

Plant Diseases
FY 2003 National Program 303 Annual Report

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Introduction

This program addresses the characterization of plant diseases and strategies to control them. The program is divided into five components: identification and classification of pathogens; biological control; cultural control; pathogen biology, genetics, population dynamics, spread, and relationship with hosts and vectors; and host plant resistance to disease. The overall goal of the Plant Diseases National Program is to develop and improve ways to reduce crop losses caused by plant diseases. The program focuses on developing effective control strategies that are not environmentally harmful, do not threaten the safety of consumers, and are compatible with sustainable and profitable crop production. The ARS program is conducted in cooperation with related research in other public and private institutions.

Selected Accomplishments by Component

Component I. Identification and Classification of Pathogens

Critical gene identified in peanut pathogen. Tomato Spotted Wilt Virus (TSWV) is a significant viral pathogen on peanut in the southwest United States. The ability of this virus to infect plants and the host range of the virus is controlled by the NsM gene. ARS scientists at Stillwater, Oklahoma, cloned and sequenced the NsM gene and determined the molecular origin of the genotypic differences that exist among the collection of TSWV isolates taken from peanut. The NsM gene will aid the identification of stable resistance sources of peanut germplasm.

Critical genes identified in insect vector of Pierce's Disease. Pierce's Disease of grapes is threatening the national grape industry. The insects that spread this bacterial-caused disease are leafhoppers, like the glassy-winged sharpshooter (GWSS). ARS scientists at Fort Pierce, Florida, have identified genes in these insects linked to development and survival. Approximately 10,000 potential genes and proteins have been identified inside leafhoppers. Identification of important traits necessary for insect survival is key to the development of new pest management strategies to protect grapes and other crops.

New sources of wheat and barley stripe rust resistance. Losses due to stripe rust have been severe for U.S. wheat producers. ARS scientists at Pullman, Washington, have identified new, emerging races of the stripe rust pathogen. Also, they have evaluated over 12,000 wheat and

barley accessions from the ARS National Small Grain Collection for rust resistance. Wheat and barley accessions with stripe rust resistance can now be used as breeding sources to develop more stripe rust resistant wheat and barley varieties.

Genetic variability of corn virus identified. Little is known about the genetic variability on maize chlorotic dwarf virus, a corn virus that causes significant disease problems in the southeastern United States. ARS scientists at Wooster, Ohio, sequenced both severe and mild isolates of the virus. The severe strain shared about 60 percent sequence identity with the mild type. These results show that there is wide variability among these viruses and suggest that the disease may be caused by a complex of more than one virus, a finding that will likely impact the designing of disease control strategies.

Component II. Biological Control

Microbial production and formulation for biological control of fungal plant diseases.

Phytophthora infestans, the causal agent of potato late blight is considered to be the most significant pathogen of potatoes worldwide, and an increase in severity and aggressiveness of the pathogen has stimulated interest in developing new biological control alternatives. ARS scientists at Peoria, Illinois, produced and formulated several bacterial strains patented for biological control of *Fusarium* dry rot, which previously suppressed late blight in laboratory potato bioassays. Late blight reduction provided by the biological control treatments ranged from 20 to 90 percent depending on strain and formulation composition. These results demonstrate the potential of combinations of these bacteria to simultaneously control both late blight and *Fusarium* dry rot.

Factors influencing antibiotic production and biocontrol efficacy. Antibiotics produced by biological control agents are important determinants of disease suppression, but their production, and consequently the success of biological control, is influenced by many unknown environmental and physiological factors. ARS scientists at Corvallis, Oregon, demonstrated that the antibiotic pyoluteorin, which is toxic against Oomycete plant pathogens such as *Pythium ultimum*, serves as a signal molecule influencing the expression of antibiotic biosynthesis and regulatory genes in the biological control organism *Pseudomonas fluorescens* Pf-5. Using a low-density microarray, they also demonstrated that pyoluteorin influences the expression of diverse genes in this organism, which suggests a general signaling role for this antibiotic. This information provides insight into factors influencing the antibiotic production and biocontrol efficacy of a model biological control agent, which can be used to improve the consistent efficacy of biological control agents in agriculture.

Component III. Cultural Control

Beneficial fungi in vineyards. Different forms of beneficial fungi can greatly aid plants in their growth, development and productivity, but are often poorly understood. ARS scientists at the Crops Pathology and Genetics Research Laboratory, Davis, California, conducted research to determine how different sources of arbuscular mycorrhizal (AM) fungal propagules contribute to the AM fungal community on and around grapevine roots. Various herbicide and cover crop regimes were studied across the season in vineyards and it was found that while mycorrhizal

cover crops and weeds are an important source of AM fungi in vineyards, vineyard floor management practices impact how AM fungal propagules from cover crops and weeds contribute to colonization of grapevines. A better understanding of the biology of AM fungi will facilitate determining their contribution to grapevine growth and their potential application for improved productivity of vineyards.

Component IV. Pathogen Biology, Genetics, Population Dynamics, Spread, and Relationship with Hosts and Vectors

Characterization and Epidemiology of Citrus Tristeza Virus (CTV) in California. Citrus tristeza virus is the most important virus disease of citrus. Evaluation of the rate of spread and virulence of CTV in the San Joaquin Valley of California remains critical to the local citrus industry and the fate of the CTV eradication program. ARS scientists at Parlier, California, found that CTV spread continues at a high rate despite extensive eradication efforts. Isolates from different infected trees in a 4 square mile area yielded the same highly transmissible virus strain by the cotton aphid but the virulence was benign in commercial varieties grown in this area, which suggests that the eradication program, in its present state, may no longer be useful or cost effective.

Biology and control of sugarcane disease. A high incidence of sugarcane yellow leaf virus (SCYLV) occurs in commercially grown sugarcane in Florida and the extent of yield losses is not known. Two yield tests were established by ARS scientists at Canal Point, Florida, comparing the yields between SCYLV infected and virus-free plants. The analysis of the combined data for 5 cultivars determined that the yield parameters were significantly higher (up to 11 percent higher) in the virus-free plants over the SCYLV-infected plants. This indicates that the use of virus-free planting material will increase yields.

A major cooperative research effort to protect U.S. crops from Sclerotinia diseases. White mold caused by *Sclerotinia sclerotiorum* is an economically devastating disease of numerous broad leaf crops throughout the United States. ARS scientists at Fargo, North Dakota, coordinate cooperative research to manage this disease in five commodity crops (canola, dry bean, pea & lentil, soybean, and sunflower). Research was conducted at 11 land-grant universities, the National Sunflower Association of Canada and 6 ARS research locations. Highlighted findings include improved ability to forecast white mold incidence for various crops, where a risk map for canola is currently in use and is being expanded into other crops. This map has potential to reduce fungicide costs while maintaining use of fungicides in high-risk areas, thus avoiding unacceptable white mold losses. Genetic resistance to white mold was developed in canola germplasm at North Dakota State University. In addition, white mold resistance was discovered in dry bean germplasm at Michigan State University. This resulted in release of the navy bean cultivar 'Seahawk'. Progress also was made toward the development of plant resistance to Sclerotinia stem rot at the University of Wisconsin. A simple, inexpensive and reliable greenhouse method was developed for initial screens of canola to differentiate response to the disease in development of resistant cultivars. Other research on Sclerotinia stem rot at the University of Illinois was initiated to map resistance genes from plant introductions and initiate the incorporation of these genes into elite soybean germplasm. Progress was made in mapping quantitative trait loci in three populations developed from crosses between partially resistant

soybean plant introductions and partially resistant or susceptible varieties.

Transmission of serious virus confirmed. Plum pox virus (PPV), the most destructive virus of *Prunus* has caused millions of dollars in losses in Pennsylvania, and continues to spread outside the quarantine zone. ARS Scientists at Frederick, Maryland, in cooperation with Pennsylvania State University showed that the infected fruit was a source of virus inoculum for spread by the green peach aphid and the spirea aphid, the two most common aphid species in the Pennsylvania orchards. Peaches and other stone fruits have not been considered a source of transmissible virus; however, fruit from quarantine areas could potentially provide a pathway for the virus to spread to new areas and affect the ability to eradicate the virus.

Component V. Host Plant Resistance to Disease

Improving natural resistance to diseases through plant recognition of pathogens. Crop species often lack effective genetic resistance to some of their significant pathogens. ARS scientists at Albany, California, have determined several steps in disease progression that are critical for the expression and function of disease resistance. Plant recognition of pathogens is one of the first steps to resistance and is mediated by a large family of receptor-like proteins that results in activation of signaling cascades and induction of defense and resistance responses. ARS scientists determined that the resistance R gene is alternatively spliced after virus infection and that the alternative splice version is required for resistance. These results provide a useful model for disease resistance.

Critical resistance gene in wild potato identified. ARS scientists at Madison, Wisconsin, have been working to locate a disease resistance gene in order to permit studies on fine mapping of the wild potato (*Solanum bulbocastanum*), which has resistance to late blight disease. Using molecular markers, ARS scientists in collaboration with the University of Wisconsin were able to determine the location of the resistance gene in the potato genome. The gene was located and cloned. The impact of this work will be to insert the gene into a susceptible potato variety, making the plant resistant to late blight and eliminating the need for fungicide spraying.

New wheat disease resistance genes identified. Wheat is vulnerable to an array of disease losses and insect damage. Researchers at West Lafayette, Indiana, Purdue University, and the CuraGen Corporation have discovered thousands (over 3,000) of new wheat genes that respond to disease pathogens and pests. These genes are differentially regulated when wheat is attacked by scab, viruses or Hessian flies. This new information can be used to develop wheat with improved resistance to each of these disease or insect threats.

Barley Genome GeneChip contains over 400,000 ESTs (parts of genes). ARS scientists at Ames, Iowa, working with national and international barley researchers, and Affymetrix have developed a microarray chip that contains over 400,000 ESTs (expressed sequence tags) for barley genes. Project received funding from USDA-CSREES Initiative for Future Agriculture and Food Systems. The chip enables cereal researchers to assess effects of drought, pests, and disease on most barley genes simultaneously, which will result in more efficient, precise barley improvement.

Looking to wild relatives to improve wheat leaf rust resistance. ARS scientists at Manhattan, Kansas, have identified a novel source of leaf rust resistance in the wild wheat relative, *Triticum armeniacum*. U.S. wheat producers suffer significant losses to leaf and stem rusts each year, and a new source of resistance will be useful in developing new varieties with higher levels of leaf rust resistance.