# Quantitative Trait Loci for Partial Resistance to *Sclerotinia sclerotiorum* in PI391589A

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# Introduction

- The best means to manage this disease is by planting soybean cultivars with high levels of partial resistance to *Sclerotinia sclerotiorum* (Grau, 2003).
- Two previous studies identified QTLs in soybean cultivars associated with partial resistance to *S. sclerotiorum* (Arahana et al., 2001; Kim and Diers, 2000).
- 68 plant introductions were identified that have higher levels of partial resistance than what is currently available (Hoffman et al., 2002).
- Are the QTL's associated with resistance in the plant introductions all the same or different?
- And are the QTL's in the plant introductions different from those previously identified in the current soybean cultivars?
- If QTLs are different, then there is the potential to combine resistance from different sources, possibly leading to cultivars more resistant than any now available

# Objective

- Identify the quantitative trait loci associated with partial resistance to *S. sclerotiorum* in PI391589A, one of the PI's identified in the earlier study

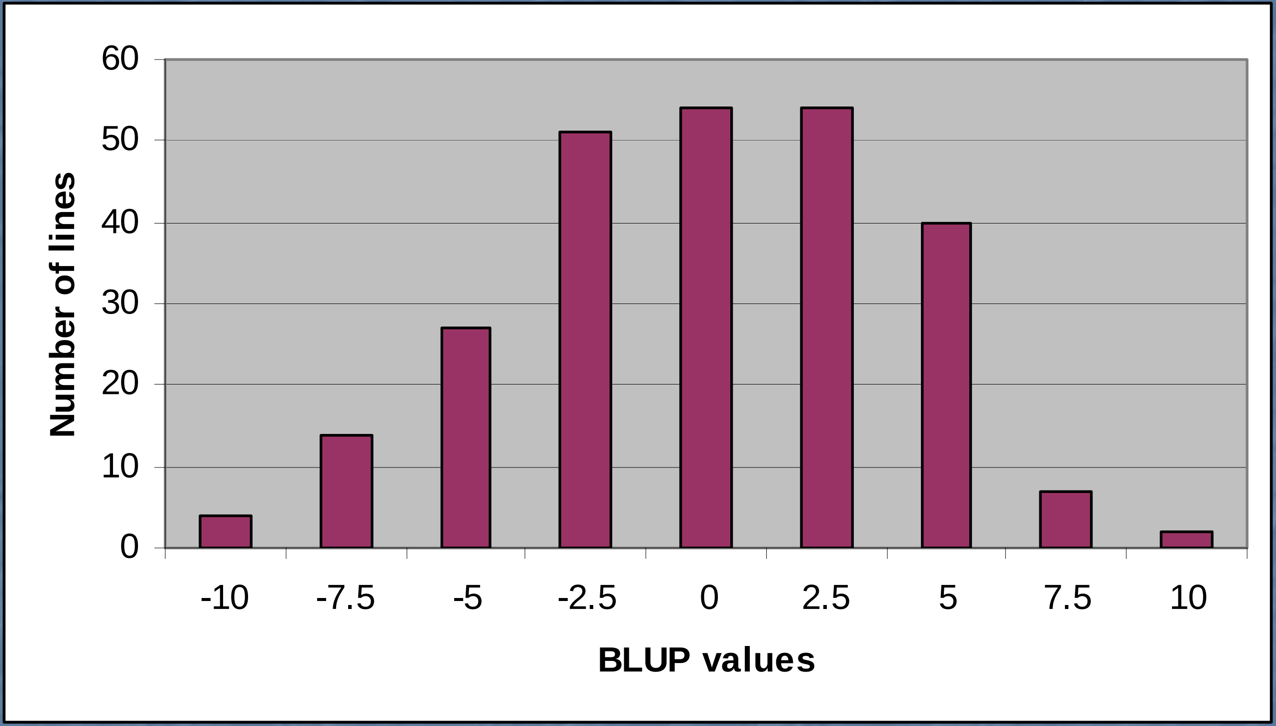
# Materials and Methods

- The Population: Kottman (susceptible) x PI391589A (resistant) consisting of 230 BC1F4:5 lines was made. This was advanced to a BC1F4:6 generation during 2003 and will be screened during 2004

# Materials and Methods

- Twelve to 15 plants were inoculated with *S. sclerotinia*. For each plant a hole was punched in the cotyledon, in the 1/3 closest to the stem and a colonized oat kernel placed in the hole. Plants were placed in a mist chamber for 48 hrs at 20oC. Plants were then removed from the mist chamber and placed in the greenhouse for 24 to 48 hours and data was collected when the control plants (Williams 82) were 70 to 90% dead.

# Preliminary Results



Frequency distribution for the best linear unbiased predictors (BLUP) values for percentage of plants that die from Sclerotinia stem rot.

-10 are the lines that are highly resistant and 10 are the lines that are highly susceptible. Data presented is from 3 replications.

**Table 1.** The number of simple sequence repeat markers (SSR) that have been screened for polymorphisms between Kottman and PI391589A, and their location in the soybean genome.

| MLG | No. Amplified | Number SSR’s polymorphic | MLG | Number Amplified | Number SSR’s polymorphic |
|---|---|---|---|---|---|
| A1 | 9 | 6 | F | 13 | 4 |
| A2 | 11 | 7 | G | 12 | 9 |
| B1 | 9 | 7 | H | 9 | 4 |
| B2 | 9 | 5 | I | 9 | 5 |
| C1 | 6 | 4 | J | 7 | 4 |
| C2 | 9 | 5 | K | 17 | 11 |
| D1a+Q | 11 | 6 | L | 11 | 8 |
| D1b+W | 9 | 6 | M | 14 | 11 |
| D2 | 17 | 9 | N | 10 | 7 |
| E | 7 | 3 | O | 12 | 9 |
| Total | 211 | 130 | | | |

# Conclusions

- Based on the preliminary phenotypic data, this population is segregating for resistance to *Sclerotinia sclerotiorum*
- There are a substantial number of SSR markers that are polymorphic for this population with good coverage of the soybean genome.
- Identifying QTLs associated with this resistance to Sclerotinia with molecular markers in this population is highly probable
- Development of enhanced germplasm to combat this disease meets the goals of the Sclerotinia Initiative.
- Using molecular techniques greatly expedites the discovery of economic solutions for Sclerotinia stem rot, ie: resistant cultivars

# Acknowledgements

- We gratefully thank T. Vuong, Univ. of Illinois for assistance with data for SSR markers, phenotypic data was collected as part of a summer internship by Ms. Jessica Russell of Vorhees College, South Carolina and S.A. Berry. Funding for this project is from USDA Sclerotinia Initiative through a collaboration with the University of Illinois.

# Literature Cited

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## *Introduction*

Sclerotinia stem rot continues to impact soybean yields in many parts of the north central region. The best means to manage this disease is by planting soybean cultivars with high levels of partial resistance to *Sclerotinia sclerotiorum* (Grau, 2003). Two previous studies identified QTLs in soybean cultivars associated with partial resistance to *S. sclerotiorum* (Arahana et al., 2001; Kim and Diers, 2000). In addition 68 plant introductions were identified that have higher levels of partial resistance than what is currently available (Hoffman et al., 2002). There are several questions that have arisen from these findings. Are the QTL's associated with resistance in the plant introductions all the same or different? And are the QTL's in the plant introductions different from those previously identified in the current soybean cultivars? If there are different QTLs involved, then there is the potential to combine resistance from different sources, possibly leading to cultivars more resistant than any now available. These questions were the focus of a larger project led by University of Illinois entitled "Characterization of soybean genotypes with partial resistance to Sclerotinia Stem Rot" funded by the USDA Sclerotinia Initative. As part of this larger project, the objective of our study is to: Identify the quantitative trait loci associated with partial resistance to *S. sclerotiorum* in PI391589A, one of the PI's identified earlier.

## *Materials and Methods*

<u>The Population</u>: Kottman (susceptible) x PI391589A (resistant) consisting of 230 BC1F4:5 lines was made. This was advanced to a BC1F4:6 generation during 2003 and will be screened during 2004.

<u>Phenotype for resistance</u>. Twelve to 15 plants were inoculated with *S. sclerotinia*. For each plant a hole was punched in the cotyledon, in the 1/3 closest to the stem and a colonized oat kernel placed in the hole. Plants were placed in a mist chamber for 48 hrs at 20°C. Plants were then removed from the mist chamber and placed in the greenhouse for 24 to 48 hours and data was collected when the control plants (Williams 82) were 70 to 90% dead. Inbred lines were treated as entries and for every 15 entries 2 controls were also inoculated. The experiment was planted as a randomized complete block design with replications in time. Both an analysis of variance on the percentage of plants that die from Sclerotinia and a mixed models analysis to obtain the best linear unbiased predictor (BLUP) for each inbred line (Stroup, 1989) were completed.

Genotype: *in progress*

## *Preliminary Results*

***Figure 1.*** Screening for resistance to Sclerotinia with colonized oat grain in a growth chamber. The percentage of dead seedling is measured when the susceptible check is 80 to 90% dead.

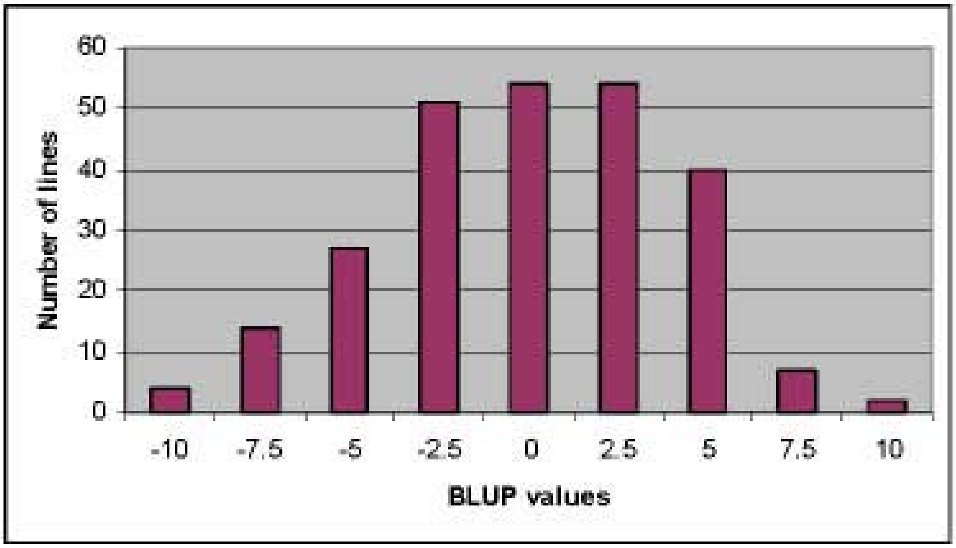

**Figure 2**. Frequency distribution for the best linear unbiased predictors (BLUP) values for percentage of plants that die from Sclerotinia stem rot. -10 are the lines that are highly resistant and 10 are the lines that are highly susceptible. Data presented is from 3 replications.

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