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Meeting Strategic Milestones of the National Sclerotinia Research Initiative for 2010

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 *National Strategic Plan for the Sclerotinia Initiative 2008-2012* 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 US 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 2010* 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

	2008	2009	2010	2011	2012
	number of accomplishment citations				
Total Accomlishments Cited	76	61	75		
Milestones w/ multiple citations	17	10	14		
Milestones w/ no citations	30	30	24		
Milestones not funded	NA	14	2		
Milestones completed	0	1	1		
Total Milestones Rated	76	76	73		
Achievement Rating (%)	56.7	62.2	67.2		
Total Projects	34	28	19		
Accomplishments / project	2.2	2.2	3.9		
All Publications by SYs	47	53	122		
Total SYs funded by NSI	20	33	35		
Germplasm/Varieties released	10	10	15		

Achievement Rating:
((all accomps x (milestones (multi citations/(no citations-not funded)))/milestones(all-not funded) x 100) + (milestones completed*0.75)

Milestone	2008	2009	2010	2011	2012
Crop Germplasm Resources & Genetics	number of accomplishment citations				
PM 1.1: New sources of resistant plant germplasm					
• *Exploration trips to obtain seeds of wild species*	0	3	1		
• *Improved germplasm screening methods*	3	3	3		
• *Increased availability of resistant germplasm*	1	3	1		
• *Doubled haploid lines for resistance, tested in multiple environments*	1	1	1		
PM 1.2: Transfer new resistance genes into plant germplasm					
• *Germplasm derived from interspecific crosses*	7	2	2		
• *Resistant selections of unadapted x agronomic traits*	0	1	1		
PM 1.3: Genetic analysis & QTL discovery					
• *Highly inbred mapping populations with validated QTLs*	2	4	2		
• *QTL analysis to generate a high density genetic maps*	3	2	2		
• *Integrated linkage maps*	4	1	1		
PM 1.4: Pyramid white mold resistance genes					
• *Improved conventional breeding methods for quantitative traits*	1	2	1		
• *Breeding populations segregating for multiple resistance alleles and other traits*	3	1	1		
PM 1.5: Marker-assisted selection					
• *Disease reaction of RILs in multiple field environments*	1	1	1		
• *Marker-assisted selection protocol for more efficient genotyping*	4	1	1		
• *Field verification of resistance*	3	1	1		
PM 1.6: GM improved resistance					
• *GM oxalate oxidase expression, inheritance and field evaluation*	1	1	1		
• *Catalog of candidate resistance genes, promoters, and constructs for transformation*	2	1	2		
• *Perlka-resistant soybean lines (COMPLTED IN 2008)*	1				
• *Transgenic expression of antifungal peptides*	0	0	2		
PM 1.7: Plant germplasm/cultivars with improved resistance					
• *Enhanced adapted germplasm*	2	1	1		
• *Herbicide tolerance with resistance to Sclerotinia*	1	1	1		
• *Agronomic resistant varieties for commercial production.*	1	2	3		
• *Identifycrop germplasm with partial resistance to virulent isolates*	1	1	12		
Pathogen Biology & Mechanisms of Disease Resistance					
PM 2.1: Population structure & dynamics					
• *Standardized genotypic characterization on wild and cultivated crops*	1	1	1		
• *Defined environmental requirements for pathogen biotype germination & disease*	1	0	0		
• *Documented gene-flow or outcrossing contribution to population variability*	1	0	1		
• *Geographical inventory of US populations*	1	1	1		
PM 2.2: Durable host resistance					
• *Isolate virulence/aggressiveness across geographic areas and hosts*	2	0	1		
• *Pathogen population dynamics on partially resistant crops*	0	1	1		
• *Pathogen x environmental interaction*	0	1	0		
• *Knowledge of plant x pathogen x environmental interactions*	1	1			
• *Criteria for testing virulence/aggressiveness on specific hosts.*	1	1	1		
PM 2.3: Factors that mediate sclerotia germination					
• *Host factors that mediate myceliogenic germination*	2	1	1		
• *Defined envronmental requirements for pathogen biotype germination & disease*	0	0	0		
• *Effect of sclerotiasphere microbes on germination and dormancy*	0	0	0		
• *Effect of sclerotiasphere microbes on mycelial growth*	0	0	0		
PM 2.4: Genetic markers and molecular tools for pathogen biology					
• *Reporter gene constructs with inducible promoters, insertional mutant libraries*	0	0	0		
• *Standard molecular protocols to genotype isolates*	2	1	1		
• *Transformed isolates for host/pathogen & pathogen/microbe interactions*	1	2	1		
PM 2.5: EST libraries from pathogen stains					
• *Useful cDNA libraries from pathogen expressed genes*	1	1	0		
• *Useful genome sequence information*	1	0	0		
• *Full length, normalized cDNA libraries*	1	0	0		

Pathogen Biology & Mechanisms of Disease Resistance	2008	2009	2010	2011	2012
PM 2.6: Candidate genes for pathogenicity	number of accomplishment citations				
• *Large ATMT collections for phenotypic screens*	0	0	0		
• *Transcriptome profiles and high through put functional analyses*	0	0	0		
• *Promoters for RNAi constructs during infection*	0	0	0		
• *Catalog genes from ATMT random mutagenesis*	0	0	0		
• *Discovery of candidate gene function*	0	0	0		
Crop Genome Analysis and Genomic Tools					
PM 3.1: DNA markers for QTL identification and marker assisted selection					
• *Affordable high-throughput genotyping and phenotyping technology*	1	2	2		
• *High density genetic map of DNA markers for resistance*	2	1	1		
PM 3.2: Structure of resistance gene enriched genomic regions					
• *Extensive cDNA libraries from host tissues at different stages of infection*	1	1	2		
• *DNA markers from BAC-ends to anchor contigs to genetic maps*	1	1	2		
• *Physical map of genomic regions containing resistance genes*	0	0	2		
• *High through-put resequencing capacity and haplotype maps*	0	0	1		
PM 3.3: Function of candidate resistance genes					
• *Microarrays for high throughput gene screening*	2	1	1		
• *Sequenced cDNA libraries from infected host tissue*	0	0	1		
• *Discovery of candidate genes for Sclerotinia resistance*	1	1	1		
• *Function of candidate genes using gene silencing methods*	2	1			
PM 3.4: Mechanisms of Sclerotinia resistance					
• *Yeast screens for ecotypes and defense-related mutants for oxalate sensitivity*	0	0			
• *Efficacy of GM traits against Sclerotinia*	1	1	2		
• *Conventional analysis of genetic mechanisms*	1	1	1		
PM 3.5: Bioinformatic resources					
• *Web-based communication for the Sclerotinia Initiative*	1	1	1		
• *Interactive website for genetic, genomic & biotech resources*	1	1	1		
Disease Management & Pathogen Epidemiology					
PM 4.1: Optimized fungicide application programs					
• *S. sclerotiorum isolate collection to assess fungicide sensitivity*	0	1	2		
• *Efficacy of new chemistries*	2	1	1		
• *Updated management guides for disease management*	0	1	0		
• *Improved spraying technologies*	0	0	0		
PM 4.2: Bio-control alternatives for disease management					
• *Grower recommendations for commercial sclerotial antagonists*	0	1	0		
• *Catalog of commercial microbial biocontrol agents*	0	0	0		
• *Efficacy of Sporidesmium sclerotivorum as a biocontrol agent*	0	0	1		
• *Updated management guides for biofungicides in disease management*	0	0	0		
PM 4.3: Quantitative models for environmental and host-crop interactions					
• *Disease warning systems*	1	0	0		
• *Validated predictive models in other crops.*	0	0	0		
• *Yield loss models*	0	0	1		
• *Threshold levels for decision aids*	0	0	0		
PM 4.4: Optimized cultural practices for disease management					
• *Improved variety selection criteria*	0	0	1		
• *Management decision aids*	1	1	1		
• *Precision agriculture program*	0	0			

Total Accomlishments	**76**	**61**	**75**
Total Milestones with multiple accomplishments	**17**	**10**	**14**
Total Milestones with no accomplishment	**30**	**30**	**24**
Total Milestones not funded	**NA**	**14**	**2**
Total Milestones	**76**	**76**	**73**
Achievement Rating (%)	**56.7**	**61.5**	**67.2**

Not funded

Overall Program Major Accomplishments 2008-2012

- A *Sclerotinia* risk map for **dry bean** producers and continued validation and expansion of risk maps for **canola**.
- Screening methods that enable identification of Sclerotinia resistance in wild & cultivated species of **sunflower**, **canola, pea, lentil, dry bean, soybean** in greenhouse and field settings.
- New sources of resistance in wild species of **pea, canola, common bean, sunflower**
- Transfer of resistance from wild species to cultivated types of **dry bean, sunflower**
- QTL discovery (gene locations) for resistance to white mold in **canola, pinto bean, pea, common bean** and **soybean**.
- Pyramiding QTL for resistance in **sunflower, dry bean** and **soybean**
- Microarrays for expressed genes in soybean
- Marker Assisted Selection for resistance in **pinto bean, sunflower, common bean, soybean**
- A high density SNP marker map for Sclerotinia resistance in **soybean**
- Protocol for transformation of **sunflower** and **lentil** germplasm
- Standardized protocol for genotypic characterization of **kidney, pinto** and other cool season bean crops
- First characterized geographic inventory of Sclerotinia isolates from **canola, dry bean, filed pea, lentil, soybean and sunflower**
- Library of **pathogen** genes expressed during white mold infection of host crops
- Oxalate oxidase-minus pathogen mutants that showed oxalate was not necessary for pathogenicity, but did enhance virulence in **tomato, canola, sunflower, soybean**
- Germplasm releases with improved tolerance to white mold in **pinto bean (1), pea (3), sunflower (10), common bean (3), soybean (3), chickpea (1)**
- Variety releases with improved resistance to white mold in **pinto bean (4), soybean (3), common bean (3), lentil (2), great northern bean (2).**
- Libraries of gene markers from RNA-seq **analysis of whole transcriptomes in soybean** and **pea**
- SNP maps for **haplotype designation in soybean**.
- A comprehensive **National Sclerotinia Initiative resource on the USDA-ARS website, and bioinformatic resources for soybean and cool season legume genomics** to serve the needs of the agricultural community and provide educational information to the general public.
- Efficacy of *Coniothyrium minitans* as a **biological control agent** for white mold in various crops.
- Crop management decision aids for control of Sclerotinia in **dry beans** and **sunflower**.
- Collaboration with the ***Sclerotinia sclerotiorum* whole genome sequencing project**, the **Soybean Genomic Research program**, the **Phaseolus CAP** grant, and the **Legume Information System.**

Meeting Strategic Milestones for Sclerotinia Research-2010

Crop Germplasm Resources & Genetics

PM 1.1: New sources of resistant plant germplasm

- *Exploration trips to obtain seeds of wild species*

ARS scientists at Ames IA and Fargo ND increased the availability of wild sunflower accessions in the USDA sunflower germplasm collection. As of Dec-2010, there were 1365 wild annual sunflower accessions in the collection of which 93% (1267) were available and 805 wild perennial accessions, with 64% available

- *Improved germplasm screening methods*

ARS scientists at Ames IA and Fargo ND improved the efficiency and efficacy of a greenhouse screening method to evaluate a wide array of wild Helianthus accessions for resistance and to increase the number and variety of available wild Helianthus accessions in the USDA sunflower collection. Systematic testing began with all available accessions of H. argophyllus, H. debilis, H. exilis, H. neglectus, H. praecox, H. petiolaris, and H. niveus. In 2010, 27 entries that exhibited high levels of resistance over multiple years were entered into a trial at Staples, MN along with F1 plants crosses of the susceptible inbred HA89 with H. argophyllus, H. petiolaris and H. praecox.

Scientists at North Dakota State University evaluated 48 herbicide-tolerant elite high-oil canola breeding lines under field conditions for reaction to Sclerotinia stem rot. The average incidence and severity for lines, 9023, 9024, 9091, and 9092 was 12% and 0.3, respectively. The average incidence of four commercial controls was 28% with a mean severity of 1.1. These lines were advanced to the breeding program. In addition, 46 of 144 F2 plants from the PI169080 x Westar population were resistant to S. sclerotiorum in greenhouse. DNA from these plants was extracted and genotyped using Diversity Array Technology (DArT) with more than 3,200 markers positioned on a chromosome map. DNA from 282 B. napus accessions were genotyped with DArT markers. 1,200 polymorphic markers were detected. Resistant plants from this population were self-pollinated for future evaluation.

Scientists at Michigan State University evaluated dry bean RILs for resistance to white mold resistance in the greenhouse through the straw test, the oxalate test and detached leaf assay. All tests separated the two parents (AN 37 = 3.0 and P02630 = 5.0 $p<0.05$) and the highly resistant from the susceptible RILs however the oxalate test was not found to be very suitable. The detached leaf assay showed comparable results to the straw test and can be used for non destructive rapid screening. Correlation between the straw test and the detached leaf assay was 0.67.

- *Doubled haploid lines for resistance, tested in multiple environments*

North Dakota State University evaluations of double haploid lines were resumed. Approximately 288 clones from a DH line produced by 458940 x Ames 26628 were developed. Both parental lines were resistant to S. sclerotiorum. The petiole inoculation technique was most reliable and consistent in detecting differences in resistance as well as differences between isolates. A similar study was conducted using DH lines derived from cv. Westar

- *Increased availability of resistant germplasm*

ARS Scientists at Pullman WA identified new sources of resistance to Sclerotinia sclerotiorum stem and crown rot in wild relatives of grain legumes (chickpea, lentil and pea). 95 lines of Pisum Fulvum, Pisum sativum subsp. Abyssinicum, Pisum sativum subsp. Elatius, and Pisum sativum subsp. transcaucasicum were evaluated for resistance to Sclerotinia sclerotiorum. The cultivated pea cultivar Dark Skin Perfection was most resistant and cultivar Columbia the most susceptible. All tested accessions of wild peas were susceptible to Sclerotinia sclerotiorum. However, four wild accessions performed better than the most resistant cultivated pea Dark Skin Perfection.

PM 1.2: Transfer new resistance genes into plant germplasm

- *Germplasm derived from interspecific crosses*

ARS scientists at Fargo ND improved Sclerotinia stalk and head rot resistance in sunflower by transferring genes form perennial Helianthus species via interspecific amphidiploids.Stalk rot resistant diploid perennial H. maximiliani, H. giganteus, and H. grosseserratus were crossed with HA 410 and their BC1F2/ BC2F1 progenies with 2n=34-35 chromosomes were obtained in 2008-2009. Selfed BC1F3 and BC2F2 progeny were grown in the field in 2009 and 2010 for seed increase. Replicated field tests in 2009 with 163 and 313 progeny families screened for head and stalk-rot resistance, respectively, indicated moderate to good resistance indicating successful gene introgression. A molecular tracking study indicated a higher frequency of gene introgression from diploid perennials than from hexpaloid or interspecific amphiploids. Replicated field tests in 2010 with 309 and 413 progeny families screened for head and stalk-rot resistance, respectively, failed to produce usable results due to the complications of unexpected midge damage and adverse environmental conditions.

Scientists at the University of Idaho and Colorado State University verified white mold resistance of contemporary dry and green common bean and interspecific breeding lines derived from Phaseolus species of the secondary gene pool. White mold reaction of known contemporary resistant large-seeded Andean (A 195, CORN 601, G 122, L 192, MO 162, PC 50, and VA 19) and small (ICA Bunsi) and medium-seeded (USPT-WM-1 and 'Chase') Middle American dry and green (CORN 501) common bean and IBL derived from the secondary gene pool species (VCW 54, VCW 55, VRW 32, 92BG-7, I9365-25, 0785-120-1, 0785-121-1, and 0785-227-1) was verified in two greenhouse environments in Idaho and Colorado (June 2008 to December 2010). Five large-seeded dry bean genotypes (A 195, G 122, MO 162, PC 50, and VA 19) and three small-seeded IBL derived from P. coccineus (VCW 54, 92BG-7, and 0785-220-1) and one IBL derived from P. costaricensis (VRW 32) with the highest WM resistance across greenhouse environments were selected for the complementation study.

- *Resistant selections of unadapted x agronomic traits*

Scientists at the USDA-ARS Sunflower Research Unit, Fargo, ND; Ag Research Center Central Lakes Community College, Staples, MN; and Panhandle Research and Extension Center, Scottsbluff, NE incorporated Sclerotinia stalk rot resistance using internal breeding material and foreign hybrids. Stalk rot data were generated on 250 PIs and 11 elite USDA lines. Stalk rot inoculations were largely successful, with disease severity averaging ~ 45% on commercial hybrids. Existing populations and breeding lines for stalk and head rot resistance, and introduce new populations will be advanced. 52 lines are candidates for release.

PM 1.3: Genetic analysis & QTL discovery

- *Highly inbred mapping populations with validated QTLs*

ARS scientists at the University of Illinois found 2 QTL for Sclerotinia stem rot resistance in soybean population Merit x PI 194639 that explained 23% of the phenotypic variation and two minor QTLs accounted for 6% of the phenotypic variation. Resistant and susceptible parents were screened for polymorphic markers. Sixteen plant introductions (PIs), most of which have been in population development, were screened for potential Sclerotinia resistance. Several entries had lower mean lesion lengths comparable to resistant parents used in current mapping projects.

Scientists from North Dakota State University, USDA-ARS Prosser, WA; and North Dakota State University, Carrington Research Extension Center investigated QTLs in two pea populations that reportedly confer resistance to white mold. F6 seed was planted in the GH in the spring of 2010 and F7 Seed was grown in the fall of 2010 to finish development of a F7-derived recombinant inbred line mapping population. Seed increase for the F7-derived RILs for Population 4 will be conducted in the field at Prosper near Fargo, ND during the summer of 2011. F3 family lines from the mapping populations of Population 4 and Population 6 were screened twice in replicated growth chamber trials for resistance to *Sclerotinia sclerotiorum.* Approximately fifty percent of Population 6 survived when assessed nine days after inoculation per screening trial. Resistant information gathered from each pea line from each population will be compared to DNA extractions from each line to identify genes and QTLs associated with the resistance. F4 family lines from Populations 4 and 6 were also recently screened in replicated growth chamber trials.

- *QTL analysis to generate a high density genetic maps*

Scientists at Michigan State University discovered new 300 SSR markers (108 were polymorphic). Sixty-six of these markers were assayed and mapped. A QTL for resistance to white mold was identified near markers BM157 and IAC90 on bean linkage groups B1, B3 and B7. Yield QTL were detected on B2 and B5 accounting for up to 39% of observed variation. These QTL were contributed by alleles from P02630. QTL for the straw test on B2 B3 and B8 were from the resistant parent AN37. The QTL on B2 is likely the same as previously mapped (Soule et al., 2011). The QTL on B3 is also likely to be the same one as one that was mapped by Miklas (2007) using the same parents. These markers will be used to select for white mold resistance and yield in the AP647 population

Scientists at USDA-ARS, Prosser, WA; Oregon State University, and North Dakota State University investigated WM resistance QTL in common bean. Novel QTL examining phenotypic interactions among new and existing QTL were identified and fine-mapped using synteny with the soybean genome and gene expression transcript profiling. Novel resistance QTL in scarlet runner bean was transferred to common bean. QTL were mapped in two backcross-inbred populations: 91G/PI 433251B (Gx43), and MO162/PI433251B (Mx43). Composite interval mapping revealed QTL on Pv02, Pv06 and Pv09 that collectively explained 34.7% of the phenotypic variation. The QTL on Pv02 and Pv06 were also associated with straw test resistance and explained 18.6% of phenotypic variation. Gx43 (264 lines) and Mx43 (120 lines) populations were advanced and characterized with two field trials. The Gx43 population had QTL on 8 of 11 LGs. A QTL associated with field severity on Pv05 accounted for 6.4% of the phenotypic variation. In the Mx43 population, 70 of 79 SSRs produced three linkage groups corresponding to Pv02, Pv03 and Pv04. SFA identified 30 loci significantly associated with white mold resistance. A QTL associated with field severity located on Pv02 accounted for 9.8% of the phenotypic variation.

- *Integrated linkage maps*

Scientists at the University of Nebraska and the University of Missouri identified 28 putative QTL on 15 different chromosomes in soybean. Five RIL populations were evaluated using Williams 82 as the common susceptible parent. Seven QTL were associated with disease resistance. A mutation in the LysM-RLK1 gene resulted in susceptibility to fungal infection. Enhanced expression of this gene enhanced innate immunity. Research revealed: 1) 37 LysM genes on various linkage groups, 2) At least 6 LysM genes on white mold QTL, 3) SNPs in 8 LysM-encoding genes, 4) the LysMe11 gene LG I was associated with smaller lesion size from the more resistant parent. SNP genotypes from the 1536 SNP chip for soybean will provide a more complete QTL analysis.

PM 1.4: Pyramid white mold resistance genes

- *Improved conventional breeding methods for quantitative traits*

Scientists at the University of Idaho and Colorado State University made progress in pyramiding white mold resistance from across Phaseolus species of the primary and secondary gene pool and introgressing high level of pyramided resistance into Pinto bean. Four single or bi-parental crosses between diverse breeding lines and germplasm accessions with partial WM resistance were made between June and September 2010. These were used to make three-way and double-crosses between October and December 2010, which subsequently will be used to make multiple-parent crosses (January to May, 2011). All crosses will be made only among parents possessing partial resistance to WM and of diverse evolutionary origins (A 195, G 122, ‘Chase’, CORN 501, CORN 601, I9365-25, MO 162, USPT-WM-1, VA 19, VCW 54, VCW 55, VRW 32, 92BG-7, 0785-220-1, 0785-221-1, and 0785-127-1). These crosses should allow simultaneous pyramiding of high levels of WM resistance from across Phaseolus species of the primary and secondary gene pools and transfer into pinto bean. Also, 78 F5 families developed from two double-crosses, namely USPT-WM-1/CORNELL 601//USPT-CBB-1/92BG-7 and Chase/I9365-25//ABL 15/A 195 made for a doctoral dissertation, and over two thousand early generation progenies from additional crosses were screened in the greenhouse. From the initial screenings it is encouraging to note that some of the recombinants exhibited higher levels of WM resistance than the individual parents. Also, some of these recombinants had pinto-like seed. However, because these are only in early segregating generations it will take several selection and progeny testing cycles to develop breeding lines uniform for WM resistance reaction and assess their true potential.

- *Breeding populations segregating for multiple resistance alleles and other traits*

Scientists from North Dakota State University, USDA-ARS Prosser, WA; and North Dakota State University, Carrington Research Extension Center found four sources of resistance, PI 103709, PI 169603, PI 240515 and ICI 1204-3 represent two distinct mechanisms of resistance (inhibited lesion expansion and nodal resistance). Genetic mapping populations involving these resistant sources have been developed and will be used to place the genetic factors controlling resistance on the pea map. In addition, hybridizations aimed at combining the resistance mechanisms will be made to provide an increased level of durable resistance. QTL for to white mold in pea were mapped and genes were pyramided for mechanisms of resistance.

PM 1.5: Marker-assisted selection

- *Disease reaction of RILs in multiple field environments*

ARS scientists at Fargo ND conducted association mapping using a genome-wide SNP panel for sunflower. This technology enables focus on candidate genes and 10,000 EST-SNPs with no particular functional assignment. This resolution distinguishes “random” SNPs from “candidate” SNPs.

- *Marker-assisted selection protocol for more efficient genotyping*

ARS scientists at Fargo ND created sunflower breeding lines with higher level of resistances to both Sclerotinia head and stalk rot by improving marker-assisted selection in combination with traditional breeding methods. Head rot QTL from the HA 441 x RHA 439 population were backcrossed into confectionery and elite oilseed backgrounds. BC2F1 hybrids were produced. Half of these QTL were fixed in confection and oilseed recurrent parents. The other 50% of these loci may improve the resistance in our recurrent parents, as these lines are only considered susceptible to moderately resistant.

- *Field verification of resistance*

Traditional breeding lines in the F4 to F8 selfing generations were tested for yield and Sclerotinia head and stalk rot resistance at two locations. A germplasm release is expected from ARS scientists at Fargo ND.

PM 1.6: GM improved resistance

- *GM oxalate oxidase expression, inheritance and field evaluation*

ARS scientists at Pullman WA and Prosser WA developed transgenic lentil lines that express the barley oxalate oxidase gene and tested these lines for resistance to Sclerotinia wilt. The plasmid pCAMBIA1301, which confers resistance to hygromycin, was transformed into *Agrobacterium tumefaciens* GV3850. A MTA between the ARS and Pioneer Hi-Bred Intl. gave access to a proprietary gene that confers resistance to chlorsulfuron. This gene was subcloned into pBINARS. *Agrobacterium rhizogenes* 18r12v harboring pAKK 1444B was used to transform cotyledonary nodes of lentils. Putative transgenic lines have been identified that grow vigorously growing after selection using kanamycin. Transient expression of GUS in excised shoots has been observed. This work has identified a cell culture technique for regenerating whole lentil plants and thresholds of sensitivity in lentil genotypes to selectable markers

- *Catalog of candidate resistance genes, promoters, and constructs for transformation*

Scientists at the Ohio State University developed facile transformation methodologies for sunflower. Regeneration was increased in transformed RHA280 cells 46% to 100%. Large numbers of shoots were formed on each piece of cotyledonary tissue. Seed quality was optimized. Using *Agrobacterium*-mediated transformation of this target tissue, GFP-expressing shoots were validated with the *gfp* gene under regulatory control of the sunflower polyubiquitin (HaUbi) promoter. Although transgenic plants have not yet been recovered, most of the components required for a much more efficient system for sunflower transformation are certainly in place.

ARS scientists at Pullman WA and Prosser WA sequenced the oxalate oxidase gene construct from pDW25. Five point mutations in this sequence were detected when compared to the wild type gene sequence of the oxalate oxidase gene from barley (GenBank accession # Y14203). A mutation at position 2 of codon 79 resulted in the substitution of valine for alanine. The oxalate oxidase gene from barley DNA

was cloned into pCR® 2.1-TOPO and several individual clones were sequenced. A single clone (pEVOO1) was identified that has 100% sequence homology to the wild type oxalate oxidase gene.

- *Perlka-resistant soybean lines* ***Completed in 2008.***

- *Transgenic expression of antifungal peptides (****see PM 2.4, PM 3.4)***

PM 1.7: Plant germplasm/cultivars with improved resistance

- *Enhanced adapted germplasm*

Scientists at Michigan State University evaluated the AP630 (AN37/P02630) dry bean population for yield, days to flowering, days to maturity, height, and lodging and disease incidence. Significant variation for all the traits was observed across the population ($p<0.05$). Mean values for yield ranged from 29 to 46 cwt/acre. Most of the RILs also exhibited mid season (90 days) to late maturity (>100 days) in relation to the AN37 parent which has late maturity. Significant differences in height ($p<0.05$) were also recorded ranging from 46-59 cm in 2009 and 40 to 59 cm in 2010. Disease scores ranged from 10 to 90% with P07863 consistently having the desirable combination of high yield (> 40cwt/acre) and low disease incidence (<20%) for three consecutive years. Heritability estimates (which show how much observed can be attributed to genetic factors) were low for traits like lodging (0.16), days to maturity (0.21), plant height (0.22) and field disease incidence (0.29). On the other hand traits like yield, seed weight and the straw test had moderately higher estimates of 0.48, 0.63 and 0.43, respectively.

- *Herbicide tolerant germplasm with resistance to Sclerotinia* ***(see PM 1.1)***

- *Identification of crop germplasm with partial resistance to virulent isolates* ***(see PM 1.7)***

- *Agronomic resistant varieties for commercial production.*

Scientists from University of Nebraska, NDSU-Carrington, Colorado State University, Michigan State University, University of Idaho, Oregon State University, Cornell University, USDA ARS at Prosser WA, Seminis Seeds and Harris Moran Seeds demonstrated from greenhouse tests that three kidney lines and A195 had high levels of resistance, but only two pinto lines, PO7751 and WM31-2008 were considered to be significantly different from the susceptible Beryl in the field and greenhouse. It is possible that the two black lines and one pinto line with intermediate field resistance were exhibiting some avoidance or escape mechanism. A black and a snap bean were also identified with intermediate resistance in the greenhouse tests. Aided by the multi-site nursery data over the past 4 years, a snap bean, two pinto lines, a bayo line and six kidney lines with WM resistance were released. New lines with WM resistance from wide crosses are now being increased for greenhouse screening

Scientists at North Dakota State University Carrington Research Extension Center; Agriculture and Agri-Food Canada, Morden Research Station, Morden, Manitoba; NDSU Langdon Research Extension Center; NDSU Carrington Research Extension Center, Oakes, ND; University of Minnesota Northwest Research and Outreach Center, Crookston, MN; and USDA-ARS at Fargo, ND developed reliable, reproducible screening methods for sunflower hybrids, experimental lines, and other germplasm for resistance. 73 commercial hybrids and experimental lines not previously publically evaluated for Sclerotinia head rot had average head rot incidence from 4.2 to 80.8% in Carrington, ND and 0 to 29% in Morden, MB at physiological maturity. 25 commercial hybrids and experimental lines (including the most promising lines evaluated in 2009) had average Sclerotinia head rot incidence from 10.4 to 81.2% in Carrington, ND, 7.1 to 69.7% in Langdon, ND, 5.3 to 77.6% in Crookston, MN, 26.3 to 93.3% in Oaks, ND, and 0 to 45 % in Morden, MB. The trials were successful at differentiating the relative Sclerotinia head rot susceptibility of hybrids.

Pathogen Biology & Mechanisms of Disease Resistance

PM 2.1: Population structure & dynamics

- *Standardized genotypic characterization on wild and cultivated crops*

Scientists from University of Nebraska, NDSU-Carrington, Colorado State University, Michigan State University, University of Idaho, Oregon State University, Cornell University, USDA ARS at Prosser WA, Seminis Seeds and Harris Moran Seeds facilitated identification of resistance to *S. sclerotiorum* in secondary gene pool as well as in adapted common bean lines by reducing screening inconsistencies across multiple locations. A standardized screening test was developed using the modified Petzoldt and Dickson scale for rating the greenhouse straw test, and the CIAT scale for rating field screening tests at all sites. In four field tests with adequate disease pressure A195 and kidney bean lines Cornell 605, 607 and 611showed the best levels of resistance similar to the check G122. There also were three pinto and two black-seeded lines that were considered intermediate and had significantly lower disease ratings compared to Beryl, the susceptible check.

- *Documented gene-flow or outcrossing contribution to population variability*

- *Discovery of ecological and bio-types with fungicide resistance(*

ARS scientists at Pullman WA found that isolates described in PM 2.2 also exhibited significant difference in sensitivity to fungicides benomyl, fluzinam and Iprodione. The 40 isolates also showed three distinct colony colors: dark (11 isolates), beige (22 isolates) and white (7 isolates). Results on general biology of S. sclerotiorum were presented in an invited keynote address at the 7th Sunflower Science and Technology Conference in Harbin, Hailongjiang, China.

- *Geographical inventory of US populations*

Scientists at North Dakota State University obtained 33 isolates of *S. sclerotiorum* from states outside the North Central Region. The isolates were purified and characterized for MCG determination. Extraction of DNA and microsatellite marker analysis will begin after testing virulence on various crops. Haplotype groups were determined.

PM 2.2: Durable host resistance

- *Isolate virulence/aggressiveness across geographic areas and hosts*

Scientists from University of Nebraska, NDSU-Carrington, Colorado State University, Michigan State University, University of Idaho, Oregon State University, Cornell University, USDA ARS at Prosser WA, Seminis Seeds and Harris Moran Seeds determined that many of the isolates of *S. sclerotium* collected over the past 6 years from nine bean production regions in the USA as well as one bean production region each in Mexico and France belong to of 85 MCG. These same isolates were tested for aggressiveness using a straw test under greenhouse conditions and were found to have varying degrees of aggressiveness (2.8 to 7.9) based on a scale of 1 = no disease and to 9 = death of the plant. Differences in isolate aggressiveness were found among the isolates ($p<0.0001$) and highly significant differences were found among the MCGs ($p<0.0001$); however, isolates within an MCG did not differ in aggressiveness ($p=0.4216$). Thus, isolates that are clones had similar aggressiveness.

- *Pathogen population dynamics on partially resistant crops*

ARS scientists at Pullman WA have collected more than 300 isolates Sclerotinia sclerotiorum from pea, lentil and canola fields in nine different geographic areas in the Pacific Northwest. Phenotypic and genetic diversity of S. sclerotiorum from one square meter of soil was demonstrated by 15 MCGs and 16 microsatellite haplotypes. STRUCTURE analysis indicated five clusters (populations) among the 40 isolates.

- *Pathogen x environmental interaction*

- *Criteria for testing virulence/aggressiveness on specific hosts.*

PM 2.3: Factors that mediate sclerotia germination

- *Defined environmental requirements for pathogen biotype germination and disease development.*

Scientists at the University of Florida used biochemical stability tests, size exclusion ultra-filtration and ion exchange chromatography to show that necrosis activity is associated with a 10kD compound that is resistant to heat and protease degradation. Although the necrosis factor has not yet been identified, insight was gained into dynamics of host-pathogen interaction in the absence of oxalic acid.

- *Host factors that mediate myceliogenic germination*

- *Effect of sclerotiasphere microbes on germination and dormancy*

- *Effect of sclerotiasphere microbes on mycelial growth*

PM 2.4: Genetic markers and molecular tools for pathogen biology

- *Reporter gene constructs with inducible promoters, organelle specific targets; insertional mutant libraries*

- *Standard molecular protocols to genotype isolates*

Scientists from University of Nebraska, NDSU-Carrington, Colorado State University, Michigan State University, University of Idaho, Oregon State University, Cornell University, USDA ARS at Prosser WA, Seminis Seeds and Harris Moran Seeds used four polymorphic microsatellite markers to genotype the isolate populations collected from 2003-2007. A total of 240 isolates have been sequenced and formed 65 microsatellite haplotypes which associated closely with the MCGs. Of the 81 MCGs formed by the 2003-2007 isolates, 68 have only one microsatellite haplotype. Using analysis of molecular variance analysis (AMOVA) with the microsatellite haplotype data, 75% of the haplotype variation comes from within the nine USA locations, 21% from among the locations within regions (East, Midwest or West) and only 4% of the variation is found among the regions. This variability data does not address aggressiveness.

- *Transformed isolates for host/pathogen & pathogen/microbe interactions*

Scientists at the University of Florida developed OxOx minus mutants via transformation. Tests were conducted on tomato, sunflower, pinto bean and canola. Filtrate activity was not quantitatively associated with the virulence level exhibited by plate cultures of the oxalate minus mutant. Variations in plate culture virulence were associated with penetration efficiency that appear to be epigenetically controlled. This variation could be eliminated by wounding plants prior to inoculation. As such all oxalate minus mutants displayed attenuated virulence relative to the wild-type, yet culture filtrate activities were comparable between wild type and the oxalate minus mutant. This indicates that a toxic factor exists that is independent of oxalic acid production and not correlated with quantitative measures of virulence.

PM 2.5: EST libraries from pathogen stains

- *Useful cDNA libraries from pathogen expressed genes*

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- *Useful genome sequence information*

- *Full length, normalized cDNA libraries*

PM 2.6: Candidate genes for pathogenicity

- *Large ATMT collections for phenotypic screens*

- *Transcriptome profiles and high through put functional analyses*

- *Promoters for RNAi constructs during infection*

- *Catalog genes from ATMT random mutagenesis*

- *Discovery of candidate gene function*

Crop Genome Analysis and Genomic Tools

PM 3.1: DNA markers for QTL identification and marker assisted selection

- *Affordable high-throughput genotyping and phenotyping technology*

ARS scientists at Urbana IL evaluated an additional 233 accessions from 18 Glycine species for sensitivity to Sclerotinia stem rot in replicated greenhouse trials. Highly resistant accessions of G. canescens, G. clandestina, G. latifolia, and G. tabacina were identified. Susceptible accessions died after the first inoculation. The DCL3 gene was sequenced to identify SNP haplotypes. Oligonucleotide primers were designed to detect SNPs in each of the parental pairs. Additional crosses were performed with susceptible and resistant accessions of G. canescens and G. clandestina. Transcriptomes of at least two sets of parental lines were sequenced from normalized cDNA libraries. Phenotypic data were collected on flowers, germinating seedlings, immature pods, leaves, roots and stems.

ARS scientists at Urbana Illinois developed approximately 50 additional SSR markers making a total of 184 polymorphic SSR markers for Sclerotinia stem rot resistance in soybean genome. RIL from Merit x PI 194634 revealed over 100 SSR markers for genotyping with 40 markers being polymorphic. Markers were used to identify map intervals, which should provide additional quantitative trait loci that are significantly associated with disease resistance. More SNP markers from the Golden Gate assay and TRAP markers will be identified to fine map these regions

- *High density genetic map of DNA markers for resistance* ***(see PM 1.3)***

PM 3.2: Structure of resistance gene enriched genomic regions

- *Extensive cDNA libraries from host tissues at different stages of infection* ***(see PM 1.3, PM 3.3)***

- *DNA markers from BAC-ends to anchor contigs to genetic maps* ***(see PM 1.3, PM 1.5)***

- *Physical map of genomic regions containing resistance genes* ***(see PM 3.5)***

- *High through-put resequencing capacity and haplotype maps* ***(see PM 3.1)***

PM 3.3: Function of candidate resistance genes

- *Microarrays for high throughput gene screening*

Scientists from North Dakota State University developed cDNA libraries from doubled haploid canola lines inoculated with isolate NE 152. cDNAs are being sequenced.

- *Sequenced cDNA libraries from infected host tissue*

Scientists from Michigan State University, North Dakota State University and Dow AgroSciences, LLC used RNA-seq to examine expression profiles of Sclerotinia-pea host pathogen interactions in susceptible X partially resistant lines The expression profile of both pea and *S. sclerotiorum were* examined to identify genes involved in host resistance as well as pathogen pathogenicity. Trans-ABySS software was used for *de novo* assembly and analysis of RNA-seq data. Phenotypic association was used to map resistance gene QTL. RNA-seq revealed a large number of gene-linked markers (SSRs and SNPs). EST sequence reads were assigned by BLAST analysis. Fifty eight percent of reads were assigned to pea, 25% were assigned to *S. sclerotiorum*, 1% were assigned to both pea and *S. sclerotiorum* and only 16% were unassigned. The pea transcripts were assembled into 11,810 contigs and 17,619 singletons. Seventy three putative SSRs with a length of repeat greater than 20 nucleotides were identified in the pea contigs and will be evaluated as potential makers for pea genetic mapping.

- *Discovery and function of candidate genes for Sclerotinia resistance*

ARS scientists at Urbana IL, Agriculture and Agri-Food Canada and University of Florida used gene expression profiling and gene clustering to identify candidate defense-associated genes. Transcriptome microarray studies comparing PI194639 to susceptible Williams 82 revealed 60 differentially expressed candidate defense-related genes plus 105 genes (19 located within 500 kb of a white-mold resistance QTL). qRT-PCR confirmed the

microarray results. Stable transformants of selected candidates associated function with signaling, the phenylpropanoid pathway, and OxO related genes. Four Arabidopsis knockout lines have been obtained and homozygousity confirmed. Ten genes, targeted for overexpression have been cloned and used to transform Arabidopsis. Selected embryos were bombarded with an RNAi construct to specifically silence a gene involved in G-protein signaling. Function of additional candidate defense genes continues with more gene expression screens.

PM 3.4: Mechanisms of Sclerotinia resistance

- *Yeast screens for ecotypes and defense-related mutants for oxalate sensitivity* ***(not funded)***

- *Transgenic incorporation of genes into crops and determine their effectiveness against Sclerotinia*

Scientists at the University of Illinois and Ag AgriFoods Canada overexpressed OxOx in transgenic soybean. Disease development was arrested early in OxOx minus plants, but spread rapidly through leaves of parent lines.

Scientists at NDSU and Washington State University characterized two partial resistance mechanisms in pea node and stem.

PM 3.5: Bioinformatic resources

- *Web-based communication for the Sclerotinia Initiative*

See: *http://www.ars.usda.gov/Research/docs.htm?docid=20317&page=3*

- *Interactive website for genetic, genomic & biotech resources*

See: http://lis.comparative-legumes.org/lisg/lis_links.html

Disease Management & Pathogen Epidemiology

PM 4.1: Optimized fungicide application programs

- *S. sclerotiorum isolate collection to assess fungicide sensitivity*

Scientists at North Dakota State University and Langdon ND evaluated fungicide sensitivity for Sclerotinia sclerotiorum isolates collected in the north central region of the US. Eighty S. sclerotiorum isolates from the US North Central region have been added to our collection and are currently being evaluated for their reaction to thiophanate methyl, and prothioconazole. The sensitivity of these isolates to the chemical (EC50 values) will be determined. Aescospores produced from these isolates are required for determining sensitivity to azoxystrobin and boscalid.

Scientists at North Dakota State University and the University of Nebraska investigated drop size on the efficacy of fungicide application, and timing of application for dry bean production. The environments include the plains of western Nebraska and central and northeast North Dakota. An economic analysis will also be made for the cost/=benefit effects. Analysis of variance will be calculated and means will be separated using Fischer's protected least significant differences.

- *Efficacy of new chemistries*

Scientists at North Dakota State University and Langdon ND evaluated the efficacy of chemical fungicide tank mixtures and biological control agents as alternatives to mange S stem rot in canola. Fungicides included thiophanate methyl (Topsin), boscalid (Endura), prothioconazole (Proline) and metconazole (Quash) alone or in combination with other compounds. Trials at Langdon were conducted under moderate disease pressure whereas at Carrington, disease pressure was reduced. Disease incidence and severity at Langdon ranged between 1 and 37% and between 0.1 and 1.35 in a 0-5 scale respectively. Control plots had the highest incidences and severities. The combination of thiophanate methyl and prothioconazole in single or double applications produced the highest yield, although other combinations, like thiophanate methyl and boscalid also reduced disease incidence and severity. Tank mixtures could reduce the cost of applications between $2-4 per acre.

- *Updated management guides for disease management*

- *Improved spraying technologies*

PM 4.2: Bio-control alternatives for disease management

- *Grower recommendations for commercial sclerotial antagonists*

- *Catalog of commercial microbial biocontrol agents*

- *Efficacy of Sporidesmium sclerotivorum as a biocontrol agent*

Scientists at North Dakota State University and Langdon ND evaluated biological fungicides at Langdon and Carrington. Serenade and Polyversum (Bacillus subtilis and Pythium oligandrum) reduced disease incidence and severity slightly. Polyversum increased yields significantly.

- *Updated management guides for biofungicides in disease management*

PM 4.3: Quantitative models for environmental and host-crop interactions

- *Disease warning systems*

- *Validated predictive models in other crops.*

- *Yield loss models*

Scientists at North Dakota State University, Fargo ND; USDA-ARS Fargo, ND; NDSU Research Extension Center Langdon, ND; Panhandle Research Extension Center Scottsbluff, NE; South Dakota State University Brookings, SD; and NDSU Research Extension Center Carrington, ND evaluated the efficacy of a wide range of fungicides for control of Sclerotinia head rot, including both products registered on other crops and new experimental compounds, and 2) develop a yield loss model based on head rot.

- *Threshold levels for decision aids*

PM 4.4: Optimized cultural practices for disease management

- *Improved variety selection criteria* ***(see PM 1.1)***

- *Management decision aids*

Scientists at Colorado State University and Idaho State University optimized cultural practices for dry bean production. During 2010, low white mold pressure in fields was attributed to delayed plantings (early-spring rains) which delayed flowering until late July. In addition, the commercial field was moderately to severely damaged by bacterial brown spot which opened up the canopy of the commercial variety surrounding our trial and prevented the production of ascospore inoculum. Only 1 commercial field could be included this year due to the reduce budget allocation. However, the preliminary analysis of data from the 2 locations revealed that there were no interactions between fungicide treatment or nitrogen by entries or locations. Yields of the 4 entries averaged 1135 lb/acre (1281 seed/lb) at the research station and 2966 lb/acre (1204 seed/lb) at the better commercial field in the absence of white mold and with moderate bacterial disease at the commercial field in 2010; similar to results obtained in 2009. Plant canopy monitoring during late vegetative to seed fill periods of crop growth showed that average daily relative humidity was higher in a prostrate variety (Montrose) than an upright type (Stampede); and canopy temperature showed the reverse trend. Field data during the 2011 study will include microclimatic monitoring, soil fertility, plant stand, disease intensity, yield, seed size, and economic impacts. Results will be shared with colleagues and growers via progress reports, refereed publications, extension releases, web sites, and meetings. Agronomic and chemical (fertilizer, fungicide) implications from this IPM approach will be applicable to other host cropping systems affected by foliar phases of white mold.

- *Precision agriculture program* ***(not funded)***

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2010 Sclerotinia Funding Matrix

	Project	PI	2009	Cooperator	Commodity	Requested	Aveage Rating
1	Evaluation of Wild Helianthus Species for Resistance to Sclerotinia Stalk Rot	Block	$17,427	ARS	Sunflower	$14,767	5.0
7	Functional verification of candidate defense-related genes in Sclerotinia sclerotiorum in soybean & arabidopsis	Clough	New	ARS	Soybean	$66,099	5.0
19	Identification of QTL for white mold resistance in pinto bean	Kelly	$34,396	MI	Dry Bean	$34,396	5.0
30	Enhancing soybean for resistance to Sclerotinia stem rot	Wang	$40,001	MI	Soybean	$41,601	5.0
21	White mold resistance QTL: Identification, interactions & fine mapping in common bean	Miklas	$75,000	ARS	Dry Bean	$160,000	4.9
16	Fine mapping of quantitative resistance genes to Sclerotinia stem rot in two soybean populations	Hartman	New	ARS	Soybean	$62,500	4.9
17	Pyramiding Sclerotinia head rot and stalk rot resistances into elite sunflower breeding lines with the aid of DNA markers	Hulke	$85,000	ARS	Sunflower	$105,000	4.8
6	Expression profiling of the pea-Sclerotinia sclerotiorum interaction for genomics assisted breeding	Chilvers	$55,426	MI	Pea & Lentil	$63,870	4.7
18	Transferring Sclerotinia resistance genes from wild Helianthus species into cultivated sunflower	Jan	$102,000	ARS	Sunflower	$106,000	4.7
25	Evaluation of Sunflower Hybrids and Germplasm for Resistance to Sclerotinia	Schatz	$72,500	ND	Sunflower	$81,125	4.7
15	Discovery of novel sources of resistance to head rot and stalk rot in cultivated sunflower & wild Helianthus	Gulya	$67,847	ARS	Sunflower	$81,012	4.6
28	Improved resistance in common bean through multi-site screening and pathogen characterization throughout major production areas	Steadman	$56,550	NE	Dry Bean	$58,907	4.6
14	Identification of Resistance and Pathogenicity Genes Associated with Sclerotinia Sclerotiorum Infection using next generation sequencing	Goswami	$0	ND	Canola	$65,100	4.6
5	Searching for resistance sources to Sclerotinia in wild relatives of cool season grain legumes	Chen	$60,000	ARS	Pea & Lentil	$73,912	4.3
4	Variation in pathogenicity and fungicide sensitivity in relation to variation of neutral markers of Sclerotinia sclerotiorum	Chen	$66,268	ARS	All	$79,716	4.3
20	Characterization of the genetic basis for partial resistance to Sclerotinia sclerotiorum in pea	McPhee	$60,250	ND	Pea & Lentil	$39,270	4.2
23	Characterization of the genetic basis for partioal resistance to Sclerotinia sclerotiorum in pea	Porter	New	ARS	Pea & Lentil	$14,960	4.2
22	Genetic variation and virulence of S. sclerotiorum in the US	Nelson	$59,490	ND	All	$60,500	4.0
26	On-Farm Validation of Cultural Practice Adjustments to Improve White Mold Management in Dry Bean Irrigation Systems	Schwartz	$42,538	CO	Dry Bean	$46,316	3.9
29	Expression of the oxalate oxidae gene in transgenic lentils and evaluation of transgenic plants for resistance to Sclerotinia sclerotiorum	Vandemark	$57,920	ARS	Pea & Lentil	$43,000	3.9
13	The effects of soil type on efficacy of Contans WE and survival of Coniothyrium minitans for control of Sclerotinia stem rot of soybean	Esker	$0	WI	Soybean	$42,268	3.9
12	Optimizing management of Sclerotinia diseases through fungicide use	del Rio	$26,411	ND	Canola	$45,112	3.4
27	Gamete selection for simultaneously pyramiding and introgressing white mold resistance from Phaseolus species into pinto beans	Singh	$0	ID	Dry Bean	$69,246	3.4
2	Multi-state uniform fungicide testing program for control of Sclertinia stem rot in soybean	Bradley	New	IL	Soybean	$36,000	3.4
9	Defining critical environmental and biological parameters needed to develop Sclerotinia stem rot on canola	del Rio	$26,580	ND	Canola	$37,599	3.3
10	Development of canola breeding populations and identification of herbicide tolerant breeding lines with resistance to sclerotinia sclerotiorum	del Rio	Not- New	ND	Canola	$66,955	3.3
3	Is Oxalic acid required for pathogenicity by Sclerotinia sclerotiorum?	Chen	New	ARS	All	$65,334	3.1
8	Inactivation of salic=ylate and jasmonate by Sclerotinia sclerotiorum and its role in patogenisesis on canola, sunflower, dry bean & soybean	Daniel	New	IL	Canola, Sunflower, Dry Bean, Soybean	$35,086	3.1
11	Quantifying risk of Sclerotinia diseases in wheat-soybean-canola crop sequencing in northeastern North Dakota	del Rio	New	ND	Canola	$65,423	2.6
24	Pathogenicity of Sclerotinial sclerotiurum on crops in rlation to mycelium pigmentation and oxalic acid production	Sanogo	New	NM	All	$50,360	2.4