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| **Reporting Period** | Final Report |
| **Proposal** | [1242 Expedited Delivery of Phytophthora QTL and How They Impact Yield?](http://moss.unitedsoybean.org/Lists/Proposals/DispForm.aspx?ID=2143&RootFolder=*) |
| **Committee** | Production |
| **Target Area** | Supply |
| **Project Start Date** | 10/1/2010 |
| **Project End Date** | 12/30/2011 |
| **Project Number** | 1242 |
| **Project Status**    **Reporting Period: Final Report 2011**   * Summary of what was accomplished or learned during the project   In several host-pathosystems, the detection of an individual QTL differed depending on the specific pathogen isolate or phenotypic assay that was used.  In addition, the contribution of a QTL towards yield is an important factor for selecting specific QTL candidates for resistance breeding. We completed a series of experiments that assessed these differences.  The first experiment in this study compared the QTL identified previously in a ‘Conrad × Sloan’ F4:6 population challenged with *Phytophthora sojae* isolate 1.S.1.1 to the QTL identified when this same population was challenged with isolates PT2004C2.S1 and OH25 using a tray test assay. In a second experiment, QTL were mapped in the same population with *P. sojae* isolate 1.S.1.1 using a different phenotypic assay, the layer test. Finally, in a third experiment, the impact of these QTL on soybean yield was evaluated using 20 selected RILs  grown in a field infested with *P. sojae*.  Resistance QTL with smaller effects, especially those from the susceptible parent, were not consistently detected with the three isolates or  the two phenotypic assays. Basic and composite interval mapping identified a major Conrad QTL on chromosome 18 and two on 19 that were detected with all three isolates and both phenotypic assays. RILs with resistance alleles at these four QTL had significantly higher yields (~1000 kg/ha more) than RILs with susceptible alleles. These results indicate the important role these four QTL play in conferring partial resistance to *P. sojae.*   * Continued to examine new sources of partial resistance to <i>*Phytophthora sojae</i>,* Fine map the QTL that have been identified, and develop marker assisted breeding strategy to pyramid partial resistance genes into MGs II, III, and IV soybeans with high yielding backgrounds.     Phytophthora root rot (PRR) caused by *Phytophthora sojae* Kaufm. & Gerd. and flooding injury can limit growth and productivity of soybean [*Glycine max* (L.) Merr.], especially on poorly drained soils.  The objective of this research was to map quantitative trait loci (QTL) associated with flooding tolerance and/or resistance to *P. sojae*.  Mapping was conducted using F7 recombinant inbred lines derived from a cross between the flooding tolerant, but PRR resistant accession PI 408105A, and the flooding intolerant line S99-2281.  A genetic linkage map consisting of 613 simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers was developed.  Flooding tolerance was determined by measuring both plant injury and flooding yield index.  Both *Rps*-gene and partial resistance to *P. sojae* were measured for each RIL using the hypocotyl and layer tests.  Genomic regions on four chromosomes were associated with genetic control of decreased plant injury and higher yield under flooded conditions.  Of these, one region near markers Sct\_033 and BARC-024569-04982 on chromosome 13 and one near BARC-016279-02316 on chromosome 11 were associated with partial resistance to *P. sojae.* The results indicate that genes for both flooding tolerance and *P. sojae* resistance are necessary to reduce injury and yield loss under saturated soil conditions, and that these genes can contribute to increasing soybean productivity on soils prone to waterlogging.  Identified two additional QTL on chromosome 18, in the Conrad x Sloan population using the new SNP markers developed by Cregan’s Lab.  Several populations are near completion for identification and fine mapping of QTL associated with Partial resistance to *Phytophthora sojae.*  Among these QTL have been identified on chromosomes 1, 3, 13 and 18 from PI 398841; chr 6, 8, 9, and 18 from PI 407861A; and chr. 11 and 12 from OX20-8; and chr. 19 from PI 427106.  There are several manuscripts in progress and additional screening to verify these results.  Compared the genomic regions on chromosome 19 which are associated with the expression of two QTLs and verified the role of the genes that were associated with this expression.    One of our key objectives was to identify candidate genes that may contribute to the expression of partial resistance to *Phytophthora sojae*.    Two quantitative trait loci (QTL) on Chr. 19 in soybean cultivar ‘Conrad’ contributed to the expression of partial resistance towards multiple *Phytophthora sojae* isolates.  These two QTL were then dissected through sequence and expression analysis of genes from both resistant and susceptible genotypes. There were 1025 single nucleotide polymorphisms (SNPs) in 87 of 153 genes sequenced from Conrad and the susceptible cultivar Sloan In the sequence comparison of Conrad to both Sloan and Williams 82, there were 304 SNPs in 54 genes, and of which 11 genes had SNPs unique to Conrad. Expression patterns of 19 genes in these regions were studied in response to inoculation with *P. sojae* in Conrad, Sloan, and four selected recombinant inbred lines (RILs) from the Conrad × Sloan F6:8 population. A list of candidate genes with significantly different infection response between the resistant and susceptible lines were identified, including those involved in signal transduction, hormone-mediated pathways, plant cell structural modification, ubiquitination, and basal resistance. These findings suggest a complex defense network with multiple mechanisms underlying individual soybean QTL conferring resistance to *P. sojae*. This study also provides putative candidate genes and SNP markers for fine mapping and marker-assisted resistance breeding for this trait.     * Assessment of progress achieved toward each project performance measure, and if a performance measure was not achieved, an explanation * Evaluate the yield impact of different QTL in adapted backgrounds both with and without disease pressure. * This was abandoned last year due to the delayed planting and challenging season. We did not want to use the limited seed we have some lines to pursue this goal * Several lines were advanced to develop remnant RIL populations – these may be used for this portion of the project     **Plans:**  Ohio:  Primary Goal is to complete the phenotyping of the last two populations, layer tests are currently in progress.  Final marker analysis to fill in gaps and fine map the QTL in these populations.  Complete and have all manuscripts submitted by June.  For the QTL on chromosome 18, begin the bioinformatics to examine the genes associated with this QTL region.  Initiate the analysis of the last MO population.  The remainder of the plans were outlined in the new proposal. | |
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| **Attachments** | |  | | --- | | [PAG-Poster-Jinrong-01-2012.pdf](http://moss.unitedsoybean.org/Lists/ProjectStatusReports/Attachments/4777/PAG-Poster-Jinrong-01-2012.pdf) | |

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