United States Department of Agriculture

Research, Education & Economics

Agricultural Research Service

Northern Plains Area

February 2014

Version 3.0

National Strategic Plan for the Sclerotinia Research Initiative

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

2013 to 2017

Table of Contents

Executive Summary

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

Process & Development of the National Strategic Plan for the Sclerotinia Research Initiative - 2013-2017: On January 19-20, 2012, approximately 60 scientists and stakeholders with knowledge of the fungal pathogen, *Sclerotinia sclerotiorum* participated in an annual workshop hosted by the United States Department of Agriculture's Agricultural Research Service (ARS) in Minneapolis, MN. ARS, the National Sunflower Association, the U.S. Canola Association, the USA Dry Pea and Lentil Council, the U.S. Dry Bean Council, and the United Soybean Board co-organized this program. Participants reviewed annual research accomplishments and peer assessment of program performance to develop research priorities that targeted improved understanding and management of Sclerotinia disease in canola, dry edible beans, peas & lentils, soybean, and sunflower. A summary of overall program performance against priorities of the USDA ARS National Sclerotinia Research Initiative (NSI) strategic plan for 2008 to 2012 follows:

Sclerotinia Initiative Research Progress Evaluation

	2008	2009	2010	2011	2012
	number of accomplishment citations				
Total Accomlishments Cited	76	61	75	71	80
Milestones w/ multiple citations	17	10	14	18	21
Milestones w/ no citations	30	30	24	29	34
Milestones not funded	NA	14	2	3	2
Milestones completed	0	1	1	1	1
Total Milestones Rated	76	76	73	70	70
Achievement Rating (%)	56.7	62.2	67.2	73.4	80.9
Total Projects	34	28	19	15	21
Accomplishments / project	2.2	2.2	3.9	4.7	3.8
All Publications by SYs	47	53	214	235	303
Total SYs funded by NSI	20	33	35	29	27
Germplasm/Varieties released	10	10	15	9	13

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

ARS leadership considered stakeholder input in the overall assessment of the NSI program performance and in determining the research needs of industry. Reviews of ARS projects associated with NSI also were conducted by the Office of Scientific Quality Review to ensure relevance, quality and performance in meeting goals of ARS national programs. USDA-ARS leadership of NSI included:

Dr. Roy Scott, National Program Leader, Office of National Programs, Beltsville MD
Dr. Michael McGuire, Acting Area Director, Northern Plains Area, Ft. Collins, CO
Dr. William Kemp, Agricultural Administrator, Red River Agricultural Research Center, Fargo ND

Based on all evidence, there was consensus that genetic as well as management solutions to the Sclerotinia problem were attainable. This optimism was largely due to NSI scientist applications of advances in molecular biology to characterize genes involved in Sclerotinia resistance within the DNA and RNA sequences of soybean, dry bean, *Medicago truncatula*, the pathogen and other plant genomes; and the implementation of molecular tools in breeding programs. However, the most critical factor for future success of the NSI was deemed to be the ability to maintain, manage and manipulate the vast quantities of bioinformation that will be generated by the ancillary projects.

The availability of genome sequences and related genetic resources will greatly enhance gene discovery and characterization if NSI data can be integrated and made accessible using state of the art on-line genomic research tools. While it is crucial to provide, at a minimum, unimpeded access to the intermediate products of a genomics project (the sequence assemblies, the gene models and coordinates, the gene read counts, etc.), these raw data sets in themselves are relatively limited value to end users such as breeders and molecular biologists. Bioinformatic resources are needed to improve ability to compile, analyze, and interpret genomic data in a useful and timely manner.

Break-out sessions were convened at the 2012 NSI annual meeting to draft a foundation for a new five-year plan. Four goals plus performance measures and anticipated products were proposed for the NSI Strategic Plan 2013 to 2017. The following individuals lead the development of this Strategic Plan:

Goal 1: Germplasm Resources & Translational Genomics--Phil Miklas, USDA ARS, Prosser WA
Goal 2: Pathogen Biology & Mechanisms of Resistance----Weidong Chen, USDA ARS, Pullman WA
Goal 3: Gene Discovery & Phenotypic Association----------Steven Clough, USDA ARS, Urbana IL
Goal 4: Disease Management & Crop Production----------Luis Del Rio, ND State University, Fargo ND

This strategic plan encompasses the breadth of research disciplines necessary to better understand the disease and to provide significant management options for the affected producers across the U.S. To achieve the strategic goals and research objectives, this plan emphasizes achievements that hinge on teamwork throughout the Sclerotinia research community. All actions and results will be attained in a manner that is both inclusive and open to public scrutiny.

Introduction

Sclerotinia sclerotiorum, the most important species of *Sclerotinia,* has an unusually large host range of over 400 plant species in numerous families. This fungus causes diseases known as white mold, Sclerotinia stem rot, wilt or stalk rot, or Sclerotinia head rot on a wide variety of broadleaf crops. It commonly causes economic yield loss in dry edible beans, sunflower, soybean, canola, pea and lentils. Many other crops also are susceptible such as alfalfa, potato, peanut, mustard, safflower, flax, borage, crambe, buckwheat, chickpea, lupine, faba bean and numerous vegetables such as lettuce and carrots. The pathogen is found in diverse environments from southern to northern climates and in different agricultural systems under both dryland and irrigated conditions. Although found primarily as a pathogen in the field, it can also be a problem under storage conditions for some crops. The success of this pathogen and its demonstrated ability to adapt to a wide range of conditions can be largely attributed to its aggressive mode of pathogenesis and to the production of specialized multicellular developmental structures for survival and dispersal. Improved knowledge of population structure, ecological types, virulence diversity, germination factors, pathogenicity factors, and advances in molecular biology are needed to develop effective control methods for the numerous diseases caused by this pathogen.

The collective annual economic loss attributed to Sclerotinia damage in the five crops participating in the ARS National Sclerotinia Research Initiative has been as high as $482 million. Specifically, annual losses for each of the crops have been as high as $100 million for sunflowers; $300 million for soybean; $46 for dry edible beans; $24 million for canola; and $12 million for pulse crops. The disease is a serious threat to the future of the confection sunflower, where quality is a significant concern. Diseased seeds cannot always be separated in cleaning and processing resulting in bitter tasting seeds which are rejected by consumers.

The primary survival (overwintering) structure of *S. sclerotiorum* is the sclerotium. A sclerotium is a hard resting structure consisting of a light colored interior portion called a medulla and an exterior black protective covering called the rind. The rind contains melanin pigments which are highly resistant to degradation, while the medulla consists of fungal cells rich in beta glucans and proteins. The shape and size of sclerotia depend on the host and where they are produced in or on infected plants. The Sclerotinia disease cycle begins when sclerotia germinate after overwintering in soil. Sclerotia may undergo carpogenic germination which results in the production of a small mushroom called an apothecium and ascospores which are ejected into the environment. The pathogen produces oxalic acid and numerous enzymes that break down and degrade plant tissue. Disease development is favored by moisture and moderate temperatures of 15 to 25 C.

Another method of germination is myceliogenic, where sclerotium produce mycelium. This is common in the disease cycle in Sclerotinia wilt of sunflower. Most other Sclerotinia or white mold diseases of dry edible beans, soybean, canola and sunflower head rot are initiated by carpogenic germination and infection of above ground plant parts by ascospores. Few studies have quantified sclerotia survival in the field. Microbial degradation is the principal reason for a decline in populations of sclerotia. Many fungi, bacteria and other soil organisms parasitize or utilize sclerotia as carbon sources. Crop rotations allow the natural microbial population to degrade sclerotia. Two important fungal parasites involved in the natural degradation of sclerotia are *Coniothyrium minitans* and *Sporidesmium sclerotivorum.* Both may become biocontrol agents for sclerotia.

The effect of tillage on survival of sclerotia is poorly understood. Fungicides have been used with some success in dry edible bean and canola. Crop rotation continues to be used for certain crops such as sunflower where inoculum densities in the soil play a major role in disease development. Most Sclerotinia diseases are not controlled by host resistance. However, moderate levels of host resistance in dry edible beans and soybean have been used in integrated control programs.

The *National Strategic Plan for the Sclerotinia Initiative 2013-2017* provides the research community with a foundation for a comprehensive and integrated research approach toward these problems. The performance measures outlined in this plan are relevant to the current needs of US agriculture. The plan defines the actions that will be taken to solve these problems, describes what is promised or will be produced, assigns accountability for the work to be accomplished, and provides a mechanism for peer review and assessment of research progress.

Strategic Plan for Sclerotinia Research

Crop Germplasm Resources & Translational Genomics

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. Commercially available canola, pea, lentil, chickpea, common bean, soybean and sunflower cultivars are not resistant to *S. sclerotiorum*, although some differences in susceptibility exist. USDA & International Germplasm Collections will be fully evaluated for genes that mediate effective resistance to *S. sclerotiorum*.

Anticipated Products

- Germplasm accessions of canola, chickpea, lentil, pea, and sunflower, and wild crop relatives with resistance to S. sclerotiorum are used in breeding programs.
- Improved phenotypic methods for identifying and validating resistance to *S. sclerotiorum* in accessions from USDA and World germplasm collections.

PM 1.2: Transfer and adapt new sources of resistance genes into useful plant germplasm (pre-breeding) Landraces, cultigens, and wild species of cultivated crops often possess novel resistance genes that are not found in adapted germplasm. Interspecific and other wide crosses are often constrained by genetic incompatibilities or other problems resulting in non viable progeny. Sophisticated strategies will be developed and deployed to utilize beneficial genetic variation for Sclerotinia resistance from unadapted and wild species in modern variety production.

Anticipated Products:

- Common bean breeding lines derived from interspecific crosses with effective resistance in multiple environments and against a range of aggressive isolates.
- Canola, chickpea, lentil, pea, soybean and sunflower lines selected from unadapted accessions with confirmed resistance to Sclerotinia stem rot and evaluated for agronomic traits.
- Sunflower breeding lines with enhanced resistance to Sclerotinia stalk-rot & head-rot derived from wild annual and perennial species via interspecific hybridizations. Alien chromosome addition stocks characterized and used for resistance breeding.

PM 1.3: Genetic analysis and discovery of quantitative trait loci (QTL) that confer resistance to Sclerotinia. Knowledge of the genetics of resistance to *S. sclerotiorum* is essential to formulation of effective screening strategies for disease resistance. Genetic maps of the genome are needed to facilitate breeding efficiency and genetic associations are necessary to understand the nature and the number of genes involved in resistance. Information gained from genetic analyses will lead to the identification and positioning of closely linked molecular markers on genetic maps for disease resistance genes, and the discovery of relevant QTLs.

Anticipated Products:

- Bi-parental breeding populations generated in canola, common bean, pea, soybean, and sunflower for identification of QTL associated with Sclerotinia resistance from diverse sources.
- 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.
- Use of genome-wide association mapping (PM3.5) and linkage analysis to identify and map QTL with major and minor effects in common bean, soybean and sunflower.
- 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.
- Define metabolic mechanisms associated with Sclerotinia resistance QTL in common bean, soybean, pea and sunflower.

PM 1.4: Pyramid white mold resistance in plant germplasm using traditional or genome sequence guided approaches, and release germplasm lines and cultivars with enhanced resistance. Parental lines seldom contain all identified favorable QTL alleles for reaction to Sclerotinia. QTL from multiple sources must be combined into single lines to enhance overall resistance. Translational genetics will help determine which of the marked genes for disease resistance are most important for use in breeding enhanced germplasm and cultivars. Such knowledge will help plant breeder's better handle the complexity of gene recombination in breeding populations. Elite cultivars or germplasm with improved resistance to *S. sclerotiorum* will enhance crop productivity & profitability.

Anticipated Products:

- Canola, chickpea, lentil, and pea lines with resistance to Sclerotinia and a broad portfolio of desirable agronomic traits developed and released.
- 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.
- Interaction of combined QTL on level of disease reaction in common bean and soybean is elucidated.
- Establish disease nurseries for characterizing field and greenhouse resistance to all pathogenic forms of Sclerotinia in common bean, soybean and sunflower.
- 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.
- 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. Clonal and sexual processes are involved in expressing genetic variability in *S. sclerotiorum*, but the true genotype structure of the population within North America is not well characterized. More detailed characterization of pathogen genotype collections from a wide variety of economic and wild hosts is necessary. Identifying ecological types within populations will provide an understanding of how disease develops in agro-ecosystems and provide insight into pathogen survival. Information is needed on ecotypes associated with certain hosts and agro-ecosystems, and there is limited knowledge on the virulence range of isolates.

Anticipated Products:

- Understanding the interaction of pathogen with environmental factors such as temperature and light.
- Identification of biotypes with resistance to new fungicide chemistry
- Characterization of the genetics of fungicide resistance
- Characterization of ecological types in the population.
- Associate traits 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. Differences in virulence exist within the pathogen population, but the extent of the variation and how it relates to pathogen genotype and host range is poorly understood. Physiological characteristics may be important to disease development and pathogenesis. Standard methods will be developed to describe virulence/ aggressiveness in the pathogen. Host specificity and the range of virulence/aggressiveness of collections from different hosts and environments will be tested to determine impact on partial resistance.

Anticipated Products:

- Documented reactions of a broad spectrum of isolates on new sources of host resistance.
- Diverse collection of isolates with a broad spectrum of aggressiveness and other characteristics
- 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. Germination of sclerotia is a critical event in disease development. Certain environmental factors like plant exudates are involved in the myceliogenic germination, whereas moisture and temperature are important in carpogenic germination. The biological mechanisms and genetic control of sclerotial germination are not precisely understood. Additionally, different *Sclerotinia* spp. may have different requirements for sclerotial germination. The role of soil microorganisms, other than mycoparasites, in the sclerotiasphere also will be determined on the germination process to aid in the prediction of disease and identify points in the cycle where germination can be disrupted. Revealing the genetic mechanisms of carpogenic germination will aid in developing strategies managing the disease

Anticipated Products:

- Identification of host factors that may enhance myceliogenic germination.
- Genetic control and required environmental conditions governing the processes of myceliogenic and carpogeneic 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. The genome sequence of *Sclerotinia sclerotiorum* is now available. Gene discovery in *Sclerotinia* will be accelerated by significant amounts of sequence data from transcribed genes to achieve high confidence in the annotation. Transcriptomes (expressed genes) is the most effective means of studying functional genes at specific growth and infection stages, host-pathogen interactions, or under specific environmental conditions. Next generation sequencing of transcriptomes (RNA-Seq) has largely replaced traditional cloning and clone sequencing approaches or even hybridization based approaches like microarrays. Transcriptomes at a variety of physiological and developmental stages of *Sclerotinia* will help identify genes that are functional at specific conditions. These include: sclerotial initials, polygalacturonic acid-grown mycelia, neutral pH-shifted mycelia, differentiating apothecia, low pH vegetative mycelia, agar grown mycelia, and infection cushions. Comparing *S. sclerotiorum* with related *Sclerotinia* spp. will provide insight into factors and mechanisms that limit host ranges of *S. minor* and *S. trifoliorum*, and will in turn help us better understand the mechanisms involved with the extremely wide host range of *S. sclerotiorum*.

Anticipated Products:

- Transcriptomic, genomic, and metabolomics data bases for growth stage-specific genes and infection-related genes from both host and pathogen.
- Improved gene annotation using transcriptomic data.
- Genetic control of differential infection processes of the *Sclerotinia* spp. in response to different host plants

PM 2.5: Identification and verification of candidate genes involved in

Sclerotinia pathogenicity. Profiling transcriptomes of *Sclerotinia* in interactions with various host plant tissues would allow identification of pathogen and host gene expression patterns and will provide further clues as to key factors for pathogenicity and defense. Universal mechanisms exist in organisms to inactivate target genes with interfering RNA molecules to prevent them from being translated into functional proteins. RNAi approaches in *Sclerotinia* will be standardized and widely available.

Anticipated Products:

- 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).
- Inventory of genes potentially involved in pathogenesis recovered from mutagenesis and transcriptome profiling.
- Functional verification of candidate genes using a systems biology approach to gene silencing and quantitative expression assays.

Gene Discovery & Phenotypic Association

Goal 3: Develop molecular technologies that facilitate breeding progress

PM 3.1 Develop useful molecular marker resources for QTL Discovery. Marker-assisted selection (MAS) is now a well-established and powerful technology in plant breeding for indirect selection of traits at the seedling stage. Pre-breeding with markers that help create reduced-representation populations that are enriched in desired traits thus speeds up the process of conventional plant breeding. To use this powerful technology in crop improvement, validated molecular markers are needed to identify genomic regions that control economically important traits. A variety of genetic mapping populations are being developed (PM1.3) for identification of quantitative trait loci (QTLs) for agronomic traits and Sclerotinia resistance. A catalog of all useful markers for assignment of important trait loci to specific chromosomes on a consensus map for each commodity will facilitate development of comparative maps within related and between genetically diverse populations. Given a reference genome sequence, the utility of thousands of SNP markers will empower advances in genotyping by sequencing (GBS) methods. Future advances in molecular marker technology will lead to the development of allele specific markers. The outcome of these efforts will enable effective and precise molecular breeding for crop improvement

Anticipated Products:

- 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 maps for Sclerotinia resistance. Several genetic maps have been constructed and are being developed by NSI projects. Genotyping data for these mapping populations should be used to compile a consensus map, which will help align physical maps of genomic regions that harbor Sclerotinia resistance genes. Sets of selected markers will be useful in the creation of high throughput genotyping systems for multiple loci. Identified QTLs and linked markers will be compiled for development of a consensus QTL map. This QTL map will help breeders select parental lines with the aid of linked markers for introgression or pyramiding of traits of interest to locally adapted germplasm.

Anticipated Products:

- Compilation of marker genotyping data for different mapping populations
- Improved genetic maps for Sclerotinia resistance genes
- A consensus genetic/QTL map for Sclerotinia resistance genes

- Core sets of markers for discovery of candidate genes for disease 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. As suggested from the reference soybean genome sequence, the number of protein encoding genes in each NSI crop species may exceed 60,000. Genome sequencing allows detection of all genes present within an organism, but does not reveal which genes are active in different metabolic pathways, tissues, or stages of development. Until recently, analysis of cDNA libraries of expressed gene sequences (ESTs) was limited to a gene-by-gene approach. New high-through-put sequencing platforms (such as RNAseq) provide a rapid and sensitive means to survey gene expression. RNA-Seq (whole transcriptome shotgun sequencing) deploys high-throughput sequencing technology to discern how individual alleles are expressed, detect post-translational mutations, and discover other functional aspects of gene expression profiles. This information will help create a comprehensive gene expression atlas that catalogs gene activity in different tissues and treatments. Such an atlas would be a valuable resource for the study of gene function and add definitive context to the annotation of consensus genetic and physical genome maps

Anticipated Products:

- A standardized methodology for annotation of maps among specified crop species
- Transcriptomic, proteomic and metabolomics annotation of genomic sequences in QTL associated with resistance to Sclerotinia diseases
- Characterization of candidate genes involved in biological mechanisms for resistance, such as: oxalic acid
- A commodity-based gene atlas with a comprehensive list of all expressed genes, alternative splice products, identification of co-regulated genes and gene networks
- Identification of specific genes within QTL of importance to Sclerotinia-host interactions

PM 3.4 Genome mapping and allelic analysis through Genome-Wide-Association-Studies. The research community has created genetic resources that facilitate both the generation of high resolution genetic maps through mapping by sequencing as well as the mapping of important agricultural traits through genome wide association studies (GWAS). Genetic mapping through sequencing and analysis of RIL populations will capture gene space in parental lines and each related RIL. Analysis of RIL data will be used to generate an ultra-dense, gene-based genetic map for each population. Genetic mapping and GWAS through low-coverage sequencing of germplasm collections will capture sequence variation and SNP-based association studies will reveal the level of linkage disequilibrium in breeding populations. Haplotype maps will help refine genetic maps and provide the foundation for efficient QTL mapping and candidate gene discovery.

Anticipated Products:

- High resolution exome maps of genomic regions that harbor QTL for Sclerotinia resistance.
- Identification of specific alleles in gene families that mediate Sclerotinia resistance.
- GWAS studies of the trait associated with phenotypic variation in disease resistance.
- 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.

PM 3.5 Develop plant germplasm with improved resistance using biotechnology and other novel genetic methods. Novel methods of developing Sclerotinia resistant germplasm include mutagenesis and transformation. Accumulation of endogenous plant genes to enhance Sclerotinia resistance, introduction of genes from unrelated plants or other sources may provide complementary and useful approaches for effective control of white mold in crop species.

Anticipated Products:

- 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.
- Functional tests in model plants to determine potential importance of candidate defense genes
- Determination of the efficacy of transformed genes on disease control in crop germplasm.
- Effective use of genome editing technologies to genetically modify genomic regions in ways that enhance resistance to Sclerotinia diseases
- 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. Efforts will identify fungicides, concentrations and application methods that provide best control of *Sclerotinia* in canola, soybean, common bean, pea, lentil, chickpea and sunflower.

Anticipated Products:

- 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

PM 4.2: Develop bio-control alternatives for disease management. Activities will focus in the evaluation of already available commercial bio-control agents, like *Coniothyrium minitans*. Additional surveys and screening exercises will identify new antagonists of *S. sclerotiorum* and optimal application

Anticipated Products:

- Identification of application strategies that will maximize the efficacy of currently available biocontrol agents for control of *S. sclerotiorum*
- Identification of novel antagonists of *S. sclerotiorum* and assessment of their efficacy in field trials
- Updated management guides for growers on use of biofungicides for disease management

PM 4.3: Develop disease-warning systems to optimize management of *S. sclerotiorum*. Epidemiological studies will help characterize the association between environment and cultural practices on disease development and its spatial distribution in the fields. Disease-warning systems based on these studies are needed to help optimize fungicide use for control of *S. sclerotiorum* in canola, dry bean, sunflower, soybean, and pulse crops. The effect of disease intensity on yield or crop quality will be determined to establish disease management criteria and decision models for commercial production systems.

Anticipated Products:

- 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.
The impact of common cultural practices on disease development will be evaluated through field experiments emphasizing crop rotation schemes, variety/hybrid selection, planting dates, etc. Use of precision agriculture technology will help optimize disease management.

Anticipated Products:

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

Appendix

Collaborators & Organizations

Advisory Committee

Roy Scott
Mickey McGuire
Barry Coleman
Greg Varner
William P. Kemp
John Sandbakken
Tim McGreevy
Kelly Whiting
Todd Scholz
Rich Wilson

USDA Agricultural Research Service locations

Ft. Collins, Colorado
Pullman, Washington
Prosser, Washington
Fargo, North Dakota
Urbana, Illinois
Ames, IA

Universities/Institutions

North Dakota State University
University of Nebraska, Lincoln
Michigan State University
Oregon State University
University of Idaho
Ohio State University
Colorado State University

Agricultural Organizations

US Dry Pea & Lentil Council
National Sunflower Association
United Soybean Board
US Dry Bean Council
U.S. Canola Association