; (8) Virginia Tech, Blacksburg, VA, USA; (9) Phytobiomes Alliance, Bethesda, MD, USA

Ralstonia solanacearum (*Rs*) is a plant pathogen that causes disease on hundreds of plant species. A small group of *Rs* strains, known as Race 3 Biovar 2 (R3B2), cause potato brown rot disease at cooler temperatures and lead to crop losses of up to 100%. R3B2 strains are not found in the USA and because of the ease of transmission, pose a serious threat to the US potato industry. Since it is challenging to distinguish R3B2 strains from other *Rs* strains and also because R3B2 strains are not a formally described taxon, the entire *Rs* species is included in the list of highly regulated Select Agents. To help USDA APHIS improve the regulation of *Rs* strains, the aim of this study is to apply a genome-based classification scheme capable of precisely identifying and distinguishing the cool-virulent R3B2 strains from non-cool-virulent *Rs* strains. Towards this goal, a core genome phylogenetic tree of over 100 *Rs* strains was constructed. This tree clearly separated the 18 confirmed R3B2 strains from other *Rs* strains. Next, a distance-based tree was constructed using LINbase. Both trees grouped the cool-virulent strains similarly. Genome-based classification and identification of cool-virulent *Rs* strains is thus possible. However, virulence assays of R3B2 strains still need to be performed to precisely define which strains should be included in a revised select agent definition. Once done, USDA APHIS will have a new tool to protect US agriculture from cool-virulent *Rs* strains.

Use of *Trichoderma* to reduce viability of *Calonectria* species in boxwood leaf litter

N. Shishkoff (1), E. SMALLWOOD (2), R. Whitesell (3), (1) USDA ARS FDWSRU, Frederick, MD, USA; (2) USDA ARS FDWSRU, Fort Detrick, MD, USA; (3) Mount Saint Mary's University, Emmitsburg, MD, USA

Boxwood plants are threatened by invasive *Calonectria pseudonaviculata* (*Cps*) in the US and by both *Cps* and *C. henricotiae* (*Che*) in Europe. The pathogen has been shown to persist in boxwood litter in or on soil, so an attempt was made to reduce survival with application of a biocontrol agent. A water suspension of *Trichoderma* conidia was tested as a drench over boxwood litter in sand. Infested leaves of Buxus 'Justin Brouwers' were allowed to mature for one mo, and then placed in 0.6 L plastic boxes containing dry sand. Approx. 140 leaves were placed in each box and the moisture content of the box adjusted to carrying capacity using either sterile water or a spore suspension of *Trichoderma koningiopsis* at approx. 13 ml at 10⁶ spores/mL. Boxes were incubated at 0, 10, and 20°C, with two boxes per treatment. A random subsample of 20 leaves/box were removed monthly for six mo and plated on GYET media. Number of leaves with sporulating CPA or Che were recorded. Results for the first two trials indicated that temperature, sampling time and the presence of *Trichoderma* significantly affected viability, but there was no difference in survival between *Cps* and *Che*. These preliminary experiments provide support for the investigation of additional *Trichoderma* isolates as potential biological controls of *Cps* and *Che* in litter.

Xanthomonas euvesicatoria type III effector XopN promotes an aqueous apoplast and enhances bacterial proliferation in both tobacco and pepper

Z. WANG, B. Zhao, Virginia Tech, Blacksburg, VA, USA

Bacterial spot (BS) disease is one of the most common and destructive diseases that infect both tomatoes and peppers. BS can be easily identified due to the appearance of dark, irregular, water-soaked areas on the leaf. While a number of studies have indicated that an aqueous environment is essential for bacterial proliferation, it remains unclear which components of *Xanthomonas euvesicatoria* (*Xe*) contribute principally to the water-soaked symptoms of BS in affected pepper and tomato plants. In this study, we report that a *Xe* type III secreted effector, XopN, is required for triggering the water-soaking symptom on *Nicotiana benthamiana* (*N. benthamiana*) and pepper plants infected with *Xe*. With the function of XopN, a higher apoplastic water content is maintained in *N. benthamiana* leaf infected by *Xe*. In addition, XopN positively regulates stomatal conductance, by directly or indirectly increasing the stomata aperture, which can enhance the colonization of a nonpathogenic *Xe* strain on tobacco and pepper leaves. Furthermore, our results showed that a glycerol uptake facilitator (*glpF*) and the type two secretion system of *Xe* also contribute to the development of the water-soaking phenotype. Therefore, *Xanthomonas euvesicatoria* utilizes different mechanisms to promote an aqueous apoplast, which is vital for enhancing bacterial proliferation in both tobacco and pepper plants.

Culture-independent plant pathogen identification from metagenomic DNA using The Oxford Nanopore Technologies (ONT) MinION™

M. AGUILERA (1,2), P. Sharma (1,2), M. E. Mechan Llontop (2), S. Yang (2), S. Li (2), B. A. Vinatzer (2), (1) Genetics, Bioinformatics, and Computational Biology program, Virginia Tech, Blacksburg, VA, USA; (2) School of Plant and Environmental Sciences, Virginia Tech, Blacksburg, VA, USA

Emerging plant diseases are a global threat to crop biosecurity. Therefore, fast and precise identification of emerging pathogens is crucial for correct diagnosis and effective disease control. Unfortunately, conventional methods based on visual or molecular diagnosis

mainly detect already known pathogens and may miss emerging pathogens. Metagenomic DNA sequencing could address this limitation since all organisms present in a sample could be sequenced and identified at the same time. The ONT MinION™ offers the ability to sequence long-reads in a laboratory or field setting in almost real-time and is thus well suited for metagenomic sequencing for plant disease diagnosis. We have successfully used the MinION™ to detect and identify bacterial and fungal pathogens from tomato and boxwood plant samples. However, to achieve real-time identification, there are challenges that still need to be overcome, including the improvement in basecalling and barcoding tools, development of bioinformatics tools for precise identification of closely related strains, and construction of more complete pathogen databases.

Survey of plant pathogenic nematodes in Delaware and Maryland soybean fields

A. C. KESSLER, A. Koehler, University of Delaware, Georgetown, DE, USA

Soybean cyst nematode (SCN, *Heterodera glycines*) is considered the most damaging pathogen of soybeans across the US, as well as one of the most significant nematode species affecting soybeans in Delaware and eastern shore Maryland. Management has relied on widespread use of the PI88788 resistance gene, but a breakdown in resistance is emerging. Detailed surveys were conducted across Delaware and Maryland in 1993 and in 2009 where elevated reproduction on PI88788 was observed at rates of 44–80%. Over the past decade, it is likely that reproduction has continued to elevate and most growers are unaware of their SCN population levels. In 2019, nematode soil sampling was conducted across 60 organic and conventional soybean fields in Maryland and Delaware. Field representative soil samples were collected and submitted to the NCDA Agronomic Services Nematode Assay lab for analysis. Within sites sampled, SCN was recovered in 57% of fields, root knot nematode in 17%, lesion nematode in 60%, and dagger nematode in 17%. A grower survey was conducted representing over 2,220 acres of soybean production. All respondents indicated some level of concern about SCN reducing yields and around half of the respondents were concerned about root knot nematode levels. The confirmation of widespread nematode prevalence combined with a break down in SCN resistance across the region highlights the need for future research to investigate management options.

Proteome analysis of *Xanthomonas campestris* isolated from invasive garlic mustard

J. THOMAS (1), M. B. McMahon (1), W. Garrett (2), D. G. Luster (1), M. Tancos (1), (1) USDA ARS Foreign Disease Weed Science Research Unit, Fort Detrick, MD, USA; (2) USDA-ARS, Beltsville, MD, USA

Xanthomonas campestris is a Gram-negative bacterium that infects many cruciferous, agronomic crops and is widely distributed throughout the United States. In 2019, a novel isolate of *X. campestris* was first reported on the non-native, invasive weed, garlic mustard (*Alliaria petiolata*) in Frederick County, MD (strain FDWSRU 18048). Garlic mustard is native to Eurasia and was intentionally introduced into the United States in the 19th century, but has since rapidly displaced native flora across the midwestern and eastern U.S. and Canada, forming dense monocultural stands in the forest understory. A multilocus sequence analysis of eight conserved loci was used in pathovar determination and revealed that the novel isolate clustered with nonpathogenic *X. campestris* strains versus the agronomically-important pathogenic strains. This novel isolate has the potential to be utilized as a biological control agent of invasive garlic mustard, but an increased understanding of pathogen emergence and host range is required. To elucidate the biological processes involved in pathogenicity and host specificity, *X. campestris* proteins were collected from the media of mid-log phase cells and analyzed by LC-MS/MS. A total of 2310 unique proteins were identified. Results of this preliminary proteome analysis will be compared with analyses of pathogenic pathovars to identify differences in protein expression.

Effector diversification underwrites the rapid evolution of *Xanthomonas oryzae* pv. *oryzae* in the Indian Subcontinent

K. NEELAM (1,2), I. S. Yadav (3), B. Yadav (3), J. Lore (4), M. S. Hunjan (5), N. Rawat (6), R. Rai (7), P. Kaur (8), Y. Vikal (9), P. Chhuneja (8), K. Singh (10), (1) Punjab Agric Univ, Ludhiana, Punjab, INDIA; (2) University of Maryland, Columbia, MD, USA; (3) Punjab Agricultural University, Ludhiana, INDIA; (4) Punjab Agricultural University, Ludhiana, INDIA; (5) PAU, Ludhiana, INDIA; (6) University of Maryland College Park, College Park, MD, USA; (7) ICAR, New Delhi, INDIA; (8) PAU, Ludhiana, INDIA; (9) PAU, INDIA; (10) ICAR-NBPGR, INDIA

Bacterial blight (BB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is an important disease of rice (*Oryza sativa* L.) causing significant yield losses annually in irrigated and rain-fed lowland ecologies throughout Asia. Till date 10 pathotypes of *Xoo* have been identified/characterized in Punjab state of India, based on virulence/avirulence reactions to the near isogenic lines with known bacterial blight resistance genes. The ten *Xoo* pathotypes from Punjab (India) were sequenced using PacBio and the Illumina HiSeq 2500 with the paired end library. Complete genome assembly (approximately 5Mb) was obtained for nine of the pathotypes except one. A comparison of all the nine genomes indicated intensive genomic rearrangements among all the 10 pathotypes. Major translocations were reported in Pbxo 3, Pbxo 4, Pbxo 7, and Pbxo 9 as compared to the reference genomes of *Xoo* strains i.e. PXO99A, KACC, MAFF and PXO86. Approximately four thousand genes were predicted in all of the studied *Xoo* pathotypes. The numbers of TALE genes identified varied from thirteen to eighteen among the nine *Xoo* pathotypes. The detailed analysis of TALEs in all the nine *Xoo* assembled data revealed the presence of three newer TALE gene classes in them. Class-wise comparison of repeat variable residues (RVD) sequences revealed insertion/deletion among different TALE classes, thus providing a clue towards the rapid evolution of *Xoo* pathotypes in Punjab state of India.

Translatome analysis of phloem defense responses during plum pox virus infection in European plum

T. COLLUM (1), A. L. Stone (1), D. Sherman (1), E. E. Rogers (1), C. D. Dardick (2), J. N. Culver (3,4), (1) USDA, Agricultural Research Service, Foreign Disease-Weed Science Research Unit, Frederick, MD, USA; (2) USDA, Agricultural Research Service, Appalachian Fruit Research Station, Kearneysville, WV, USA; (3) Department of Plant Science and Landscape Architecture, University of Maryland, College Park, MD, USA; (4) Institute of Bioscience and Biotechnology Research, University of Maryland, College Park, MD, USA

Plant phloem tissues are the main conduit for the movement of hormones, nutrients, proteins, RNAs, and carbohydrates essential for plant growth and development. The phloem is also utilized by plant viruses as the main route for viral long-distance movement. Movement of molecules through the plant phloem is regulated, and specific viral-plant interactions are required for movement. However, these phloem specific interactions and plant responses are not well characterized especially in agriculturally important perennial crops. In this study, we use translating ribosome affinity purification (TRAP) followed by RNA sequencing to identify phloem specific responses to plum pox virus (PPV) infection in plum (*Prunus domestica* L.) during leaf development. PPV is the causative agent of Sharka, one of the most devastating diseases of stone fruits. We found that in four to six-week old leaves the phloem has a disproportionate response to PPV with two- to six-fold more differentially expressed genes in phloem than non-phloem tissues despite similar infection levels. Phloem alterations included genes associated with salicylic acid mediated defense responses and RNA silencing. The results reveal new insights into the dynamics of plant defense responses in phloem tissue types during virus infection. Identified genes provide new candidates for manipulating the timing of plant defense responses to disrupt the normal virus lifecycle and develop new strategies for disease resistance.

Fungicide sensitivities of *Pythium* spp. causing damping off of corn in Delaware

J. BICKEL, A. Koehler, University of Delaware, Georgetown, DE, USA

Corn (*Zea mays* L.) is an important grain crop in Delaware and good stand establishment is necessary for a productive and profitable growing season. Reduced tillage practices and wet growing seasons have favored the development of pre- and post-emergent damping off caused by *Pythium* spp. In 2019, multiple cases of post-emergent damping were observed in fields of fungicide-treated seed, with several fields having to be replanted due to stand loss. To date, there has been limited investigation into the species distribution and fungicide sensitivities of *Pythium* species across the Mid-Atlantic. In 2019, fungal isolates collected from symptomatic corn roots were classified at the species level through amplification of the ITS region. Species detected in the collection included *P. graminicola*, *P. torulosum*, *P. aristosporum*, *P. inflatum*, *P. sylvaticum*, and *P. coloratum*. A subset of fifteen isolates were selected and screened for sensitivity to three active ingredients: picarbutrazox, ethaboxam, and metalaxyl-M. In vitro assessments were conducted by transferring isolates to V8-agar media amended with 0, 0.01, 0.1, 1.0, or 10 ppm of each fungicide. Hyphal growth was measured at 48 hours to calculate percent inhibition and corresponding effective concentration to inhibit 50% of growth (EC₅₀ value). No isolates displayed insensitivity to any of the fungicides tested. Among species evaluated, *Pythium sylvaticum* exhibited the most growth in vitro.

Foliar blight affecting *Sarcococca hookeriana*

V. L. CASTROAGUDIN (1), O. Stanley (2), R. R. Whitesell (2), T. N. Olson (3), N. Shishkoff, and J. A. Crouch (1), (1) United States Department of Agriculture, Agricultural Research Service (USDA-ARS) Beltsville, MD, USA; (2) USDA-ARS, Frederick, MD, USA; (3) Pennsylvania Department of Agriculture, Harrisburg, PA, USA

Evergreen sweetbox (*Sarcococca hookeriana*, *Buxaceae*) shrubs are high value ornamental plants that flourish in full shade areas and produce fragrant, winter-blooming flowers. One-year old sweetbox with moderate leaf spotting and defoliation were observed in October 2018 in a residential landscape in Lancaster County, Pennsylvania. A fungal isolate recovered from the infected sweetbox leaves showed morphological characteristics and ITS sequence consistent with *Coccinonectria pachysandricola*, a known causal agent of blight on *Pachysandra* and *Sarcococca* species in the United States. Ongoing research is being conducted to better understand the infection of *Buxaceae* hosts by *C. pachysandricola*.

Effect of planting date and fungicide spray on foliar diseases of four chickpea varieties grown in central Virginia

S. Chawla, L. Rutto, S. Matthews, S. Campbell, Z. MERSHA, Virginia State University, Petersburg, VA, USA

Chickpea (*Cicer arietinum* L.) is nutrient-dense legume with a number of health and ecological benefits. Chickpea faces many biotic and abiotic challenges in Virginia where weather is highly conducive for many of its pathogens. In 2019, a split-split plot field trial with six biweekly planting dates (PD) as main plots, fungicide spray (F) (treated and non-treated) as subplots, and four chickpea varieties (V) (Myles, Frontier, Leader and Pedrosillano) as sub-subplots, was conducted at Randolph Farm of Virginia State University. Fungicide treated plots received 3–6 sprays of five fungicides that were applied alternatively. Severity (DS) of foliar diseases, such as blights and leaf spots caused by *Ascochyta* and others, was rated visually by estimating percent foliage covered with lesions on plants in the middle rows. Relative area under the disease progress curve (rAUDPC) was calculated to account for the variation in maturity dates. Data from a weather station was used to correlate weather favorability with DS. After harvest, pods were categorized into threshable (clean or symptomatic) and non-threshable (insect damaged, shattered or aborted). In terms of rAUDPC, all the three individual factors ($P <$

0.0001) and interactions between PD*V ($P < 0.0001$) and PD*F ($P = 0.0437$) were significant. Accordingly, rAUDPC was highest for the Kabuli type Pedrosillano planted on 15-June and lowest on the Desi type Myles planted on 01-May. Studies on plant spacing will be added in 2020.

Detecting the boxwood blight pathogen, *Calonectria pseudonaviculata* (Cps), using the Oxford Nanopore MinION sequencing device

S. YANG (1), M. Aguilera (1,2), M. A. Hansen (3), E. A. Bush (1), S. Li (1), B. A. Vinatzer (1), (1) School of Plant and Environmental Sciences, Virginia Tech, Blacksburg, VA, USA; (2) Genetics, Bioinformatics, and Computational Biology program, Virginia Tech, Blacksburg, VA, USA; (3) Plant Disease Clinic, Virginia Tech, Blacksburg, VA, USA

Boxwood is an evergreen shrub or small tree and a popular horticultural crop in the U.S. with annual sales of \$126 million. Boxwood blight, caused by *Calonectria pseudonaviculata* (Cps), is a devastating fungal disease of great concern to the landscape and nursery industry. This pathogen was first introduced to the U.S. in 2011 and has spread to more than twenty states. The best way to protect boxwood from boxwood blight is to avoid its dissemination with infected plant material. Thus, early and rapid detection is critical to managing this disease. However, infected plants are initially asymptomatic, and different types of microbes living on plants complicate detection and diagnosis. The MinION sequencer, a portable single-molecule sequencing platform developed by Oxford Nanopore Technologies, has the potential to enable initial, rapid, and real-time diagnosis of plant diseases. In this study, to maximize the concentration of pathogen DNA without losing quality, several DNA extraction methods were compared. Metagenomic DNA was extracted either with or without disrupting plant cells from infected and healthy boxwood, and sequenced by the MinION sequencer. Data were analyzed by bioinformatics tools. It was possible to confirm the presence of Cps with all methods, but sensitivity varied. The ultimate goal is to detect Cps in mildly symptomatic or even asymptomatic plants.

Identification of susceptibility factors in wheat for *Fusarium graminearum* infection for designing resistance in crops

N. RAWAT (1), B. Chhabra (1), V. Tiwari (2), (1) University of Maryland College Park, College Park, MD, USA; (2) 2114 Plant Sciences Building, College Park, MD, USA

Fusarium Head Blight, caused by ascomycete *Fusarium graminearum*, is a devastating disease of wheat and barley. Genetic resistance is one of the major strategies for controlling FHB in these crops. However, very limited effective genetic resistance has been found for FHB. One of the research goals of the Rawat lab is to find susceptibility factors in wheat and use them to design resistance in plants against this serious disease. Multipronged efforts towards this goal include: screening of chemically mutagenized populations of wheat for loss of susceptibility against *F. graminearum*, mapping of a gene controlling susceptibility to *F. graminearum* infection in wheat and, functional genomics studies of lipoxygenases in wheat. Update on these research efforts will be provided in the presentation.

The effect of leaf shape and plant architecture on downy mildew of lima bean caused by *Phytophthora phaseoli*

A. GINN (1), E. Ernest (2), N. F. Gregory (1), A. Koehler (2), T. A. Evans (1), N. M. Donofrio (1), (1) University of Delaware, Newark, DE, USA; (2) University of Delaware, Georgetown, DE, USA

Maximum lima bean yields in the mid-Atlantic region of the United States are obtained during late summer and early fall months. These harvest dates coincide with climatic conditions conducive for the destructive lima bean pathogen *Phytophthora phaseoli*. Widely planted lima bean cultivars such as C-Elite Select and M-15 have both low and sprawling growth patterns and large and ovate-shaped leaves. These phenotypic traits place plants at high risk of infections due to their proximity to soil and lack of adequate airflow through the canopy. Six pairs of lima bean near isogenic lines (NILs) with lanceolate and ovate leaf shape, and five experimental varieties with upright architectures, were planted in early July 2019, to assess the effect of leaf shape and plant architecture on disease development. Two months after planting, *P. phaseoli* inoculum was applied twice, two weeks apart. Three weeks post initial inoculation, severity ratings were recorded and infected pods collected for qPCR analysis. Plants were harvested for yield data at the succulent seed stage. Lines with lanceolate leaf shape had significantly lower overall severity ratings compared to ovate NILs, while no significant differences were observed due to plant architecture. Yield data also showed significant differences between leaf shapes. Pod samples are currently being tested via qPCR. Development of less susceptible lima bean cultivars may lead to lower yield losses due to *P. phaseoli*.