

2021 Report
Spatial Distribution and Diversity of *S. sclerotiorum*
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Three new fields across PA were sampled to study *S. sclerotiorum* spatial distribution and genotypic diversity at a field scale. Soil samples were collected in April and May 2021. Sclerotia obtained from soil samples were sterilized and plated on agar. Three hundred thirty-eight isolates were grown out, and 129 isolates from 2021 were selected for DNA extraction and genotyping by fragment analysis.

Overall, 286 isolates from eight locations across Pennsylvania (2019-2021) were extracted (Figure 1). Using a fluorescently tagged forward primer, ten loci from each isolate's DNA were amplified by polymerase chain reaction (PCR). The ten PCR products were combined in a 96-well plate and sent to the Penn State Genomics Core Facility, where they were analyzed by capillary electrophoresis. The base-pair size (allele) for each locus was determined from the data using the Peak Scanner software. The multilocus genotype (MLG) for each isolate was determined, and population analyses were performed.

The population analysis results showed that there were 83 unique MLGs across Pennsylvania. However, many MLGs only represented one (or a few) isolates, while several MLGs made up most of the population (Figure 2). The evenness across all PA locations was 0.47, where 1 is a completely even population. The uneven population suggests that some genotypes are more prevalent than others. At the field scale several MLGs were predominant in most field populations. Each field showed evidence for a clonal population, meaning that 1-3 MLGs made up most of the isolates sampled. However, two fields had a high number of MLGs, which may lead to fungicide resistance. Overall, these results show a low probability of fungicide resistance to develop in PA *S. sclerotiorum* populations. Further work will be done on fungicide sensitivity and looking at which management practices impact genotypic diversity.

Regional Distribution and Diversity of *S. sclerotiorum*

To determine *S. sclerotiorum* diversity across Pennsylvania, white mold isolates were obtained from diseased soybean plants and soil samples in 2019, 2020, and 2021 from 19 fields across 10 different counties (Figure 3). In addition, we received isolates from New York from our collaborator, Dr. Sarah Pethybridge at Cornell University, to use for a comparison study. To date, there are 235 isolates to undergo diversity analysis. Currently, nine loci from each isolate's DNA are being amplified by PCR and prepared for capillary electrophoresis at the Penn State Genomics Core Facility.

Sporecaster Validation for the Northeast

For the Sporecaster validation project, we monitored 23 fields across Pennsylvania and New York. Flowering dates were recorded, and white mold scouting was completed at R5-R7. The Sporecaster risk varied across locations from an average risk of 19% to 63%. The disease incidence in the scouted Pennsylvania soybeans was low, from 0 to 4.6%. However, several New York snap bean fields were also monitored and ranged from 0 to 23.3% disease incidence. The model accuracy ranged from 65-74% disease incidence when looking at a 5% disease incidence level, depending on the threshold used. At a 10% disease incidence level, accuracy was 65-87% at forecasting white mold development. Like the 2020 validation, the 50% and 60% action thresholds were more accurate at predicting white mold in Pennsylvania. Four biweekly articles were published for the Penn State Field Crop News. These

articles updated growers on the latest risk for white mold, given the weather in various counties across PA.

Grower Survey on Feasibility and Adoption of Best Management Practices

We developed an online survey to elucidate growers' experience and perception of white mold but only received five completed responses. Therefore, we created poll questions to ask attendees at virtual workshops and conferences regarding their knowledge of white mold and which management tools they recommend or use. We received 51 responses from farmers, industry personnel, and consultants attending these virtual events. While most attendees think white mold is a problem in Pennsylvania, approximately one-third of respondents indicated that they did not have an issue with the disease. Approximately 42% of growers deal with white mold, with 10% having problems every year. One-quarter of respondents indicated being uncertain about having white mold. Half of the attendees indicated that the efficacy of a management practice is most considered when making decisions for disease management, whereas one-quarter consider recommendations from extension educators, crop consultants, or researchers. These survey responses suggest that white mold is a significant disease that has impacted or continues to be problematic for Pennsylvania soybean growers. Future steps include redesigning the online survey into an effective in-person survey and elucidating specific white mold disease management strategies currently used by growers.

Developing a Self-Guided Interactive Lesson on Plant Disease Epidemiology

The online teaching platform prototype was created using PowerPoint and presented at the 2021 American Phytopathological Society annual meeting. In addition to text, short videos, embedded YouTube videos, photos, figures, case studies, and activities were used to guide the viewer through the learning modules. Five learning modules with three submodules were created to teach the topic of white mold disease epidemiology (Figure 4). To evaluate the impact of the self-guided learning modules and receive feedback, graduate students enrolled in Epidemiology of Plant Diseases (PPATH 542) will complete a pre-and post-lesson survey and go through the lesson. The Digital Ed Team at Penn State will be contacted to transform this lesson into an Open edX, a web-based platform used for extension.

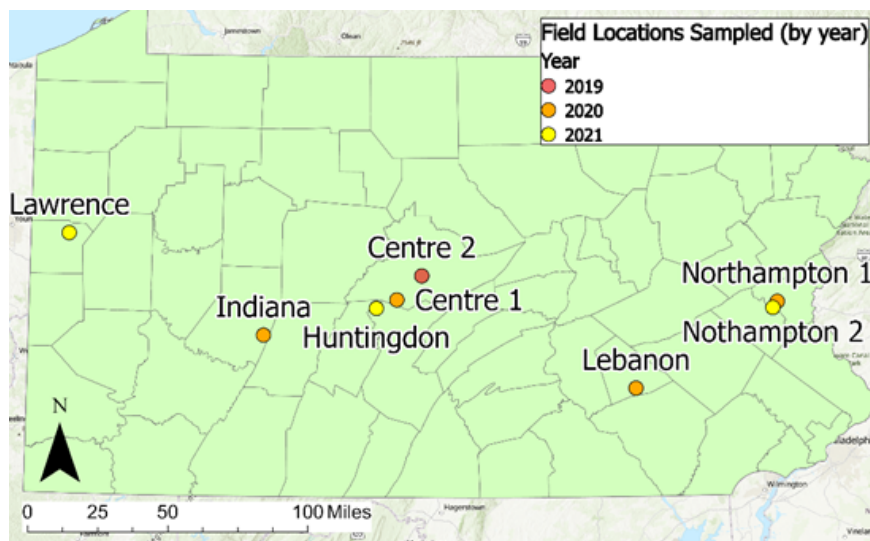


Figure 1: Map of Pennsylvania showing field locations by sampling year.

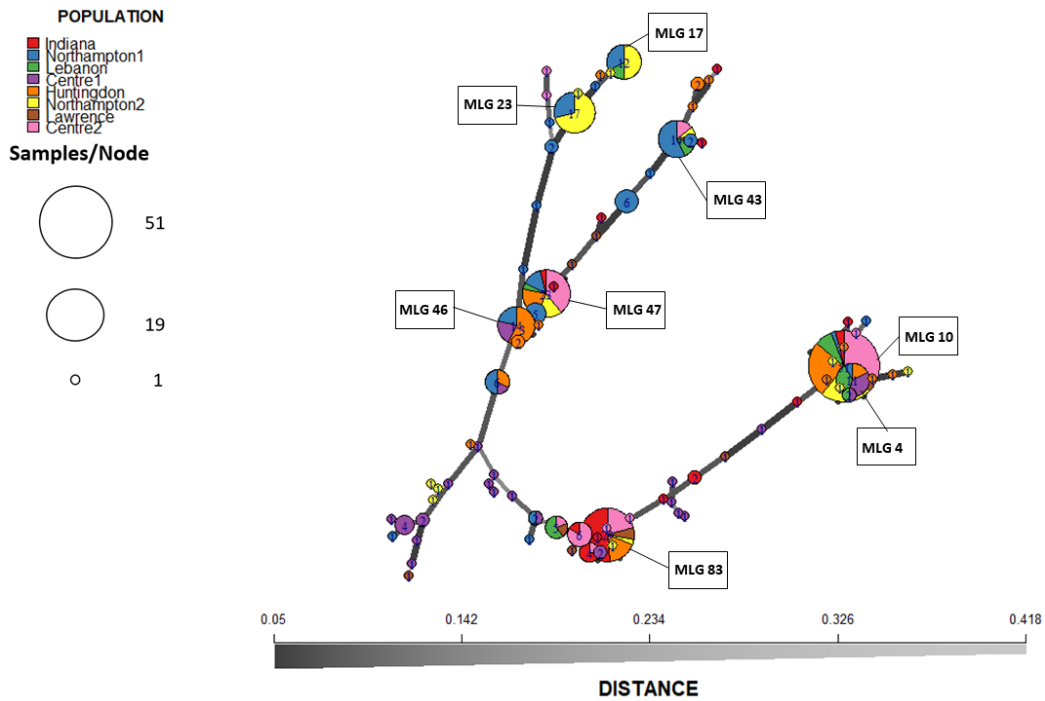


Figure 2: Minimum spanning network for all field subpopulations, as indicated by node colors. Node size represents the number of isolates with that multilocus genotype (MLG). The pie chart within the node gives the proportional number of isolates from a given subpopulation that are that MLG. Distance is measured by Bruvo's distance. Small, blue labels represent the number of isolates that make up a node.

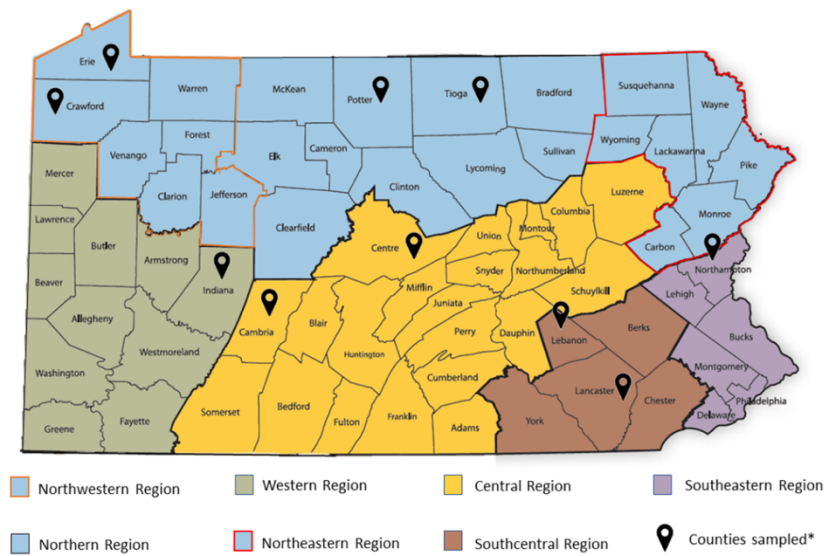
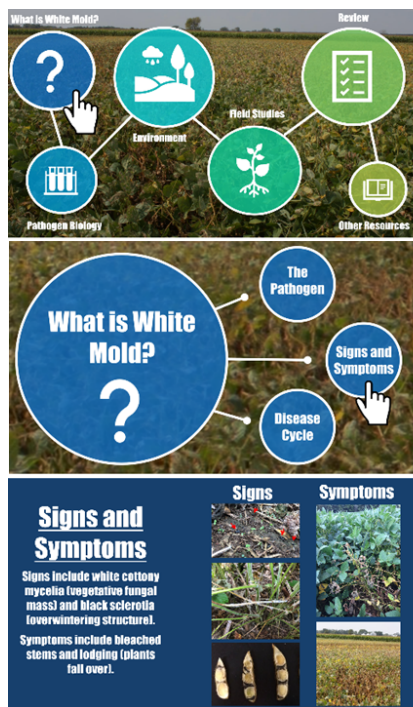


Figure 3: Map of sampling locations for the regional distribution and diversity project. *Pinpoints denote the county sampled and are not indicating specific areas within the county.



Learning Modules

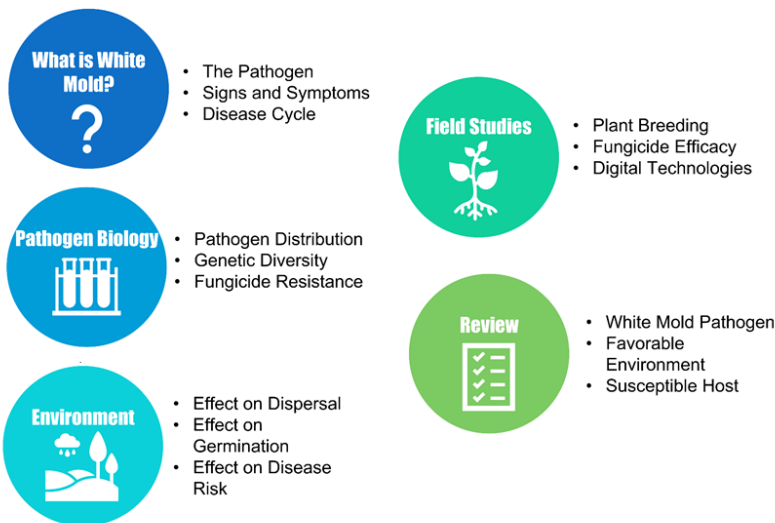


Figure 4: An example of what a participant will see while navigating the white mold epidemiology lesson prototype and learning modules and submodules.

APS Poster

Poster presentation: McFeaters, T.S, Luong, K. P, Mizubuti, E. G, and Esker, P.D. 2021. Field scale genotypic diversity of *Sclerotinia sclerotiorum* in soybeans in Pennsylvania and Minas Gerais, Brazil. American Phytopathological Society, August 5, 2021.

Luong, K., McFeaters, T.S., and Esker, P.D. (2021, August). Interactive Science Communication of Plant Disease Epidemiology for the Classroom and Extension [abstract]. Paper presented at the 2021 Plant Health APS Annual Meeting, online. Retrieved from: <https://events.rdmobile.com/Lists/Details/1179386>