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| **Reporting Period** | Final Report |
| **Proposal** | [2242 Partial Resistance to Phytophthora sojae, Pythium spp., and Fusarium spp.: Mechanisms, Markers, and Deployment (Year 1 of 3)](http://moss.unitedsoybean.org/Lists/Proposals/DispForm.aspx?ID=2659&RootFolder=*) |
| **Committee** | Production |
| **Target Area** | Supply |
| **Project Start Date** | 1/1/2012 |
| **Project End Date** | 12/31/2012 |
| **Project Number** | 2242 |
| **Project Status** | ·         Summary of what was accomplished or learned during the project    Identified common and unique QTLs for both flood tolerance and resistance to *P. sojae.*  Released a variety with both flood tolerance and resistance to *Phytophthora sojaeAs a*    Mapped numerous QTL that confer resistance to *Phytophthora sojae* in both US cultivars and germplasm from South Korea and China.    As a result of the parental design for developing six of these soybean populations were developed, this team was also able to analyze the impacts of combining these populations to look for additional QTL.    Identified several new sources of resistance to *Phytophthora sojae*, *Fusarium graminearum*, *Pythium irregulare,* and *Pythium ultimum*.      Key Manuscripts since January, 2012    *1.      Lee, S., Mian, R.M.A., Sneller, C.H., Wang, H., Dorrance, A.E., and McHale, L. 2013. Joint linkage QTL analysis for partial resistance to Phytophthora sojae using six nested inbred populations with heterogeneous conditions.  Theor. Applied Genet. doi: 10.1007/s00122-013-2229-z.*  *2.      Lee, S., Mian, R.M.A., McHale, L., Sneller, C.H., and Dorrance, A.E. 2013. Identification of quantitative trait loci conditioning partial resistance to Phytophthora sojae in soybean PI 407861A. Crop Sci. 53: 1022-1031.*  *3.      Ellis, M.L., McHale, L.K., Paul, P.A., St. Martin, S.K., and Dorrance, A.E. 2013.  Soybean germplasm resistant to Pythium irregulare and molecular mapping of resistance quantitative trait loci derived from the soybean accession PI 424354.  Crop Sci. 53: 1008-1021.*  *4.      Lee, S., Mian, R. McHale, L., Wang, H., Wijeratne, A., Sneller, C. and Dorrance, A.E. 2013. Novel quantitative trait loci for partial resistance to Phytophthora sojae in soybean PI 398841.  Theo. Applied Genetics.  126: 1121-1132.*  *5.      Wang, H., Wijeratne, A., Wijeratne, S., Lee, S., Taylor, C., St. Martin, S.K., McHale, L., and Dorrance, A.E. 2012. Dissection of two soybean QTL conferring partial resistance to Phytophthora sojae through sequence and gene expression analysis.  BMC Genomics.2012, 13:428.*  *6.      Nguyen, V.T., Vuong, T.D., VanToai, T., Lee, J.D., Wu, X., Mian M.A.Rouf, Dorrance, A.E., Shannon, J.G., and Nguyen, H.T. 2012. Mapping of quantitative trait loci associated with resistance to Phytophthora sojae and flooding tolerance in soybean. Crop Sci. 52:2481-2493.*   1. *Ellis, M.L., Wang, H., Paul, P., St. Martin, S.K., McHale, L., and Dorrance, A.E. 2012.  Identification of soybean genotypes resistant to Fusarium graminearum and genetic mapping of resistance quantitative trait loci in the cultivar Conrad.  Crop Sci. 52:2224-2233.* 2. *Wang, H., St. Martin, S.K., and Dorrance, A.E. 2012. Comparison of phenotypic methods and yield contributions of quantitative trait loci for partial resistance to Phytophthora sojae in soybean.  Crop Science 52:609-622.*     *Training of Students:*    *Sungwoo Lee, Ph.D. 2013, The Ohio State University, now Post-doc with Andy Michel & Rouf Mian.*  *Margaret Ellis, Ph.D., 2012, The Ohio State University, now Post-doc at Iowa State University with Leanor Leandro and Gary Munkvold.*  *Hehe Wang, Ph.D., 2012, The Ohio State University, now Post-doc at University of Florida.*        *·         Assessment of progress achieved toward each project performance measure, and if a performance measure was not achieved, an explanation*    ***Strategy 1.  Identify Key QTL to those that are essential for yield under high disease pressure****.*    *Performance Measure:  Evaluate the performance of  near isogenic lines (NILs) in field trials for yield with and without disease pressure.*    *One set of NILs was evaluated in Ohio during 2013.  Additional NILs were developed during the last two seasons to more accurately assess this effect.*    ***Strategy 2.  Exploring mechanisms:  Fine map partial resistance and identify key genes involved in the expression of resistance in these populations.***    *Performance Measure:  Each of the advanced populations will be phenotyped and the QTL verified with 15 to 20 newly developed markers per QTL.  Key recombinant inbred lines or near isogenic lines will be selected for sequence comparison.*    *During the past two years, we mapped and reported the QTL for Phytophthora sojae, Pythium irregulare and Fusarium graminearum.  In addition, we are currently fine-mapping the resistance to these three pathogens in an advanced, large population of Conrad x Sloan with the new Soy 6K SNP chip.  These results should be available by mid-February.*    *In addition, 1,400 lines of germplasm from South Korea as well as North American breeding lines were evaluated for genome wide association analysis to identify key QTL for resistance to P. sojae. This will enable us to identify the novel QTL and bypass the process of developing individual populations with each germplasm line.  We have genotypic data from the USDA-ARS Beltsville group for the South Korean lines, the North American breeding lines have recently been genotyped with the Woy 6K SNP chip.   Preliminary analysis has identified 12 loci for partial resistance. Additional  inoculations of these lines with P. sojae are in progress to repeat and verify earlier findings.*    ***Strategy 3:  Functional analysis of key genes associated with partial resistance to P. sojae.***    ***Performance measure(s) for Strategy 3:****Composite soybean plants (wild-type shoots with transgenic roots) and/or hairy root cultures in which identified genes are expressed in soybean roots will be developed and screened for their resistance to P. sojae.  We anticipate testing between 15 and 30 genes per year.*    *This objective has taken longer than expected as the students who are on this project were taking classes and could not spend 100% of their time conducting the research. The good news is that the system is up and running and the promoters from 6 genes are almost ready for analysis. The gene sequence comparisons are in progress to prioritize the list of 100 candidate genes that have been identified as part of this project.*    ***Strategy 4:  Identify additional sources of resistance to other seedling pathogens.***    ***Performance measure for Strategy 4:****A thorough analysis of soybean genotypes that were used to develop populations for specific key traits will be screened for resistance to key seedling pathogens.*    *Several QTL were identified and published with resistance to F. graminearum and Py. irregulare.  In addition, the screening of additional lines was completed.  Statistical analyses of these results are in progress and manuscripts are expected to be submitted by July 2014.*    ***Strategy 5.  Development of highly adapted germplasm with QTL identified in these PI’s.***    *Performance measure:  Germplasm developed from diverse resources with QTL for partial resistance to P. sojae, Py. irregulare, Py. ultimum, and F. graminearum will be available.   MO:  Marker-assisted backcrossing (MABC) was continued to develop near-isogenic lines (NILs) for a major QTL on Chr. 13 (F) in the winter nursery. Several BC4F1’s seed were produced. True hybrid verification was completed. Harvest of the BC4F2 seed should be completed later this month. Seed will be sent back to the Nguyen Lab for further evaluation and NIL development.    Additionally, new mapping populations were developed and advanced in the winter nursery.*      *OH:  Backcrossing and NIL development of the two PIs, with the major QTL at the top of chromosome 18, begun.*      *·         If the findings to date for this USB funded research project have been instrumental in leveraging additional non-USB funding, please briefly list the funding source, the amount of incremental funding and how these results might have influenced that funding decision*    *The Ohio Team applied for a USDA AFRI grant, preliminary data from this project greatly helped in the development of the proposal, which was not funded, but received a high priority ranking.*    *Internal Funding was leveraged through an Ohio State University program, Center of Applied Plant Sciences.  This program has provided tuition dollars for students on the USB project and salary for a post-doc with bioinformatic expertise, which was greatly needed for this project.*    *The Dorrance Lab is providing expertise to three companies at the moment for support in evaluation of cultivars for resistance to P. sojae, in the form of verification of results; isolate maintenance.  NOTE: Uploaded by Katie Williams on 1/31/2014 on behalf of Anne Dorrance.* |
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