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Meeting Strategic Milestones of the National Sclerotinia Research Initiative for 2014

Integrated Research for Disease Management in Sunflower, Canola, Dry Bean, Pea & Lentils and Soybean

Executive Summary

Vision Statement: An integrated research approach will guide the effective development of diagnostic technologies, disease management systems, genomic resources, and crop germplasm exhibiting durable resistance to *Sclerotinia sclerotiorum*. Strategic deployment and use of these resources will help sustain the competitiveness of U.S. canola, pea, lentil, chickpea, common bean, soybean, and sunflower producers in domestic and global markets.

Introduction: The *Strategic Plan for the National Sclerotinia Initiative 2013-2017* provides programmatic transparency to all sectors of the agricultural value-chain and gives the research community a foundation for an integrated research approach for mitigating this devastating disease. The performance measures outlined in the Strategic Plan are relevant to the current needs of U.S. agriculture. Each performance measure defines the actions that will be taken to solve the problem, describes what is promised or will be produced, and provides a mechanism for peer review and assessment of research progress. The current document, *Meeting Strategic Milestones of the National Sclerotinia Research Initiative for 2014* provides an interim accounting of how the research community has addressed the goals and objectives the plan, and provides the basis for rating overall program performance on an annual basis. This document and information regarding the governance and activities of the National Sclerotinia Research Initiative may be accessed at: **http://www.ars.usda.gov/Research/docs.htm?docid=20317&page=3**

Rating Summary:

Sclerotinia Initiative Research Progress Evaluation

	2013	2014	2015	2016	2017
	number of accomplishment citations				
Total Accomlishments	43	58			
Total Milestones	79	79			
Achievement Rating (%)	54.4	73.4			
Total Projects	21	22			
Accomplishments / project	2.0	2.6			
Total Publications	266	283			
Germplasm/Varieties released	41	9			

Achievement Rating: # cited accomplishments/ # published milestones *100

Distribution of Accomplishments across Strategic Plan

Milestone	Milestone #	2013	2014	2015	2016	2017
Crop Germplasm Resources & Genetics		number of accomplishment citations				
PM 1.1: Identify new sources of resistance.						
Germplasm of all NSI crops.	**1**	1	1			
Improved phenotypic methods for validating resistance.	**2**	2	3			
PM 1.2: Transfer new sources of resistance (pre-breeding).						
Common bean breeding lines from interspecific crosses.	**1**		1			
Canola, chickpea, lentil, pea, soybean and sunflower lines.	**2**	1	1			
Sunflower breeding lines from wild species	**3**	1	1			
PM 1.3: Genetic analysis and discovery of QTL						
Breeding pops in canola, bean, pea, soy, and sunflower.	**1**	1	4			
Backcross in sunflower/MAGIC populations in common bean.	**2**	1	1			
GWAS and linkage analysis in common bean & sunflower.	**3**	1	5			
QTL markers in NSI crops.	**4**	1	2			
Metabolic mechanisms with resistance QTL.	**5**	1				
PM 1.4: Pyramid white mold resistance and release cultivars.						
Canola, chickpea, lentil, and pea lines released.	**1**	1	1			
Pinto and other bean market classes released	**2**	1	1			
Interaction of QTL in common bean and soybean.	**3**	1				
Establish disease nurseries.	**4**		1			
Soybean breeding line with Sclerotinia resistance	**5**	1	1			
Commercial & experimental release of sunflower lines.	**6**					
Pathogen Biology & Mechanisms of Resistance						
PM 2.1: Characterize population structure & ecology						
Interaction of pathogen with environmental factors.	**1**					
Biotypes with resistance to new fungicide chemistry	**2**		1			
Characterization of the genetics of fungicide resistance	**3**					
Characterization of ecological types in the population.	**4**					
Associate activity in *Sclerotinia* with specific genetic markers.	**5**					
PM 2.2: Characterize virulence/aggressiveness						
Reactions of isolates on new sources of host resistance.	**1**	1	1			
Collection of isolates with broad aggressiveness	**2**	1	1			
New sources of host resistance isolates	**3**	2				
Criteria for virulence/aggressiveness on specific hosts.	**4**					
PM 2.3: Identify environmental & genetic factors in germination						
Factors that may enhance myceliogenic germination.	**1**	2				
Genetic control ofmyceliogenic/carpogenic germination	**2**					
Genetic events that lead to carpogenic germination.	**3**					
PM 2.4: Temporal gene expression profiles of Sclerotinia.						
Transcriptomic, genomic, and metabolomic data bases.	**1**	1	3			
Improved gene annotation using transcriptomic data.	**2**	1				
Genetic control of infection processes	**3**	1	2			
PM 2.5: Identification and verification of candidate genes.						
Development and maintenance of culture collections.	**1**					
Transcriptome profiling analyses.	**2**	1				
Promoters for RNAi constructs.	**3**		1			
Inventory of genes involved in pathogenesis.	**4**					
Functional verification of candidate genes.	**5**		1			
Gene Discovery & Phenotypic Association						
PM 3.1 Molecular marker resources for QTL Discovery.						
Core set for deployment in genotyping systems	**1**	1				
DNA markers for annotation of crop genomes	**2**	1				
Allele specific DNA markers for disease resistance	**3**					
Allele specific DNA markers for quality traits	**4**					

Milestone	Milestone #	2013	2014	2015	2016	2017
Allele specific DNA markers for yielding ability	5					
PM 3.2 Genetic and physical maps for Sclerotinia resistance.						
Compilation of genotypic data from mapping populations	1		1			
Improved genetic maps for Sclerotinia resistance genes	2	1	1			
Consensus genetic map for Sclerotinia resistance genes	3		1			
Core sets of markers for disease resistance	4		1			
Core sets of markers for quality traits	5					
Core sets of markers for agronomic traits	6					
Place candidate genes on consensus genetic map	7					
3.3 Characterize gene models for pathology & resistance.						
Standardized annotation of maps among crop species.	1					
Transcriptomic, proteomic & metabolomic annotation of QTL	2	1	4			
Biological mechanisms for resistance, such as: oxalic acid	3	2	4			
Gene atlas with a comprehensive list of all expressed genes.	4		1			
Identification of specific genes within QTL	5		1			
3.4 Genome mapping and allelic analysis through GWAS.						
High resolution exome maps of QTL	1		1			
Specific alleles that mediate Sclerotinia resistance.	2		2			
GWAS studies of phenotypic variation in disease resistance.	3	3	1			
Haplotype maps correlated with genetic variation for resistance.	4	1				
Allele specific markers for pyramiding genes	5		1			
PM 3.5 Develop improved resistance with biotechnology.						
Inventory validated resistance genes, promoters, & constructs	1					
Transcription factors and elements of gene regulation	2		1			
Functional tests in model plants to determine candidate genes	3	3				
Efficacy of transformed genes on defense control	4	2	1			
Genome editing to modify resistance to Sclerotinia	5		1			
Crop germplasm transformed with putative anti-fungal genes.	6					
Disease Management & Crop Production						
PM 4.1: Optimize fungicide application programs.						
Collection of *S. sclerotiorum* isolates for fungicide sensitivity	1	1				
Economic return of fungicide applications	2	1				
Management guides for fungicides	3	1				
Spray technologies for fungicide performance	4					
Ttiming of fungicide applications.	5	1	1			
PM 4.2: Develop bio-control alternatives.						
Efficacy of current bio control agents	1					
Novel antagonists of *S. sclerotiorum*	2		1			
Management guides for bio fungicides	3					
PM 4.3: Develop disease-warning systems.						
Models that calculate risk of disease development	1					
Effect of tillage practices on Sclerotinia survival;	2					
Economic loss models	3					
Define risk levels for crop-specific fungicide decisions	4					
PM 4.4: Optimize cultural practices for disease management.						
Variety selection based on disease reaction	1					
Publication of disease management information	2		1			
Epidemiological information on disease development.	3					
Total Accomlishments		**68**	**58**			
Total Milestones		**79**	**79**			
Achievement Rating (%)		**86.1**	**73.4**			
Total Projects		**21**	**22**			
Publications		**266**	**283**			

2014 Accomplishment Highlight Summary

- Selected sunflower germplasm with combined resistance to S. sclerotiorum head rot, stalk rot, phomopsis and stem canker among backcrossed progenies of interspecific hybrids or amphiploids 2n=34 chromosomes.
- Improved the ascospore production method developed by retired pathologist Dr. Michael Boosalis; the original isolate (NEB-274) and one other produced ascospores with no preconditioning other than scarification.
- Determined that Sclerotinia disease onset at early bloom stage affected greatest disease levels and seed yield loss in dry beans, soybeans, and sunflowers.
- Validated white mold (WM) resistance from P. coccineus and P. vulgaris in advanced snap bean breeding lines; advanced populations with WMG904/20-3 h, WMG39 and A195 sources of resistance.
- Determined inheritance of resistance genes in F1 to F3 populations of interspecific cross combinations between H. tuberosus, H. strumosus, H. decapetalus, H. hirsutus, H. divaricatus, H. occidentalis, and H. salicifolius with HA 410 and a susceptible inbred line HA 234.
- Identified QTL in a F6:7 RIL population from the cross of cultivated sunflowers HA 441 and RHA 439; and an AB-RIL population BC2F5:6 from the cross of HA 89 and wild annual species H. argophyllus (PI 494573, resistant parent).
- Evaluated F1 populations among elite sunflower breeding lines showing increased levels of resistance in the field plus 3700+ individual F2 plants from 25 RIL populations to determine mechanisms of resistance.
- Developed a common bean linkage map from 160 F5:7 lines (Orion/USPT-WM-12) for white mold reaction; genotyped RIL population with the BARCBean6K_3 BeadChip (6000 SNPs), and established a QTL analysis (WM7.1 and WM8.3) pipeline for RNA-seq and fine mapping.
- Developed 500+ dry bean breeding lines with resistance by GWAS; associated SNP markers with phenotypes; mapped and validated QTL for resistance
- Developed a WM-MAGIC (Multi-parent Advanced Generation Inter-Cross) population for future fine-mapping and improved common bean germplasm.
- Evaluated two doubled haploid lines, NEP32 and NEP63 (susceptible and resistant) in a F2 population exhibiting transgressive segregation for white mold resistance; conducted RNA-Seq to identify ~ 9000 splice variants and ~ 3400 novel transcripts, 5 QTLs for resistance to SSR, one gene was identified as a potential candidate for resistance on C01 of the canola genome.
- Evaluated Sclerotinia stalk rot infection QTL analysis by GBS; developed two public SNP genetic maps containing more than 15,000 markers; determined GBS was cost effective for SNP discovery and genotyping in sunflower.
- Conducted GWAS on snap bean, Mesoamerican, and Andean Diversity Panels using GBS; discovered 35,000 SNPs distributed throughout the genome; Four SNPs showed significant associations with

field WM disease severity and mapped on Pv08 different from WM8 3; SNPs mapped on Prva 03, 06, 07, 08, 09, 10 and 11.

- Evaluated a diverse set of early maturing (maturity groups I, II and III) 280 soybean plant introductions selected based on 52,041 SNP marker data for resistance nursery and greenhouses with the drop-mycelium method.
- Used meta-QTL analysis to refine and validate QTL reported with resistance: WM2.2, WM2.3, WM7.2, WM8.4, WM 9.2 and WM 11.1 which mapped to five different chromosomes in the bean genome.
- Developed F2 populations of RoundUp Ready canola and mapped five significant SNP markers associated with resistance to chromosomes A01, A03, C01, and C08.
- Pyramided QTL that represent different sources with plant architectural avoidance traits for field resistance to white mold along with yield, lodging, and agronomic desirability in common bean.
- Identified partial resistance to S. sclerotiorum in secondary gene pool and in adapted dry and snap bean lines; released a snap bean, a pinto, a bayo and six kidney lines with moderate WM resistance.
- Tested 10 soybean lines in the Uniform Soybean Tests – Northern Region (19 locations in 10 US states and 1 Canadian province), for yield and other agronomic traits.
- Genotyped all 366 isolates of S. sclerotiorum collected over the past 6 years from nine bean production regions in the USA Mexico and France using 16 polymorphic microsatellites and UPGMA cluster analysis.
- Developed a standardized screening greenhouse straw test and the CIAT scale for rating all field screening tests.
- Identified 17 QTL in the S. sclerotiorum genome for virulence on soybean and dry bean; 5 loci had highly significant marker trait associations and 12 loci associated with virulence.
- Obtained 150X sequence coverage of whole S. sclerotiorum genome; Identified 15 mutants with reduced virulence in a T-DNA insertion library; developed partial expressed gene atlas for pathogen and lentil
- Mapped metabolic phenotypes to identify genetic loci (mQTL) that co-localize with the resistance phenotype and identify candidate resistance genes in common bean.
- First use of Linkage Disequilibrium to validate recombination due to cross-over not mutation in the S. sclerotiorum genome.
- Found that genes governing lignin, pectin and flavonoid metabolism are potential candidate genes for nodal resistance in chickpea.
- Cloned Inducible promoters for soybean transformation that included PGIP1 and pER8 to drive the OxO gene, transformed soybean GV3101 Agrobacterium with pER:OxO.
- Identified candidate genes by resequencing the genomes of nine S. sclerotiorum isolates from three different mycelial compatibility groups to identify hypervariable genes; validated function of candidate genes by RNAi and VIGS; assayed for mycelial compatibility and frequency of mycovirus transmission through hyphal anastomosis.

- Found 5 Arabidopsis genes encoded two putative precursors of peroxidases (Psat_118093 and Psat_116532), a chalcone synthase (Psat_107301), a ferulate 5-hydroxylase (Psat_117663) and a β-1,3-hydrolase (Psat_111657). All are linked to host defenses up-regulated in PI240515.
- Found 24 hr post inoculation gave best differential transcriptome profile from PI 240515 and Lifter; mechanism of resistance was attributed to genes governing programmed cell death.
- Verified candidate defense genes in silenced soybean transgenic GPCR-RNAi plants susceptible to powdery mildew, confirmed silencing of 14-3-3 gene and ODC2 cellular localization; Candidate genes include: prenyltransferase, protease inhibitor, Glutathione S-transferase, TIR-domain protein, dirigent-like protein, NADH oxidoreductase, chalcone synthase, cytochrome p450.
- Conducted GBS on a F2 canola population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers
- Conducted functional tests of MED16 mutants, the ODC2 gene was functionally characterized to regulate oxalate degrading enzymatic activity when overexpressed in Arabidopsis.
- Mapped the HSS1 gene in Arabidopsis and demonstrated loss of function confers extreme susceptibility to Sclerotinia infection when mutated; identified a B. napus ortholog of HSS1 (BnHss1).
- The oxalate decarboxylase gene (ODC2) gene from pathogen was fine mapped the A. thaliana
- Showed the HSS1 gene encoded Mediator subunit MED16, a transcription factor complex required for resistance by blocking JA ET defense and required for WRHY33 activation of PDF1.2.
- Developed effective and durable disease resistance for Sclerotinia stem rot of canola through transgenic and/or cisgenic engineering of the host using two genes, one from a host plant and another from the pathogen that block disease when over-expressed in canola.
- Found that current recommendations for applying fungicides at early bloom (soybeans, dry beans) and again10 to 14 days later (dry beans) was moderately effective at managing Sclerotinia under early disease onset and moderately to highly effective at managing Sclerotinia under intermediate and late disease onset.
- Evaluated Asteraceae family root exudate effects on myceliogenic germination of sclerotia.
- Published guides to improve use of fungicides for management of Sclerotinia in dry beans and soybeans; economic yield loss models, and maintained mist nurseries for disease assessments in sunflower.

Milestones for Sclerotinia Research - 2014

Accomplishment Coding: Goal . Performance Measure . Milestone . Plan of Work (i.e. 1.1.1.19)

Crop Germplasm Resources & Genetics

Goal 1: Identify novel germplasm sources with higher levels of field resistance effective against a wide range of aggressive *Sclerotinia sclerotiorum* isolates.

PM 1.1: Identify new sources of resistance in plant germplasm.

- Germplasm accessions of canola, chickpea, lentil, pea, and sunflower, and wild crop relatives with resistance to S. sclerotiorum are identified and used in breeding programs.

1.1.1.19 USDA ARS scientists at Fargo ND phenotyped 260USDA Plant Introductions for resistance to head rot and stalk rot in multiple, separate, inoculated field trials; and Identified germplasm with superior Sclerotinia resistance for incorporation into breeding program and for candidate gene and genome wide association mapping for effective marker-assisted selection. Resistance to Phomopsis and stem canker also was evaluated. One gene family was particularly important in basal stalk rot resistance in sunflower; multiple genes are responsible for resistance to stalk rot, Phomopsis and stem canker. Advanced existing populations and breeding lines for stalk and head rot resistance. Improved phenotypic methods for identifying and validating resistance to *S. sclerotiorum*, in accessions from USDA and World germplasm collections.

- Improved phenotypic methods for identifying and validating resistance to S. sclerotiorum in accessions from USDA and World germplasm collections.

1.1.2.11 USDA ARS scientists at Fargo ND used field misting facilities at Staples, MN, and Carrington, ND to evaluate stalk rot resistance in backcrossed progenies of interspecific hybrids or amphiploids 2n=34 chromosomes.

1.1.2.19 USDA ARS scientists at Fargo ND improved the ascospore production method developed by retired pathologist Dr. Michael Boosalis at the University of Nebraska, Lincoln, NE. The original isolate (NEB-274) and one other produced ascospores with no preconditioning other than scarification, while four isolates failed to produce any apothecia. This method produced predictably large quantities of ascospores, but it is highly isolate-dependent.

1.1.2.22 Scientists at NDSU determined that timing of Sclerotinia disease onset affected disease levels and seed yields differently in dry beans, soybeans, and sunflowers. In dry beans, overall Sclerotinia disease levels were highest when Sclerotinia developed at early bloom, and the yield loss was highest when Sclerotinia developed at early bloom. In soybeans, overall Sclerotinia disease levels were highest when Sclerotinia developed at early bloom. In sunflowers, overall disease levels were highest at either at early or late bloom.

PM 1.2: Transfer and adapt new sources of resistance genes into useful plant germplasm (pre-breeding).

- Common bean breeding lines derived from interspecific crosses with effective resistance in multiple environments and against a range of aggressive isolates.

1.2.1.25 Scientists from USDA ARS at Pullman WA, Oregon State University and NDSU validated white mold (WM) resistance from P. coccineus and P. vulgaris in advanced snap bean breeding lines; advanced populations. WMG904/20-3 was the best source of P. coccineus resistance. Also crossed WMG39 to the great northern 'Spinel'. Developed populations with A195 source of resistance in a snap bean background.

- Canola, chickpea, lentil, pea, soybean and sunflower lines selected from un-adapted accessions with confirmed resistance to Sclerotinia stem rot and evaluated for agronomic traits.

1.2.2.11 USDA ARS scientists at Fargo ND made seven cross combinations between H. tuberosus, H. strumosus, H. decapetalus, H. hirsutus, H. divaricatus, H. occidentalis, and H. salicifolius were made with HA 410, followed by backcrossing to obtain new resistant lines and to diversify resistance gene sources. Conducted inheritance studies between new resistant lines crossed with susceptible inbred line HA 234. Evaluated F1, F2, and F3 progeny families. Transferred major resistance QTLs into lines HA 410 or HA 441.

- Sunflower breeding lines with enhanced resistance to Sclerotinia stalk rot derived from wild annual and perennial species via interspecific hybridizations. Alien chromosome addition stocks characterized and used for resistance breeding.

1.2.3.11 USDA ARS scientists at Fargo ND Increased the number of 2n=34 progeny families for field testing, and 2n=36 plants from selfed 2n=35 plants, expected to be disomic additions, were tested in the field to identify major resistance QTLs associated with specific chromosomes. Mapped the disomics to specific linkage groups of the sunflower RFLP map.

PM 1.3: Genetic analysis and discovery of quantitative trait loci (QTL) that confer resistance to Sclerotinia

- Bi-parental breeding populations generated in canola, common bean, pea, soybean, and sunflower for identification of QTL associated with Sclerotinia resistance from diverse sources.

1.3.1.13 USDA ARS scientists at Fargo ND Identified QTL in a F6:7 RIL population from the cross of cultivated sunflowers HA 441 and RHA 439; and an AB-RIL population BC2F5:6 from the cross of HA 89 and wild annual species H. argophyllus (PI 494573, resistant parent).

1.3.1.14. Scientists from NDSU established and evaluated several F1 populations among elite breeding lines or varieties and accessions showing increased levels of resistance in the field. More than 3700 individual F2 plants from 25 populations were harvested and used to develop RIL populations to study the genetics of the resistance mechanisms. .

1.3.1.15 Scientists from USDA ARS at Pullman WA, Oregon State University and NDSU

examined phenotypic interaction among major QTL conferring partial resistance to WM in common bean. 160 lines from the RI population (Orion/USPT-WM-12) in F5:7 were phenotyped for white mold reaction (Resistant parent USPT-WM-12, a pinto; Great northern Orion was susceptible). Genotyped RIL population is for SNPs with the BARCBean6K_3 BeadChip (6000 SNPs). Developed a common bean linkage map and established a QTL analysis (WM7.1 and WM8.3) pipeline for RNA-seq and fine mapping.

1.3.1.21 Scientists at Michigan State University developed over 500 breeding lines by crossing resistant with susceptible parents and evaluated resistance in nursery and greenhouses. Lines were genotyped with SNP markers associated with resistance by GWAS. SNP marker and phenotypes mapped and validated QTL for resistance

- Advanced backcross populations in sunflower and MAGIC populations in common bean used to identify, validate and fine map QTL identified from exotic sources including interspecific populations.

1.3.2.15 Scientists from USDA ARS at Pullman WA, Oregon State University and NDSU developed a WM-MAGIC (Multi-parent Advanced Generation Inter-Cross) population for future fine-mapping and improved germplasm development with approximately 20 genotypes.

- Use of genome-wide association mapping and linkage analysis to identify and map QTL with major and minor effects in common bean and sunflower.

1.3.3.04 Scientists at NDSU evaluated two doubled haploid lines, NEP32 and NEP63, to inoculations with S. sclerotiorum (susceptible and resistant respectively). F2 population from the cross between these two DH lines transgressive segregation. Conducted an RNASeq to identify resistance genes in canola genome ref. Identified ~ 9000 splice variants and ~ 3400 novel transcripts. Identified 5 QTLs for resistance to SSR. Generated several transformants for these potential genes. One gene was identified as a potential candidate for resistance on C01

1.3.3.10. USDA ARS scientists at Fargo ND tested all applicable statistical methods for GS using cross-validation of subsampled training and selection data sets, to simulate the accuracy that could be achieved in an actual breeding program. These data sets were stratified to avoid bias from the same pedigree, leading to more realistic predictions of accuracy. Phenotypic data individual results were pooled and converted into the statistics of average accuracy and predictive intervals. The latter statistic, in particular, indicated the level of statistical certainty when real selection candidates were evaluated.

1.3.3.13 USDA ARS scientists at Fargo ND evaluated response to Sclerotinia stalk rot infection field trials. Conducted QTL analysis by GBS on individual lines in mapping populations and developed a molecular linkage map with a genome-wide set of SSR and SNP markers. Developed two public SNP genetic maps containing more than 15,000 markers. Determined that GBS (21000 SNP) was cost effective for SNP discovery and genotyping in sunflower.

1.3.3.15 Scientists from USDA ARS at Pullman WA, Oregon State University and NDSU conducted GWAS on snap bean, Mesoamerican, and Andean Diversity Panels using genotype-by-sequencing (GBS). Pinto, navy, black, great northern, pink, and small red market cultivars were re-analyzed by GWAS. Discovered 35,000 SNPs were distributed throughout the genome. Four SNPs showed significant associations with field WM disease severity and mapped on Pv08 in a different location from WM8.3.SNPs mapped on Pv 03, 06, 07, 08, 09, 10 and 11. A

wax bean cv ‘Unidor’ consistently topped the trial in terms of field resistance.

1.3.3.21 Scientists at Michigan State University evaluated a diverse set of early maturing (maturity groups I, II and III) 280 soybean plant introductions selected based on 52,041 SNP marker data for resistance nursery and greenhouses with the drop-mycelium method.

- Breeder friendly QTL-linked DNA markers generated in canola, chickpea, common bean, lentil, pea, soybean, and sunflower and validated for application in marker-assisted breeding.

1.3.4.10 USDA ARS scientists at Fargo ND determined the sunflower genome contains sufficient polymorphic sites to support the use of GBS in the breeding program. Found 60,000 markers GBS data from progenitor lines with whole genome sequence (WGS).

1.3.4.12 Scientists at Michigan State University used meta-QTL analysis to refine and validate QTL previously reported to be associated with resistance. The QTL targeted for validation were WM2.2, WM2.3, WM7.2, WM8.4, WM 9.2 and WM 11.1. These QTL mapped to five different chromosomes in the bean genome. Crossed elite breeding lines from the Mesoamerican gene with validated resistance sources. Marker-assisted backcrosses were performed with the elite lines as recurrent parents. The introgression lines were evaluated in a 3-replicate field nursery.

- Define metabolic mechanisms associated with Sclerotinia resistance QTL in common bean, soybean, and sunflower.

PM 1.4: Pyramid white mold resistance in plant germplasm using traditional and genome sequence guided approaches, and release germplasm lines and cultivars with enhanced resistance.

- Canola, chickpea, lentil, and pea lines with resistance to Sclerotinia and a broad portfolio of desirable agronomic traits developed and released.

1.4.1.06 Scientists at NDSU developed F2 populations and mapped five significant SNP markers associated with resistance located in chromosomes A01, A03, C01, and C08. Developed RoundUp ready canola.

- Breeding lines and cultivars of pinto and other bean market classes released with broadly effective resistance pyramided from diverse sources - Andean, Middle American, and secondary gene pools (*P. coccineus*), in combination with desirable agronomic traits.

1.4.2.12 Scientists at Michigan State University pyramided QTL that represent different sources with plant architectural avoidance traits for field resistance to white mold along with yield, lodging, and agronomic desirability in common bean. Powderhorn, Rosetta, UST-WM12 Zeneth, Zorro had top yield and lowest WM in nursery tests 2014.

- Interaction of combined QTL on level of disease reaction in common bean and soybean elucidated.

- Establish disease nurseries for characterizing field and greenhouse resistance to all pathogenic forms of Sclerotinia in common bean, soybean and sunflower.

1.4.4.20 Scientists from University Nebraska, Michigan State University Seminis Seeds, USDA ARS-Pullman WA, Oregon State University, NDSU, Colorado State University, University Idaho, and Storm Seeds identified partial resistance to S. sclerotiorum in secondary gene pool as well as in adapted dry and snap bean lines. Outcome helped by multiple location screening nurseries; and released a snap bean, a pinto, a bayo and six kidney lines with moderate WM resistance.

- At least one released soybean breeding line with Sclerotinia resistance from multiple sources of resistance as verified by QTL-linked markers, including high yield, and resistance to other diseases or insects.

1.4.5.21 Scientists at Michigan State University evaluated over 70 advanced breeding lines derived from multiple sources of resistance to Sclerotinia at seven locations in Michigan for yield and agronomic traits; also in a disease nursery and greenhouse. 15% of the selected lines will be re-evaluated in disease nursery. Five to 10 lines will be selected and tested in the Uniform Soybean Tests – Northern Region (19 locations in 10 US states and 1 Canadian province), for yield and other agronomic traits. The best lines were released to the public.

- Commercial & experimental release of sunflower lines exhibiting both Sclerotinia head rot and stalk rot resistance.

Pathogen Biology & Mechanisms of Resistance

Goal 2: Understand *Sclerotinia sclerotiorum* biology and development

PM 2.1: Characterize migration/population structure and ecological variability of genotypes.

- Understanding the interaction of pathogen with environmental factors such as temperature and light.

- Identification of biotypes with resistance to new fungicide chemistry

2.1.2.20 Scientists from University Nebraska, Michigan State University Seminis Seeds, USDA ARS-Pullman WA, Oregon State University, NDSU, Colorado State University, University Idaho, and Storm Seeds genotyped all 366 isolates of S. sclerotiorum collected over the past 6 years from nine bean production regions in the USA Mexico and France using 16 polymorphic microsatellites and UPGMA cluster analysis. No significant differences in aggressiveness were found with the straw test. Comparison of isolate sensitivity to five common fungicides did show variation between some isolates.

- Characterization of the genetics of fungicide resistance

- Characterization of ecological types in the population.

- Associate activity in *Sclerotinia* with specific genetic markers.

PM 2.2: Characterize virulence/aggressiveness within the population, identify isolates for use in screening, and monitor durability of host resistance.

- Documented reactions of a broad spectrum of isolates on new sources of host resistance.

2.2.1.20 Scientists from University Nebraska, Michigan State University Seminis Seeds, USDA ARS-Pullman WA, Oregon State University, NDSU, Colorado State University, University Idaho, and Storm Seeds developed a standardized screening greenhouse straw test and the CIAT scale for rating all field screening tests. 9 lines with large cream, pinto, great northern and cranberry seed types and three snap beans with significantly greater WM resistance compared with Beryl. New lines with high WM resistance from wide interspecific crosses are now in seed increases for greenhouse screening.

- Diverse collection of isolates with a broad spectrum of aggressiveness and other characteristics

2.2.2.16 Scientists at NDSU identified seventeen QTL within the S. sclerotiorum genome for virulence. QTL were common to both soybean and dry bean. Five of the loci had highly significant marker trait associations and 12 loci associated with virulence.

- Identification of new sources of host resistance using a new set of aggressive isolates

- Criteria for testing virulence/aggressiveness on specific hosts and tissue types.

PM 2.3: Identify environmental and genetic factors involved in myceliogenic and carpogenic germination of sclerotia.

- Identification of host factors that may enhance myceliogenic germination.

- Genetic control and required environmental conditions governing the processes of myceliogenic and carpogenic germination

- Determination of common and unique genetic events that lead to carpogenic germination in different *Sclerotinia* spp.

PM 2.4: Identify genes that are functional at specific growth and infection stages of Sclerotinia.

- Transcriptomic, genomic, and metabolomic data bases for growth stage-specific genes and infection-related genes from both host and pathogen.

2.4.1.01 USDA ARS scientists at Pullman WA Identified 15 mutants with reduced virulence in a T-DNA insertion library. Sequenced mutants and identified locations of mutated genes in T-DNA insertions. Obtained 150X coverage of whole S. sclerotiorum genome. Developed partial expressed gene atlas for pathogen and lentil

2.4.1.09 Scientists at Colorado State University mapped metabolic phenotypes to identify genetic loci associated with the metabolic source of resistance (mQTL) for leaves and stems. mQTL that co-localize with the resistance phenotype. Data was used to identify candidate resistance genes associated with a metabolic source of resistance to Sclerotinia in common bean.

2.4.1.16 Scientists at NDSU conducted GBS on a diverse natural population of isolates of S. sclerotiorum. Collected lesion length phenotyping data for the isolates on four different hosts.

- Improved gene annotation using transcriptomic data.

- Genetic control of differential infection processes of the *Sclerotinia* spp. in response to different host plants

2.4.3.01 USDA ARS scientists at Pullman WA used LD to validate recombination due to cross-over not mutation in S. sclera genome.

2.4.3.02 Scientists at Michigan State University, NDSU and Dow AgroSciences determined that lignin plugs were involved in nodal resistance. Total lignin content was determined. Greater lignin deposition was found in inoculated PI240515. More lignin in the resistant line. Pectin and flavonoid metabolism is a source of candidate genes..

PM 2.5: Identification and verification of candidate genes involved in Sclerotinia pathogenicity.

- Development and maintenance of relevant natural and derived culture collections for use in phenotypic association.

- Transcriptome profiling approaches for a variety of gene targets and high through put functional analyses.

- Promoters useful for expressing RNAi constructs during infection (e.g., plant-inducible promoters).

2.5.3.03 Promoters useful for expressing RNAi constructs during infection (e.g., plant-inducible promoters). USDA ARS scientists at Urbana IL and Agriculture Food Canada Identified Inducible promoters for soybean transformation. Sclerotinia and wound inducible promoter PGIP1 was cloned to drive the OxO gene. Cloning of DEX promoter was unsuccessful. pER8 vector, an estrogen-inducible promoter was cloned in OxO gene. Transformed soybean GV3101 Agrobacterium with pER:OxO.

- Inventory of genes potentially involved in pathogenesis recovered from ATMT random mutagenesis and transcriptome profiling.

- Functional verification of candidate genes using a systems biology approach to gene silencing and quantitative expression assays.

2.5.5.07 USDA ARS scientists at Urbana IL and the University of Illinois and NDSU used a combination of comparative genomics and targeted gene silencing approaches to test three interrelated hypotheses: 1) S. sclerotiorum genes involved in vegetative incompatibility are

significantly more variable than other genes in the S. sclerotiorum genome; 2) transfection of S. sclerotiorum with a mycovirus modified to express fragments of S. sclerotiorum vic-gene homologues will silence (i.e., significantly reduce the accumulation of mRNAs from) targeted and closely related genes 3) silencing of S. sclerotiorum vic-gene homologues altered anastomosis properties of S. sclerotiorum isolates and b) enhance mycovirus transmission. Candidate genes were identified by resequencing the genomes of nine S. sclerotiorum isolates from three different mycelial compatibility groups to identify hypervariable genes. The expression of individual candidate genes and gene families in S. sclerotiorum potentially involved in vegetative incompatibility were silenced by RNA interference. VIGS infectious clone of Sclerotinia sclerotiorum hypovirus 2 and by DNA-mediated transformation with synthetic genes expressing inverted-repeat sequences. Sclerotinia sclerotiorum isolates silenced for candidate genes were assayed for mycelial compatibility and frequency of mycovirus transmission through hyphal anastomosis.

Gene Discovery & Phenotypic Association

Goal 3: Develop molecular technologies that facilitate breeding progress

PM 3.1 Develop useful molecular marker resources for QTL Discovery.

- Identification of a core set of informative markers for deployment in genotyping systems suitable for use in breeding programs
- DNA markers that contribute to the annotation of the crop genomes
- Allele specific DNA markers that can be used in pre-breeding for disease resistance
- Allele specific DNA markers that can be used in pre-breeding for quality traits
- Allele specific DNA markers for yielding ability and other agronomic traits

PM 3.2 Genetic and physical maps for Sclerotinia resistance.

- Compilation of marker genotyping data for different mapping populations

3.2.1.21 Scientists at Michigan State University developed over 500 breeding lines by crossing resistant with susceptible parents and evaluated resistance in nursery and greenhouses. Lines were genotyped with SNP markers associated with resistance by GWAS. SNP marker and phenotypes mapped and validated QTL for resistance

- Improved genetic maps for Sclerotinia resistance genes

3.2.2.21 Improved genetic maps for Sclerotinia resistance genes. Scientists at Michigan State University developed over 500 breeding lines by crossing resistant with susceptible parents and evaluated resistance in nursery and greenhouses. Lines were genotyped with SNP markers associated with resistance by GWAS. SNP marker and phenotypes mapped and validated QTL for resistance

- A consensus genetic/QTL map for Sclerotinia resistance genes

3.2.3.21 Scientists at Michigan State University developed over 500 breeding lines by crossing resistant with susceptible parents and evaluated resistance in nursery and greenhouses. Lines were genotyped with SNP markers associated with resistance by GWAS. SNP marker and phenotypes mapped and validated QTL for resistance

- Core sets of markers for discovery of candidate genes for disease resistance

3.2.4.21 Scientists at Michigan State University developed over 500 breeding lines by crossing resistant with susceptible parents and evaluated resistance in nursery and greenhouses. Lines were genotyped with SNP markers associated with resistance by GWAS. SNP marker and phenotypes mapped and validated QTL for resistance.

- Core sets of markers for discovery of candidate genes for quality traits

- Core sets of markers for discovery of candidate genes for agronomic traits

- Placement of candidate genes on the consensus genetic map

3.3 Characterize gene models associated with pathology and resistance.

- A standardized methodology for annotation of maps among specified crop species.

- Transcriptomic, proteomic and metabolomic annotation of genome sequences in QTL associate with resistance to Sclerotinia diseases

3.3.2.02 Scientists at Michigan State University, NDSU and Dow AgroSciences found in reference to Arabidopsis, five genes encoded two putative precursors of peroxidases (Psat_118093 and Psat_116532), a chalcone synthase (Psat_107301), a ferulate 5-hydroxylase (Psat_117663) and a β-1,3-hydrolase (Psat_111657). All are linked to host defenses up-regulated in PI240515.

3.3.2.04 Scientists at NDSU evaluated two doubled haploid lines, NEP32 and NEP63, to inoculations with S. sclerotiorum (susceptible and resistant respectively). F2 population from the cross between these two DH lines transgressive segregation. Conducted an RNASeq to identify resistance genes in canola genome ref. Identified ~ 9000 splice variants and ~ 3400 novel transcripts. Identified 5 QTLs for resistance to SSR. Generated several transformants for these potential genes. One gene was identified as a potential candidate for resistance on C01

3.3.2.09 Scientists at Colorado State University identified components of primary and secondary metabolism that regulate physiological resistance observed in the Andean line A195. The metabolic traits differed between leaves and stems. A RIL population of 200 lines generated from a cross between the bean lines A195 (resistant) and Sacramento (susceptible) was evaluated to establish resistance and metabolic phenotypes to Sclerotinia in leaves and stems. The RIL population was genotyped using a single nucleotide polymorphism array.

3.3.2.15 Scientists from USDA ARS at Pullman WA, Oregon State University and NDSU correlated GWAS results with RNA-seq gene expression data. Mapped the WM 7.1 QTL of common bean using RNA-seq data to the common bean reference genome using Tophat. Assembled transcripts from a backcross population: Matterhorn (recurrent parent)*4/ NY6020-4 (resistant source), tissue from four susceptible and four resistant NILs were used to form two pools from RNA-Seq reads.

- Characterization of candidate genes involved in biological mechanisms for resistance, such as: oxalic acid

3.3.3.02 Scientists at Michigan State University, NDSU and Dow AgroSciences found 24 hpi best differential transcriptome profile from PI 240515 and Lifter. Unique expressed genes during pea-S. sclerotiorum interaction. PI240515 vs Lifter in subcategories, cell wall (2.8% vs 2.1%) death (4.9% vs 1.6%), immune system (3.4% vs 2.8%) and regulation of transcription (6.8% vs 4.2%). Mechanism is programmed cell death (PCD).

3.3.3.03 USDA ARS scientists at Urbana IL and Agriculture Food Canada transformed soybean with PGIP1:OxO construct. Forty PCR positive events have been identified and regeneration of culture into plants is ongoing. Verified candidate defense genes in silenced transgenic GPCR-RNAi plants susceptible to powdery mildew. 14-3-3 Silenced transgenic soybean: confirm silencing of 14-3-3 gene. ODC2 cellular localization. Genes candidates: Prenyltransferase, protease inhibitor, Glutathione S-transferase, TIR-domain protein, dirigent-like protein, NADH oxidoreductase, chalcone synthase, cytochrome p450

3.3.3.04 Scientists at NDSU conducted GBS on a F2 population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers

3.3.3.18 Scientists at University of Florida conducted functional tests of MED16 mutants. The ODC2 gene was functionally characterized and confirmed oxalate degrading enzymatic activity, and overexpressed ODC2 in Arabidopsis.

- A commodity-based gene atlas with a comprehensive list of all expressed genes, alternative splice products, identification of co-regulated genes and gene networks.

3.3.4.02 Scientists at Michigan State University, NDSU and Dow AgroSciences found in reference to Arabidopsis, five genes encoded two putative precursors of peroxidases (Psat_118093 and Psat_116532), a chalcone synthase (Psat_107301), a ferulate 5-hydroxylase (Psat_117663) and a β-1,3-hydrolase (Psat_111657). All are linked to host defenses up-regulated in PI240515.

- Identification of specific genes within QTL of importance to Sclerotinia-host interactions

3.3.5.04 Scientists at NDSU conducted GBS on a F2 population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers

3.4 Genome mapping and allelic analysis through Genome-Wide Association Studies.

- High resolution exome maps of genomic regions that harbor QTL for Sclerotinia resistance

3.4.1.04 Scientists at NDSU conducted GBS on a F2 population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers

- Identification of specific alleles in gene families that mediate Sclerotinia resistance.

3.4.2.04 Scientists at NDSU conducted GBS on a F2 population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have

the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers

3.4.2.18 Scientists at University of Florida mapped the HSS1 gene in Arabidopsis and demonstrated loss of function confers extreme susceptibility to Sclerotinia infection when mutated; identified the specific mutation conferring the hss1 phenotype, overexpressed the HSS1 gene in Arabidopsis, and identified a B. napus ortholog of HSS1 (BnHss1). Oxalate decarboxylase gene (ODC2) gene from pathogen functions breakdown of oxalate, a major virulence factor was fine mapped the A. thaliana

- GWAS studies of the trait associated with phenotypic variation in disease resistance.

3.4.3.04 Scientists at NDSU conducted GBS on a F2 population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers

- Haplotype maps correlated with genetic variation for resistance to Sclerotinia diseases.

- Allele specific markers and high-throughput screening methods for pyramiding genes that mediate resistance to Sclerotinia diseases.

3.4.5.04 Allele specific markers and high-throughput screening methods for pyramiding genes that mediate resistance to Sclerotinia diseases. Scientists at NDSU conducted GBS on a F2 population and generated a high density genetic map consisting of ~1850 SNP markers. The SNP markers associated with the QTLs have the potential to be developed as Cleaved Amplified Polymorphic Sequences (CAPS) markers

PM 3.5 Develop plant germplasm with improved resistance using biotechnology and other novel genetic methods.

- An inventory of validated disease resistance genes, promoters, and constructs for transformation into crop germplasm.

- Discovery of transcription factors and elements of gene regulation that mediate expression of disease resistance genes.

3.5.2.18 Scientists at University of Florida showed the HSS1 gene encodes Mediator subunit MED16, a transcription factor complex required for resistance by blocking JA ET defense and required for WRHY33 activation of PDF1.2. MED16 central regulator of resistance. Homozygous transgenic lines express MED16 or ODC2 were generated. Canola MED15 ortholgogs were cloned. Transgenic plants coexpressed MED16 and ODC2 were crossed.

- Functional tests in model plants to determine potential importance of candidate defense genes

- Determination of the efficacy of transformed genes on defense control in crop germplasm.

3.5.4.08 USDA ARS scientists at Urbana IL measured in vitro growth suppression of mycelium using solid and liquid media amended with different levels of glyceollin, resveratrol, and pterostilbene. Colony diameters on solid agar media and dried mycelial mass, produced in liquid media were monitored on the surface of the detached leaflets. The percent of leaflet areas colonized and damaged after inoculation was high. A transgenic soybean was generated that expressed genes

enabling constitutive production of resveratrol, a non-native phytoalexin for soybean.

- Effective use of genome editing technologies to genetically modify genomic regions in ways that enhance resistance to Sclerotinia diseases

3.5.5.18 Scientists at University of Florida developed effective and durable disease resistance for Sclerotinia stem rot of canola through transgenic and/or cisgenic engineering of the host using two genes, one from a host plant and another from the pathogen that block disease when over-expressed in canola.

- Development and testing of agronomic crop germplasm transformed with putative anti-fungal genes or RNA interfering constructs for reaction to white mold.

Disease Management & Crop Production

Goal 4: Broaden knowledge of *Sclerotinia sclerotiorum* epidemiology and improve disease management strategies

PM 4.1: Optimize fungicide application programs.

- A region-wide collection of *S. sclerotiorum* isolates to establish a baseline of fungicide sensitivity
- Identification of the economic return of fungicide applications relative to timing of disease onset
- Updated management guides for growers on use of fungicides for disease management
- New spraying technologies that improve fungicide performance by enhancing canopy penetration, plant coverage, and fungicide deposition
- Determine most effective timing of fungicide applications relative to canopy closure after blooming.

4.1.5.22 Scientists at NDSU found that current recommendations for applying fungicides at early bloom (soybeans, dry beans) and again 10 to 14 days later (dry beans) was moderately effective at managing Sclerotinia under early disease onset and moderately to highly effective at managing Sclerotinia under intermediate and late disease onset. It was unclear whether this application strategy was optimal, as alternate fungicide application strategies were not comprehensively tested.

PM 4.2: Develop bio-control alternatives for disease management.

- Identification of application strategies that will maximize the efficacy of currently available bio control agents for control of *S. sclerotiorum*
- Identification of novel antagonists of *S. sclerotiorum* and assessment of their efficacy in field trials

4.2.2.19 USDA ARS scientists at Fargo ND tested a hypothesis based on the observation that sunflower is the only crop plant documented to develop root infection by Sclerotinia, but ornamental plants within the Asteraceae family are susceptible to Sclerotinia infection using sclerotia. This implied root exudates stimulate myceliogenic germination of sclerotia, or may inhibit carpogenic germination. A cross section of Asteraceae genera was evaluated to test this hypothesis on induction of myceliogenic and carpogenic germination of sclerotia.

- Updated management guides for growers on use of bio fungicides for disease management

PM 4.3: Develop disease-warning systems to optimize management of *S. sclerotiorum*.

- Models that calculate risk of disease development as functions of leaf wetness duration and temperature, and risk of apothecia formation as function of soil moisture conditions
- Effect of tillage practices on Sclerotinia survival;
- Economic loss models based on plant density at time of disease onset
- Define risk levels to guide crop-specific fungicide selection decisions

PM 4.4: Optimize cultural practices for disease management.

- Variety selection using disease reaction measured as the amount of sclerotia produced
- Collate disease management information and distribute to growers through print media, internet postings and extension publications

4.4.2.22 Scientists at NDSU contributed to (1) improved use of fungicides for management of Sclerotinia in dry beans and soybeans, (2) improved Sclerotinia disease risk assessment through the development of economic yield loss models based on timing of disease onset, and (3) improved progress in breeding sunflowers for resistance to Sclerotinia head rot by identifying sources of head rot resistance and by developing tools for using disease assessments to predict sunflower yield potential under Sclerotinia head rot disease pressure.

- Epidemiological information on disease development (spatial distribution, remote sensing, etc.) that could be used to support precision agriculture programs for disease control.

Publications: (includes papers from 2012 to 2015; none cited in prior annual reports)

1. Abdel-Ghany S, Day I, Heuberger AL, Broeckling C, Reddy ASN (2013) "Metabolic engineering of Arabidopsis for butanetriol production using bacterial genes." Metabolic Engineering. 20, 109-120.
2. Abi---Ghanem, R., Carpenter---Boggs, L., Smith, J. L., and G. J. Vandemark. 2012. Nitrogen fixation by US and middle eastern chickpeas with commercial and wild middle eastern inocula. ISRN Soil Science 2012: Article ID 981842, 5 pages.
3. Abraham N.D., Acevedo M., Chitrampal P., LeBoldus J.M. (2014) Quantification of Sphaereulina musiva in infected Populus clones using qPCR. Phytopathology 104: S2.2
4. Acevedo, M., J.R. Steadman and J.C. Rosas. 2013. Uromyces appendiculatus in Honduras: Pathogen Diversity and Host Resistance Screening. Plant Disease 97:652-661.
5. Akamatsu, H.O., Chilvers, M.I., Kaiser, W.J., Peever, T.L. 2012. Karyotype polymorphism and chromosomal rearrangement in populations of the phytopathogenic fungus, *Ascochyta rabiei*. Fungal Biology. 116:1119-1133.
6. Akond M., S. Liu, S. Kantartzi, K. Meksem, N. Bellaloui, D. Lightfoot, J. Yuan, D. Wang, and A. Kassem. 2014. Quantitative trait loci for seed isoflavone contents in 'MD96-5722' by 'Spencer' recombinant inbred lines of soybean. J. Agric. Food Chem. 62:1464-1468.
7. Ali, H., Alam S.S, Attanayake R. N, Rahman M and Chen W. 2012. Population structure and mating type distribution of the chickpea blight pathogen *Ascochyta rabiei* from Pakistan and United States through molecular marker analyses. Journal of Plant Pathology 94: 99-108.
8. An, C. and Mou, Z. (2012). Non-host defense response in a novel Arabidopsis-Xanthomonas citri subsp. Citri pathosystem. PLoS ONE 7(1): e31130.
9. An, C. and Mou, Z. 2013. The function of the Mediator complex in plant immunity. Plant Signal & Behavior 8:e23182.
10. Anderson JV, M Dogramaci, DP Horvath, , ME Foley, WS Chao, JC Suttle, J Thimmapuram, AG Hernandez, S Ali, MA Mikel. 2012. Auxin and ABA act as central regulators of developmental networks associated with paradormancy in Canada thistle (*Cirsium arvense*). Functional and Integrative Genomics 12:515-531.
11. Anderson JV, M Doğramacı, DP Horvath, WS Chao, ME Foley, JC Suttle, J Thimmapuram, AG. Anthocyanin, leaf chlorosis and days to flowering in F2 population of *Brassica rapa* L. Plant Breed. 133(3):381-389. (doi:10.1111/pbr.12165).
12. Arkzwazee, H., J. Davis, Phil Miklas, S. Moghaddam, P. McClean, and J.R. Myers. 2014. Analysis of variation for white mold resistance in the bean CAP snap bean panel. Ann. Rep. Bean Impr. Coop. 57:175-176.
13. Arora, D., T. Gross and R. Brueggeman (2013) Allele characterization of genes required for rpg4-mediated wheat stem rust resistance identifies Rpg5 as the R-gene. Phytopathology 103:1153-1161.
14. Astudillo-Reyes, C. 2014. Integration of transcriptome analysis and consensus QTL in the identification of candidate genes associated with zinc concentration in common bean (Phaseolus vulgaris). Master thesis, Michigan State University, East Lansing MI. 113pp.

15. Attanayake, R. N., Tennekoon, V., Johnson, D. A., Porter, L.D., del Rı´o-Mendoza, L. D Jiang, and Chen, W. 2014. Inferring outcrossing in the homothallic fungus *Sclerotinia sclerotiorum* using linkage disequilibrium decay. Heredity 113: 353-363. doi:10.1038/hdy.2014.37
16. Attanayake, R.N., Porter, L., Johnson, D.A., and Chen, W. 2012. Genetic and phenotypic iversity and random association of DNA markers of isolates of the fungal plant pathogen *Sclerotinia sclerotiorum* from soil on a fine geographic scale. Soil Biology and Biochemistry 5:28-36.
17. Barimani, M., Pethybridge, S. J., Vaghefi, N., Hay, F. S., and Taylor, P. W. J. 2013. A new anthracnose disease of pyrethrum caused by Colletotrichum tanaceti sp. nov. Plant Pathol. 62:1248-1257.
18. Barnes B, Wilson M, Carr P, Vitha MF, Broeckling CD, Heuberger AL, Prenni J, Janis GC, Corcoran H, Snow NH, Chopra S, Tawfall A, Sumner LW, Boswell PG (2013) "'Retention Projection'" Enables Reliable Use of Shared Gas Chromatographic Retention Data Across Labs, Instruments, and Methods" Analytical Chemistry. 85 (23): 11650-11657.
19. Beaver, J.S., E.H. Prophete, J.C. Rosas, G. Godoy-Lutz, J.R. Steadman, and T.T. Porch. 2014. Release of 'XRAV-40-4' Black Bean (Phaseolus vulgaris L.) Cultiver. Journal of Agriculture of University of Puerto Rico 98:83-87.
20. Bekel, S., Domier, L.L., Gonfa, B., McCoppin, N.K., Lambert, K.N., Bhalerao, K. 2014. A novel flavivirus in the soybean cyst nematode. Journal of General Virology. 95:1272-1280.
21. Bello MH, Moghaddam SM, Massoudi M, McClean PE, Cregan PB, Miklas PN (2014) Application of in silico bulked segregant analysis for rapid development of markers linked to Bean common mosaic virus resistance in common bean. BMC Genomics 15:903
22. Bitocchi E, Nanni L, Bellucci E, Rossi M, Giardini A, Zeuli PS, Logozzo G, Stougaard J, McClean P, Attene G, Papa PR (2012) The Mesoamerican origin of the common bean (Phaseolus vulgaris L) is revealed by sequence data. Proceeding of the National Academy of Science, USA 109 (14) E788–E796
23. Block, C., L. F. Marek, and T. J. Gulya. 2013. Evaluation of wild Helianthus species for resistance to Sclerotinia stalk rot. Sclerotinia Initiative Annual Meeting, Bloomington, MN. January 18-20, 2012. Abstract p.16.
24. Boches, P.S. and J.R. Myers. 2012. Classical genetics and traditional breeding: Classical mapping efforts. In: B. Liedl, A. Slade, S. Hurst, J.A. Labate, and J.R. Stommel (eds.)Tomato. Genomics of Fruits and Vegetable Crops series. Science Publishers Ltd.
25. Bodo Slotta TA, DP Horvath, ME Foley. 2013. Phylogeny of *Cirsium* spp. in North America: Host Specificity Does Not Follow Phylogeny. Plants 1:61-73.
26. Bolton MD. V Rivera, LE del Río Mendoza, MFR Khan, GA Secor. 2012. Efficacy of variable tetraconazole rates against *Cercospora beticola* isolates with differing in vitro sensitivities to DMI fungicides. Plant Dis.96:1749-1756.
27. Boutigny, A., Beukes, I, Small, I, Zuhlke, S. Spiteller, M, Janse Van Rensburg, B. Flett, B.C.& Viljoen, A. 2012. Quantitative detection of Fusarium pathogens and their mycotoxins in South African maize. Plant Pathology 61: 522-531.
28. Broeckling CD., Afsar, FA, Neumann S, Ben-Hur A., Prenni JE "RAMClust: A Novel Feature Clustering Method Enables Spectral-Matching-Based Annotation for Metabolomics Data" (2014) Analytical Chemistry 86(14), 6812-6817.

29. Brusini, J., and Robin, C. 2013. Mycovirus transmission revisited by in situ pairings of vegetatively incompatible isolates of Cryphonectria parasitica. J. Virol. Methods 187:435-442.
30. Burlakoti P, V Rivera, G Secor, A Qi, LE del Río Mendoza, MFR. Khan. 2012. Comparative pathogenicity and virulence of *Fusarium* species on sugar beet. Plant Dis. 96:1291-1296.
31. Burlakoti P, V Rivera, G Secor, A Qi, LE del Río Mendoza, MFR. Khan. 2012. Comparative pathogenicity and virulence of *Fusarium* species on sugar beet. Plant Dis. 96:1291-1296.
32. Byrne A.M. and Chilvers, M.I. 2014. Efficacy of foliar fungicides for white mold control in soybeans in Michigan, 2013. Plant Disease Management Reports 8:FC174.
33. Castro P., K.S. Lewers, C.K. Weebadde, D. Wang, and J.F. Hancock. 2014. Genetic mapping of day-neutrality in cultivated strawberry. Mol Breed:(in press).
34. Chalhoub, B., Denoeud, F., Liu, S., Parkin, I. A. P., Tang, H., Wang, X., et al…Wincker, P. 2014. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science. 345:950–953.
35. Chang, H.-X., L.A. Miller, and G. L. Hartman. 2014a. Melanin-independent accumulation of turgor pressure in appressoria of Phakopsora pachyrhizi. Phytopathology 104:977-984.
36. Chang, S., C. Thurber, P. Brown, G. L. Hartman, K.N. Lambert, and L.L. Domier. 2014. Comparative mapping of the wild perennial Glycine latifolia and soybean (G. max) reveals extensive chromosome rearrangements in the genus Glycine. PLOS ONE 9:e99427.
37. Chang, S., G. L. Hartman, R.J. Singh, K.N. Lambert, H.A. Hobbs, and L.L. Domier. 2013. Identification of high quality single nucleotide polymorphisms in Glycine latifolia using a heterologous reference genome sequence. Theor. . Appl. Genet. 126:1627-1638.
38. Chao WS, M Dogramaci, JV Anderson, ME Foley, DP Horvath. 2014. The resemblance and disparity of gene expression in dormant and non-dormant seeds and crown buds of leafy spurge (Euphorbia esula). BMC Plant Biol. 14:216. DOI: 10.1186/s12870-014-0216-4.
39. Chen,W., Dugan, F.M. and McGee,R. 2014. First report of dodder (*Cuscuta pentagona*) on chickpea (*Cicer arietinum*) in the United States. Plant Disease 98: 165.
40. Chilvers, M.I., Jones, S., Meleca, J., Peever, T., Pethybridge, S., Hay, F. 2014. Characterization of mating type genes supports the hypothesis that *Stagonosporopsis chrysanthemi* is homothallic and provides evidence that *Stagonosporopsis tanaceti* is heterothallic. Current Genetics. 60:295-302. DOI 10.1007/s00294-014-0435-0
41. Chirumamilla, A., C.B. Hill, and G. L. Hartman. 2014. Stability of soybean aphid resistance in soybean across different temperatures. Crop Science doi:10.2135/cropsci2014.05.0393
42. Chirumamilla, A., J.J. Knodel, L.D. Charlet, B.S. Hulke, S.P. Foster, and P.J. Ode. 2014. Ovipositional preference and larval performance of the banded sunflower moth and its larval parasitoids on resistant and susceptible lines of sunflower, Helianthus annuus. Environ. Ent. 43:58-68.
43. Chitrampalam, P., and Nelson, B. D., Jr. 2014. Effect of Fusarium tricinctum on growth of soybean and a molecular-based method of identification. Plant Health Progress doi:10.1094/PHP-RS-14-0014
44. Chittem K, SM Mansouripour, LE del Río Mendoza. 2014. First report of clubroot on canola caused by *Plasmodiophora brassicae* in North Dakota. Plant Dis. 98:1438.

45. Chittem, K. W. Yajima, L.E. del Río Mendoza, and R. S. Goswami. 2013. Identification of resistance and pathogenicity genes associated with Sclerotinia sclerotiorum infection on canola. National Sclerotinia Initiative Annual Meeting. Bloomington, MN Jan. 2013. pp 24.
46. Chittem, K., and Goswami, R. S. 2013. Identification of resistance and pathogenicity genes associated with Sclerotinia sclerotiorum infection in canola. Presented at 11th Annual National Sclerotinia Initiative meeting held at Bloomington, MN, 23 Jan – 25 Jan.
47. Chittem, K., Matthew, F. M., Gregoire, M., Lamppa, R. S., Chang, Y. W., Barasubiye, T., Markell, S. G., Bradley, C. A., and Goswami, R. S. 2014. Identification and characterization of Fusarium spp. associated with root rots of field pea in North Dakota. Submitted to European Journal Plant Pathology.
48. Chittem, K., Yajima, W., del Rio Mendoza, L. E., and Goswami, R. S. 2012. Fungal gene expression patterns during infection of canola by Sclerotinia sclerotiorum. Phytopathology 102:S4.23.
49. Chun S., K. Yu, W. Xie, G. Perry, A. Navabi, K. P. Pauls, P. N. Miklas, and D. Fourie. 2012. Development of candidate gene markers associated to common bacterial blight resistance in common bean. Theor. Appl. Genet. 125:1525-1537.
50. Coram TE et al. (2014). Performance and stabilty of precise genome modification in maize using zinc-finger nucleases. In preparation.
51. Cui, D., Q. Zhang, M. Li, T.L. Slaminko, and G. L. Hartman. 2014. A method for determining the severity of sudden death syndrome in soybeans. Trans. ASABE 57:671-678.
52. Davis, J.W., J.R. Myers, D. Kean, N. Al Bader, B. Yorgey, P. Cregan, Q. Song, and C. Quigley. 2014. A SNP-based linkage map of snap bean (Phaseolus vulgaris).Ann. Rep. Bean Impr. Coop. 57:119-120.
53. de Milliano, Walter A.J., Edith T. Lammerts van Bueren, Roeland E. Voorrips, and James R. Myers. Resistance and resistance breeding. In: Maria Finckh (ed.) Plant Disease Management in Organic Agriculture. (in press)
54. de Vries, P.M., R.P., Dyer, P.S., Fillinger,S., Fournier, E., Gout, L., Hahn, M., Kohn, L., Lapalu, N.,
55. del Río LE, A Nepal, J Bjerke, M Boyles, T Peeper. 2011. Identification of blackleg (*Leptosphaeria maculans*) pathogenicity group 4 on winter canola (*Brassica napus* L.) in Oklahoma. Plant Dis. 95:614.
56. del Río Mendoza LE, A Nepal, S Markell. 2012. Outbreak of blackleg in canola in North Dakota is caused by new pathogenicity groups. Plant Health Prog. doi:10.1094/PHP-2012-0410-01-RS.
57. Derevnina L., T. Fetch, D. Singh, R. Brueggeman, C.M. Dong and R.F. Park (2014) Analysis of stem rust resistance in Australian barley cultivars. Plant Disease (In Press).
58. Diers, B.W., K.S. Kim, R.D. Frederick, G. L. Hartman, J.R. Unfried, S.J. Schultz, and T.R. Cary. 2013. Registration of eight soybean germplasm lines resistant to soybean rust. J. Plant Reg. 8:96-101.
59. Ding, Y., Shaholli, D. and Mou, Z. (2014). A large-scale genetic screen for mutants with altered salicylic acid accumulation in Arabidopsis. Frontiers in Plant Science (accepted).
60. Doğramaci M, JV Anderson, WS Chao, ME Foley. 2014. Foliar application of glyphosate affects molecular mechanisms in underground adventitious buds of leafy spurge (Euphorbia esula) and alters their vegetative growth patterns. Weed Sci. 62:217-229.
61. Doğramacı M, ME Foley, WS Chao, MJ Christoffers, JV Anderson. 2013. Induction of endodormancy in crown buds of leafy spurge (Euphorbia esula L.) implicates a role for ethylene and cross-talk between photoperiod and temperature. Plant Mol. Biol. 81:577-593.

62. dos Santos, H.M., V. Hoyos-Villegas and J.D. Kelly. 2014. Genome-wide association analysis for reaction to white mold in the BeanCAP Mesoamerican panel. Ann. Rep. Bean Improv. Coop. 57:235-236.
63. Dunnell K.L,. Berguson W., McMahon B., LeBoldus J.M. (2014) Variation in host response to Septoria canker in a population of Populus nigra. Phytopathology 104: S3.36.
64. Felicetti, E., Q. Song, G. Jia, P. Cregan, K. E. Bett, and P. N. Miklas. 2012. Simple sequence repeats linked with slow darkening trait in pinto bean discovered by SNP assay and whole genome sequencing. Crop Science 52: 1600-1608.
65. Feng, J., Z. Liu, G. J. Seiler, and C. C. Jan. 2014. Registration of cytoplasmic male-sterile oilseed sunflower genetic stocks CMS2 and CMS GIG2-RV, and fertility restoration lines RF GIG2-MAX 1631 and RF GIG2-MAX 1631-RV. J. Plant Reg. DOI:10.3198/ jpr2014.05.0029crgs.
66. Feng, X., A.R. Poplawsky, O.V. Nikolaeva, J.R. Myers, and A.V. Karasev. 2014. Recombinants of Bean common mosaic virus (BCMV) and genetic determinants of BCMV involved in overcoming resistance in common beans. Phytopathology 104:786-793. http://dx.doi.org/10.1094/PHYTO-08-13-0243
67. Foley ME, WS Chao, DP Horvath, M Doğramaci, JV Anderson. 2013. The transcriptomes of dormant leafy spurge seeds under alternating temperature are differentially affected by a germination-enhancing pretreatment. J Plant Physiol. 170:539-547.
68. Foley ME, WS Chao, M Doğramaci, DP Horvath, JV Anderson. 2012. Changes in the transcriptome of dry leafy spurge (*Euphorbia esula*) seeds imbibed at a constant and alternating temperature. Weed Sci. 60:48-56.
69. Fortuna, A., W. Honeycutt, G. Vandemark, T. S. Griffin, R. P. Larkin, Z. He, B. J. Weinhold, K. R. Sistani, S. L. Albrecht, B. L. Woodbury, H. A. Torbert, J. M. Powell, R. K. Hubbard, R. A. Eigenberg, R. J. Wright, J. R. Alldredge and J. Harsh. 2012. Links among nitrification, nitrifier communities, and edaphic properties in contrasting soils receiving dairy slurry. Journal of Environmental Quality 41:262---272.
70. Fox, C., K.S. Kim, P.B. Cregan, C.B. Hill, G. L. Hartman, and B.W. Diers. 2013. Inheritance of soybean aphid resistance in 21 soybean plant introductions. Theor. Appl. Genet. 127:43-50.
71. Freund DM, Prenni JE, Curthoys NP 2012 “Response of the Mitochondrial Proteome of Rat Renal Proximal Convoluted Tubules to Chronic Metabolic Acidosis” AJP - Renal Physiology Jan;304(2);F145-55.
72. Friebe B. **Qi L.L.,** Liu L., Liu W., Gill B.S. 2012 Registration of a hard red winter wheat genetic stock homozygous for *ph1b* for facilitating alien introgression for crop improvement. J. Plant Regist. 6:121-123.
73. Ghafoor, A. and K. McPhee. 2012. Marker assisted selection for developing powdery mildew resistant pea cultivars. Euphytica, 186:593-607.
74. Gong L., Li C.F., Capatana A., Feng J.H., Qi L.L., Seiler G.J., Jan C.C. 2014. Molecular mapping of three male sterility mutant genes in cultivated sunflower (Helianthus annuus L.). Mol. Breeding 34:159-166.
75. Goretti D, Bitocchi E, Bellucci E, Rodriguez M, Rau D, Gioia T, Attene G, McClean P, Nanni L, Papa R Development of single nucleotide polymorphisms in Phaseolus vulgaris and related Phaseolus spp. Molecular Breeding (in press)

76. Grisham M., Hoy J., Haudenshield J.S., Hartman G.L. (2013) First Report of Orange Rust Caused by Puccinia kuehnii in Sugarcane in Louisiana. Plant Disease 97:426.
77. Hamon, C., C.J. Coyne, R.J. McGee, A. Lesné, R. Esnault, P. Mangin, M. Hervé, I. Le Goff, G. Deniot, M. Roux-Duparque, G. Morin, K.E. McPhee, R. Delourme, A. Baranger and M.-L. Pilet- Nayel. 2013. QTL meta-analysis provides a comprehensive view of loci controlling partial resistance to *Aphanomyces euteiches* in four sources of resistance in pea. BMC Plant Biology, 13:45.
78. Han, J.P., Domier, L.L., Dorrance, A., Qu, F., 2012. Complete Genome Sequence of a Novel Pararetrovirus Isolated from Soybean. J. Virol. 86, 9555-9555.
79. Heilig, J.A., and J.D. Kelly. 2012. Performance of dry bean genotypes grown under organic and conventional production systems in Michigan. Agron. J.104:1485-1492. doi:10.2134/agronj2012.0082.
80. Hernandez, S Ali, MA Mikel. 2012. Auxin and ABA act as central regulators of developmental networks associated with paradormancy in Canada thistle (Cirsium arvense). Funct. Integr. Genomics 12:515-531.
81. Heuberger AL, Robison FM, Lyons SM, Broeckling CD, Prenni JE (2014) “Evaluating plant immunity using mass spectrometry-based metabolomics workflows.” Frontiers in Plant Science 5:291. doi: 10.3389/fpls.2014.00291.
82. Hill, C.B., A. Chirumamilla, and G. L. Hartman. 2012. Resistance and virulence in the soybean-Aphis glycines interaction. Euphytica 186: 635–646.
83. Hong, MG, Karlsson R, Magnusson PKE, Lewis MR, Isaacs W, Zheng LS, Xu J, Gronberg H, Ingelsson E, Pawitan Y, Broeckling CD, Prenni JE, Wiklund F, Prince JA 2012 “A Genome-Wide Assesment of Variability in Human Serum Metabolism” Human Mutation Mar;34(3)”515-24.
84. Horneburg, B. and J.R. Myers. 2012. Tomato: Breeding for improved disease resistance in fresh market and home garden varieties. In: Lammerts van Bueren, E., and J.R. Myers (eds.) Organic Plant Breeding. Wiley-Blackwell pp. 239-249.
85. Horvath DP, D Kudrna D, J Talag, JV Anderson, WS Chao, R Wing, ME Foley, M Doğramacı. (2013) BAC library development, and clone characterization for dormancy-responsive DREB4A, DAM, and FT from leafy spurge (Euphorbia esula L.) identifies differential splicing and conserved promoter motifs. Weed Sci. 61:303-309.
86. Horvath DP, M Santana, JV Anderson. 2013. Microarray analysis of the semi-compatible pathogenic response and recovery of leafy spurge inoculated with the cassava bacterial blight pathogen Xanthomonas axonopodis pv. manihotis. Weed Sci. 61:428-436.
87. Hu, Z. J., Wu, S. S., Cheng, J. S., Fu, Y. P., Jiang, D. H., and Xie, J. T. 2014. Molecular characterization of two positive-strand RNA viruses co-infecting a hypovirulent strain of Sclerotirtia sclerotiorum. Virology 464:450-459.
88. Hulke, B.S., and L.W. Kleingartner. 2014. Sunflower. p. 433-457. In: Yield Gains in Major US Field Crops: CSSA Special Publication 33. S. Smith, B. Diers, J. Specht, and B. Carver (Eds.) ASA-CSSA-SSSA, Madison, WI.
89. Hulke, B.S., and T.J. Gulya. 201x. Registration of the oilseed restorer sunflower germplasms RHA 472, RHA 473, RHA 474, and RHA 475, possessing resistance to Sclerotinia head rot. J. Plant Registrations (in review).

90. Hulke, B.S., B.S. Bushman, E. Watkins, and N.J. Ehlke. 2012. Association of freezing tolerance to LpCBFIIIb and LpCBFIIIc gene polymorphism in perennial ryegrass accessions. Crop Sci 52:2023-2029.
91. Hulke, B.S., C.J. Grassa, J.E. Bowers, J.M. Burke, L.L. Qi, Z.I. Talukder, and L.H. Rieseberg. 201x. An unified single nucleotide polymorphism map of sunflower (Helianthus annuus L.) derived from current genomic resources. Crop Sci. (in review).
92. Jain, S. A. Kumar, S. Mamidi and K. McPhee. 2014. Genetic diversity and population structure among pea (*Pisum sativum* L.) cultivars as revealed by simple sequence repeats and novel genic markers. Molecular Biotechnology, DOI 10.1007/s12033-014-9772-y.
93. Jan, C. C., G. J. Seiler, and J. M. Hammond. 2014. Effect of wild Helianthus cytoplasms on agronomic and oil characeristics of cultivated sunflower (Helianthus annuus L.). Plant Breed. 133:262-267.
94. Jan, C.C., Z. Liu, G.J. Seiler, L. Velasco, B. Perez-Vich, J. Fernandez-Martinez. 2014. Broomrape (Orobanche cumana Wallr.) resistance breeding utilizing wild Helianthus species. Helia DOI: 10.1515/helia-2014-0018.
95. Javid, M., Zhang, P., Taylor, P. W. J., Pethybridge, S. J., Groom, T., and Nicolas, M. E. 2013. Interactions between waterlogging and ray blight in pyrethrum. Crop and Past. Sci. 64:726-735.
96. Jhala, R., B. Higgins, and J.R. Steadman. 2013. Use of multi site screening to identify and verify partial resistance to white mold in common bean in 2012. Ann. Rpt. Bean Improvement Coop. 56:47-48.
97. Jhala, R., R. Higgins, and J.R. Steadman. 2014. Use of Multi Site Screening to Identify and Verify Partial Resistance to White Mold in Common Bean in 2013. Ann. Rpt. Bean Improvement Coop. 57:233-234.
98. Jhala, R., R. Higgins, E. Eskridge and J.R. Steadman. 2014a. Characterized Isolates of Sclerotinia sclerotiorum Can Facilitate Identification and Verification of Resistance to White Mold in Dry and Snap Beans. Ann. Rpt. Bean Improvement Coop. 57:57-58.
99. Jonas, E., and D.-J. De Koning 2013. Does genomic selection have a future in plant breeding? Trends in biotechnology 31:497-504.
100. Jones, S. J., Gent, D. H., Pethybridge, S. J., and Hay, F. S. 2012. Site-specific risk factors of white mould epidemics in bean (Phaseolus vulgaris) in Tasmania, Australia. N. Z. J. Crop and Hort. Sci. 40:147-159.
101. Jones, S. J., Pilkington, S., Gent, D. H., Hay, F. S., and Pethybridge, S. J. 2014. Detection of ascosporic inoculum of Sclerotinia sclerotiorum using PCR. Proceedings of the 8th Australasian Soilborne Diseases Symposium, 10 to 13 November, Hobart, Tasmania.
102. Jossey, S., Hobbs, H.A., Domier, L.L., 2013. Role of Soybean mosaic virus-encoded proteins in seed and aphid transmission in soybean. Phytopathology 103, 941-948.
103. Kandel, Y., Bradley, C., Wise, K., Chilvers, M., Tenuta, A., Davis. V., Esker, P., Smith, D., Licht, M., Mueller, D. *In Press*. Effect of glyphosate application on sudden death syndrome of glyphosate-resistant soybean under field conditions. Plant Disease
104. Kantar, M., K. Betts, B.S. Hulke, R.M. Stupar, and D. Wyse. 2012. Breaking tuber dormancy in Helianthus tuberosus L. and interspecific hybrids of Helianthus annuus L. x Helianthus tuberosus. HortScience 47:1342-1346.

105. Kantar, M.B., K. Betts, J.-M. Michno, J.J. Luby, P.L. Morrell, B.S. Hulke, R.M. Stupar, and D.L.Wyse. 2014. Evaluating an interspecific Helianthus annuus × Helianthus tuberosus population for use in a perennial sunflower breeding program. Field Crops Res. 155:254-264.
106. Kelly, J.D., G.V. Varner, K.A. Cichy, and E.M. Wright. 2014. Registration of Powderhorn great northern bean. J. Plant Registrations 8:1-4. doi:10.3198/jpr2013.05.0020crc.
107. Khalifa, M. E., and Pearson, M. N. 2014. Characterisation of a novel hypovirus from Sclerotinia sclerotiorum potentially representing a new genus within the Hypoviridae. Virology 464–465:441-449.
108. Khalifa, M. E., and Pearson, M. N. 2014. Molecular characterisation of an endornavirus infecting the phytopathogen Sclerotinia sclerotiorum. Virus Res. 189:303-309.
109. Kim, K.S., A. Chirumamilla, C.B. Hill, G. L. Hartman, and B.W. Diers. 2014. Identification and molecular mapping of two soybean aphid resistance genes in soybean PI 587732. Theor. Appl. Genet. (in press).
110. Kim, W., Park, C.-M., Park, J.-J. Akamatsu, H. O., Peever, T.L., Xian, M, Gang, D.R., Vandemark, G. and Chen,W. 2015. Functional Analyses of the Diels-Alderase Gene *sol5* of *Ascochyta rabiei* and *Alternaria solani* Indicate that the Solanapyrone Phytotoxins Are Not Required for Pathogenicity. . Molecular Plant-Microbe Interactions : In press.
111. Kodira, C., Kretschmer, M., Lappartient, A., Leroch, M., Levis, C., Mauceli, E., Neuvéglise, C., Oeser, B., Pearson, M., Poulain, J., Poussereau, N., Quesneville, H., Rascle, C., Schumacher, J.,
112. Koga, L. J., Bowen, C. R., Godoy, C. V., de Oliveira, M. C. N., and Hartman, G. L. 2014. Mycelial compatibility and aggressiveness of Sclerotinia sclerotiorum isolates from Brazil and the United States. Pesquisa Agropecuaria Brasileira 49:265-272.
113. Kuhn, J.H., Bekal, S., Cai, Y., Clawson, A.N., Domier, L.L., Herrel, M., Jahrling, P.B., Kondo, H., Lambert, K.N., Mihindukulasuriya, K.A., Nowotny, N., Radoshitzky, S.R., Schneider, U., Staeheli, P., Suzuki, N., Tesh, R.B., Wang, D., Wang, L., Dietzgen, R.G. 2013. Nyamiviridae: Proposal for a new family in the order Mononegavirales. Archives of Virology. 159:2209-2226.
114. Kusolwa, P.M. and J.R. Myers. 2012. Peptide sequences from seed storage proteins of tepary bean (Phaseolus acutifolius) accession G40199 demonstrate the presence of multiples variants of APA proteins. Int. J. Biochem. Biotech. 1:12-18.
115. Kusolwa, P.M., and J.R. Myers. 2011. Seed storage proteins ARL2 and its variants from the APA locus of wild tepary bean G40199 confers resistance to Acanthoscellides obtectus when expressed in common beans. Afr. Crop Sci. J. 19:255-265.
116. Kwon S.-J., A.F. Brown, J. Hu, R.J. McGee, C.A. Watt, T. Kisha, G.M. Timmerman-Vaughan, M. Grusak, K.E. McPhee and C.J. Coyne. 2012. Population genetic sub-structure within the USDA ARS *Pisum* core collection and its potential as a platform for association mapping. Genes & Genomics, 34(3):305-320. DOI:10.1007/s13258-011-0213-z.
117. Kwon, S.-J., P. Smykal, J. Hu, M. Wang, S.-J. Kim, R.J. McGee, K. McPhee and C.J. Coyne. 2013. User friendly markers linked to Fusarium wilt race 1 resistance *Fw* gene for marker assisted selection in pea. Plant Breeding, 132:642-648.
118. Lambert, S. J., Scott, J. B., Pethybridge, S. J., and Hay, F. S. 2012. Strain characterization of Potato virus S isolates from Tasmania, Australia. Plant Dis. 96: 813-819.

119. Lammerts van Bueren, E.T. and J.R. Myers. 2012. Organic crop breeding - integrating organic agricultural approaches and traditional and modern plant breeding methods. In: Lammerts van Bueren, E., and J.R. Myers (eds.) Organic Plant Breeding. Wiley-Blackwell pp. 3-13.
120. LeBoldus, J., K. Kinzer, Z. Ya, C. Yan, T. L. Friesen and R. Brueggeman (2014) Genotype-by-sequencing of the plant pathogenic fungi Septoria musiva and Pyrenophora teres utilizing ion torrent sequence technology. Molecular Plant Pathology (In Press).
121. LeBoldus, J.M. Kinzer, K., Richards, J., Zhu, Y., Yan, C., Friesen, T.L., Brueggeman, R. (In Press) Genotype-by-sequencing of the plant pathogenic fungi Pyrenophora teres and Sphaerulina musiva utilizing Ion torrent sequence technology. Molecular Plant Pathology.(doi: 10.1111/mpp.12214)
122. LeBoldus, J.M. Ostry, M.E. and Blodgett, J.T. (In press) Septoria leaf spot and canker. Ch. 30. In Diseases of Trees in the Great Plains. Edited by: A. Bergdahl and A. Hill. Fort Collins, CO: US Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station.
123. LeBoldus, J.M., Isabel N., Floate K.D., Blenis P.V., Thomas B.R. (2013) Testing the 'hybrid susceptibility' and 'phenological sink' hypotheses using the P. balsamifera – P. deltoides hybrid zone and Septoria leaf spot [Septoria musiva] PLoS ONE. e84437.
124. LeBoldus, JM. Zhang, Q., Kinzer, K. (2012) First report of dollar spot caused by Sclerotinia homoeocarpa on Agrostis stolonifera in North Dakota. Plant Disease 96: 1071.
125. Li S., JI, P., Domier, L.L., Zhang, N., Bluhm, B.H. 2015. Draft genome sequence of Phomopsis longicolla MSPL 10-6 Genome Announcements. Accepted.
126. Li, M., Kim, J., Seo, E., Hwang, E., Domier, L.L., Hammond, J., Youn, Y., Lim, H. 2014. Sequence variability in HC-Pro coding regions of Korean Soybean mosaic virus isolates is associated with differences in RNA silencing suppression. Archives of Virology. 159:(4)1373-1383.
127. Liang, X., Liberti, D., Li, M., Kim,Y-T, Hutchens, A., Wilson, R. and. Rollins, J.A. 2014. Oxaloacetate acetylhydrolase gene mutants of Sclerotinia sclerotiorum do not accumulate oxalic acid but do produce limited lesions on host plants. Molecular Plant Pathology. doi: 10.1111/mpp.12211
128. Liang, H., Staton, M., Xu, Y., Xu, T., and LeBoldus, J.M. (2014) Comparative expression analysis of resistant and susceptible Populus clones inoculated with Septoria musiva. Plant Science 223: 69-78.
129. Lim, H.S., Jang, C., Bae, H., Kim, J., et al., 2011. Soybean mosaic virus infection and helper component-protease enhance accumulation of Bean pod mottle virus-specific siRNAs. Plant Pathol. J. 27, 315-323.
130. Lim, H.S., Jang, C.Y., Nam, J., Li, M., et al., 2012. Characterization of the in vitro Activities of the P1 and helper component proteases of Soybean mosaic virus strain G2 and Tobacco vein mottling virus. Plant Pathol. J. 28, 197-201.
131. Liu, Z, F. Wei, X. Cai, G. J. Seiler, T. J. Gulya, K. Y. Rashid, and C. C. Jan. 2012. Progress on the transferring of Sclerotinia resistance genes from wild perennial Helianthus species into cultivated sunflower. Proc. 34th Sunflower Res. Workshop, Nat. Sunflower Association, January 11-12, Fargo, ND. Available: http://www.sunflowernsa.com/uploads/research/ 1181/liu_progress_12.pdf.
132. Liu, Z., D. Holmes, J.D. Faris, S. Chao, R.S. Brueggeman, M.C. Edwards and T.L. Friesen, (2014) QTL mapping reveals effector-triggered susceptibility underlying the barley-Pyrenophora teres f. teres interaction. Mol Plant Path (In Press).

133. Liu, Z., F. Wei, X. Cai, G. J. Seiler, T. J. Gulya, K. Rashid, and C. C. Jan. 2013. Update on transferring Sclerotinia resistance genes from wild perennial Helianthus species into cultivated sunflower. Proc. 10th Nat. Sclerotinia Initiative Meeting, January 23-25, Bloomington, MN. p. 32.
134. Liu, Z., J. Zhang, X. Cai, G. J. Seiler, T. J. Gulya, K. Rashid, C. Block, and C. C. Jan. 2014. Advancement on transferring Sclerotinia resistance genes from wild perennial Helianthus species into cultivated sunflower. Proc. 11th Nat. Sclerotinia Initiative Meeting, January 23-25, Bloomington, MN. Abstract p. 11.
135. Liu, Z., X. Cai, G. J. Seiler, and C. C. Jan. 2014. Interspecific amphiploids-derived alloplasmic male sterility with defective anthers, narrow disk florets, and small ray flowers in sunflower. Plant Breed. DOI: 10.1111/pbr.12216.
136. Lonergan, E., Pasche, J., Skoglund, L., and Burrows, M. 201X. Sensitivity of Ascochyta species infecting pea, lentil, and chickpea to boscalid, fluxapyroxad, and prothioconazole. Plant Dis. (Accepted 8/28/14: PDIS-06-14-0620-RE).
137. Lygin, A.V., C.B. Hill, M. Pawlowski, O.V. Zernova, J.M. Widholm, G. L. Hartman, and V.V. Lozovaya. 2014. Inhibitory effects of stilbenes on the growth of three soybean pathogens in culture. Phytopathology 104:843-850.
138. Madrid, E., Chen, W., Rajesh, P. N., Castro, P, Millan, T. and Gil, J. 2012. Allele-specific amplification for the detection of ascochyta blight resistance in chickpea. Euphytica DOI 10.1007/s10681-012-0753-6.
139. Madrid, E., Rajesh, P. N., Rubio, J., Gil, J., Millan, T. and Chen, W. 2012. Characterization and genetic analysis of an EIN4-like sequence (CaETR-1) located in QTLAR1 implicated in scochyta light resistance in chickpea. Plant Cell Reports 31:1033-1042. DOI 10.1007/s00299-
140. Mamidi S, Lee RK, Goos RJ, McClean PE (2014) Genome-wide association studies identifies seven major regions responsible for iron deficiency chlorosis in soybean (Glycine max). PLoS ONE 9(9): e107469
141. Mamo, B., K. P. Smith, R. Brueggeman, and B. J. Steffenson (2014) Genetic characterization of wheat stem rust resistance in landrace and wild barley accessions identifies rpg4/Rpg5 locus. Phytopathology (In Press).
142. Marvelli, R., H.A. Hobbs, S. Li, N.K. McCoppin, L.L. Domier, G. L. Hartman, and D.M. Eastburn. 2014. Identification of novel double-stranded RNA mycoviruses of Fusarium virguliforme and evidence of their effects on virulence. Arch. Virol. 159:349-352.
143. Marzano, S. L., Ajayi, O., Nelson, B. D., Bradley, C. A., Hughes, T. J., Hartman, G. L., . . . Domier, L. L. 2015. Metagenomic characterization of the viromes of five plant pathogenic fungi and identification of novel and diverse mycoviruses infecting prevalent of major crops. J.Gen. Virol.:manuscript in preparation.
144. Marzano, S. L., Hobbs, H. A., Nelson, B. D., Hartman, G. L., Eastburn, D. E., McCoppin, N. K., and Domier, L. L. 2015. Transfection of Sclerotinia sclerotiorum with in vitro transcripts of a naturally occurring interspecific recombinant of Sclerotinia sclerotiorum hypovirus significantly reduces virulence of the fungus. J. Virol.:Accepted.
145. Marzano, S.-Y. L., Wander, M. M., Villamil, M. B., Ugarte, C. M., Wen, L.-W., Eastburn, D. 2015. Organic transition effects on soilborne diseases of soybean and populations of Pseudomonadaceae. Agronomy journal. Accepted.

146. Marzano, S.-Y. L., Wander, M. M., Villamil, M. B., Ugarte, C. M., Zaborki, E. R., Eastburn, D. M. 2014. Organic amendment and transitional cropping system effects on crop diseases. Agronomy journal. Vol 106(2) p.1-9.
147. Mathew, F., M., Castelbury, L., A., Jordahl, J. G., Taylor, C., A., Meyer, S., M., Lamppa, R. S., Pasche, J., S., and Markell, S., G. 201X. Identification of Diaporthe longicolla on dry edible peas, dry edible beans and soybeans in North Dakota. Plant Health Progress (Submitted 10/10/14: PHP-RV-14-0045).
148. McClellan, M.S., Domier, L.L., Bailey, R.C., 2012. Label-free virus detection using silicon photonic microring resonators. Biosens. Bioelectron. 31, 388-392.
149. Mendoza, F.A., K. Cichy, R. Lu and J.D. Kelly. 2014. Evaluation of canning quality traits in black beans (Phaseolus vulgaris L.) by visible/near-infrared spectroscopy. Food Bioprocess Technol. 7:2666-2678. DOI 10.1007/s11947-014-1285-y
150. Merk, H.L., S.C. Yarnes, A. Van Deynze, N. Tong, N. Menda, L.A. Mueller, M.A. Mutschler, S.A. Loewen, J.R. Myers, and D.M. Francis. 2012. Trait Diversity and Potential for Selection Indices Based on Variation among Regionally Adapted Processing Tomato Germplasm. J. Amer. Soc. Hort. Sci. 137:427–437. .
151. Michelmore, R.W., Christopoulou, M., and Caldwell, K.S. 2013. Impacts of resistance gene genetics, function, and evolution on a durable future." Annu. Rev. Phtyopathology 51: 291–319.
152. Miklas, P. N., D. Fourie, J. Trapp, J. Davis, and J. R. Myers. 2014. New loci including Pse-6 conferring resistance to halo bacterial blight on chromosome Pv04 in common bean. Crop Sci. 54: 2099-2108.
153. Miklas, P. N., J. D. Kelly, J. R. Steadman, and S. McCoy. 2014. Registration of partial white mold resistant pinto bean germplasm line USPT-WM-12. Journal of Plant Registrations 8:183-186.
154. Millan, T., Madrid, E., Imtiaz, M., Kharrat, M. and Chen, W. 2012. Chapter 12: Disease resistance in chickpea. In: Genomics Applications in Plant Breeding. Wiley- Blackwell Publishers, USA. In press.011-1221-9
155. Mkwaila, W. 2013. Identification of quantitative trait loci for white mold resistance in common bean (Phaseolus vulgaris L.). Doctoral Dissertation, Michigan State University, East Lansing MI. 149pp.
156. Mukeshimana, G., A.L. Lasley, W.H. Loescher and J.D. Kelly. 2014. Identification of shoot traits related to drought tolerance in common bean seedlings. J. Amer. Soc. Hort. Sci. 139:1-11.
157. Mukeshimana, G., L. Butare, P.B. Cregan, M. W. Blair and J. D. Kelly. 2014. Quantitative Trait Loci associated with drought tolerance in common bean. Crop Sci. 54: 923-938.doi: 10.2135/cropsci2013.06.0427.
158. Myers, J., J. Davis, P. Miklas and P. McClean. 2013. Preliminary evaluation of the Bean CAP snap bean panel for white mold resistance. National Sclerotinia Initiative Meetings, 23-25 Jan., Minneapolis, MN.
159. Myers, J.R., L.McKenzie, and R.E. Voorrips. 2012. Brassicas: Breeding cole crops for organic agriculture. In: Lammerts van Bueren, E., and J.R. Myers (eds.) Organic Plant Breeding. Wiley-Blackwell pp. 251-262.

160. Myers. J., C. Will, and J. Davis. 2013. Can the negative association between yield and white mold resistance for NY6020 bean resistance be broken? National Sclerotinia Initiative Meetings, 23-25 Jan., Minneapolis, MN.
161. Nelson BD, MD Bolton, HD Lopez-Nicora, TL. Niblack, L del Río Mendoza. 2012. First confirmed report of Sugar beet cyst nematode, *Heterodera schachtii*, in North Dakota. Plant Dis. 96:772.
162. Nepal A., Friesen T.L., LeBoldus J.M. (2013) Polyethylene Glycol (PEG) mediated transformation of Septoria musiva. Phytopathology: 103:S3.7.
163. Neupane, A., P. Tamang, R. S. Brueggeman and T. L. Friesen (2014) Evaluation of a barley core collection for spot form net blotch reaction reveals distinct genotype specific pathogen virulence and host susceptibility. Phytopathology (In Press).
164. Njambere, E. N., Peever, T., Vandemark, G. and Chen, W. 2014. Genotypical variation and population structure of *Sclerotinia trifoliorum* infecting chickpea in California. Plant Pathology 63: 994-1004. DOI: 10.1111/ppa.12176
165. O'Connell*, R. J., Thon*, M.R., Hacquard, S., van Themaat E.M.V., Amyotte, S., Kleemann, J., Torres-Quintero, M., Damm, U., Buiate, E., Epstein, L., Alkan, N., Altmüller, J., Alvarado-Balderrama, L., Bauser, C., Becker, C., Birren, B.W., Chen, Z., Crouch, J.A., Duvick, J., Farman, M., Gan, P., Heiman, D., Henrissat, B., Howard, R.J., Kabbage, M., Koch, C., Kubo, Y., Law, A., Lebrun, M-H., Lee, Y-H., Miyara, I., Moore, N., Neumann, U., Panaccione, D.G., Panstruga, R., Place, M., Proctor, R.H., Prusky, D., Rech, G., Reinhardt, R., Rollins, J.A., Rounsley, S., Schardl, C., Schwartz, D.C., Shenoy, N., Shirasu, K., Stüber, K., Sukno, S.A., Sweigard, J.A., Takano, Y., Takahara, H., van der Does, H.C., Voll, L., Will, I., Young, S., Zeng, Q., Zhang, J., Zhou, S., Dickman, M.B., Schulze-Lefert, P., Ma, L-J. and Vaillancourt, L.J. 2012. Life-style transitions in plant pathogenic Colletotrichum fungi deciphered by genome and transcriptome analyses. Nature Genetics 44:1060-1065.
166. O'Rourke JA, Iniguez LP, Fu F, Bucciarelli B, Miller SS, Jackson SA, McClean PE, Li J, Dai X, Zhao PX, Hernandez G, Vance CP (2014) An RNA-seq based gene expression atlas of the common bean. BMC Genomics 15:886
167. Ostry, M.E. and LeBoldus J.M. (In press) Marssonina leaf spot and blight of Populus species. Ch. 9. In Diseases of Trees in the Great Plains. Edited by: A. Bergdahl and A. Hill. Fort Collins, CO: US Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station.
168. Ostry, M.E. and LeBoldus. J.M. (In press) Hypoxylon canker of aspen Ch. 27. In Diseases of Trees in the Great Plains. Edited by: A. Bergdahl and A. Hill. Fort Collins, CO: US Department of Agriculture, Forest Service, Rocky Mountain Forest and Range Experiment Station.
169. Pasche, J. S., and Gudmestad, N. C. 201X. Laboratory Methods for Evaluating Resistance in vitro. Pages (In Press) in: Fungicide Resistance in North America, 2nd Edition. K. L. Stevenson, M. T. McGrath, and C. A. Wyenandt, eds. APS Press, St Paul, MN.
170. Pasche, J. S., Mallik, I., Anderson, N. R., and Gudmestad, N. C. 2013. Development and validation of a real-time PCR assay for the quantification of Verticillium dahliae in potato. Plant Dis. 97:608-618.
171. Pasche, J. S., Taylor, R. J., David, N. L., and Gudmestad, N. C. 2013. Effect of soil temperature, injection depth, and metam sodium rate on the management of Verticillium wilt of potato. Amer. J. Potato Res. DOI 10.1007/s12230-013-9348-6.

172. Pasche, J. S., Thompson, A. L., and Gudmestad, N. C. 2013. Quantification of field resistance to Verticillium dahliae in eight russet-skinned potato cultivars using real-time PCR. Amer. J. Potato Res. 90:158-170.
173. Paul C., Hartman G.L., Marios J.J., Wright D.L., Walker D.R. (2013) First report of Phakopsora pachyrhizi adapting to soybean genotypes with Rpp1 or Rpp6 rust resistance genes in field plots in the United States. Plant Disease 97:1379.
174. Pearson, C., J.B. Ogg, M.A. Brick, and A. Berrada. 2012. Popping and Yield Characteristics of Nuña Bean Lines Developed for Temperate Climates. Agron. J. 104: 6: 1574-1578.
175. Pearson, T.C., J.R. Prasifka, D.L. Brabec, R.P. Haff, and B.S. Hulke. 2014. Automated detection of insect-damaged sunflower seeds by X-ray imaging. Applied Engineering in Agriculture 30:125-131.
176. Peers G, Smith K, Jonikas M, Grossman A, Posewitz M. "Chlamydomonas reinhardtii during Dark Anoxia and the Dominant Role of Chloroplasts in Fermentative Acetate Production." Plant Cell. DOI: http://dx.doi.org/10.1105/tpc.114.129965.
177. Peever, T.L., Chen, W., Abdo, Z. and Kaiser, W.J. 2012. Genetics of virulence in *Ascochyta rabiei*. Plant Pathology 61: 754-760. DOI: 10.1111/j.1365-3059.2011.02566.x
178. Pegadaraju V. Nipper R. Hulke B.S., Qi L.L. Schultz Q. 2013. De novo sequencing of sunflower genome for SNP discovery using RAD (Restriction site Associated DNA) approach. BMC Genomics 15:556.
179. Peltier, A.J., Bradley, C.A., Chilvers, M.I., Malvick, D.K., Mueller, D.S., Wise, K.A., Esker, P.D. 2012. Biology, yield loss, and control of Sclerotinia stem rot of soybean. Journal of Integrated Pest Management. 3(2):B1-B7
180. Pérez-Vega, E., A. Pascual, A. Campa, R. Giraldez, P. N. Miklas, and J. J. Ferreira. 2012. Mapping QTL conferring partial physiological resistance to white mold in the common bean RIL population Xana/Cornell 49242. Mol. Breed. 29:31-41.
181. Pethybridge, S. J., Gent, D. H., Groom, T., and Hay, F. S. 2013. Minimizing crop damage through understanding relationships between pyrethrum phenology and ray blight disease severity. Plant Dis. 97:1431-1437.
182. Pethybridge, S. J., Gent, D. H., Hingston, L., and Frost, P. 2014. Quantifying the effects of uniconazole on growth and yield of pyrethrum in Australia. N. Z. J. Crop and Hort. Sci. 42:50-59.
183. Pethybridge, S. J., Scott, J. B., Latham, R., and Hay, F. S. 2012. Evidence against the Phoma ligulicola var. inoxydablis population undergoing recombination or containing spatial structure in Australian pyrethrum fields. Plant Dis. 96: 746-751.
184. Porch, T.G., J.S. Beaver, and M.A. Brick. 2013. Registration of tepary germplasm with multiple-stress tolerance, TARS-Tep 22 and TARS-Tep 32. Journal of Plant Registrations. 2013 7: 3: 358-364 doi:10.3198/jpr2012.10.0047crg
185. Poromarto, S. H., Gramig, G. G., Nelson Jr, B. D., and Jain, S. 2014. Evaluation of Weed Species from the Northern Great Plains as Hosts of Soybean Cyst Nematode. Plant Health Progress (in press).
186. Prasifka JR, LW Cook, DE Palmquist, ME Foley. 2014. Sesquiterpene lactone composition of wild and cultivated sunflowers and biological activity against an insect pest. Submitted to Phytochemistry on 09-08-14.

187. Prasifka, J.R., B.S. Hulke, and G.J. Seiler. 2014. Pericarp strength of sunflower and its value for plant defense against the sunflower moth, Homoeosoma electellum. Arthropod-Plant Interactions 8:101-107.
188. Qandah I, LE del Río Mendoza. 2012. Modeling inoculum dispersal and Sclerotinia stem rot gradients in canola fields. Can. J. Plant Pathol. 34:390-400.
189. Qi L.L, Gulya T.J., Hulke B.S., Vick B.A. 2012 Chromosome location, DNA markers and rust resistance of the sunflower gene R5. Mol. Breeding 30:745-756
190. Qi L.L, Seiler G.J. 2013 Registration of a male fertility restorer oilseed sunflower germplasm, HA-R9, resistant to sunflower rust. J. Plant Reg. 7:353-357.
191. Qi L.L., Gulya T.J., Block C.C., Hulke B.S. 2012. Deployment of novel sources of Sclerotinia resistance in sunflower. National Sclerotinia Initiative Annual Meeting, January 18-20, 2012, Bloomington, MN. p:31.
192. Qi L.L., Gulya T.J., Hulke B.S., Vick B.A., Seiler G.J. 2012. Molecular mapping of the rust resistance genes in sunflower: results and prospects. Presentation at the National Sunflower Association Research Forum, January 11-12, 2012, Fargo, ND. Available: http://www.sunflowernsa.com/uploads/resources/621/molecular-mapping-of-the-rust---qi.pdf.
193. Qi L.L., Long Y.M., Gulya T.J., Block C.C., Hulke B.S. 2013. Genetic resistance of cultivated sunflower to Sclerotinia stalk rot introduced from wild Helianthus. 15th International Sclerotinia workshop, August 20-24, 2013, Wuhan, China. p:66
194. Qi, L., L. Gong, S. Markell, G.J. Seiler, T.J. Gulya, and B. Hulke. 2014. Registration of two confection sunflower germplasm lines, HA-R10 and HA-R11, resistant to sunflower rust. J. Plant Reg. 8:329-333.
195. Qi, L.L., G. Ma, Y. Long, L. Gong, B.S. Hulke, and S. Markell. 201x. Relocation of a rust resistance gene R2 and its marker-asssisted gene pyramiding in confection sunflower (Helianthus annuus L.). Theor Appl Genet (in review).
196. Qin R., Stanosz G.R., LeBoldus J.M. (2013) Non-wound greenhouse screening of hybrid poplar trees with Septoria musiva. Phytopathology 103: S2.1.
197. Qin, R. and LeBoldus, J.M. (2014) The infection biology of Sphaerulina musiva: clues to understanding a forest pathogen. PloS ONE. e103446.
198. Qin, R. Stanosz G.R., LeBoldus J.M. (2014) A non-wounding greenhouse screening protocol for prediction of field resistance of hybrid poplar to Septoria canker. Plant Disease 98: 1106-1111.
199. Ragimekula N, K Chittem, VN Nagabudi, LE del Río Mendoza. 2014. First report of 16SrII-D phytoplasma '*Candidatus* Phytoplasma *aurantifolia*' associated with mung bean phyllody in Andhra Pradesh, India. Plant Dis. 98:1424.
200. Rahman, M. (2014) Independent assortment of seed color and leaf hairiness genes in *Brassica rapa* L. Can. J. Plant Sci. 94:615-620.
201. Rahman, M., Mamidi S., and McClean P.E. (2014) QTL mapping of seed color, hairy leaf, seedling anthocyanin, leaf chlorosis and days to flowering in F2 population of Brassica rapa L. Plant Breed. 133(3):381-389. (doi:10.1111/pbr.12165).
202. Raupp F, O Spring. 2013. New sesquiterpene lactones from sunflower root exudate as germination stimulants for Orobanche cumana. Journal of Agricultural and Food Chemistry 61:10481-10487.

203. Reif, J.C., Y. Zhao, T. Wurschum, M. Gowda, and V. Hahn. 2013. Genomic prediction of sunflower hybrid performance. Plant Breeding 132:107-114.
204. Reinprecht Y, Yadegari Z, Perry GE, Siddiqua M, Wright LC, McClean PE, Pauls K P (2013) In silico comparison of genomic regions containing genes coding for enzymes and transcription factors for the phenylpropanoid pathway in Phaseolus vulgaris L and Glycine max L Merr. Frontiers in Plant Science, 4:317
205. Renaud, Erica N.C., Edith T. Lammerts van Bueren, James R. Myers, Maria João Paulo, Fred A. van Eeuwijk, Ning Zhu, John A. Juvik. 2014. Variation in broccoli cultivar phytochemical content under organic and conventional management systems: Implications in breeding for nutrition. PLoS ONE (in press).
206. Renaud, Erica N.C., Edith T. Lammerts van Bueren, Maria João Paulo, Fred A. van Eeuwijk, John A. Juvik, Mark G. Hutton, James R. Myers. 2014. Broccoli cultivar performance under organic and conventional management systems and implications for crop improvement. Crop Science (https://www.crops.org/publications/cs/view/first-look/c13-09-0596.pdf)
207. Rennie, D.C., LeBoldus J.M., Turkington, T.K., Strelkov S.E. (2012) Fine scale clubroot mapping in Alberta. Canadian Journal of Plant Pathology. 35: 123-123.
208. Rollins, J.A., Cuomo, C.A., Dickman, M.B. and Kohn, L.M. 2014. Genomics of Sclerotinia sclerotiorum. In Genomics of Plant-Associated Fungi and Oomycetes: Dicot Pathogens, Eds. Ralph Dean, Ann Lichens Park and Chittaranjan Kole. Springer-Verlag Berlin Heidelberg, p. 1-17.
209. Schapaugh, W., J.G. Shannon, R. Uniatowski, M. Sciences, D. Wang, and B. Diers. 2014. Genetic Improvement of US Soybean in Maturity Groups II, III, and IV. Crop Sci. 54:1-14.
210. Rubiales, D., Fondevilla, S., Chen, W., Gentzbittel, L., Higgins, T. J. V., Castillejo, M. A., Singh, K. B. and Rispail, N. 2015. Achievements and challenges in legume breeding for pest and disease resistance. Critical Reviews in Plant Sciences 34: 195-236. DOI:10.1080/07352689.2014.898445.
211. Saha, G. C., and G. J. Vandemark. 2012. Evaluation of expression stability of candidate reference genes among green and yellow pea cultivars subjected to abiotic and biotic stress. Am. J. Plant Sci. 3:235---242.
212. Saha, G. C., Sarker, A, Chen, W., Vandemark, G. J. and Muehlbauer, F. J. 2013. Inheritance and linkage map positions of genes conferring agromorphological traits in *lens culinaris* Medik. International Journal of Agronomy 2013:618926.
213. Schmutz J, McClean P, Mamidi S, Wu GA, Cannon SB, Grimwood J, Jenkins J, Shu S, Song Q, Chavarro C, Torres-Torres M, Geffroy V, Moghaddam SM, Gao D, Abernathy B, Barry K, Blair M, Brick MA, Chovatia M, Gepts P, Goodstein DM , Gonzales M, Hellsten U, Hyten DL, Jia G, Kelly JD, Kudrna D, Lee R, Richard MMS, Miklas PN, Osorno JM, Rodrigues J, Thareau V, Urrea CA, Wan M, Yu Y, Zhang M, Wing RA, Cregan PB, Rokhsar DS, Jackson SA. 2014. A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics 46: 707-713.
214. Schumacher, J., Ségurens, B., Sexton, A., Silva, E., Sirven, C., Soanes, D.M., Talbot, N.J., Schwartz HF, Singh SP (2013) Breeding Common Bean for Resistance to White Mold: A Review. Crop Science 53: 1832-1844.
215. Scott, J. B., Gent, D. H., Pethybridge, S. J., and Hay, F. S. 2014. Spatiotemporal characterization of Sclerotinia crown rot epidemics in pyrethrum. Plant Dis. 98:267-274.

216. Scott, J. B., Pethybridge, S. J., Gent, D. H., Groom, T., and Hay, F. S. 2014. Crop damage from Sclerotinia crown rot and risk factors in pyrethrum. Plant Dis. 98:103-111.
217. Seiler, G.J. 2014. Comparison of fatty acid composition of oil from original and regenerated populations of wild Helianthus species. Plant Genetic Res. DOI:10.1017/S1479262114000677.
218. Seiler, G.J. and C.C. Jan. 2014. Wild sunflower species as a genetic resource for resistance to sunflower broomrape (Orobanche cumna Wallr.). Helia DOI: 10.1515/helia-2014-0013.
219. Settles ML, Coram T, Soule T and Robison BD (2012). An improved algorithm for the detection of genomic variation using short oligonulceotide expression microarrays. *Molecular Ecology Resources* 12:1079-1089,
220. Shen, M, Broeckling CD, Chu EY, Ziegler G, Baxter IR, Prenni JE, Hoekenga OA, 2013 "Leveraging non-targeted metabolite profiling via statistical genomics" PLOSONE 8(2):e57667.
221. Shjerve, R., J.D. Faris, R.S. Brueggeman, V. Koladia and T.L. Friesen (2014). Evaluation of a Pyrenophora teres f. teres mapping population shows multiple independent interactions with the barley 6H chromosome region. Fungal Genetics and Biology (In Press).
222. Sidhu H., Haagenson D., Rahman M., and Wiesenborn D. (2014) Diode array near infrared spectrometer calibrations for composition analysis single plant canola (*Brassica napus* L.) seeds. Appl. Eng. Agric. 30(1): 69-76.
223. Sikora, E.J., T.W. Allen, K.A. Wise, G. Bergstrom, C.A. Bradley, J. Bond, D. Brown-Rytlewski, M. Chilvers, J. Damicone, E. DeWolf, A. Dorrance, N. Dufault, P. Esker, T.R. Faske, L. Giesler, N. Goldberg, J. Golod, I.R.G. Gomez, C. Grau, A. Grybauskas, G. Franc, R. Hammerschmidt, G. L. Hartman, A. Henn, D. Hershman, C. Hollier, T. Isakeit, S. Isard, B. Jacobson, D. Jardine, B. Kemerait, S. Koenning, M. Langham, D. Malvick, S. Markell, J.J. Marois, S. Monfort, D. Mueller, J. Mueller, R. Mulroony, M. Newman, L. Osborne, G.B. Padgett, B.E. Ruden, J. Rupe, R. Schneider, H. Schwartz, G. Shaner, S. Singh, E. Stromberg, L. Sweets, A. Tenuta, S. Vaiciunas, X.B. Yang, H. Young-Kelly, and J. Zidek. 2014. A coordinated effort to manage soybean rust in North America: a success story in soybean disease monitoring. Plant Dis. 98:864-875.
224. Sim S-C., A. Van Deynze, K. Stoffel, D.S. Douches, D. Zarka, M.W. Ganal, R.T. Chetelat, S.F. Hutton, J.W. Scott, R.G. Gardner, D.P. Panthee, M. Mutschler, J.R. Myers, D.M. Francis. (2012) High-Density SNP genotyping of tomato (Solanum lycopersicum L.) reveals patternsof genetic variation due to breeding. PLoS ONE 7(9): e45520. doi:10.1371/journal.pone.0045520
225. Singh, S., H.F. Schwartz and J.R. Steadman. 2014. A New Scale for White Mold Disease Rating for The Common Bean Cut-stem Method of Inoculation in the Greenhouse. Ann. Rpt. Bean Improvement Coop. 57:231-232.
226. Sousa, L.L., A. S. Cruz, P. S. Vidigal Filho, V. A. Vallejo, J. D. Kelly and M.C. Gonçalves-Vidigal. 2014. Genetic mapping of the resistance allele Co-52 to Colletotrichum lindemuthianum in the common bean MSU 7-1 line. Aust. J. Crop Science 8:317-323.
227. Steyn, C., Mclaren, N.W., Flett, B. C. & Minnaar-Ontong, A. (2013). Genetic variation of Sclerotinia sclerotiorum isolates in South Africa. 15th International Sclerotinia Workshop, Wuhan, China. 20-24 August 2013.
228. Talukder Z.I., Gong L., Hulke B.S., Pegadaraju V., Song Q.J., Schultz Q., *Qi L.L. 2014. A high-density SNP map of sunflower derived from RAD-sequencing facilitating fine-mapping of the rust resistance gene R12. PLoS ONE 9(7): e98628.

229. Talukder Z.I., Hulke B.S., Qi L.L., Scheffler B.E., Pegadaraju V., McPhee K. and Gulya T.J. 2014b. Candidate gene association mapping of Sclerotinia stalk rot resistance in sunflower (Helianthus annuus L.) uncovers the importance of COI1 homologs. Theor Appl Genet 127:193–209.
230. Talukder, Z. I., B. S. Hulke, L. Marek, and T. J. Gulya. 2014. Sources of resistance to sunflower diseases in a global collection of domesticated USDA plant introductions. Crop Sci. 54:694-705.
231. Talukder, Z.I., B.S. Hulke, and T.J. Gulya. 201x. Genome-wide association studies of Sclerotinia basal stalk rot, Sclerotinia head rot and Phomopsis stem canker resistance in sunflower (Helianthus annuus L.). BMC Plant Biol. (in review).
232. Talukder, Z.I., L. Gong, B.S. Hulke, V. Pegadaraju, Q. Song, Q. Schultz, and L. Qi. 2014. A high-density SNP map of sunflower derived from RAD-sequencing facilitating fine-mapping of the rust resistance gene R12. PLoS One 9 (7):e98628.
233. Tamang, P., A. Neupane, S. Mamidi, T. Friesen and R. Brueggeman (2014) Association mapping of seedling resistance to Spot Form Net Blotch in a worldwide collection of barley. Phytopathology (In Press).
234. Terán, H., Jara, C., Mahuku, G., Beebe, S. and Singh, S.P. 2013. Simultaneous selection for resistance to five bacterial, fungal, and viral diseases in three Andean x Middle American inter-gene pool common bean populations. Euphytica 189:283-292.
235. Twizeyimana, M., P.S. Ojiambo, R. Bandyopadhyay, and G. L. Hartman. 2014. Use of quantitative traits to assess aggressiveness of Phakopsora pachyrhizi isolates from Nigeria and the United States. Plant Dis. 9:1261-1266.
236. Vaghefi, N., Ades, P., Hay, F. S., Pethybridge, S. J., Ford, R., and Taylor, P. W. J. 2014. Identification of the MAT1locus in Stagonosporopsis tanaceti, and exploring its potential for sexual reproduction in Australian pyrethrum fields. Fungal Biology (in press).
237. Vaghefi, N., Hay, F. S., Ades, P. K., Pethybridge, S. J., Ford, R., and Taylor, P. W. J. 2014. Rapid changes in the genetic composition of Stagonosporopsis tanaceti populations in Australian pyrethrum fields. Phytopathology (in press).
238. Vaghefi, N., Pethybridge, S. J., Ford, R., Nicolas, M. E., Crous, P. W., and Taylor, P. W. J. 2012. Stagonosporopsis spp. associated with ray blight disease of Asteraceae. Austral. Plant Pathol. 41:675-686.
239. Van Bruggen, J., Dunn, A. R., Smart, C. D., and Pethybridge, S. J. 2014. Variation of phenotypic characteristics in populations of Sclerotinia sclerotiorum causing white mold in snap bean in New York. Proceedings of the 2014 Summer Scholars Program, Undergraduate Research Program Session, 1 August, Cornell University, New York Agricultural Experiment Station, Geneva, NY, Pp. 10.
240. Van Verk MC, R Hickman, CMJ Pieterse, SCM Van Wees. 2013. RNA-Seq: revelation of the messengers. Trends in Plant Science 18:175-179.
241. Vandemark, G.J., M.A. Brick, J.M. Osorno, J.D. Kelly, and C.A. Urrea. 2014. Edible grain legumes. In: S. Smith, B. Diers, J. Specht, and B. Carver, editors. Yield gains in major U.S. field crops. CSSA Spec. Publ. 33. CSSA, Madison, WI. p. 87-123. doi:10.2135/cssaspecpub33.c5
242. Velasco L, B Pérez-Vich, AAM Yassein, , C-C Jan, M Fernández-Martínez. 2012. Inheritance of resistance to sunflower broomrape (Orobanche cumana Wallr.) in an interspecific cross between Helianthus annuus and Helianthus debilis subsp. tardiflorus. Plant Breeding 131:

243. Velasco, L., B. Pérez-Vich, A. Yassein, C.C. Jan, and J.M. Fernández-Martínez. 2012. Inheritance of resistance to sunflower broomrape (Orobanche cumana Wallr.) in an interspecific cross between Helianthus annuus and H. debilis subsp. tardiflorus. Plant Breed. 131-220-221.
244. Viteri, D. M., H. Terán, M. C. Asensio-S.-Manzanera, C. Asensio, T. G. Porch, P. N. Miklas, and S. P. Singh. 2014. Progress in breeding Andean common bean for resistance to common bacterial blight. Crop Sci. 54: 2084-2092.
245. Viteri, D. M., P. B. Cregan, J. J. Trapp, P. N. Miklas, and S. P. Singh. 2014. A new common bacterial blight resistance QTL in VAX 1 common bean and interaction of the new QTL, SAP6, and SU91 with bacterial strains. Crop Sci. 54:1598-1608.
246. Viteri, D., and S. P. Singh, 2014. Breeding common bean for high levels of resistance to white mold. Abstract 277-9. ASA Meetings, Long Beach CA.
247. Viteri, D.M. and S.P. Singh. 2015. Inheritance of white mold resistance in an Andean common bean A 195 and its relationship with Andean G 122. Crop Sci. 55:1-6.
248. Vittal, R., C. Paul, C.B. Hill, and G. L. Hartman. 2014. Characterization and quantification of fungal colonization of Phakopsora pachyrhizi in soybean genotypes. Phytopathology 104:86-94.
249. Wang J., Jacobs, J.L., Chilvers, M.I. In Press. Improved diagnoses and quantification of Fusarium virguliforme, causal agent of soybean sudden death syndrome. Phytopathology
250. Wang J., P. Chen, D. Wang, G. Shannon, A. Shi, A. Zeng, and M. Orazaly. 2014. Identification of quantitative trait loci for oil content in soybean seed. Crop Sci. doi:10.2135/cropsci2014.04.0280.
251. Wang, D., Z. Wen, R. Tan, and M. Chilvers. 2013. Genome-wide association mapping of loci underlying soybean resistance to Sclerotinia sclerotiorum. In National Sclerotinia Initiative, ed. Proceedings of 2013 Sclerotinia Initiative Annual Meeting, Jan. 2013, Bloomington, MN.
252. Wang, J., Jacobs, J.L., Byrne, J.M., Chilvers, M.I. *In Press.* Improved diagnoses and quantification of *Fusarium virguliforme*, causal agent of soybean sudden death syndrome. Phytopathology http://dx.doi.org/10.1094/PHYTO-06-14-0177-R
253. Wang, X., J. Richards, T. Gross, A. Druka, A. Kleinhofs, B. Steffenson, M. Acevedo and R. Brueggeman (2013) The rpg4-mediated resistance to wheat stem rust (Puccinia graminis) in barley (Hordeum vulgare) requires Rpg5, a second NBS-LRR gene and an actin depolymerization factor. Mol Plant Microbe In 26(4):407-418.
254. Wang, Y., An, C., Zhang, X., Yao, J., Zhang, Y., Sun, Y., Yu, F., Amador, D.M. and Mou, Z. (2013). The Arabidopsis Elongator complex subunit2 epigenetically regulates plant immune responses. Plant Cell 25, 762-776.
255. Wen Z., R. Tan, J. Yuan, C. Bales, W. Du, S. Zhang, M. Chilvers, C. Schmidt, Q. Song, P. Cregan, and D. Wang. 2014. Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. BMC Genomics 2014 15:809.
256. Wen, Z., Tan, R., Yuan, J., Bales, C., Du, W., Zhang, S., Chilvers, M.I., Schmidt, C., Song, Q., Cregan, P., Kull, L., Wang, D. 2014. Genome-wide association mapping of quantitative resistance to sudden death syndrome in soybean. BMC Genomics 15:809
257. Weyman PD, Beeri K, Lefebvre SC, Rivera J, Heuberger AL, Peers G, Allen AE, Dupont CL. "Inactivation of Phaeodactylum tricornutum urease gene using TALEN-based targeted mutagenesis." (Plant Biotechnology Journal, in press).

258. Wunsch, M., Pasche, J., Knodel, J., McPhee, K., Markell, S., Chapara, V., and Pederson, S. 2014. Pea Seed-borne Mosaic Virus in Field Peas and Lentils. NDSU Extension Service publication PP1704.
259. Wunsch, M., Pasche, J., Knodel, J., McPhee, K., Markell, S., Chapara, V., and Pederson, S. 2014. Pea Seed-borne Mosaic Virus in Field Peas and Lentils. NDSU Extension Service publication PP1704.
260. Wunsch, M.J., Schaefer, M.D., and Kraft, B.D. 2013. Field evaluation of fungicides to control Mycosphaerella blight on field peas, Carrington, ND, 2012. Plant Disease Management Reports 7:FC108.
261. Wunsch, M.J., Schaefer, M.D., and Kraft, B.D. 2013. Field evaluation of fungicides to control Ascochyta blight on lentils, Carrington, ND, 2012. Plant Disease Management Reports 7:FC102.
262. Xiang, Y., T. Herman, and G. L. Hartman. 2014. Utilizing soybean milk to culture soybean pathogens. Adv. Microbiol. 4:126-132.
263. Xiao, X. Q., Cheng, J. S., Tang, J. H., Fu, Y. P., Jiang, D. H., Baker, T. S., . . . Xie, J. T. 2014. A novel partitivirus that confers hypovirulence on plant pathogenic fungi. J. Virol. 88:10120-10133
264. Yadava, S., N. Arumugam, A. Mukhopadhyay, Y. Sodhi, V. Gupta, D. Pental and A. Pradhan. 2012. QTL mapping of yield-associated traits in Brassica juncea: meta-analysis and epistatic interactions using two different crosses between east European and Indian gene pool lines. Theor Appl Genet 125: 1553-1564. doi:10.1007/s00122-012-1934-3.
265. Yajima, W., Chittem, K., and Goswami, R. S. 2012. (Book Chapter) Relevance of genomics-based studies on management of diseases caused by Fusarium species. In 'Fusarium: Epidemiology, Environmental Sources and Prevention' Pp: 191-208. Ed by Rios, T. F. and Ortega, E. R. Nova Scientific Publishers Inc, Hauppauge, NY.
266. Yang, H.-C., J.S. Haudenshield, and G. L. Hartman. 2014. Colletotrichum incanum sp. nov., a curved-conidial species causing soybean anthracnose in the USA. Mycologia 106:32-42.
267. Yu, Y., Jiang, D. H., Xie, J. T., Cheng, J. S., Li, G. Q., Yi, X. H., and Fu, Y. P. 2012. Ss-Sl2, a novel cell wall protein with PAN modules, is essential for sclerotial development and cellular integrity of Sclerotinia sclerotiorum. PLOS ONE 7:14.
268. Yuan J., Z. Wen, C. Gu, and D. Wang. 2014. Introduction of high throughput and cost effective SNP genotyping platforms in soybean. Plant Genetics, Genomics, and Biotechnology 2:90-94.
269. Zeng A., P. Chen, A. Shi, D. Wang, B. Zhang, M. Orazaly, L. Florez-Palacios, K. Brye, Q. Song, and P. Cregan. 2014. Identification of quantitative trait loci for sucrose content in soybean seeds. Crop Sci. 54:554-564.
270. Zeng, L-M., Zhang, J., Han,Y-C., Yang, L., Wu, M.-d., Jiang, D.-H., Chen, W. and Li, G-Q. 2014. Degradation of oxalic acid by the mycopsrasite *Coniothyrium minitans* plays an important role in interacting with *Sclerotinia sclerotiorum*. Environmental Microbiology 16: 2591-2610 DOI: 10.1111/1462-2920.12409
271. Zernova, O.V., A.V. Lygin, M.L. Pawlowski, C.B. Hill, G. L. Hartman, J.M. Widholm, and V.V. Lozovaya. 2014. Regulation of plant immunity through modulation of phytoalexin synthesis. Molecules 19:7480-7496.
272. Zhang Y, Itaya A, Fu P, Zheng S, J Hulm J, Blahut-Beatty L, Marillia E-F, Lindenbaum M, Fabijanski S, Simmonds D. (2013) Generation of stable engineered chromosomes in soybean. Plant Biotech 30(5):455-465.

273. Zhang Y, Schernthaner J, Labbé1 N, Hefford MA, Zhao J, Simmonds DH. (2014) Improved Protein Quality in Transgenic Soybean Expressing a De Novo Synthetic Protein, MB-16. Transgenic Research 23:455-467.
274. Zhang, D. X., Spiering, M. J., Dawe, A. L., and Nuss, D. L. 2014. Vegetative incompatibility loci with dedicated roles in allorecognition restrict mycovirus transmission in chestnut blight fungus. Genetics 197:701-U413
275. Zhang, X. and Mou, Z. (2012). Expression of the human NAD(P)-metabolizing ectoenzyme CD38 compromises systemic acquired resistance in Arabidopsis. Molecular Plant-Microbe Interactions 25, 1209-1218.
276. Zhang, X., Wang, C., Zhang, Y., Sun, Y. and Mou, Z. (2012). The Arabidopsis Mediator complex subunit16 positively regulates salicylate-mediated systemic acquired resistance and jasmonate/ethylene-induced defense pathways. Plant Cell 24, 4294-4309.
277. Zhang, Z., J. Hao, J. Yuan, Q.J. Song, D.L. Hyten, P.B. Cregan, G. Zhang, C. Gu, M. Li, and D. Wang. 2014. Phytophthora root rot resistance in soybean E00003. Crop Sci. 54:492-499.
278. Zhao, Y., M. Gowda, W. Liu, T. Wurschum, H.P. Maurer, F.H. Longin, N. Ranc, H.P. Piepho, and J.C. Reif. 2013. Choice of shrinkage parameter and prediction of genomic breeding values in elite maize breeding populations. Plant Breeding 132:99-106.
279. Zhuang X, Santos P, Rojas JA, Wang J, McPhee KE, Coram TE and Chilvers MI (2014). Delayed cell death mediates partial resistance to *Sclerotinia sclerotiorum* in *Pisum sativum* (pea). Plant Physiology (submitted).
280. Zhuang, X, McPhee, K.E., Coram, T.E., Peever, T.L., Chilvers, M.I. 2012. Rapid transcriptome characterization and parsing of sequences in a non-model host-pathogen interaction; pea-sclerotinia sclerotiorum. BMC Genomics 13:668.
281. Zhuang, X, McPhee, K.E., Coram, T.E., Peever, T.L., Chilvers, M.I. 2013. Development and characterization of 37 novel EST-SSR markers in *Pisum sativum* (Fabaceae). Applications in Plant Sciences 1(1):1200249.
282. Zitnick-Anderson, K., and Nelson Jr., B. D. 2014. Identification and pathogenicity of Pythium on soybean in North Dakota. Plant Dis. 98: http://dx.doi.org/10.1094/PDIS-02-14-0161-RE. posted 08/01/2014
283. Zurn, D, M. Newcomb, M. N. Rouse, Y. Jin, S. Chao, J. Sthapit, D. R. See, R. Wanyera, P.Njau, M. Bonman, R. Brueggeman,. and M. Acevedo (2014) High Density Mapping of a Resistance Gene to Ug99 from an Iranian Landrace. Molecular Breeding 34:871-881.

FY2015 Sclerotinia Review Matrix

	Project	PI	2014 Request	Affiliation	Commodity
1	Comparative transcriptomics of *Sclerotinia sclerotiorum* infecting grain legumes for genomics assisted breeding	Chen	$76,884	ARS-Pullman WA	Pea & Lentil
2	Expression profiling of the pea-Sclerotinia sclerotiorum interaction for genomics assisted breeding	Chilvers	$50,577	Mich State Univ	Pea & Lentil
3	Identifying and verifying genes for defense to Sclerotinia	Clough	$89,929	ARS-Urbana IL	Soybean
4	Characterizing resistance and pathogenicity genes associated with infrection of B. napus by *Sclerotinia sclerotiorum*	del Rio	$64,093	NDSU	Canola
5	Myceliogenic germination in response to crop-specific factors	del Rio	$54,958	NDSU	Canola
6	Improving resistance to *Sclerotinia sclerotiorum in Spring canola*	del Rio	$39,489	NDSU	Canola
7	Functional analysis of Sclerotinia sclerotiorum genes involved in mycelial compatibility by virus-induced gene silencing	Domier	$28,000	ARS Urbana IL	Pathogen
8	Evaulation of native and non-native phytoalexins in suppressing in vitro, in vivo, and in planta growth of Sclerotinia sclerotiorum	Hartman	$60,000	ARS Urbana IL	Pathogen, Soybean
9	Linking metabolic phenotypes with genetic factors that confer resistance to Sclerotinia sclerotiorum in common bean	Heuberger	$75,115	Colorado State Univ	Dry Bean
10	Using genomic selection to optimize prediction of Sclerotinia and agronomic phenotypes for more efficient breeding	Hulke	$89,049	ARS Fargo ND	Sunflower
11	Transferring Sclerotinia resistance genes from wild *Helianthus* species into cultivated sunflower	Jan	$149,163	ARS Fargo ND	Sunflower
12	Validating QTL for White Mold Resistance in Mesoamerican Beans	Kelly	$49,985	Mich State Univ	Dry Bean
13	Identification of major genes-QTL for Sclerotinia resistance in cultivated sunflower and wild Helianthus	Qi	$101,790	ARS Fargo ND	Sunflower
14	Characterization and validation of two distinct mechanisms for partial resistance to Sclerotinia sclerotiorum in pea	McPhee	$55,001	NDSU	Pea & Lentil
15	White mold resistance-QTL: Identification, interactions & fine mapping in common bean	Miklas	$169,547	ARS-Prosser WA	Dry Bean
16	Identification and functional analyses of candidate Sclerotinia sclerotiorum virulence genes.	Brueggeman	$55,250	NDSU	Pathogen
17	Tackling White Mold from the Ground-Up: Manipulating Carpogenic Germination	Pethybridge	$21,160	Cornell Univ	Pathogen
18	Synergistic enhancement of resistance to Sclerotinia sclerotiorum	Rollins	$60,411	Univ Florida	Canola, Model Crop
19	Discovery and use of novel sources of head and stalk rot resistance in sunflower and studies of Asteraceae genera stimulating myceliogenic germination	Seiler	$78,454	ARS Fargo ND	Sunflower, Pathogen
20	Improved white mold resistance in dry and snap beans through multi-site screening and pathogen characterization throughout major production areas	Steadman	$51,071	Univ Nebraska	Pathogen, Dry Bean
21	Enhancing soybean for resistance to Sclerotinia stem rot	Wang	$44,409	Mich State Univ	Soybean
22	Improved head rot resistance screening in sunflowers and impacts and implications of sclerotinia infection timing in dry bean, soybean, and sunflower	Wunsch	$68,000	NDSU	Sunflower, Dry Bean, Soybean