Inheritance of Partial Resistance to Sclerotinia sclerotiorum in Soybean Cultivars Asgrow A2506 and Novartis S19-90

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Abstract

Partial resistance to Sclerotinia stem rot (SSR), [Sclerotinia sclerotiorum (Lib.) de Bary] has been identified in soybean [Glycine max (L.) Merr.] accessions and cultivars in the United States. There have been no reports of the inheritance of partial resistance to S. sclerotiorum in soybean. The objectives of this study were to: (i) estimate the number of genes contributing to resistance to S. sclerotiorum in the soybean cultivars Asgrow A2506 and Novartis S19-90 and (ii) estimate broad and narrow sense heritabilities. Data from greenhouse evaluations of three crosses, Asgrow WR2347 x Asgrow A2506, Novartis S19-90 x Asgrow A2506, and Novartis S19-90 x Asgrow WR2347, were used to estimate goodness of fit for theoretical inheritance models in F2 and F3 generations and to estimate heritabilities. We found significant results indicating partial resistance to S. sclerotiorum is caused by multiple genes and some may be recessive. Estimates of heritabilities indicated more dominance occurred when Novartis S19-90 was used as a parental line compared with Asgrow A2506. All heritability estimates based on F2:3 family means (>0.86) were higher than the heritability estimates based on F2 plant basis. This presages selection for partial resistance to S.

sclerotiorum in soybean based on F2:3 family means evaluation would be more efficient than selecting on a single F2 plant basis. The high heritability estimates in our greenhouse evaluations are valuable to soybean breeders selecting for partial resistance to S. sclerotiorum.

Introduction

Partial resistance to Sclerotinia stem rot (SSR), caused by Sclerotinia sclerotiorum (Lib.) de Bary, has been identified in soybean [Glycine max (L.) Merr.] cultivars and accessions in the United States. Although researchers have identified partial resistance to SSR in field, greenhouse (Nelson et al., 1991) and growthroom evaluations (Boland and Hall, 1986), there have been no reports of the number of alleles contributing to the resistance to S. sclerotiorum in soybean. Kim and Diers (in press) reported a broad sense heritability of 0.59 on a progeny mean basis over two years of field tests in Michigan.

In previous field studies, the soybean cultivars Asgrow A2506 (A2506) and Novartis S19-90 (S19-90), (Kim et al., 1999) were observed resistant, and Asgrow WR2347 (WR2347) was observed susceptible to S. sclerotiorum. The objectives of this study were to: (i) estimate the number of alleles contributing to resistance to S. sclerotiorum in the soybean cultivars Asgrow A2506 and Novartis S19-90 and (ii) estimate broad (H2) and narrow (h2) sense heritabilities.

Materials and Methods

The parents, A2506, S19-90, and WR2347, were intermated to produce the crosses WR2347 x A2506, S19-90 x A2506, and S19-90 x WR2347. All F1 and F2 seed of the crosses were obtained from the Asgrow Seed Company. Segregation among the F2 plants, F3 plants, and F2 derived F3 (F2:3) families for the reaction to S. sclerotiorum was used for analysis in this study. The evaluations of F2 and F3 plants of these crosses were conducted in the greenhouse during the winter of 1997. Isolate 1 of S. sclerotiorum from Illinois was used in a modified limited term inoculation method (Hoffman, 1998).

Ratings for the F2 plants were based on the number of living plants versus the number of dead plants. Ratings for the F3 plants were based on four

classifications: 1 = healthy living plant; 2 = plant's unifoliates wilted or apical meristem curled over in a cane-like fashion; 3 = plant's unifoliates wilted and apical meristem curled over in a cane-like fashion; and 4 = dead plant shriveled and/or wilted. Ratings were taken at multiple times for each evaluation, and the rating times with the greatest observed difference in disease severity between the parental lines were selected for use in the inheritance evaluations.

The segregation among the F2 plants, F3 plants, and F2:3 family means for each cross was tested against the best theoretical inheritance ratios using chi-square analysis for goodness of fit. The classifications for the F3 plants and F2:3 family means were used to compare with the 95% confidence intervals (CI) of the parental lines for each cross. Any F3 plants or F2:3 family means, which were within or greater than the 95% CI of the more resistant parent, were considered resistant. Any F3 plants or F2:3 family means, which were within or less than the 95% CI of the less resistant or susceptible parent, were considered susceptible. All other F3 plants or F2:3 family means were classified as having intermediate resistance to SSR.

An analysis of variance was performed on the F3 plant data using a design adapted from the analysis from Hallauer and Miranda, Fo (1981) to estimate genetic variance components and H2 and h2.

Results and Discussion

Sclerotinia stem rot ratings of the F2 plants in all crosses segregated in a 3:1 (susceptible : resistant) genetic ratio suggesting a single recessive allele controls resistance to S. sclerotiorum in all crosses (Table 1).

The F2:3 family means of all crosses fit an expected 1:2:1 genetic ratio (Table 2) and supports F2 progeny analysis that suggested a single allele is involved with resistance to S. sclerotiorum. However, multiple F2:3 family means were above the CI of the more resistant parent and multiple families were below the CI of the more susceptible parent (Fig. 1). The families above and below the CI's may be caused by transgressive segregation in the population or by errors in the technique and/or ratings. If transgressive segregation is present, it suggests there are alleles at more than one locus contributing to resistance to S. sclerotiorum. In addition, the F3 plants did not segregate in the expected 5:3 (susceptible : resistant) genetic ratio (Table 3),

and the F3 plants within each intermediate F2:3 family did not segregated as expected in each cross. This also suggests there are alleles at more than one locus contributing to resistance to S. sclerotiorum in A2506 and S19-90.

The estimates of variance components and heritabilities from all crosses suggest more dominance is occurring in crosses S19-90 x A2506 and S19-90 x WR2347 when using S19-90 as a parental line compared to A2506 as a parental line (Table 4). The H2's calculated for the F2:3 family mean analyses were larger than the H2's calculated in the F2 plant analysis in the greenhouse. This suggests selection for resistance to S. sclerotiorum in soybean based on F2:3 family means basis is better than selecting on a single F2 plant basis in greenhouse evaluations. Large variability in the estimating H2 and h2 is likely the result of the difficulty of obtaining good estimates of additive and dominance variances for S. sclerotiorum resistance with our experimental design. Based on the heritability estimates for these crosses, the greenhouse evaluations would assist the soybean breeders in quick and reliable selection for resistance to SSR in soybean.

We found significant results indicating partial resistance to S. sclerotiorum is caused by multiple genes and some may be recessive, however these data are only based on greenhouse evaluations and have not been evaluated in field nurseries. Currently, it is unclear how these greenhouse results correlate with field evaluations for resistance to S. sclerotiorum.

References

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