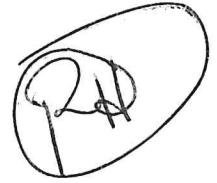


National Sclerotinia Initiative 2024 Annual Meeting

Fargo, ND
January 17-18, 2024
Author: Scott Bales



The following is a summarized report from the 2024 annual meeting of the National Sclerotinia Initiative (NSI). The 2024 meeting location was Fargo, ND and took place over two days in January. The annual meeting serves as an opportunity for both reporting of research activities from the previous funding period, and networking between multi-disciplinary researchers. Traditionally this meeting also serves as the first meeting of the stakeholder steering committee. Stakeholder represented include canola, dry bean, pea, lentil & chickpea, soybean, and sunflower.

In 2023 1.54 million dollars were allocated to Sclerotinia research through NSI based on the annual budget. While the NSI does fund research on Sclerotinia in many crops, significant funds are annually contributed to projects focusing on common bean (>\$290,000 in FY22-23). The annual report of the NSI includes a progress report on these projects specifically, included below. Projects directly affecting common bean are highlighted in green in the 2023 list of funded projects. While intensive research still needs to be done on Sclerotinia in common bean, the NSI has provided significant funding and direction to the research efforts.

National Sclerotinia Initiative Annual Report – 2024

Objective:

Coordinate the development of a Sclerotinia initiative for expanded research to control this devastating disease which effects canola, sunflower, soybean, edible beans, lentils, peas and other crops. Research should be coordinated with interested ARS, state, and industry cooperators and administered through specific cooperative agreements. Planning workshops and annual meetings involving interested parties will be organized through the funding period.

Progress Report (*Dry Bean Research*):

Of the twenty three total projects funded seven focus specifically on common beans, abstracts from these seven projects written by the researchers are found below in the supplemental materials (pages 2- 7). Also included is the full meeting agenda and 2023 list of funded projects.

Leveraging Aerial Imaging and Machine Learning to Predict White Mold in Common Bean

John Hawkins, Michigan State University

Funded Plan of Work: Evaluation and optimization of genomic selection for durable white mold resistance in dry bean

ABSTRACT:

White mold disease caused by *Sclerotinia sclerotiorum* (Lib.) de Bary is the major yield limiting disease of common bean (*Phaseolus vulgaris* L.). In the US bean industry, it causes millions of dollars in yield loss annually. White mold is a monocyclic and necrotrophic disease which causes water-soaked lesions, wilting, collapse, and bleaching of bean plants. For research purposes, white mold incidence and severity are typically scored visually by examining plants for signs and symptoms of the disease and rating severity on a 1-9 or percent scale. However, this approach is both labor intensive and subjective, with no way to correct for observer bias. Imaging-based approaches using statistical models have the potential to reduce labor and improve accuracy and repeatability in white mold scoring. Advances in the technology of uncrewed aerial systems (UAS) allow high resolution imaging of agricultural fields in multiple spectra. In this research UAS imaging of a white mold nursery in both the visible and infrared spectra at several time points from flowering to immediately before harvest was used to create a dataset of vegetation indices. This data, together with visual white mold scores, was used to train machine learning models using a random forest approach. Models were created using the caret package in the R programming language, and the initial models were fitted on a single year of data. 10-fold cross validation of the best model gave an RMSE of 1.095015 and explained 18.6% of the variance. While these models do not yet have strong predictive power, they do show promise. Further training with multiple years of data is expected to improve model performance.

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Population genetic characterization of *Sclerotinia sclerotiorum* from USA soybean and dry bean using AmpSeq, and development of an informational survey to assess NSI impacts

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Research Project: Genetic variability associated with the traits of fungicide resistance and pathogenicity in *Sclerotinia sclerotiorum*.

ABSTRACT: An AmpSeq primer array of 167 sets were developed to amplify and sequence variants in SSRs, SNPs, putative pathogenicity-related loci, and genes conferring fungicide resistance (β -tubulin, Sdh complex, and cytochrome b gene). AmpSeq was applied to 178 *S. sclerotiorum* genomic DNA hierarchically sampled from diverse sources. Our AmpSeq array included 174 polymorphic SNPs (74 SNPs in 18 genes and 100 intergenic SNPs). Fasta sequences of these genes (“poly_genes_SNP.fasta”) were retrieved from NCBI and were further inspected using SECRETOOL, Batch CD-Search tool, and available scientific literature to identify putative virulence/pathogenicity factors. In our preliminary AmpSeq analysis, 61 of 178 *S. sclerotiorum* (34%) had good quality sequence data in the *SdhB* gene, and 17 of those had the A11V mutation. These samples with mutations were collected from Mexico (N=12) and USA (N=5). None of the *S. sclerotiorum* samples with good quality *SdhC* sequence data contained the I22V or I31V point mutations. No sequence data for other resistance loci were present, possibly due to low sequence depth, quality control filters, or poor primer amplification. Ongoing work is focused on identifying polymorphic and reliable variants loci that can be used for downstream population genetic analysis. We also recently developed a new objective to design and deploy a nationwide survey to evaluate the impact of recent advances in the management of disease caused by *S. sclerotiorum* on NSI-focused commodity groups, including canola, dry bean pea, lentil, chickpea, soybean, and sunflower. Our mixed-methods survey questionnaire will include questions related to NSI-improved management practices, such as planting resistant cultivars, use of biological control methods, and integrated disease management practices. A focus group is currently being sought to evaluate the preliminary effectiveness of this survey, following which the full survey will be deployed.

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Improved white mold resistance in dry and snap beans through multi-site screening throughout major production areas

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Funded Plan of Work: Improved white mold resistance in dry and snap beans through multi-site screening throughout major production areas

ABSTRACT:

The research goal of our collaborative study is to identify improved sources of resistance to white mold in adapted dry bean breeding lines using multiple disease screening sites located in major bean-production areas of the United States. Two approaches were taken to evaluate entries submitted by collaborators: a greenhouse-based straw test and field trials carried out within white mold nurseries in five locations throughout the northern U.S. and Quebec, Canada. In 2023, trials were conducted in MI, ND, NE, OR, WA and QC with a total of 18 entries that included Black, Navy, Pinto, Pink, and Light Red Kidney seed classes, along with check cultivars G122, Bunsu, and Beryl. Preliminary analysis of greenhouse and field data shows overall moderate levels of resistance. Greenhouse data indicated multiple lines performed equal to the resistant check (G122) at some locations. Further greenhouse and field data analysis are currently underway, which will provide greater insight into the genetic progress towards developing future cultivars with improved levels of both physiological resistance and architectural avoidance to white mold.

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Using Genomic Prediction to Identify Dry Bean (*Phaseolus vulgaris* L.) Genotypes with Resistance to White Mold (*Sclerotinia sclerotiorum* Lib. De Bary)

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North Dakota State University, Fargo, ND, & Phil N Miklas, USDA-ARS, Prosser, WA.

Funded Plan of Work: White mold resistance QTL: identification, interactions, and fine mapping in common bean.

ABSTRACT:

Dry bean growers in the US northern Great Plains rank white mold (*Sclerotinia sclerotiorum* Lib. de Bary) as the worst disease. Reliable field screening for white mold resistance is challenging, because the incidence and severity of the pathogen is influenced by several factors. A multi-parent advanced generation inter-crosses (MAGIC) population (n = 1040) was screened for white mold reaction in the greenhouse and genotyped to carry out a genome-wide association study (GWAS). In addition, the predictive ability of six genomic prediction (models for white mold resistance and the agronomic performance of resistant genotypes were evaluated under field condition. GWAS identified 15 genomic regions associated with resistance spanning across seven chromosomes. A predictive ability of 0.34 was detected for all the models. Genomic selection applied in the validation populations were able to detect from 64 to 71% of the susceptible lines. MAGIC lines WMM-556 and WMM-750 showed superior seed yield compared to the mean of the rest of resistant lines and MAGIC parental lines.

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A QTL Approach Toward Understanding and Improving Genetic Resistance to White Mold in Common Bean

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Research Project: White mold resistance QTL: identification, interactions, and fine mapping in common bean.

ABSTRACT: During 2023, multiple genetic and breeding populations were generated, phenotyped and genotyped in support of detecting new and existing QTL that control white mold (WM) resistance in common bean. Selected lines from these populations with WM resistance and favorable agronomic traits were advanced toward possible release using marker-assisted selection (MAS). A new snap bean MAGIC population, generated using six snap beans and two dry bean parents with WM resistance, was advanced to the F5 generation in 2023. There were 996 families phenotyped but only 906 were harvested due to poor emergence (dwarf lethal syndrome) or very late maturity resulting from photoperiod sensitivity. White-flowered (61%), bush types (68%), with snap pod traits (88%) predominated. Harvested seed will be used for replicated white mold trials and genotyping in 2024. A nested association mapping (NAM) of four recombinant inbred line (RIL) snap/dry bean populations was completed (MS thesis). Fifteen lines from these populations were advanced because they showed a combination of white mold resistance, favorable agronomic traits, and select QTL haplotypes. A genome-wide association study (GWAS) in a pinto bean WM-MAGIC population identified 15 genomic regions, spanning seven chromosomes associated with white mold resistance. Genomic selection models applied in the pinto WM-MAGIC population were able to detect from 64 to 71% of the susceptible lines (MS thesis). Two pinto MAGIC lines with superior resistance and seed yield were included in the 2023 National White Mold Nursery and used in crosses. Three different mapping approaches: classical, bulked segregant analysis, and Khufu *de novo* QTL-seq were compared and combined to fine map the major WM2.2 QTL in two dry bean RIL populations (Oladza et al., 2023). This research found three independent QTL regions WM2.2a, WM2.2b and WM2.2c underpinning the ‘meta’ WM2.2 QTL. Integrated classical and QTL-seq mapping was used in other dry bean RIL populations to fine map the WM5.4 and WM7.5 QTL (Roy et al., 2023). A similar integrated mapping approach was used to fine map eight QTL in two pinto bean RIL populations (publication pending). A red bean RIL population, tested for WM reaction in the greenhouse in 2023, will be tested in a newly established WM field nursery in Othello, WA in 2024. Selected lines from these RIL populations are being used to improve WM resistance in the breeding programs. Overall continued progress is being made toward identifying, developing, and generating QTL linked markers for use in breeding snap and dry beans with improved resistance to white mold.

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Evaluation and optimization of genomic selection for durable white mold resistance in dry bean

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Funded Plan of Work: Evaluation and optimization of genomic selection for durable white mold resistance in dry bean

ABSTRACT:

Dry bean production in the U.S. suffers annually from yield loss due to white mold infection. Dry bean cultivars lack high levels of genetic resistance, and progress to breed new cultivars with improved levels of resistance has been slow due to the quantitative inheritance of this trait, difficulty pyramiding resistance, and field screening dependence on the presence of the pathogen under suitable environmental conditions. Genomic prediction provides an alternative method to pyramid resistance genes by utilizing genome-wide marker coverage to predict genotypic values for quantitative traits. This study evaluated the efficiency of different genomic prediction models given the complex population structure of multiple market classes present in dry bean breeding programs. A panel of 303 Middle-American breeding lines were genotyped with 3,026 markers and evaluated for white mold in the field over two seasons. Prediction accuracy across models and subsets was moderate (0.3 - 0.36) given the population size. Furthermore, when fixed effect QTL were identified and implemented through GP + GWAS, 1-3 QTL increased prediction accuracy only modestly (0.36 - 0.4). These results indicate that genomic prediction is a promising screening tool in dry bean breeding for white mold resistance.

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