|  |  |
| --- | --- |
| Project Number:  | 1420-532-5659 |
| Project Title:  | Genes and Markers for Resistance to *Phytophthora sojae*, *Pythium* spp., and *Fusarium graminearum* in Soybean (Year 3 of 3) |
| Organization:  | The Ohio State UniversityIowa State UniversityUSDA-ARS Virginia TechMissouri University |
| Principal Investigator Name: | Dr. Anne E. Dorrance |
| Project Status - What key activities were undertaken and what were the key accomplishments during the life of this project? Please use this field to clearly and concisely report on project progress. The information included should reflect quantifiable results (expand upon the KPIs) that can be used to evaluate and measure project success. Technical reports, no longer than 4 pages, may be included in this section.  |
| Please see attached document |
| Did this project meet the intended Key Performance Indicators (KPIs)? List each KPI and describe progress made (or not made) toward addressing it, including metrics where appropriate.  |
| 1. Six new loci (Rps genes) will be identified that confer resistance to *Phytophthora sojae*.

 Our analysis is still in progress, but this will be surpassed based on the data to date.1. Constructs for silencing 20 Rps-related genes will be completed and potentially screening will also be completed. This will also provide for specific markers for marker assisted selection for the correct R-gene sequence

One assay was completed – and more are in progress. 1. Identify the quantitative trait loci associated with resistance to P. sojae, Pythium spp., and Fusarium graminearum. complete mapping in at least 10 populations.

*We greatly exceeded this goal*:**Published**:Conrad x Sloan, P. sojae, Py. irregulare, & F. graminearumSix PIs for QTL via joint linkage analysis for P. sojae PI 567301B – F graminearumPI 567301C – F. graminearumGWAS study for P. sojae**Final analysis and Manuscripts in progress**:Magellan x PI 438489B: Py. irregulare & P. ultimumWyandot x PI 200538PI 408097 x Williams – Py. irregulare, Py. sylvaticum, & Py. torulosum3 Nested Association Mapping Populations were completed – LG-05-4464, PI398881, and PI 427136 for resistance to Pythium spp.*More populations are in various stages of analysis*.1. Complete transcript analysis of candidate genes identified in 567301B for Fusarium graminearum. – *Experiment was completed and bioinformatics analysis is still ongoing.*
2. Identify key candidate genes in PI 427106, PI 427105B, V71-370 (chr. 18) for a major QTL for P. sojae. Complete transcript analysis of candidate genes in Conrad for P. sojae.- *Experiment was completed, but a delay in sequencing capabilities – we are just waiting for the sequence to begin analysis*.
3. Coordinated genotyping system for introgression of 5 QTL for resistance to soil borne pathogens into high yielding adapted germplasm.- *in progress, varieties and germplasm are in various stages of the development*.
4. Complete analysis of Avr1 effector in P. sojae; and diversity of Pythium spp. in Iowa and Ohio.

*Delayed due to staffing changes, but is now back on track with new students*. |
| Expected Outputs/Deliverables - List each deliverable identified in the project, indicate whether or not it was supplied and if not supplied, please provide an explanation as to why. |
| **1. Characterize and fine map sources of potentially novel *Rps* genes towards *Phytophthora sojae*.**Germplasm/varieties/markers associated with novel *Rps* genes for *Phytophthora sojae* have been identified. Eleven of these are in the final stages and manuscripts are in progress.Mapping populations were developed with additional plant introductions and are ready for phenotyping.**2. Using Virus Induced Gene Silencing (VIGS) to assay the function of candidate *P. sojae Rps* genes.**Within these loci, numerous candidate R-genes were identified. Gene silencing vectors were developed and assays are in progress**3. Identify QTL to those that are essential for resistance towards seed and seedling pathogens:*Phytophthora sojae*, *Pythium* spp., and *Fusarium graminearum*.**4 **Fine map QTL and identify key genes involved in the expression of resistance in these populations.**Numerous sources of resistance have been identified and mapping for some has been completed while others is still in progress. **5. Functional analysis of key genes associated with partial resistance to *P. sojae, Pythium spp. and F. graminearum.***For these 5 objectives/strategies, we have developed molecular markers that are directly tied to the QTL and markers tied to the genes associated with the resistance response to these key soybean seed and root pathogens is in progress. In addition, we will have available, germplasm with key QTL to use in variety development, varieties for release from different backgrounds will be in progress. These are in progress and some will be released in the coming year.**6. Development of highly adapted germplasm with QTL identified in these studies.** Develop and release germplasm and varieties with resistance to multiple soybean root pathogens. These are in various stages in the breeding pipeline.**7. Assess the population diversity of *Phytophthora sojae* and key *Pythium* spp. throughout the Midwest, targeted towards identifying key pathotypes or effectors required for screening.**Characterized pathogen isolate collections that can be used for screening and comparison of resistance response. These are now currently available as well significantly greater understanding of the diversity of *P. sojae* in the Midwest regions. |
| Describe any unforeseen events or circumstances that may have affected project timeline, costs, or deliverables (if applicable.) |
| Several manuscripts were delayed due to unexpected personnel changes. For example, Research Associate left for a great position at Bayer Crop Sciences, with 2 week notice, another paper was delayed due to student leaving for Pioneer.We are also meeting the demand of providing students for Industry – and students taking classes does take time and delays the projects. Our staffing for the next 2 years will involve students in their final year or two as well as research assistants who can put move through more material at a faster pace.At Ohio State – Greenhouse renovations impacted assays for resistance and delayed several experiments related to functional gene analysis. |
| What, if any, follow-up steps are required to capture benefits for all US soybean farmers?Describe in a few sentences how the results of this project will be or should be used. |
| these results will be used by industry to develop new highly resistant varieties and the markers will be incorporated into the breeding programs |
| **List any relevant performance metrics not captured in KPI’s.** |
| We have supplied industry with some amazing talent over the course of this study and more students are getting to their final stages to earn their degrees. |

**Final Report**

**Project Number:** 1420-532-5659 Year 3

**Project Title:** Genes and Markers for Resistance to *Phytophthora sojae*, *Pythium* spp., and *Fusarium graminearum* in Soybean (Year 3 of 3)

1. **Characterize and fine map sources of potentially novel *Rps* genes towards *Phytophthora sojae*.**

Potentially 6 new loci (Rps genes) will be identified that confer resistance to *Phytophthora sojae*

*During 2014-2016 screening and genotyping for resistance to 11 different advanced populations (F3, F5 or greater) was completed. The phenotyping for each population required 2 to 6 isolates each.* Using Illumina BARCSoySNP6K chip, linkage maps were constructed for three populations: PI 408097 X Williams, PI 408132 X Williams, and PI 407985 X Williams (PI 424477, PI 399079). Preliminary analysis with disease reaction data from earlier generations using key *Phytophthora* isolates indicated presence of multiple *Rps* resistance genes on these parental lines. Interestingly, the *Phytophthora*-resistant line PI 408097 also gave resistance reaction with 3 *P*. *sojae* effectors. Furthermore, the line was also resistant to three *Pythium* species: *P. sylvaticum* (seed assay), *P. torulosum* (seed assay) and *P. irregulare* (seed and root assays) – See below Pythium section.

*Final analysis, additional phenotyping with more isolates to confirm earlier responses, as well as manuscript writing are in progress. In addition many of these sources for novel Rps genes are also resistant to Pythium and F. graminearum! Our prediction is that we will bypass the 6 new loci as we wrap this section up.*

*In addition a* set of 69 accessions/lines was identified, which showed very strong resistance (0 to 10% dead plants/line after inoculation with *Phytophthora* *sojae*). A list of these resistant lines was made publically available through a publication. Fifty of the 69 lines were further screened with several isolates expected to overcome the *Rps8* resistance gene. The same 50 lines were also subjected to *P*. *sojae* effector screening in conjunction with a multi-institutional USDA/NIFA CAP project. At least 30 of the lines responded to one or more essential *P*. *sojae* effectors (i.e., gave resistance reaction) indicating presence of potentially novel *Phytophthora* resistance genes. The selected 50 *Phytophthora*-resistant lines were further assayed for reaction to five *Pythium* species including *P*. *sylvaticum*, *P.* *lutarium*, *P. irregulare*, *P.* *torulosum*, and *P.* *oopapillum.* Fourteen of the accessions showed resistance each to one *Pythium* species, five each to two species and three each to three different species. Resistance level based on seed and/or root assay was higher than that of Archer, which is known to be *Pythium*-resistant. Forty *Phytophthora*-resistant lines including some also resistant to *Pythium* were crossed with the susceptible Williams to develop mapping populations. Seven of the resistant lines were *G*. *soja* and 33 were *G*. *max* lines, 21 of which had responded to effectors indicating presence of novel resistance genes. Recombinant Inbred Line (RIL) populations were developed for the 33 *G*. *max* populations and were advanced in the field. Majority of these RIL populations are at F7, F8 or F9 generation. The advanced generation populations provide critical genetic material for current activities on mapping/identification of potentially novel resistance genes and selection of disease-resistant breeding lines.

Several Lines with potentially novel sources of Rps genes were submitted for sequencing (November 2016) to characterize and confirm which sequence is the *Rps* gene

1. **Using Virus Induced Gene Silencing (VIGS) to assay the function of candidate *P. sojae* *Rps* genes.**

*Rps2:* We have developed a series of four constructs that split the genes in the Rps2 interval into four distinct groups. Two of these constructs, which corresponded to novel R-genes fused to other proteins, immediately resulted in disease-like symptoms (leaf necrosis) even though plants had not been infected with *P. sojae*. Silenced plant have been characterized using RNA-seq to the gene networks regulated by the candidate R-genes. The two remaining constructs resulted in a reduced grown phenotype.

*Rps8/Rps3a:* Twenty putative R-genes within the Rps8 and Rps3a loci were identified. Constructs for silencing of all 20 genes were made and the first round of assays a hypocotyl type assay were completed. A second round with the same constructs is currently in progress but with root inoculations. Two manuscripts, one for fine mapping and the second comparison of transcripts and sequence analysis is in progress.

*General Rps Constructs for R-gene mediated response*: For identification of novel genes required for Rps-governed resistance, we developed VIGS constructs for 20 + signaling genes identified by Lin et al. 2014. These genes represent a core set of genes common to resistance responses governed by Rps1-a, Rps1-b, Rps1-c, and Rps1-k, Rps3-a, Rps3-b, Rps4, Rps5, and Rps6 and differentially expressed in response to *P. sojae* infection. Almost all of the constructs have been tested on William82 for obvious phenotypic changes.  We plan to test for the effect of silencing on *P. sojae* infection in different lines this spring.

1. **Identify and fine map QTL (Quantitative Trait Loci) essential for resistance towards seed and seedling pathogens: *Phytophthora sojae*, several *Pythium* spp., and *Fusarium graminearum*.**

***P. sojae*:**

2014: Conrad x Sloan is completed, manuscript published 2016

2014: Genome wide association mapping of key Plant Introduction lines for *Phytophthora sojae* reaction completed manuscript published 2016

2015/2016: Completed phenotyping of S99-2281 x PI 561271 and 2 QTL were mapped to Chr. 3 and Chr 7. Manuscript in progress

2016 – Identified and increased seed of 12 Nested Association Mapping populations. Phenotyping and mapping to be completed 2017-2018

2017 – Maverick x PI 408105A phenotyping has started to narrow down QTL region first identified in an earlier cross of S99-2280 x PI 408105A

***F. graminearum***

*2016- PI 567301B has 2 QTL (Published 2015), fine mapping completed, RNAseq analysis is in progress*

*2016-Magellan x PI 567516C has 1 QTL-Manuscript submitted and in final revision*

***Pythium spp.***

*2014/2015: The SoyNAM Parents were screened for resistance to different Pythium spp by Iowa and Ohio. In Iowa, Pythium sylvaticum, P. lutarium, P. oopapillum, and P. torulosum two assays: a seed rot assay and a root rot assay were used and identified four of the parents, Maverick, CL0J095-4-6, CL0J173-6-8, and Magellan had resistance to three Pythium spp. in both assays. Seven parents, 4J105-3-4, HS6-3976, LD02-9050, LG05-4832, PI404.188A, and PI427.136, were resistant to two the Pythium spp. in both assays. Some of the parents were more susceptible to seed rot than to root rot. Manuscript in progress (IA).*

*In Ohio, 7 lines were highly resistant to Pythium ultimum var ultimum, Py. ultimum var sporangiferum, as well as Phytophthora sojae. Seed was increased during 2016 and assays are in progress to map QTL.*

*An additional 47 lines of diverse parentage, with known resistance to Phytophthora sojae, were screened for resistance to Pythium sylvaticum, P. lutarium, P. oopapillum, P. torulosum, and P. irregulare using the same two assays mentioned above. Three lines showed resistance to three Pythium spp. and seven lines showed resistance to two spp. in both assays.*

*2015/2016: Three NAM populations were chosen to identify QTL for resistance to Pythium sylvaticum, P. lutarium, and P. oopapillum. The following populations were assayed using a seed rot or root rot assay in 2015/2016. QTL mapping and identification is in progress (2017).*

 *LG05-4464 x IA3023: seed and root rot resistance to P. sylvaticum (Iowa)*

 *PI 398.881 x IA3023: root rot resistance to P. oopapillum (Iowa)*

 *PI 427.136 x IA3023: seed rot resistance to P. sylvaticum, P. oopapillum, and P. lutarium; root rot resistance to P. lutarium (Iowa)*

*An additional population PI 408097 x Williams was chosen to identify QTL for resistance to Pythium irregulare, P. sylvaticum, and P. torulosum. The population was assayed for resistance to seed rot caused by each of the three species and assayed for resistance to root rot caused by P. irregulare. QTL mapping and identification is in progress (2017 by Saghai-Maroof’s lab).*

*From the greenhouse assessments in the past year, an additional 6 Plant Introductions were resistant to more than 3 different Pythium spp. Two of three of these soybean populations were screened for resistance to Pythium spp.- analysis and mapping is in progress*

 *Magellan x PI 438489B to Py. irregulare and Py. ultimum (Ohio)*

 *Wyandot x PI 200538 (source of Rag2) to Py. irregulare (Ohio)*

1. **Fine map QTL and identify key genes involved in the expression of resistance in these populations**

2014/2015: completed NIL analysis for QTL for *P. sojae in Conrad*. The NIL pairs are genetically identical, except for narrow region where the resistance is located- these NILs did not behave as expected and was placed on hold

2014: complete resequencing of key genes in Sloan and Conrad for sequence comparison- completed

2014: complete sequencing of genes in key QTL on PI 567301B/completed

2015: complete transcript analysis of those candidate genes in PI 567301B, repeated and is in progress

2015/2016-2018: Identify key candidate genes in PI 427106, PI 427105B, V71-370 (chr.18) for a major QTL for *P. sojae. NILs for PI 427106 and PI 427105B were developed, RNAseq experiment completed, field evaluations of NILs completed over 2 years.*

1. **Functional analysis of key genes associated with partial resistance to *P. sojae, Pythium spp. and F. graminearum.***
2. Utlilize an e-QTL approach to identify targeted genes that may identify additional key genes.

Experiment was completed, library prep and the first round of sequencing completed in early 2016. An additional experiment was completed due to low RNA quantity and sequencing completed Nov 2016. Data analysis is currently in progress

1. **Key QTL loci**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Pathogen | Source of Gene | Key locus | Pathway/Genes | Student/TechnicianScreening Lines |
| *Phytophthora sojae* | Conrad | QTL-19 | Auxin- PIN genes and SAUR genes | Anna Stasko |
|  | QTL-13 | R-gene classes | Bill Rolling |
|  | QTL-18 | Jasmonic acid roleLeucine Rich Repeat | Dorrance LabBill Rolling |
| S99-2281 x 408105A | QTL -13 |  | MO |
| PI 427106PI 427105B | QTL-18 (top) | Numerous genes | Stephanie Verhoff |
| *Fusarium graminearum* | PI 567301B | QTL-8 | narrowed to 8 of 39 genes, silencing in progress | Cassidy Gedling |
| PI 567516C | QTL-6 | 3 genes | Peng Chen & MO |

1. 30 to 35 promoter/genes per year// either through VIGs or composite root samples
* 2015 (May): 4 promoters completed (no response associated with infection to *P. sojae*
* *A total of 65 genes have been selected within key QTL regions for resistance to P. sojae and Py. spp. to target for functional gene silencing in composite plant and/or hairy root systems*
	+ *In the past year. Twelve genes have been totally completed the transformation and inoculation assays. A few genes had different root phenotypes but there was no difference in greater or smaller lesions following inoculation.*
	+ *In the pipeline 22 genes are ready to be silenced in hairy roots*
	+ *And the remaining 20 are in the vector development step in the process.*
* 2016-2017: Nine BPMV VIGS vectors targeting seven auxin-related genes on chromosome 19 where developed and used in preliminary testing on Thorne and Sloan. Based on these preliminary results, three constructs showed promising phenotypes and were selected for further testing in Conrad and Sloan. One replication has been completed, and a second is in progress.
* 2015-2016: Metabolite analysis of auxin and secondary auxin metabolites indicated differences between the two cultivars. These analysis will be used to further refine and define the genes in this complex pathway that should be examined.
* The expression of two PIN1-like genes, Glyma.19G128800 and Glyma.03G126000, was measured using quantitative real-time PCR at 12, 48, and 72 hours after inoculation (hai) with *P. sojae* in both Conrad and Sloan. Preliminary data analysis suggests that the two genes behave differently from each other during infection. Glyma.03G126000 expression was significantly different between Conrad and Sloan at 48 hai. The expression of four other PIN-like genes was measured at 0 hai to look for initial differences between Conrad and Sloan. Measurement of the expression of an additional five PIN-like genes is in progress.
1. New VIGs/composite plants for infection assays for *Fusarium graminearum & Pythium* spp. will be developed: Existing soybean VIGS vectors often produce disease symptoms that interfere with the silencing phenotypes of many target genes, or are frequently ineffective in some plant tissues. To address these shortcomings, a new VIGS vector based on Apple Latent Spherical Virus (ALSV) was evaluated for its amenability to soybean. This vector was shown previously to silence a soybean phytoene desaturase (GmPDS) gene in a few soybean varieties. However, the procedure used particle bombardment delivery of viral RNA propagated in a different plant species prior to inoculation of soybean seedlings, and was highly variable and difficult to use in high-throughput gene silencing. We modified and evaluated an *Agrobacterium* infiltration-based method for inoculum propagation in *Nicotiana benthamiana*. This allowed for infection of soybean plants with the VIGs vector via simple mechanical rubbing with *N. benthamiana* homogenate. Infection and silencing capability of this VIGs vector was then evaluated on 20 diverse soybean genotypes, of which eight showed pronounced silencing phenotype in a minimum of 20% individuals. More importantly, the RNA of the VIGS vector was detected in pods, embryos, stem, leaf, and roots. Our study demonstrates that the modified ALSV VIGS vector, coupled with the simplified inoculation procedure, is a valuable functional genomics tool in a substantial number of soybean genotypes. Further modifications are in progress to expand its use to more soybean genotypes as well as a manuscript is in progress.
2. **CRISPR-** which stands for clustered regularly interspaced short palindromic repeats is a newer technology that is purported to enhance efficiency and accuracy of functional gene analysis. This technique is in progress to determine if it will work for the key genes for our various pathogens.

Expression of the CRISPR gene sequence is being driven by the Cassava Vein Mosaic Virus (CvMV) promoter sequence which is known to be active in soybean hairy roots (Govindarlajulu et al., 2008). The CRISPR gene expression cassette was then cloned into the plant expression vector (Akk1467) along selectable (Basta) and scorable (GFP) markers. Target regions for genomic modification were selected for *Myb* transcription factor (*IbMYB*), β-glucuronidase (GUS), apyrase, phytoene desaturase (PDS) of *Nicotiana benthamiana* and soybean. These selected target regions were cloned into the constructed CRISPR vectors and will be evaluated for the efficiency of gene silencing. Gene function analysis will be performed once these CRISPR vectors are validated and optimized to be complemental and enhance to our current soybean hairy root composite plant transformation system.

1. **Development of highly adapted germplasm with QTL identified in these studies.**

2014: evaluate lines with partial resistance to *P. sojae* from PI 408105A in fields – move forward for variety development and release

2014/2015: Coordinate genotyping system for introgression of 5 QTL into high yielding adapted germplasm

|  |  |  |
| --- | --- | --- |
| **QTL locus** | **Source** | **Pathogen** |
| QTL-8 | PI 567301B | *F. graminearum* |
| QTL-13, 18, 19 | Conrad | *P. sojae* |
| QTL – 2, 7,14,18 | PI 427106, PI 427105B, PI 417178, PI 398297 | *P. sojae* |
| QTL- 14, 19 | Conrad | *F. graminearum, Py. irregulare* |
| QTL-11, 13 | PI 408105A | *P. sojae* |

* Note, Lines with potentially novel R-genes will be immediately added to this list

MU breeders released five new soybean cultivars, S11-16653, S11-20124, S12-3791, S12-2418, and S12-4718, with high yield potential and field resistance/tolerance to *Phytophthora sojae.* These lines are currently in Missouri foundation seed production for commercial production. In addition, several lines with Phytophthora resistance and flooding tolerance are being developed.

Va Tech: Four Plant Introduction lines with potentially novel sources of *Rps* resistance genes were crossed with three Virginia soybean lines including: Glenn by PI 424237B and PI 398666; Hutcheson by PI 424237B and PI 408132; and Teejay by PI 424237A. Crosses of Teejay with PI424237A and Glenn by PI 424237B were advanced to F2 generation. To combine known partial resistance QTLs from two sources, a population of 178 F6 RILs was developed from the cross of Conrad by V71-370.

1. **Assess the population diversity of *Phytophthora sojae* and key *Pythium* spp. throughout the Midwest, targeted towards identifying key pathotypes or effectors required for screening.**

2014: *P. sojae* diversity analysis. Manuscript published 2016

2015-2017: Avr1a first round on a few isolates was completed, due to the findings from diversity analysis another 180 isolates were added to the study.

2015-2017: *Pythium irregulare* – diversity analysis is in progress

**Additional achievements**:

1. Degrees Awarded

R. Schneider, M.S., 2015. The Ohio State University, Now at Pioneer Seeds

S. Lee, Ph.D. 2014, The Ohio State University, Now a Post-doctoral researcher in soybean breeding at N.C. State University

1. Presentations

Dorrance, A.E. 2016. Seedling pathogens of soybean, their diversity and best practices for breeding for resistance. Soybean Breeders Workshop, February, St. Louis, MO

More than 100 private and public breeders and pathologist were in attendance

1. **Manuscripts**

Schneider, R., Rolling, W., Song, Q., Cregan, P., Dorrance, A., and Mchale, L. 2016. Genome wide association mapping of partial resistance to *Phytophthora sojae* in soybean plant introductions from the Republic of Korea. BMC Genomics*.* 17:607.

Stasko, A.K., Wickramasinghe, D., Nauth, B.J., Acharya, B., Ellis, M.L., Taylor, C.G., McHale, L., and Dorrance, A.E. 2016. High density mapping of resistance QTL towards *Phytophthora sojae*, *Pythium irregulare*, and *Fusarium graminearum* in the same soybean population. Crop Sci. 56:2476-2492.

Stewart, S., Robertson, A.E., Wickramasinghe, D., Draper, M.A., Michel, A., and Dorrance, A.E. 2016. Population structure among and within Iowa, Missouri, Ohio, and South Dakota populations of *Phytophthora sojae*. Plant Dis. 100: 367-379.

Acharya, B., Lee, S., Rouf Mian, M.A., Jun, T., McHale, L.K., Michel, A.P., and Dorrance, A.E. 2015. Identification and mapping of quantitative trait loci (QTL) conferring resistance to *Fusarium graminearum* from soybean PI 567301B. Theor. Appl. Genet*.* 128:827-838.

Prince, S.J., Song, L., Qiu, D., Maldonado dos Santos, J.V., Chai, C., Joshi, T., Patil, G., Valliyodan, B., Vuong, T.D., Murphy, M., Krampis, K., Tucker, D.M., Biyashev, R., Dorrance, A.E., Saghai Maroof, M.A., Xu, D., Shannon, J.G., and Nguyen, H.T. 2015. Genetic variants in root architecture-related genes in a *Glycine soja* accession, a potential resource to improve cultivated soybean. BMC Genomics 16:132. doi:10.1186/s12864-015-1334-6

Lee, S, Mian, R.M.A., Dorrance, A.E., McHale, L., Michel, A., 2015. A high resolution genetic linkage map of soybean based on 357 recombinant inbred lines genotyped with BARCSoySNP6K. Molec. Breeding 35: 58 DOI:10.007/s11032-015-0209-5.

Lee, S., Mian, R.M.A., Sneller, C.H., Wang, H., Dorrance, A.E., and McHale, L. 2014. Joint linkage QTL analysis for partial resistance to *Phytophthora sojae* using six nested inbred populations with heterogenous conditions. Theor. Applied Genet. 127:429-444.

**Submitted:**

Cheng, P., C.R Gedling, G. Patil, T.D Vuong, J. Grover Shannon, A.E. Dorrance, H.T. Nguyen (2017) Genetic mapping and haplotype analysis of a locus for quantitative resistance to *Fusarium graminearum* in soybean accession PI 567516C Theor. Appl. Gent. (*in press*)