Characterization of major QTL associated with partial resistance to Phytophthora stem and root rot in soybean

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INTRODUCTION

- Phytophthora stem and root rot is caused by the soilborne oomycete *Phytophthora sojae* and is a serious disease of soybeans (Figure 2)[1].
- Host resistance conferred by race-specific genes (*Rps* genes) is a common management practice.
- The widespread deployment of *Rps* genes has led to a shift in physiological races of *P. sojae*[3].
- Partial resistance is quantitatively inherited and is more robust than *Rps* gene mediated resistance.
- Genetic traits associated with high levels of partial resistance do not have a negative effect on yield in environments with low disease pressure[1].
- A major quantitative trait loci (QTL) on chromosome 18 (8-16 cM), explains 10-45% of phenotypic variance[4].
- QTL of large effect are uncommon in *P. sojae* – soybean interactions and it remains unknown if the chromosome 18 QTL represents a unique resistance mechanism.

HYPOTHESIS

- We hypothesize that this major QTL on chromosome 18 represents a novel source of partial resistance and will be valuable in soybean breeding programs.

OBJECTIVES

- Our overall objective is to assess and increase the potential of the QTL on chromosome 18 to be incorporated into soybean breeding programs.
  - The specific objective explored in this work is the phenotypic characterization of the QTL in NILs.

Figure 1. Genetic position of QTL on chromosome 18 and LOD score.

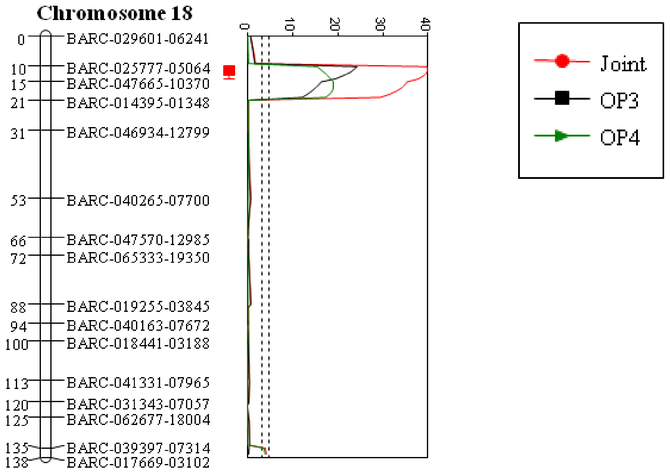


Figure 2. Field symptoms of Phytophthora stem and root rot.

METHODS

Plant Material

- Fifty-one near isogenic lines (NILs) were developed from three F_7 recombinant inbred lines (RILs) identified as segregating for the QTL of interest (RIL 3064, RIL 4060, RIL 4213).
  - RILs were derived from crosses between either OX 20-8 and PI 427105B or OX 20-8 and PI 427106

Phenotypic Evaluation

- NILs were phenotyped for partial resistance to *P. sojae* using both the tray (Figure 3) and layer test[2] (Figure 4).
- NILs were evaluated for agronomic performance and measured for yield in one field location in Defiance County (OH).
  - Field was organized in a split-split plot design with treatment nested in line and line within RIL family with two replications.

Figure 3. Tray test.

Ten plants per line were placed on a food service tray with one raised side removed. Plants were aligned on a polyester cloth placed on top of a wicking pad. Plants were inoculated with 100µl of zoospores (1 x 10^4 zoospores/mL; isolate 1.S.1.1.) adjacent and directly on the taproot. Lesion lengths were evaluated 7 days after inoculation .

Figure 4. Layer test.

An agar layer of 14-day old P. sojae (1.S.S.1) grown on lima. bean agar was placed 5 cm below seed in a 1.2-liter polystyrene containers containing coarse vermiculite . Three weeks after inoculation plant height, dry root and shoot weight, fresh root and shoot weight, and root rot score were recorded.

Figure 5. Average lesion length of NILs within family (*P<.05).

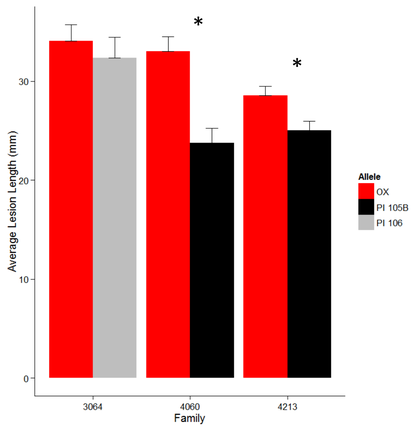


Figure 6. Root rot score, root fresh weight, shoot fresh weight (*P<.05)

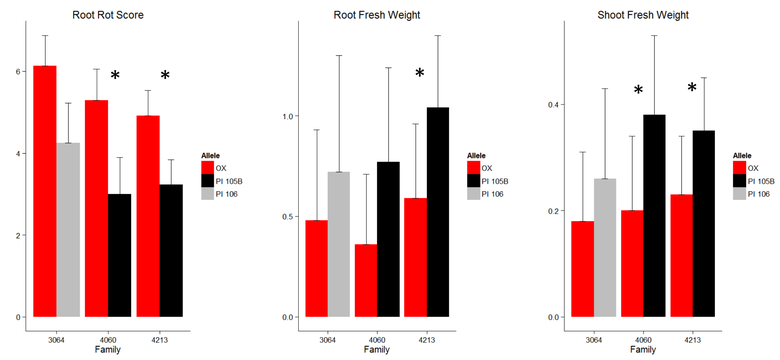
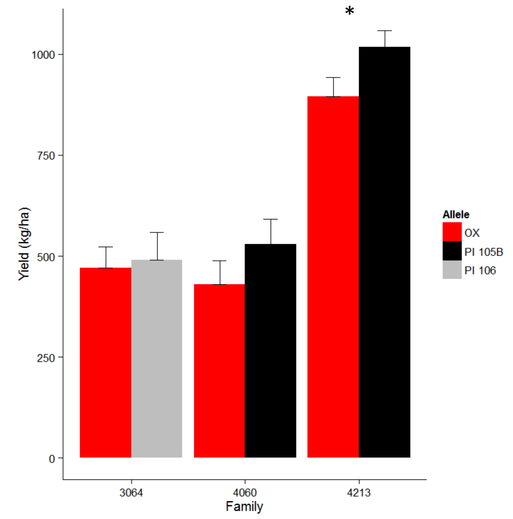


Figure 7. Yield (kg/ha) of NILs within family (*P<.05)



RESULTS

- NILs with PI allele, in general were significantly more resistant in tray and layer test (Figures 5-6).
- NILs with PI allele only had significantly higher yield in family 4213

FUTURE DIRECTIONS

- Fine map QTL by using KASP genotyping platform on recombinant BC_2 individuals.
- Perform phenotypic evaluation of NILs for resistance to soybean cyst nematode (*Heterodera glycines*), *Pythium* spp., and *Fusarium graminearum* to detect pleiotropic effects of the QTL.
- Determine level of epistatic interactions between QTL and a diverse range of genetic backgrounds.
- Enrichment analysis of differentially expressed genes from RNAseq experiment

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