NCERA 200 ANNUAL REPORT – 2011

Report Information:

Annual meeting date: 11/02/2011
Period covered by this report: 10/2010 – 09/2011

Participants:

Les Domier - Illinois
Al Eggenberger - Iowa
Craig Grau - Wisconsin
Reza Hajimorad - Tennessee
John Hill - Iowa
Houston Hobbs- Illinois
Feng Qu- Ohio
Peg Redinbaugh- Ohio
Steve Whitham- Iowa
David Wright- North Central Soybean Research Program

Brief Summary of Minutes of Annual Meeting:

The NCERA-200 meeting was held November 2, 2011 in Ames, Iowa, from 9AM to 4PM. In an effort to gauge the inputs from the stakeholders, this year's symposium featured representatives from agriculture-related industries, stakeholder groups, as well as agricultural experimental stations. The theme of the symposium was: "Industry, Experimental Stations and Commodity Groups: Are They Serving the Expectations of Their Stakeholders?" After a brief introduction by John Hill and David Wright, five speakers from diverse backgrounds covered a variety of refreshing topics.

Specifically, Palle Pedersen from Syngenta Seed Protection discussed about the innovations needed to feed nine billion global population during the next 20 years. This is followed by Donn Cummings from Monsanto Life Sciences who urged closer University-Industry partnership to meet complex research and education challenges faced by the farmers and agricultural industries alike. The third speaker, Scott Heuchelin from Pioneer further deliberated the need by seed companies for academic research support from universities.

After a brief break, the symposium resumed with Jennifer Jones from United Soybean Board reviewing the framework and the targets of farmer-driven soybean research. Finally, Joseph Colletti of Iowa State University categorized research and communication efforts made by land grant universities to meet the needs of stakeholders. The presentations were followed by a live discussion sessions in which the speakers answered many questions raised by the audience members concerning the various educational as well as research opportunities offered by the industrial groups.

The committee is especially grateful to David Wright for the time and efforts he invested to make the symposium a great success. The committee further expressed the gratitude to the North Central Soybean

Research Program for the unwavering financial support, which covered the cost of the room rental, as well as travel costs of the speakers.

The business meeting took place in the afternoon, with participants from four different states (Illinois, Iowa, Ohio, and Tennessee). Steve Slack, the administrative advisor of NCERA 200, participated through a conference call, provided a brief update on the comments provided by the reviewers of the renewal proposal, and urged the participants to apply additional research support as a multi-state team. Representatives from the states then presented the research updates during the past year. The meeting adjourned at 4PM. The state reports are attached below. Two other states (Arkansas and Kentucky) provided written reports.

Accomplishments (in the form of state reports):

Arkansas

Arkansas report

Project title: **Epidemiology of Soybean vein necrosis virus**
PI: Dr. Ioannis Tzanetakis, University of Arkansas

Soybean vein necrosis virus (SVNV) was first detected in Arkansas in mid-July this year. The late planting has obviously altered the timing of the disease and vectors. Notwithstanding, it appears that symptoms are becoming progressively more prominent in Arkansas, Missouri and Illinois where we collaborate with state and university scientists that scout routinely from SVNV symptoms.
We now have single thrips colonies in the genus *Frankliniella* and *Sericothrips* which are being used for virus transmission. The first round of experiments indicate that SVNV is indeed transmitted by a member of the two genera but taxonomical verification of the vector is pending. A total of 24 plant species belonging to four families (Chenopodiaceae, Compositae, Leguminosae and Solanaceae) have been inoculated with SVNV and tested by RT-PCR for infection. All potential alternative hosts reported here were confirmed with two sets of specific SVNV primers and sequencing of the products. Among them, at least seven species other than soybean have been confirmed as SVNV hosts through mechanical transmission. The list includes: Tobacco (three species), morning glory, cowpea, pumpkin and chrysanthemum.
We have applied a new protein-nucleic acids hybrid technique (this is a new technique that is developed in the Tzanetakis lab and no additional information can be provided until published or patented) that makes detection simpler and minimize the time of testing to only few hours. We also have experiments under way where we evaluate the reaction of elite material to early infection to the virus. At this point all material appears susceptible to the virus although the vast majority of the available genotypes are yet to be evaluated.

Project title: **Identification of the factors that cause soybean green bean syndrome**
PIs: Dr. Ioannis Tzanetakis and Dr. John Rupe, University of Arkansas

Green bean syndrome (GBS) is an elusive disorder that can have a major effect on yields. For example, in 2008, an 80-acre field in Prairie County was almost a total loss. We have focused on all aspects that can cause the disorder, both biotic and abiotic (physiological).
The GBS phenotype points to hormonal imbalance, something that phytoplasmas are known to cause. Actually, a report from Louisiana some 30 years ago provided some evidence that phytoplasmas are associated with GBS symptoms. Drs. Sabanadzovic, Valverde and Tzanetakis labs (Mississippi, Louisiana, and Arkansas) have processed at least 100 samples collected from about 10 fields in the three states showing typical GBS symptoms. It may be that a few scattered plants are infected with phytoplasmas but our results prove that GBS, in the scale we observed it in the field, **is not caused phytoplasmas**.
After eliminating the phytoplasma factor, we evaluated three other potential causes of GBS:
A. Stink bug feeding
B. Virus infection
C. Pod removal at different growth stages
The above experiments have been run in the last two years and we have good evidence of the role of those factors on the onset of the disorder.

A. Stink bug feeding

Two soybean varieties at V2 stage were placed in cages (treatment plants) whereas control plants remained on the greenhouse bench. A total of 116 - 166 green stinkbugs (*Acrosternum hilare)* were introduced to treatment plants over a one-month period. Pod size reduction was apparent in treatment plants compared to control plants (Fig. 1).

Fig.1. Effects of green stinkbugs (*Acrosternum hilare*) on soybean pod size. Cages with stinkbugs (left and middle) have smaller pod sizes than control plants of the same variety (right). The affected plants are being grafted onto seedlings to determine if the disorder is caused by a graft-transmissible agent. If so, we will process the plants further to identify the agent.

B. Virus infection

We tested the ability of *Bean pod mottle virus* (BPMV) and *Tobacco ringspot virus* (TRSV) to cause symptoms. BPMV can cause green stem syndrome but not GBS, unlike TRSV infection that can clearly cause the disorder (Fig. 2).

Fig. 2. Effects of bean pod mottle (BPMV- Valverde) and tobacco ringspot (TRSV) infection on soybean pod size. BPMV- green stem (left), TRSV - green bean (right).

C. Pod removal at different growth stages

A pod removal study was conducted this year with four cultivars: two indeterminate and two determinate cultivars that were late maturity group 4 and maturity group 5. Flowers were removed at R2 and pods were removed at R4, R5 and R6. When flowers were removed at R2, there was a slight delay in maturity, but by R5 all plants caught up and senesced at the same time. Removing pods at R4 delayed maturity throughout the season with the depodded plants remaining one to two growth stages behind the control plants. Depodding at R5 delayed maturity even more with most of the depodded plants only reaching R5 by the first frost. Depodding at R6 delayed maturity even further with plants reaching R4 and then not developing further. Plants depodded at R5 and R6 and several small pods at each node along with the more developed pods. This study showed that the later depodding occurs, the less likely the plants are to recover and produce mature seed. Some of these symptoms were similar to what was observed in fields affected by GBS.

Fig. 3. Left: Depodding study showing green plants that were depodded at different growth stages. Right: Plants depodded at R5 with a mixture of pods with developing seed and clusters of small pods.

Illinois

NCERA 200 Report – University of Illinois / USDA-ARS
November 2011
Investigators

Leslie L. Domier, Glen L. Hartman, Curtis B. Hill, Houston A. Hobbs, Nancy K. McCoppin, Thanuja Thekke Veetil, Sushma Jossey, Sungyul Chang

Virus distribution and incidence

Houston Hobbs collected 30 soybean leaf samples from each of 10 commercial soybean fields in each of 12 Illinois counties for a total of 3,600 plants. RNA was extracted from the pooled samples and sequenced with an Illumina sequencer. The analysis produced about 40 million reads which were assembled into contigs after removal of soybean sequences. BPMV and SVNaV were the two most abundant viruses in Illinois soybean fields, followed by AMV, TRSV, SbDV,TSV, CMV, TMV, in order of decreasing abundance. SMV was not detected in the samples analyzed (Table 1). While BPMV infected more soybean plants in Illinois, SVNaV was more widely distributed and was detected in 11 of 12 counties surveyed, while BPMV was detected in 7 of 12 counties.

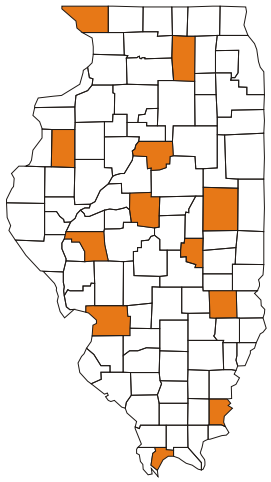

Figure 1. Counties surveyed for virus incidence

Table 1. Detection of virus sequences total RNA from 3,600 field-grown soybean plants

Sequence matches	**Virus**
76,136	*Bean pod mottle virus*
9,277	*Soybean vein necrosis associated virus*
2,055	*Alfalfa mosaic virus*
831	*Tobacco ringspot virus*
298	*Soybean dwarf virus*
14	*Tobacco streak virus*
4	*Tobacco mosaic virus*
2	*Cucumber mosaic virus*
2	*Prunus necrotic ringspot virus*
1	*Cucumber green mottle mosaic virus*
0	*Soybean mosaic virus*

Table 2. Confirmation of high throughput sequencing results by RT-PCR

County	**SVNaV**	**BPMV**	**SbDV**	**AMV**	**TRSV**	**SMV**
Champaign	+	+	-	-	-	-
DeKalb	+	+	-	-	-	-
Gallatin	+	-	-	-	-	-
Jasper	+	+	-	-	-	-
Jo Daviess	+	-	-	-	+	-
Logan	+	+	-	-	-	-
Madison	+	-	-	-	-	-
Morgan	+	-	-	-	-	-
Moultrie	+	+	-	+	-	-
Pulaski	+	+	+	-	-	-
Warren	+	-	+	-	-	-

Woodford	+	-	+	+	-	-
Total	**12**	**6**	**3**	**2**	**1**	**0**

Evaluation of Commercial Varieties for *Soybean mosaic virus* (SMV) Resistance

To provide soybean growers information about the responses of commercial soybean varieties to SMV infection, Houston Hobbs rated 325 commercial soybean varieties for their responses to inoculation with SMV G1. Just nine soybean lines, FS Hisoy HS 37L12, Merschman Grant 1236LL, Hoblit 372 LL, Merschman Tucson 1249LL, Merschman Hood 1150LL, Unisouth Genetics USG 74G99 L, Nutech 3372 L, Dyna-Gro 35P53, and Gateway 473, were resistant to SMV G1. The responses of all varieties were posted on the Varietal Information Program for Soybeans (VIPS) website (www.vipsoybeans.org).

Genetics of SMV seed transmission

Seed-borne infections are the primary sources of inoculum for SMV infections in the Midwest. Candidate genes (soybean homologues *DCL3* and *RDR6*) identified in previous mapping studies were sequenced from five soybean germplasm accession with low (<0.5%) seed transmission of SMV and five soybean germplasm accessions with high (>25%) seed transmission of SMV. Allelic frequencies of some SNPs in the germplasm lines were consistent with parental genotypes, while other positions were not. This limited data set supports the hypothesis that the candidate genes are associated with resistance to embryo invasion, but additional experiments with larger numbers of soybean lines are needed. Full-length cDNAs of the three candidate genes form each soybean parental line and the P1-HC/Pro coding regions from SMV isolates with low (SMV G2) and high (SMV 413) seed transmission SMV 413 and SMV G2 were cloned into bimolecular fluorescence complementation vectors for interactions studies.

Role of SMV genes in seed transmission in soybean

Helper component protease (HC-Pro) and coat protein (CP) of other potyviruses have been shown to be involved in aphid and seed transmission and suppression of RNA silencing. To study the role of these genes in SMV seed transmission, Sushma Jossey constructed recombinant viruses from two isolates of SMV isolates with low (SMV G2) and high (SMV 413) seed transmission and induced single amino acid changes by site-specific mutagenesis. Plants have been inoculated with the mutant and chimeric clones.

Table 3. Allelic frequencies in SNPs in predicted coding regions of candidate genes associated with seed transmission of SMV in plant introductions with low (PI548391) and high (PI88799) and pools of five PIs with low and high rates of transmission of SMV through seed.

		Nucleotide Frequencies			
Gene	Position	PI548391 (Low)	PI88799 (High)	Low Pool[1]	High Pool[2]
GmDCL3 (*Glyma04g06060*)	**3190**[3]	**1.0 T**	**1.0 C**	**1.0 T**	**1.0 C**
	3789	1.0 T	1.0 C	ND	ND
GmRDR6-04 (*Glyma04g07150*)	**177**	**1.0 A**	**1.0 T**	**1.0 A**	**0.5 A / 0.5 T**
	566	1.0 C	0.5 C / 0.5 T[4]	1.0 C	0.5 C / 0.5 T
	2004	**0.5 C / 0.5 T**	**1.0 C**	**0.5 C / 0.5 T**	**1.0 C**

GmRDR6-04 (*Glyma06g07250*)	**840**	**0.5 A / 0.5 G**	**1.0 G**	**0.5 A / 0.5 G**	**1.0 G**
	1654	1.0 G	0.5 A / 0.5 G	0.8 G / 0.2 A	1.0 G
	1905	**0.5 A / 0.5 G**	**1.0 G**	**0.5 A / 0.5 G**	**1.0 G**

[1] Pool of DNA from five soybean lines with less than 0.5% transmission of SMV through seed.
[2] Pool of DNA from five soybean lines with greater than 25% transmission of SMV through seed.
[3] Bolded values are equivalent parental soybean line and pooled samples.
[4] Two nucleotides are shown because genes on chromosomes 4 and 6 were sequenced simultaneously.

Functional genomics of soybean seed development

In collaboration with Said Ghabrial at the University of Kentucky, a series of potential vectors for virus induced gene silencing (VIGS) based on TSV were constructed (Figure 2). Sushma Jossey and Nancy McCoppin TSV RNAs 1, 2, 3 and 4 introduced a multicloning site downstream of a truncated 2b open reading frame in RNA2 of an infectious clone of an Illinois soybean isolate of TSV. The vector was highly infection in soybean seedlings when inoculated biolistically, and retained inserted sequences after seed transmission. Analysis of effects of soybean gene inserts on mRNA levels is being analyzed.

Ajay Singh and Anindya Bandyopadhyay a second set of DNA-based VIGS vectors derived from a Kentucky isolate of TSV by cloning TSV cDNAs into a binary plasmid. DNAs of these vectors are introduced into plants by a bacterium (*Agrobacterium tumefaciens*) that very efficiently moves DNA into plants, which significantly simplifies inoculation of plants with the recombinant viruses. To allow the Kentucky vectors to accommodate larger gene fragments than the Illinois vectors, the two genes normally encoded by RNA3 were split between two separate RNA*s*. The Kentucky TSV-based vectors have been tested in tobacco and shown to express inserted bacterial genes (e.g., green fluorescent protein) and to silence targeted plant genes (e.g., PDS). The Kentucky VIGS vectors were readily transferred to soybean by rub inoculation of sap from infected tobacco plants.

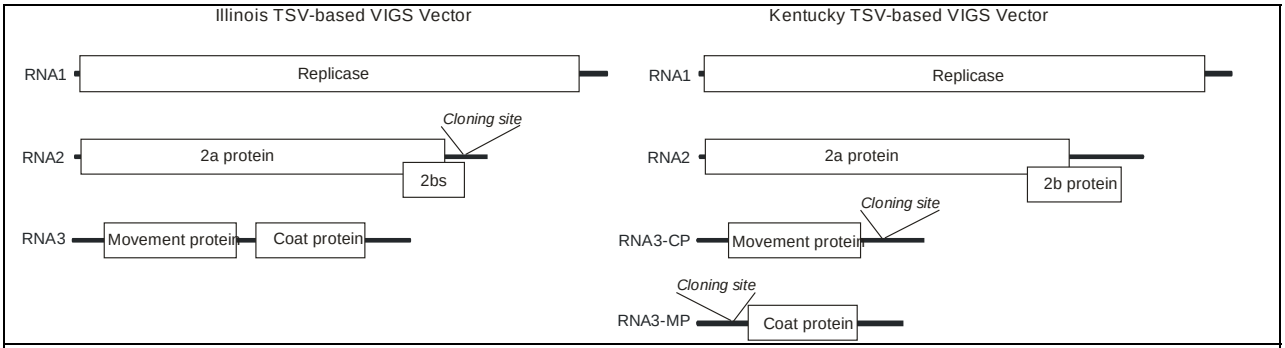

Figure 2. Construction of vectors for virus-induced gene silencing (VIGS) from *Tobacco streak virus* (TSV). The TSV genome consists of three RNA chromosomes (solid black lines). Each RNA encodes one or two proteins (open boxes). For the Illinois VIGS vector, a cloning site for insertion of foreign gene sequences was added downstream of a truncated 2b gene. For the Kentucky VIGS vectors, RNA3 was split into two RNAs where sequences encoding the movement protein or coat protein were each removed from one of the new RNA3s and cloning

sites for the insertion of foreign genes were added to each modified RNA3.

Identification of soybean viruses infecting pathogens of soybean

Publications:

Agrindotana, B.O., Ahonsia, M.O., Domier, L.L., Gray, M.E., Bradley, C.A. 2010. Application of Sequence-Independent Amplification (SIA) for the Identification of RNA Viruses in Bioenergy Crops. Journal of Virological Methods. 169(1):119-128.
Bekal S., Domier, L.L., Niblack, T.L., and Lambert, K.N. 2011. Discovery and initial analysis of novel viral genomes in the soybean cyst nematode. Journal of General Virology 92(8):1870-1879
Damsteegt, V. D., Stone, A. L., Kuhlmann, M., Gildow, F. E., Domier, L. L., Sherman, D. J., Tian, B., and Schneider, W. L. 2011. Acquisition and transmissibility of U.S. Soybean dwarf virus isolates by the soybean aphid, Aphis glycines. Plant Disease 95:945-950.
Domier, L.L., Hobbs, H.A., McCoppin, N.K., Bowen, C.R., Steinlage, T.A., Chang, S., Wang, Y., and Hartman, G.L. 2011. Multiple loci condition seed transmission of Soybean mosaic virus in soybean. Phytopathology 101:750-756.
Richardson, M.L., Lagos, D.M., Mitchell, R.F., Hartman, G.L.,and Voegtlin, D.J. 2011. Life history and morphological plasticity of the soybean aphid, *Aphis glycines*. Entomol. Experim. Appl. 140: 139-145.

Iowa

NCERA 200 report , Iowa State University, November 2, 2011
Participants: John H. Hill, Steve Whitham, Chunquan Zhang, Al Eggenberger, Steve Cannon, Michelle Graham, Randy Shoemaker, Kate Martin, Jianzhong Liu, Sehiza Grosic, Wenli Liu

Efforts have focused on using BPMV as a vector for revealing signaling networks in resistance to abiotic stress in soybeans. A cooperative interstate team includes Craig Grau (WI), Dean Malvick (MN), Melissa Mitchum (MO), Thomas Baum (ISU), Leonor Leandro (ISU) and Kerry Pedley (Ft. Detrick). Approximately 650 BPMV VIGS constructs have been developed and are catalogued on SoyBase. Data include clone names, target genes, target sequences, primer sequences, creator, and phenotype description. Information is available at http//www.soybase.org/vigsnotebook/ but at present is password protected and available only for the project participants. At present, the BPMV vector has been distributed to about 30 investigators nationally and internationally for research.

Improved/optimized DNA-based high-throughput BPMV VIGS vector
We constructed of a new DNA based high-throughput DNA-based *Bean pod mottle virus* (BPMV) vector for gene expression and/or VIGS (virus induced gene silencing) in soybeans and other legumes. This vector is based upon an endemic BPMV virus isolate found in *Desmodium illinoense* in a relic prairie in central Iowa. A patent application has been filed on this vector and it is being distributed to numerous soybean researchers under appropriate MTA's and permits.

Identified/selected key genes using various data sets to test for stress resistance
At least 650 genes of interest have been identified as of interest for study of stress resistance

Cloned selected gene fragments and insert into optimized VIGS vector. Test vector activity in soybeans
Fragments of the above 650 genes of interest have been inserted into the VIGS vector for study of stress resistance. The vector was used to inoculate Williams 82 soybean plants and soybean tissue containing the VIGS vector with gene insert has been dried down and placed in cold storage for distribution to collaborators.

Cooperators assess and record plant symptoms/phenotype.
Collaborators have described and recorded plant phenotype of those that have been inoculated with the VIGS vector. Of particular interest are phenotypes that result in conversion from a resistant to a susceptible reaction as a result of inoculation with the VIGS vector containing the gene insert. Data are assessed by all collaborators on the project through periodic (ca. every six months) meetings to coordinate and evaluate research as well as to assess challenges. A summary of research publications is listed below.

Performed molecular analyses to confirm gene silencing where assessment of plant symptoms suggests response of interest.
Molecular analyses have been performed to confirm gene silencing when plant phenotype suggests that silencing has occurred. Silencing has generally been approximately 80%.

Publications:

Zhang, C., Bradshaw, J. D., Whitham, S. A., and Hill, J. H. 2010. The development of an efficient multipurpose Bean pod mottle virus viral vector set for foreign gene expression and RNA silencing. Plant Physiol. 153:52-65.

Pandey, A. K., Yang, C., Zhang, C., Graham, M., Horstman, H. D., Lee, Y., Zabotina, O. A., Hill, J. H., Pedley, K. F., and Whitham, S. A. 2011. Functional analysis of the Asian soybean rust resistance pathway mediated by *Rpp2*. MPMI 24:194-206.
Hajimorad, M. R., Wen, R.-H., Eggenberger, A. L., Hill, J. H., and Saghai Maroof, M. A. 2011. Experimental Adaptation of an RNA Virus Mimics Natural Evolution. J. Virol. 85:2557-2564.

Liu, J. Z., Horstman, H. D., Braun, E., Graham, M. A., Zhang, C., Navarre, D., Qiu, W. L., Lee, Y., Nettleton, D., Hill, J. H., and Whitham, S. A. 2011. Soybean homologs of MPK4 negatively regulate defense responses and positively regulate growth and development. Plant Physiol. *In press.* doi: 10.1104/pp.111.185686

Pandey, A. K., Yang, C., Zhang, C., Graham, M. A., Horstman, H. D., Lee, Y., Zabotina, O. A., Hill, J. H., Pedley, K. F., and Whitham, S. A. 2011. Functional analysis of the Asian soybean rust resistance pathway mediated by *Rpp2*. Mol. Plant Microbe Interact. 24: 194–206. doi: 10.1094/MPMI-08-10-0187 (Highlighted as the Editor's Pick for the February 2011 issue of Mol. Plant Microbe Interactions)

Bradshaw, J. D., Zhang, C., Hill, J. H., and Rice, M. E. 2011. Landscape epidemiology of *Bean pod mottle comovirus*: Molecular evidence of heterogeneous sources. Arch Virol. 156:1615-1619.

He, B., Hill, J. H., and Hajimorad, M. R. 2011. Factors to improve detection of *Alfalfa mosaic virus* in soybean. Online. Plant Health Progress doi: 10.1094/PHP-2010-0926-02-RS.

Haidi, B., Bradshaw, J., Rice, M., and Hill, J. Bean leaf beetle (Coleoptera:Chrysomelidae) and *Bean pod mottle virus* in soybean: Biology, ecology, and management. Journal of Integrated Pest Management. In press.

Zhang, C., Whitham, S. A., Hill, J. H. 2011. Virus-induced gene silencing in soybean and common bean. In *Methods in Molecular Biology*. Edited by A. Becker. Humana Press, Totowa, NJ. *In press.*

Pandey, A. K., Yang, C., Zhang, C., Pedley, K. F., Graham, M., Hill, J. H., and Whitham, S. A. 2010. Identification of soybean genes that contributes to *Rpp2*-mediated defense against Asian soybean rust using VIGS. Phytopathology 100:S96.

Pedley, K. F., Pandey, A. I., Kendrick, M. D., Zhang, C., Graham, M. A., Whitham, S. A., and Hill, J. H. 2011. Functional analysis of Asian soybean rust resistance pathways using virus-induced gene silencing. Phytopathology 101:S139.

Pandey, A. K., Yang, C., Zhang, C., Graham, M. A., Hill, J. H., Pedley, K. F., and Whitham, S. A. 2011. Functional analysis of the *Rpp2*-mediated Asian soybean rust disease resistance pathway. American Society of Plant Biologists. Abs. # 19057. http://abstracts.aspb.org/pb2011/public/P19/P19057.html

Kentucky

Ghabrial, S. A.
University of Kentucky
Summary of work

1. In collaboration with Les Domier's laboratory, we developed tobacco streak virus (TSV) as a gene silencing and expression vector in soybean and tobacco. The fact that TSV readily invades meristems and embryos maskes it potentially useful for functional genomics studies of genes in those tissues.

2. We adapted the BPMV-based VIGS vector, developed in my laboratory, for functional genomics in common bean (Diaz-Camino et al., 2011).

3. We have previously demonstrated that silencing of genes encoding omega-3 fatty acid desaturase (*GmFAD3*) alters seed size and accumulation of BPMV as well as enhancing resistance to plant pathogens. Our study also showed that silencing of *GmFAD3* enhances JA

accumulation and, thereby, susceptibility to BPMV (Singh et al., 2011). We continue to investigate the role of JA in plant defense to BPMV and other viruses.

4. We have recently isolated virus-infected hypovirulent isolates of important soybean fungal pathogens (*Sclerotinia sclerotiorum*, *Phomopsis langicola*) and demonstrated co-transmission of the mycoviruses and hypovirulence traits from infected isolates to virus-free isolates using genetically-marked fungal isolates. The viruses (two mitoviruses and a partitivirus) involved have been characterized at the molecular level. We are investigated means for dissemination of the virus-infected hypovirulent isolates.

Pertinent publications

Diaz-Camino C, Annamalai P, Sanchez F, Kachroo A, **Ghabrial SA**. 2011. An effective virus-based gene silencing method for functional genomics studies in common bean. Plant Methods 2011, 7:16.

Singh AK, Fu DQ, El-Habbak M, Navarre D, **Ghabrial S**, Kachroo A. 2011. Silencing genes encoding omega-3 fatty acid desaturase alters seed size and accumulation of Bean pod mottle virus in soybean. Mol Plant Microbe Interact, 24:506-515.

Soria-Guerra, R. E., Rosales-Mendoza, S., Chang, S., Haudenshield, J. S., Rao, S. S., Hartman, G. L., **Ghabrial, S. A.** and Korban, S. S. 2010. Identifying differentially expressed genes in leaves of *Glycine tomentella* in the presence of the fungal pathogen *Phakopsora pachyrhizi*. Planta 232:1181–1189

Soria-Guerra, R. E., Rosales-Mendoza, S., Chang, S., Haudenshield, J. S., Annamalai, P., Rodriguez-Zas, S., Hartman, G. L., **Ghabrial, S. A.** and Korban, S. S. 2010. Transcriptome analysis of resistant and susceptible genotypes of *Glycine tomentella* during *Phakopsora pachyrhizi* infection reveals novel rust resistance genes. Theor. Appl. Genet. 120, 1315-1333.

McDonald, M., Kendall, A., Bian, W., McCullough, I, Lio, E., Havens, W. M., **Ghabrial, S. A.,** Stubbs, G. 2010. Architecture of the potyviruses. Virology 405, 309-313.

Ohio

2011 Ohio Report

NCERA200: Management Strategies to Control Major Soybean Virus Diseases in the North Central Region

Rouf A. Mian
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Collaborators: Rouf Mian, Peg Redinbaugh, Ron Hammond, Andy Michel, and Feng Qu

1. Developing four recombinant inbred line (RIL) populations for mapping QTL for partial resistance to BPMV using previously identified plant introductions (Mian et al. 2009) as the sources of resistance. We have harvested F5 plants for two mapping populations with 300 RIL progeny in each population. Phenotyping for leaf symptoms and ELISA will be conducted in the greenhouse following mechanical inoculation of each RIL during the Winter.

2. Three years of field evaluation of soybean aphid resistant breeding line with the Rag2 gene was completed and no yield drag was detected in the aphid resistant line.

3. Mapping of QTL for partial resistance to soybean aphid using F6 RIL in PI567301B was completed. Two genes control aphid resistance this in this population. New gene has been named as Rag5. Another novel QTL has been mapped in PI567324.

4. Research on mechanisms of aphid resistance using proteomics and metabolomics is in progress.

5. Field evaluation of transgenic soybeans resistant to AMV, BPMV, and SMV.

6. Nonhost resistance mechanism to BPMV in N. benthamiana.

7. A survey of viruses in Ohio soybean fields (ongoing).

Publications:

Jun, Tae-Hwan, M.A. Rouf Mian and Andrew P. Michel. 2011. Genetic mapping revealed two loci for soybean aphid resistance in PI 567301B. Theor. Appl. Genet. (In press).
Xiuchun Zhang, Shirley Sato, Xiaohong Ye, Anne E. Dorrance, T. Jack Morris, Thomas E. Clemente, and Feng Qu. 2011. Robust RNAi-based resistance to mixed infection of three viruses in soybean plants expressing separate short hairpins from a single transgene. Phytopathology (in press).