

Usefulness of 10 Genomic Regions in Soybean Associated With Sudden Death Syndrome Resistance

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Introduction

- Sudden death syndrome (SDS) is an important disease of soybeans caused by the soilborne fungus *Fusarium virguliforme*. The fungus infects roots causing root rot, and produces a toxin that causes leaf scorch, greatly reducing seed yield.
- The best management practice for SDS is the use of resistant varieties. Disease resistance is known to be quantitative.
- QTL have been identified for both root and foliar resistance (Kassem et al. 2012; Kazi et al. 2008; Njiti et al. 1998; Triwitayakorn et al. 2005). In order to stack QTL, crosses between resistant parents are becoming more commonly used in breeding programs.
- Currently, 14 QTL have been confirmed associated with resistance or tolerance to SDS.
- Our goal is to evaluate 10 of these 14 QTL for foliar leaf scorch severity and root rot severity to determine if it may be possible for plant breeders to focus on stacking a subset of the identified QTL to improve resistance to SDS in soybean.

Objective

The objective of this study was to determine the usefulness of the known QTL previously associated with SDS resistance in the field that were detected in the three RIL populations of Essex x Forrest (EF), Flyer x Hartwig (FH), and Pyramid x Douglas (PD).

Methods

Plant Material

- Six Populations:
 - FH-13 x EF-23
 - FH-13 x PD-98
 - FH-33 x EF-23
 - FH-33 x PD-98
 - FH-35 x PD-98
 - PD-98 x EF-23

Greenhouse Screening

- Five mycelial plugs of Iowa isolates Clinton1b and Scott were added to flasks containing 250 g of sterile white sorghum.
- The infested sorghum was incubated at room temperature for two weeks, daily shaking the containers.
- After the two weeks, the infested sorghum was dried overnight in a fume hood
- Infested sorghum was homogenously mixed with a sterile 1:2 (v/v) soil to sand mixture at a concentration of 1:20 (v/v).
- Five soybean seeds were planted in 240 ml Styrofoam cups containing the infested soil mix.
- The cups were maintained in a growth chamber at 23°C with a 14h photoperiod for 5 weeks
- Experiment was repeated three times (runs)

SDS symptom assessments

- Foliar leaf scorch severity and foliar disease incidence were scored at 21, 24, 27, 30, 33, 36 days after planting (DAP). Foliar severity was visually rated as the percentage of total leaf area showing typical SDS symptoms.



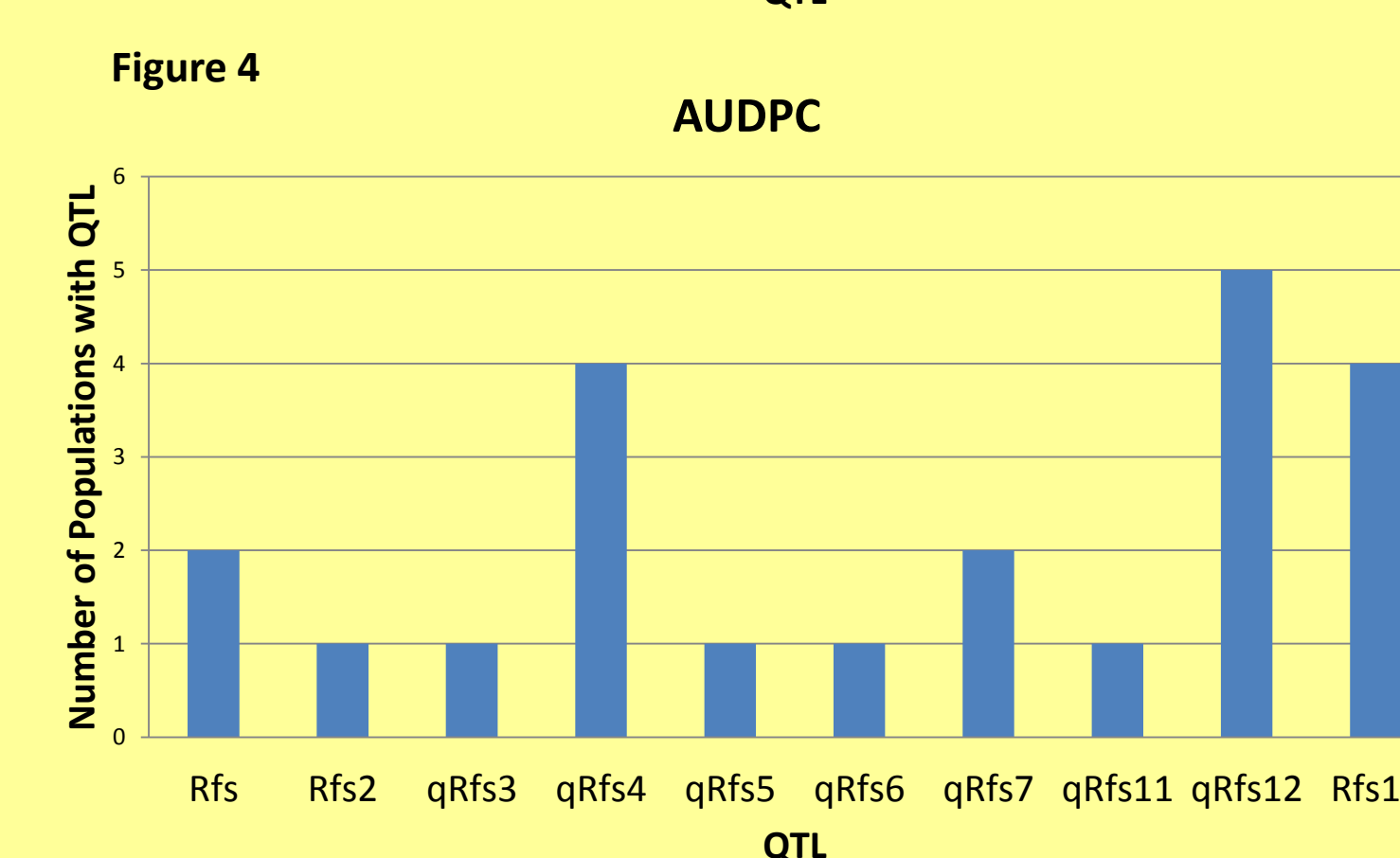
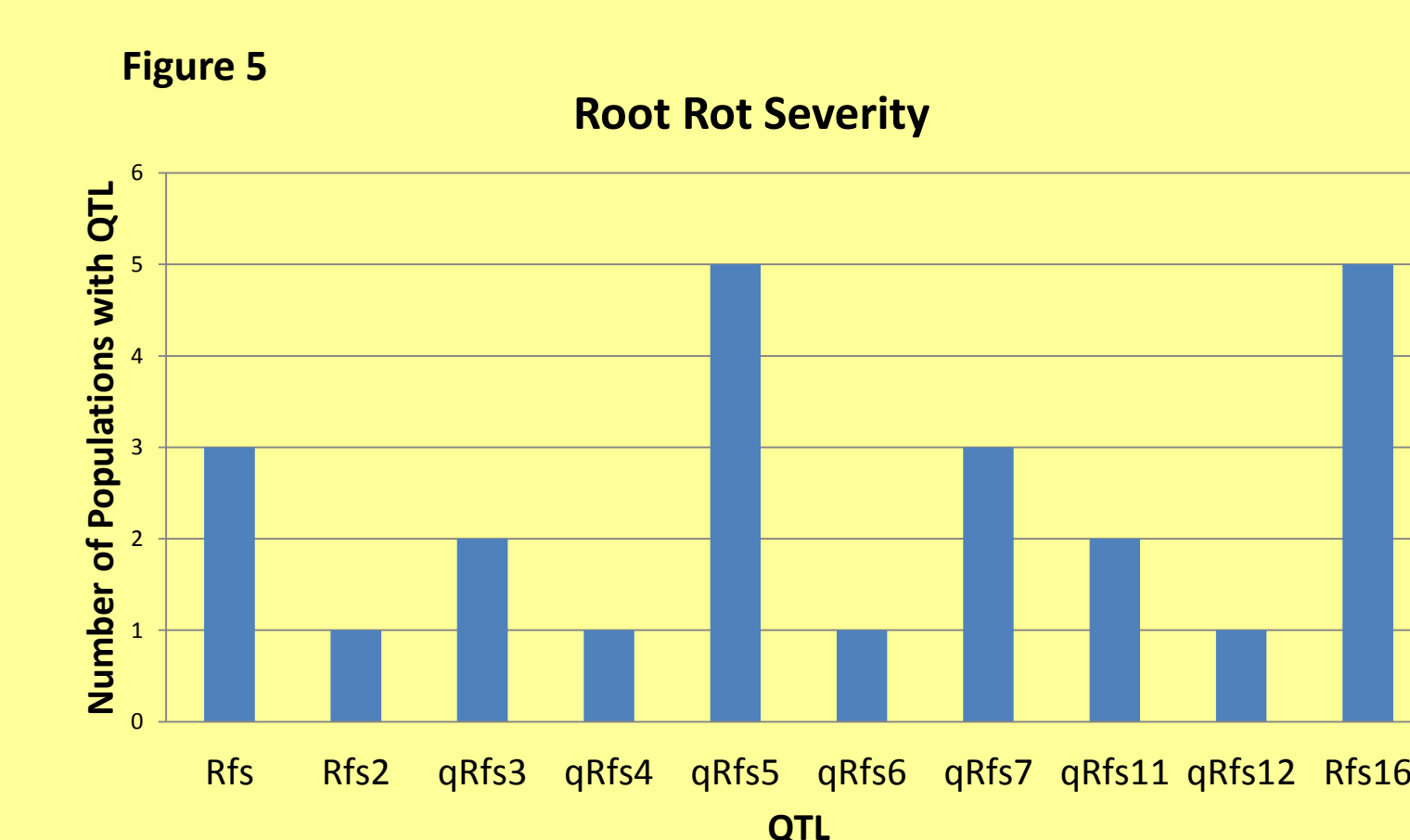
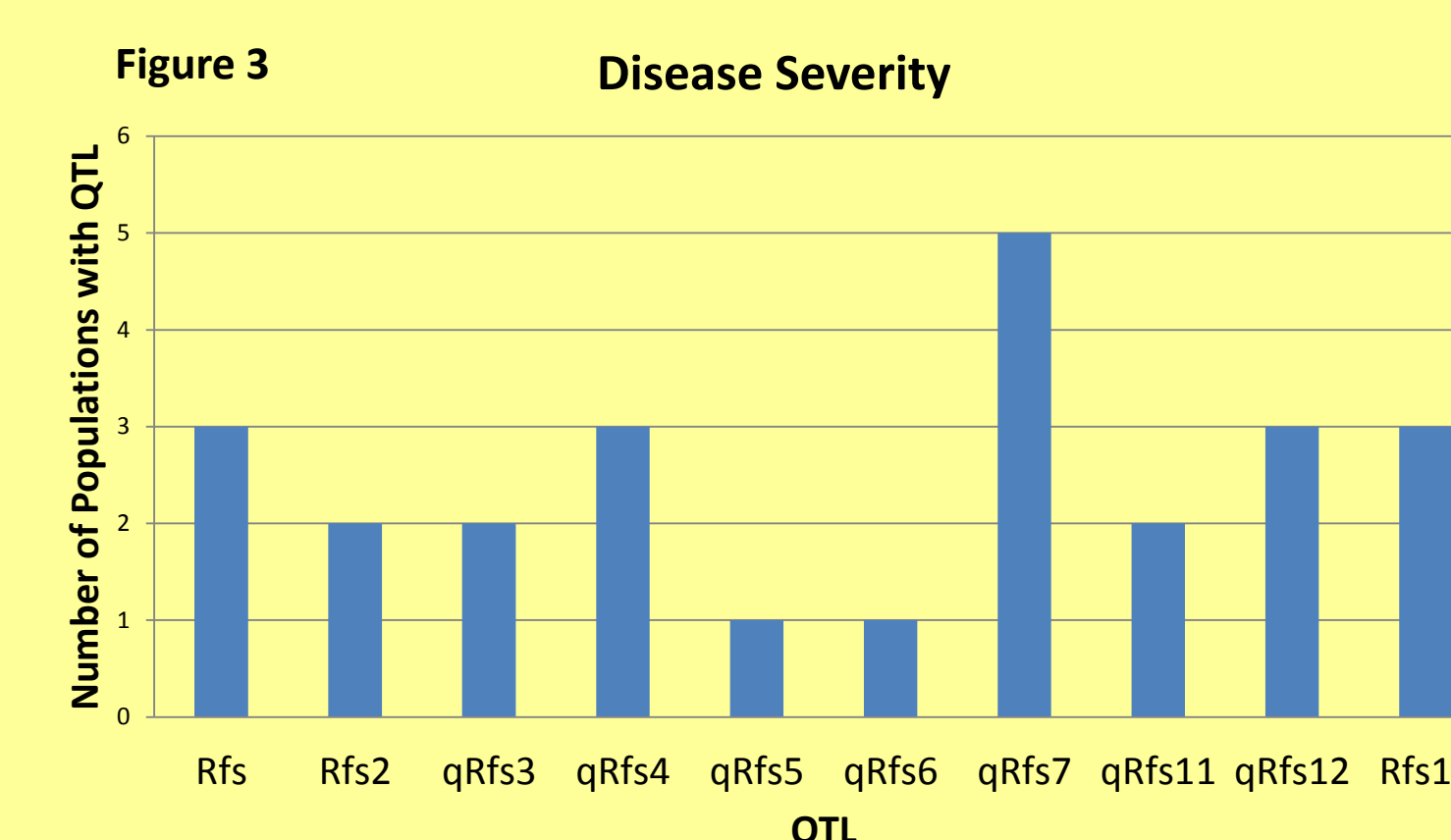
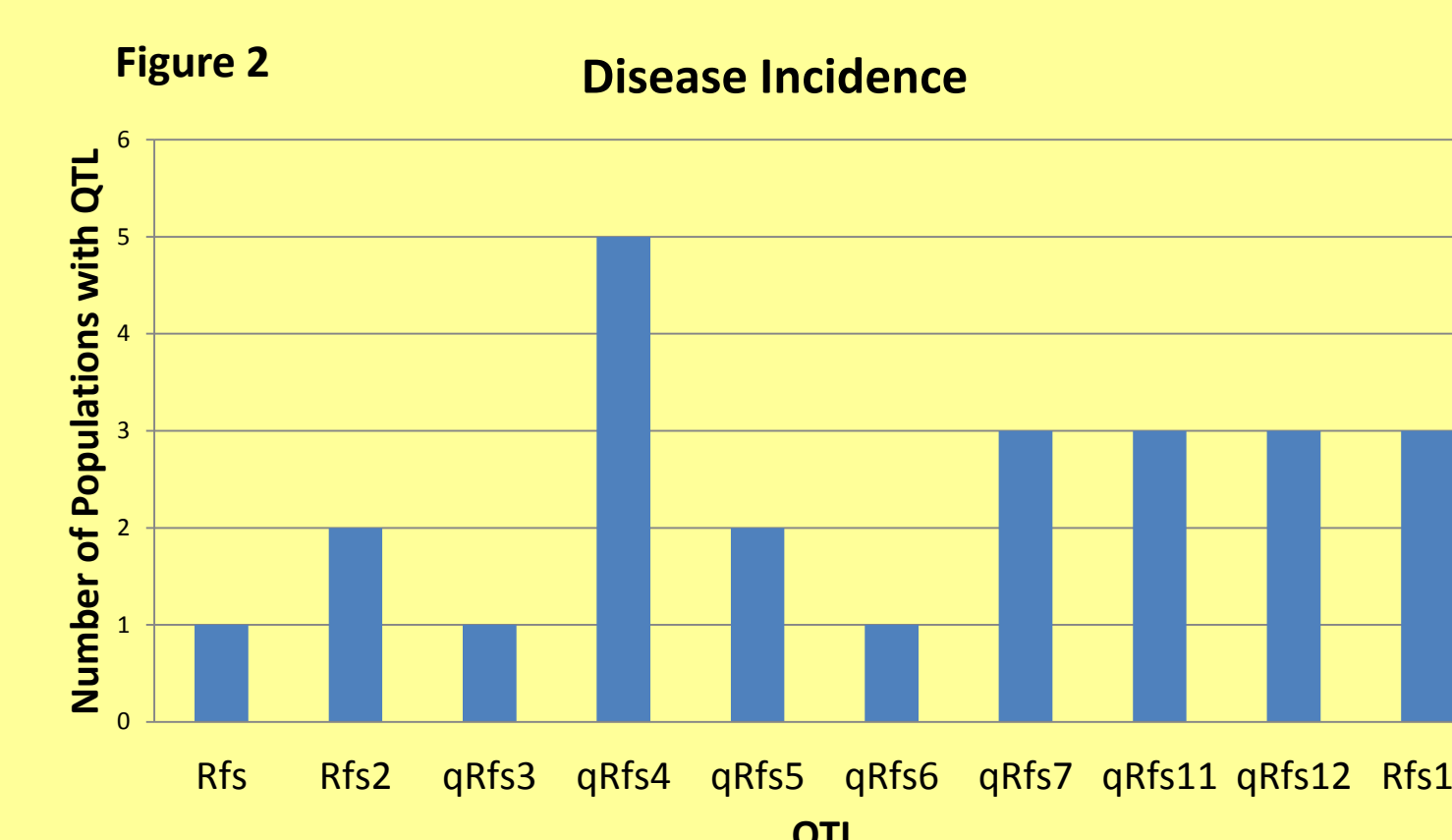
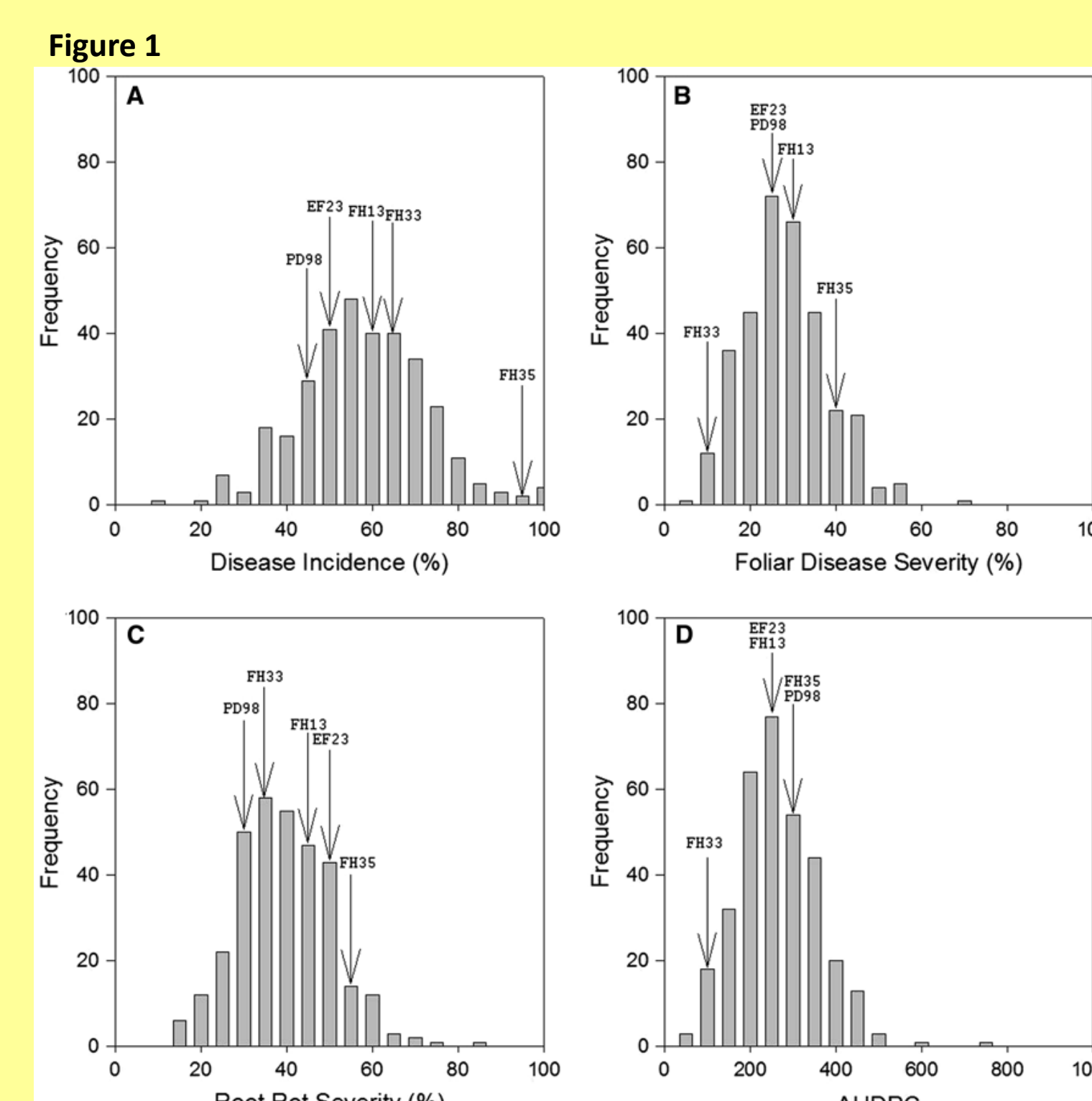
- Foliar disease incidence (DI) was calculated as number of plants per cup showing typical SDS foliar symptoms, divided by the total number of plants in each cup.
- The area under the disease progress curve (AUDPC) was calculated following the midpoint rule.
- Root rot severity was visually evaluated as the percentage of total root area showing brown or black discoloration at 36 DAP.

Analysis

- 10 SSR markers were used to screen the lines from each population
- Allele frequencies of the 10 QTL for which parents were polymorphic, were calculated within two defined groups or categories, the 10 % most resistant, 10 % least resistant for each population and the five parents. Allele frequencies were compared between groups to identify differences in frequencies for disease assessment criteria
- A Pearson correlation was also performed on DI, DS, AUDPC, root rot, and the 10 QTL using the PROC CORR statement.

Results

- In Figure 1 the Distribution of 321 F2:3-derived soybean lines and the five parents, averaged over three runs based on symptoms resulting from infection of *F. virguliforme* **A**) disease incidence (%), **B**) foliar leaf scorch severity (%), **C**) root rot severity (%), and **D**) area under the disease progress curve approached normal uni-modal distributions.
- Considering QTL and disease assessment over populations, significant differences ($P < 0.0001$) between the 10 % most resistant and 10 % least resistant groups were observed.
- The Pearson correlation between the QTL and disease assessment criteria using only the 10 % most and 10 % least resistant showed population specificity in their values. Half of the populations showed only one significant ($P < 0.05$) r value or none, while the other half of the populations had many significant relationships.
- One QTL, *qRfs12*, was associated ($P < 0.05$) with DS, root rot, and AUDPC in two populations, FH33 x PD98 and PD98 x FH35.
- For the DI assessment, QTL *qRfs4* was present in the 10 % most resistant group in five of the six populations (Figure 2) and QTL *Rfs* and *qRfs3* were present in four of the six populations in the 10 % least resistant group (not shown).
- Disease severity had QTL *qRfs7* identified in five of the populations in the 10 % most resistant group (Figure 3) and *qRfs11* in four populations in the 10 % least resistant category (not shown).
- AUDPC had *qRfs4* and *qRfs12* common in the 10 % most resistant group in four populations as well as *Rfs16* in five of the populations (Figure 4) and *Rfs2* in four populations and *qRfs11* in five populations in the 10 % least resistant group (not shown).
- Root rot severity had three common QTL across four populations, *qRfs5*, *qRfs12*, and *qRf4*. The 10 % most resistant group had *qRfs5* and *Rfs16* present in five of the six populations (Figure 5), while *qRfs4* was present in the 10 % least resistant group in four of the populations (not shown).



Conclusions

- The results indicated that of the 10 QTL for which the parental lines were polymorphic, five—*qRfs4*, *qRfs5*, *qRfs7*, *qRfs12*, and *Rfs16*—may have potentially greater effects on SDS resistance, particularly in the four disease assessment criteria, DI, DS, root rot severity and AUDPC.
- Two QTL, *qRfs4*, and *Rfs16*, were common to more than one disease assessment criteria and were also common across populations.
- Observations for *Rfs16* indicate the QTL is associated with both foliar and root resistance in the populations. QTL *qRfs4* was only associated with foliar resistance.

Future Work

- The lines will be screened in the field for SDS to verify the greenhouse work of this study and to identify any SDS QTL associations with yield.

References

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