IMPROVING SOYBEAN WHITE MOLD CONTROL: INTEGRATED MANAGEMENT AND BREEDING FOR RESISTANCE

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Introduction

White mold of soybean is caused by the fungal pathogen, *Sclerotinia sclerotiorum*, and is a devastating disease in the Great Lakes growing region of the United States. The integrated management techniques used to control this disease are multi-level including the manipulation of row spacing, adjusting planting population, and using fungicides along with genetically resistant cultivars. Previously, it had been shown that widening rows to 30” resulted in lower disease levels when compared to narrower row spacings of 10” and 15” (Grau and Radke 1984), and increasing planting populations to over 175,000 seeds/acre resulted in higher disease compared to lower planting populations (Lee et al. 2005). Fungicide programs have also been shown to significantly reduce white mold of soybean (Willbur et al. 2019). With the work presented here, we hoped to identify the most influential management practices for decreasing the incidence of disease while also maintaining high yields.

In addition to the agronomic controls, breeding for genetic resistance is also being performed in hopes of creating new elite cultivars with physiological resistance to white mold while still retaining high agronomic traits such as lateral branching and high yields. Currently there are 3 groups of breeding lines in the “pipeline” at the Univ. of Wisconsin-Madison, with the most recent having initial crosses occurring in summer of 2018. So far out of this whole endeavor, one line high in white mold resistance has gone public, “Dane,” and is commercially available. Any lines developed from this work hopefully can also be used in future breeding plans to further improve commercial germplasm.

There is a significant need to test all combinations of control strategies together to measure the full effect on white mold control. Thus, the objective of our current work are as follows:

Objectives

1. Improve management of white mold by determining the greatest methods for reducing disease pressure
2. Develop soybean lines with high white mold resistance while also retaining favorable agronomic traits

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Materials and Methods

The integrated management trial occurred over the years 2017, 2018, and 2019 at 10 different locations across the upper Midwest. Plots were planted with a white mold moderately susceptible cultivar into either 15- or 30-inch rows and were planted at one of four planting populations; 110,000, 140,000, 170,000, or 200,000 plants/acre. Each plot was then designated one of three fungicide treatments, either non-treated control, applications at the R1 and R3 growth stages, or applications following the disease risk prediction model developed by Willbur et al. (2018a, 2018b). The fungicide Aproach→ was used for all fungicide treatments. Beginning around the R5 growth stage, plots were scouted for disease. A total of 10 - 1 m pushes were made within the inner rows and disease incidence was taken by counting the total number of disease plants in all pushes. Disease severity was scored on a scale of 0-3 as described by Grau et al. (1982).

Currently there are 3 groups of breeding lines in the pipeline. As aforementioned, a newly released cultivar, Dane, has been released out of the first group of breeding lines. This work was previously described by McCaghey and Willbur et al. (2017). The second group of lines were crossed in 2016 with the help of Dr. Asheesh Singh at Iowa State and included crosses between 51-23 and 52-82B and between SSR51-70 and 51-23. With the use of a Chilean winter nursery, these lines have been able to progress through generations quickly. In 2019, the F:6 generation was planted at the Arlington Research Station and final agronomic selections (lodging, branching, plant height) were made. The third group of breeding lines were initially developed in the summer of 2018 by crossing four lines exhibiting favorable agronomics and disease resistance (Savoy, 42-136, SSR51-70, and 91-38). These lines were progressed through greenhouse increases in the spring of 2019 and field-planted in summer of 2019. Initial selections were made within each family by selecting for agronomics.

Results and Discussion

A total of 19 site years have been accumulated in the integrated management study. For analysis, locations were separated based on disease level in the non-treated check. Two levels were established, low (DIX<20) and high (DIX<20). Separate analyses were then performed for the low and high disease level sets. In the high disease locations, fungicide application ($P<0.01$) and the interaction of row spacing and planting population ($P<0.05$) influenced yield (shown in Figures 1 and 2). The main effects of row spacing, planting population, and fungicide application significantly ($P<0.05$) influenced DIX (shown in Figures 3, 4, and 5). In the low disease locations, fungicide application ($P<0.0001$) and the interaction of row spacing and planting population ($P<0.001$) influenced yield. Fungicide application ($P<0.1$) and the interaction of row spacing and planting population ($P<0.1$) also influenced DIX in low disease environments.

Of the second group of breeding lines, greenhouse disease screenings will begin in the spring of 2020 and preliminary yield trials will follow in 2020 field season. After initial selections, the third group of breeding lines are currently being grown out in Chile over the 2019-2020 winter months and will be planted back in Wisconsin during the summer of 2020 for more selections to occur.

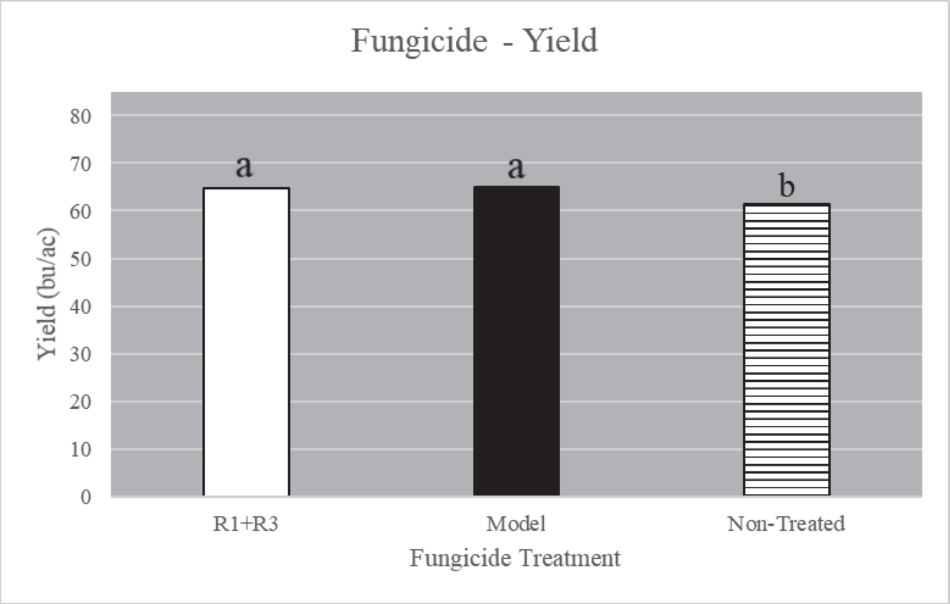

Figure 1. Fungicide application effect on yield in high disease environments across 2017, 2018, and 2019. Locations were pooled and the mean yields were examined using Fischer's least significant difference. Bars assigned the same letter are not significantly different at the α = 0.05 significance level.

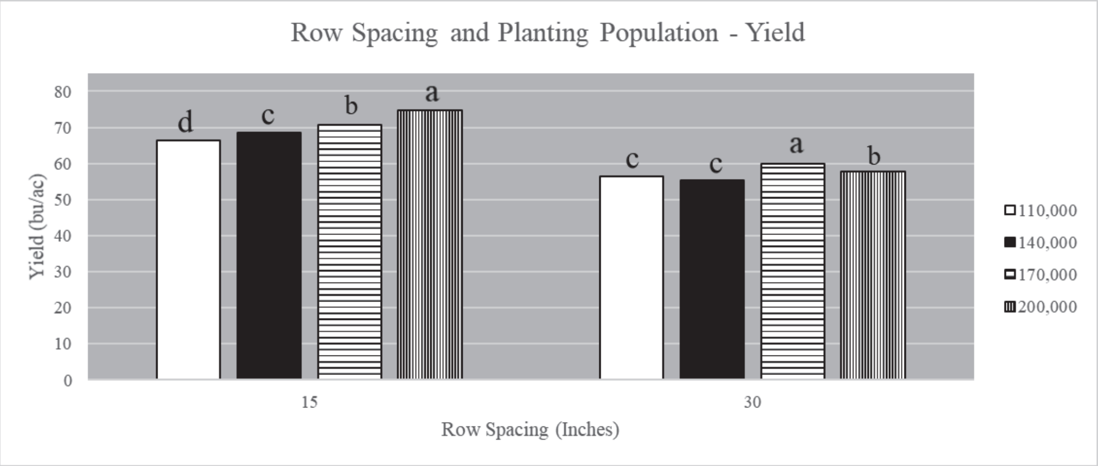

Figure 2. Row spacing and planting population effect on yield in high disease environments across 2017, 2018, and 2019. Locations were pooled and the mean yields were examined using Fischer's least significant difference. Bars assigned the same letter are not significantly different at the α = 0.05 significance level.

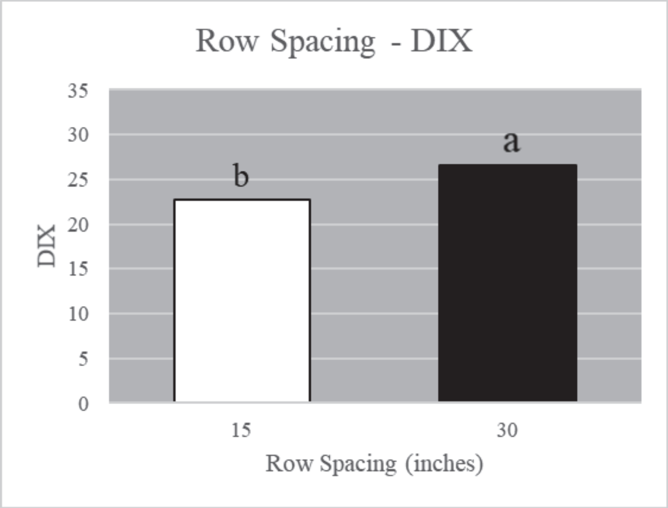

Figure 3. Row spacing effect on DIX in high disease environments across 2017, 2018, and 2019. Locations were pooled and the mean DIX were examined using Fischer's least significant difference. Bars assigned the same letter are not significantly different at the α = 0.05 significance level.

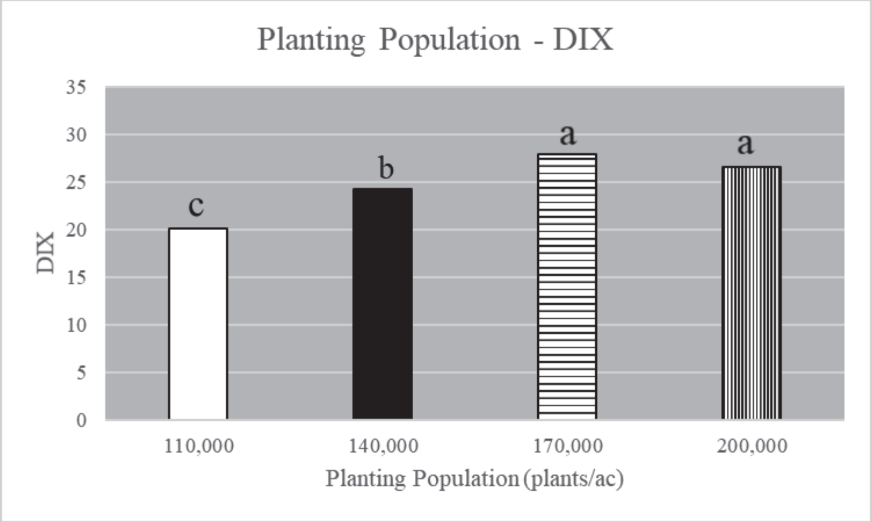

Figure 4. Planting population effect on DIX in high disease environments across 2017, 2018, and 2019. Locations were pooled and the mean DIX were examined using Fischer's least significant difference. Bars assigned the same letter are not significantly different at the α = 0.05 significance level.

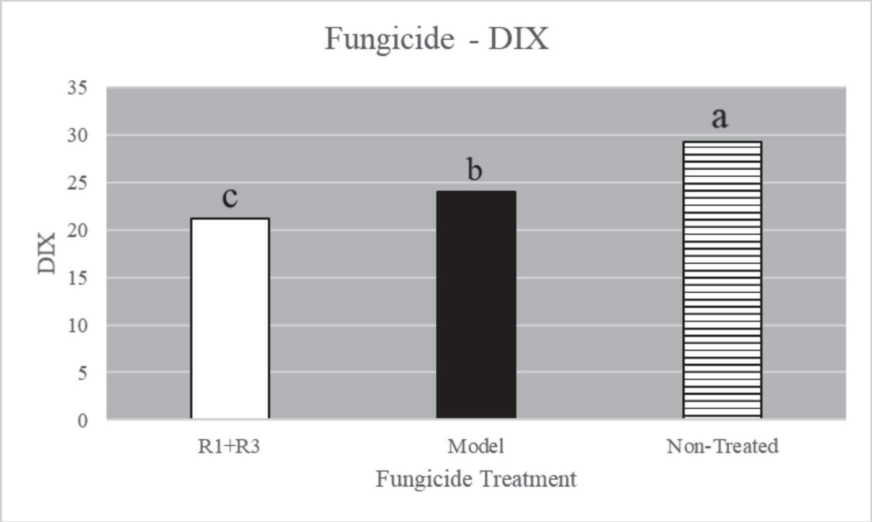

Figure 5. Fungicide application effect on DIX in high disease environments across 2017, 2018, and 2019. Locations were pooled and the mean DIX were examined using Fischer's least significant difference. Bars assigned the same letter are not significantly different at the α = 0/05 significance level.

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