

**United States Department of Agriculture
Agricultural Research Service
National Program 303 • PLANT DISEASES
FY 2016 Annual Report**

National Program 303, Plant Diseases, focuses on developing effective disease management strategies that are environmentally friendly, safe for consumers, and compatible with sustainable and profitable crop production. This USDA-Agricultural Research Service (ARS) National Program is conducted in cooperation with related research in other public and private institutions. In particular, NP 303 projects are coordinated with those in ARS' National Program 301 (Plant Genetic Resources, Genomics, and Genetic Improvement) toward the overall goal of crop improvement through increased resistance to biotic and abiotic factors and increased understanding of host-pathogen interactions.

The overall goal of NP 303 is to develop and improve ways to reduce crop losses caused by plant diseases, while safeguarding the environment. To this end, projects in this national program aim to reduce the impact of diseases on yields, product quality or shelf-life, aesthetic or nutritional value, and potential toxin contamination of food and feed.

Management of plant diseases is essential for providing an adequate, safe and consistent supply of food, feed, fiber, and aesthetic plants, and has long been a high priority for ARS. Besides the obvious monetary benefits to producers and processors, successful plant health protection is important for maintaining and increasing food supplies without increasing land under cultivation. Additionally, the knowledge and management of plant diseases of quarantine significance are vital, not only for protecting our domestic crops from foreign disease, but also for maintaining and expanding export markets for plants and plant products.

NP 303 consists of 56 projects located in 19 different states and the District of Columbia. Most of the more than 120 scientists working within this national program are specialists in plant pathology and/or nematology. Significant contributions to NP 303 also come through multidisciplinary teams that include geneticists, agronomists, botanists, horticulturists, physiologists, soil scientists, entomologists, chemists, and microbiologists.

NP 303 encompasses the following three components:

- *Component 1 – Etiology, Identification, Genomics and Systematics*
- *Component 2 – Biology, Ecology, and Genetics of Plant Pathogens and Plant-Associated Microbes*
- *Component 3 – Plant Health Management*

Together, these components include research to understand and control plant diseases and to develop and transfer strategies for disease management and control that enhance agricultural production and value. During fiscal year 2016, this program produced many important discoveries and advances. Some of these are described below, grouped by program component.

Component 1 – Etiology, Identification, Genomics and Systematics

Identifying new strains of Citrus Tristeza Virus in California that do not require quarantine measures. Citrus Tristeza Virus (CTV) has caused hundreds of millions of dollars in losses to citrus producers throughout the world. Infected trees in California are detected using a protein (antibody) test that is specific for the MCA-13 strain of CTV, which is a strain that causes rapid tree decline and death. As part of the overall effort by the California Department of Food and Agriculture to eradicate CTV, trees in California that test positive for the MCA-13 strain are removed from orchards and destroyed. ARS scientists in Parlier, California, in collaboration

with the Central California Tristeza Eradication Agency and tree fruit scientists at Bari, Italy, identified two new strains of CTV (strains RB and S1) that tested positive using the antibody test specific for the MCA-13 strain. However, these strains only produced mild symptoms, not the rapid death and decline associated with the MCA-13 strain. The scientists also determined that the mild strains RB and S1 could be distinguished from the severe strain based on their RNA sequences. These results provide improved ability to detect mild strains of CTV, such as RB and S1, for which growers are not required to remove and destroy infected trees. This permits growers to save costs associated with removal of infected trees and maintain productive orchards, while also allowing growers to avoid the need to wait several years until newly planted trees begin to bear harvestable fruit.

Development of a rapid and sensitive assay to identify select agent strains of *Ralstonia solanacearum*.

Ralstonia solanacearum is a bacterium that causes millions of dollars of crop losses in a wide range of plant species worldwide. One strain in particular, the r3b2 subgroup, is such a threat to U.S. agriculture that it has been designated a USDA select agent. New regulations require that all strains of the bacteria be considered select agents until they are shown to not be r3b2. Detection methods are needed that are sensitive, specific, accurate, and efficient in order to prevent the r3b2 strain from entering the United States, and to avoid unnecessary regulation of non-r3b2 strains. ARS researchers in Beltsville, Maryland, developed a molecular assay that improves the specificity and confidence in detecting the r3b2 subgroup of the pathogen. The new assay allows for quick, easy and reliable detection and differentiation of the r3b2 strains of *R. solanacearum*, which will help keep this pathogen out of the United States and promote food security. The technology has been transferred to USDA-APHIS as a general assay tool and is being used in two portable (onsite) analysis formats for the rapid and accurate detection of this devastating bacterial pathogen.

Antibodies developed to select agent. *Rathayibacter toxicus* is a USDA-APHIS select agent plant pathogen due to the bacteria's ability to make a toxin in forage grasses that is lethal to livestock. Annual production losses in Australia from this pathogen amount to 40 million dollars. Because of the potential threat to U.S. agriculture and food supplies, accurate and rapid diagnostics that can distinguish *R. toxicus* from other *Rathayibacter* species that already exist in the United States are critical to food security and trade. ARS researchers in Frederick, Maryland, have generated a highly specific polyclonal antibody that specifically detects *R. toxicus*, which will allow for the detection of the pathogen by a simple immunoassay (ELISA). The peptide used to generate this antibody is now being used to generate monoclonal antibodies that will be transferred to USDA-APHIS for rapid, on-site biosensor applications.

Release of nematode-resistant cotton lines. Root-knot and reniform nematodes are the pests that cause the greatest yield losses in cotton. The nematodes also act synergistically by increasing the severity of seedling diseases and Fusarium wilt, which results from tissue damage that occurs during their feeding activities. ARS researchers in College Station, Texas, jointly with workers at Texas A&M AgriLife Research and Cotton, Incorporated, released eight new nematode-resistant germplasm lines. All eight lines are resistant to the reniform nematode, and five are also resistant to the root-knot nematode. These lines have elite agronomic performance traits which will be valuable to plant breeders in their work to reduce yield losses and lower the costs of pest control in cotton.

Determining the prevalence of *Plantago asiatica* mosaic virus in imported lily bulbs and development of a rapid assay to detect the virus. Lilies are a valuable internationally-traded ornamental crop, with cut flower production in California alone worth over \$56 million (wholesale value). *Plantago asiatica* mosaic virus (PIAMV) was recently detected in lilies imported to the United States from the Netherlands, where losses of up to 80% have been reported in cut-flower lily production, indicating the potential for significant losses to U.S. producers. Unfortunately, there was no knowledge regarding the prevalence of PIAMV in different imported lily types, and there was lack of rapid diagnostic methods available for detecting the virus in infected plants. Consequently, ARS scientists in Beltsville, Maryland, in collaboration with colleagues at the University of Maryland tested different imported lily types for the presence of PIAMV. These advances contribute

critical information on what types of lilies are likely to be infected with the virus and provided diagnostic capabilities to detect the virus in this high value crop.

Identification of genes associated with fungicide resistance in the sugarbeet pathogen *Cercospora beticola*.

Cercospora leafspot of sugarbeet is caused by the fungal pathogen *Cercospora beticola*. This disease, which causes severe losses for sugarbeets throughout the United States, is primarily controlled by fungicide applications. Unfortunately, the prevalence of fungal isolates that are resistant to fungicides is increasing, and an improved understanding of the genetic control of fungicide resistance is required to develop effective disease management strategies. To address this, ARS researchers in Fargo, North Dakota, conducted genetic analysis of fungicide-resistant and fungicide-sensitive isolates of this sugarbeet pathogen. One gene, Cyp51, was found to be much more active in fungicide-resistant isolates than in fungicide-susceptible isolates, and several other genes were also identified that could be used to distinguish between fungicide-resistant and fungicide-sensitive isolates. These results increase fundamental understanding of the genetic control of fungicide resistance in this pathogen and provide an approach to develop rapid and accurate methods to detect isolates of this pathogen with fungicide resistance. These advances will encourage prescriptive uses of fungicides that promote more environmentally sustainable sugarbeet production.

Component 2 – Biology, Ecology, and Genetics of Plant Pathogens and Plant-Associated Microbes

Molecular marker developed for wheat blast pathogen. Wheat blast disease is a major threat to wheat production in South America, where it was first reported 30 years ago. The disease had not been detected outside of South America until the spring of 2016, when the disease was confirmed in Bangladesh. This discovery confirmed that the potential for the disease to spread to other wheat producing countries, including the United States, is high. To help combat wheat blast, ARS researchers in Frederick, Maryland, developed a diagnostic assay that is specific for the fungal pathogen that causes the disease, *Magnaporthe oryzae* Triticum pathotype (MoT). To accomplish this objective, a custom bioinformatics pipeline was used to identify unique regions within the MoT genome for the development of a PCR-based diagnostic assay. The genomes from four MoT isolates were compared to the genomes of sixteen *M. oryzae* isolates collected from ten different host species. The marker MoT3, which can differentiate MoT isolates from other *M. oryzae* isolates, was identified. This assay will be of utility to government, academic and private diagnosticians for detecting and identifying MoT isolates, and was recently used to identify and characterize the isolates obtained from the first outbreak of wheat blast in Bangladesh.

Identification, characterization, and functional validation of virulence genes and gene products in *Xylella fastidiosa*. Modern molecular tools are being exploited for reducing the impact of the bacterium *X. fastidiosa* on grape production, but the specific genes, gene products, and mechanisms by which the bacterium causes disease are not fully understood. ARS researchers in Parlier, California, demonstrated that *X. fastidiosa* cold-shock protein 1 (Csp1) is: 1) an RNA chaperone, 2) regulated in a temperature-independent fashion, 3) important for bacterial survival under cold and salt stress conditions, and 4) required for full virulence of the bacterium in grapevines. When studying another set of *X. fastidiosa* genes, deliberate mutations in the *X. fastidiosa* genome, followed by pathogenicity assays in grapevines, resulted in a remarkable reduction in bacterial virulence when compared to a wild type of *X. fastidiosa*. By providing a better understanding of how the bacterium causes disease in plants and withstands unfavorable environmental conditions, this research identified new molecular targets for disarming *X. fastidiosa* virulence. Findings from this study benefit grape growers, researchers and plant breeders by providing knowledge required to develop novel methods of disease control.

Draft whole genome sequencing of *Xylella fastidiosa* subspecies *fastidiosa* Stag's Leap strain. Pierce's disease, caused by the bacterium *X. fastidiosa*, is an economically important grapevine disease that endangers

the multi-billion dollar grape and wine industry causing \$104 million per year in control costs and losses. Analysis of whole genome sequences of *X. fastidiosa* strains from different geographical origins and host plants is necessary to better understand pathogenic potential, but accurate methodologies to assemble, annotate, and analyze these genomes of *X. fastidiosa* are lacking. ARS researchers in Parlier, California, in collaboration with scientists at National Chung Hsing University in Taichung, Taiwan, developed methods to reduce variability in parameters used to analyze bacterial genomes. These improved methods led to the sequencing, assemblage, annotation, and analysis of the genome of the Stag's Leap strain of *X. fastidiosa*, obtained from Napa Valley, California. Improved accuracy in bacterial genome analysis and increased knowledge of *X. fastidiosa* strain characterization will benefit grape growers through the identification of biological characteristics that could be targeted for novel methods of disease control.

RNA interference (RNAi) methods for control of whiteflies. Whiteflies are among the most destructive insect pests of American agriculture, causing tens of millions of dollars of losses annually from a diverse set of crops including vegetables, fruits, cotton, and ornamentals. There is very little resistance in most of these important crops to either whiteflies or the viruses they transmit, thus the pest is primarily controlled by insecticide applications. ARS researchers in Salinas, California, used whitefly genome sequences to design interfering RNA (RNAi) molecules that were tested for the ability to control whiteflies. Several of the RNAi molecules were very effective at killing whiteflies in laboratory conditions. These discoveries provide proof that RNAi technologies can be used to control whiteflies and that future whitefly control will be possible using methods other than insecticide applications, promoting more environmentally sustainable crop production.

Detection tools for Squash vein yellowing virus (SqVYV). Squash vein yellowing virus, the cause of viral watermelon vine decline, was first found in Florida, but the known geographic range of SqVYV has since increased with findings in Indiana, South Carolina, Georgia, California, Puerto Rico, Guatemala, and Israel. The disease is difficult to identify based on symptoms alone, thus rapid and sensitive diagnostic tools are needed to facilitate detection. ARS Scientists in Fort Pierce, Florida, developed an enzyme linked-immunosorbent assay (ELISA) and a quantitative reverse transcription-PCR (qRT-PCR) for the identification of SqVYV. The two new procedures were capable of detecting SqVYV in a wide range of cucurbit hosts. qRT-PCR was able to detect the virus in over 99% of the samples where the virus was known to be present, whereas ELISA was able to detect the virus in 58-76% of known infections, depending on the host plant. Both tests had very similar false positive rates of <6%, with ELISA sometimes outperforming qRT-PCR. The newly developed diagnostic tools provide more options for the detection of SqVYV and will assist in improved management of SqVYV-induced watermelon vine decline.

Characterization of genes expressing plant cell wall-degrading enzymes and multiple phytotoxins in the genome of *Fusarium virguliforme*. The fungus *F. virguliforme* causes root rot and sudden death syndrome in soybean, producing significant reductions in soybean yields each year. ARS scientists in Urbana, Illinois, and collaborators showed that *F. virguliforme* produces a diverse set of cell wall-degrading enzymes, including several unique enzymes not reported in other plant pathogenic fungi. The research team also identified *F. virguliforme* toxin genes that when expressed in plants induced foliar symptoms of soybean sudden death syndrome. The enumeration of the specific types of cell wall-degrading enzymes and the multiple toxins produced by *F. virguliforme* will facilitate strategies to reduce the severity of root rot and sudden death syndrome by expressing proteins that inhibit these toxins and enzymes in transgenic soybean plants that could improve the management of this economically important disease of soybeans.

Novel UV-C/dark treatment for controlling strawberry diseases. Strawberry production in high and low tunnel culture presents significant challenges to disease control. ARS researchers in Kearneysville, West Virginia, found that UV-C irradiation of strawberry plants, followed by a four-hour dark period, can control gray mold and anthracnose infection of strawberry fruit. This technology represents an effective alternative to the use of synthetic, chemical fungicides, and its use is especially applicable to urban horticulture and high/low tunnel production systems.

Identification and molecular characterization of 49 previously undescribed viruses that infect fungal pathogens of soybean. Soybean provides essential nutrients for both humans and food animals, and is an important source of bioenergy. Each year, fungal diseases significantly reduce soybean yields and seed quality, but some fungal viruses reduce the ability of pathogenic fungi to induce disease. ARS scientists in Urbana, Illinois, and collaborators identified viruses that infect the fungi that cause widely prevalent soybean diseases such as anthracnose, charcoal rot, Phomopsis seed decay, Rhizoctonia root rot, and Sclerotinia stem rot. Because some of these viruses reduced the virulence of their fungal hosts, these results could potentially widen the range and diversity of biological agents that can be used in the management of fungal diseases of soybean.

Component 3 – Plant Health Management

Using DNA sequence data to tap into genetic diversity for reniform nematode resistance in cotton.

Reniform nematode causes significant economic loss in cotton each year, and since new races occur frequently, breeders are constantly seeking new sources of resistance. The more than 1,600 Asiatic cotton accessions in the USDA National Plant Germplasm System (NPGS) cotton collection are a valuable resource that may contain resistance, but it would be time-consuming and costly to screen. Information is needed on the genetic diversity of these varieties to increase efficiency of screening to identify new sources of reniform nematode resistance, and identify DNA markers to assist in transfer of resistance to upland cotton. ARS researchers in Stoneville, Mississippi, used Genome-wide DNA sequencing data to compare 375 cotton Asiatic germplasm lines from the NPGS. Although many germplasm lines clustered together, indicating low genetic diversity, others did not cluster, indicating greater genetic diversity among them. Instead of having to screen all 375 germplasm lines, based on this research, breeders now only have to screen the subset containing the greatest diversity. Resistance to reniform nematode was observed in 122 germplasm lines, which now serve as source materials from which breeders can choose parents to use in crosses. As germplasm with different genes for nematode resistance is identified, the DNA sequencing data from this study will be used to develop DNA markers associated with resistance that can be used to more rapidly transfer the resistance genes to upland cotton.

Development and release of two watermelon breeding lines with resistance to Fusarium wilt. Fusarium wilt of watermelon is one of the oldest and most economically significant diseases of watermelon. Breeding for durable resistance to this disease is the most economical approach to manage and control disease losses. More than 20 seed companies have received and evaluated seed from two Fusarium resistant lines, USVL246-FR and USVL252-FR, released by ARS researchers from Charleston, South Carolina. Several of these companies have found these lines to be more resistant than any other breeding line currently in use. Moreover, two companies have already begun using these resistant lines in their own breeding programs. These highly resistant watermelon lines will provide strong protection against the damaging Fusarium wilt disease and will prove very useful to the U.S. watermelon industry.

Silencing of a citrus gene with a recombinant cloned DNA of a Citrus tristeza virus vector carrying a truncated citrus gene. Huanglongbing (HLB) is a new and destructive invasive disease of citrus associated with an uncultivable bacterium that lives in phloem (nutrient transport system in plants) and blocks or limits phloem transport. Tools are needed to study and design ways to control this disease. ARS researchers in Parlier, California, in collaboration with scientists at the Central California Tristeza Eradication Agency, Tulare, California, and the Citrus Research and Education Center, Lake Alfred, Florida, successfully silenced the endogenous phytoene desaturase (PDS) gene in citrus using a CTV vector containing a truncated PDS gene. This is an important proof of concept that a modified CTV vector can be engineered to alter the expression of citrus genes. Targeted citrus genes include those involved in HLB-induced premature fruit drop or callose and the phloem protein 2, which is involved in phloem plugging. In addition, the CTV vector can be further modified to produce antimicrobial peptides and RNA interference in the phloem to specifically target the HLB

pathogen and its psyllid vector. If regulatory approval is obtained, this approach could be used for short to mid-term control of HLB and reduce our reliance on insecticides to manage the insect vector (psyllid) that spreads this disease.

Resistance to cereal cyst nematode found in adapted wheat lines. Cyst nematodes are among several types of plant-parasitic nematodes that reduce yields in Pacific Northwest dryland wheat fields, accounting for about \$51 million in annual losses. There are presently no chemical controls nor resistant plant varieties to control this pathogen. ARS scientists in Pullman, Washington, screened advanced wheat lines in the greenhouse and field plots. They identified a number of elite resistant varieties developed by ARS, including SY Steelhead, Svevo and ARS Crescent. These varieties can be immediately used by growers to manage this disease. In addition, discovery of this resistance will aid plant breeders to quickly develop additional resistant varieties, without having to breed out undesirable characters present in poorly adapted germplasm.

Major-effect Ug99 wheat stem rust resistance genes. Stem rust is an important disease of wheat in the United States and around the world that can cause severe crop losses. An extremely virulent race of this pathogen from Africa, Ug99, currently threatens global wheat production. This highly virulent race of stem rust has not yet entered the United States, but preventive breeding is being conducted to develop new resistant wheat lines. ARS scientists in St. Paul, Minnesota, have transferred a new resistance gene named Sr59 from rye into wheat. The DNA sequences of three additional Ug99 resistance genes named Sr22, Sr45, and Sr50 were also identified in cooperation with international collaborators. DNA sequence information is being used through marker-assisted selection in the development of wheat lines that carry multiple genes for Ug99 resistance. Continued selection and transfer of stem rust resistance genes into wheat is essential for the development of wheat cultivars with resistance to Ug99.

Xylella fastidiosa-resistant rootstocks reduce almond leaf scorch disease incidence and severity. Significant variability in disease intensity exists among regions and cultivars affected by almond leaf scorch disease in California, the sole producer of almonds in the United States. Although cultivar selection and planting location can reduce disease intensity, better alternatives are needed. ARS researchers in Parlier, California, evaluated *X. fastidiosa* infections on almond trees grafted on 'Nemaguard', 'Okinawa', 'Nonpareil', and Y119 rootstocks. Disease symptoms and *X. fastidiosa* infections persisted throughout the study on all trees grafted on 'Nonpareil' rootstock, whereas disease remission and pathogen elimination occurred in 30% of the trees grafted on 'Okinawa' and Y119 rootstocks. 'Nemaguard' promoted complete pathogen elimination and remission of leaf scorching symptoms, indicating that a *X. fastidiosa*-resistant rootstock can be valuable for almond growers, and through its use, growers could reduce the incidence of this disease in California.

Major yield losses caused by stripe rust prevented in 2016. Stripe rust is a major wheat disease. Due to the weather conditions in the 2015-2016 season that were highly favorable to stripe rust, the disease started early and developed to a severe epidemic in the Pacific Northwest and other regions of the United States. To prevent major yield losses, ARS scientists from Pullman, Washington, made accurate forecasts of the wheat stripe rust epidemic early in the season by using recently developed prediction models in combination with stripe rust field surveys, thus making timely and accurate recommendations for fungicide applications. Major yield losses were prevented by this timely implementation of appropriate stripe rust control measures. Accurate forecasting, in combination with field surveys proved to be an effective disease management tool in 2016 for controlling stripe rust epidemics in the Pacific Northwest.

Fescue suppresses plant-parasitic nematodes. Plant-parasitic nematodes can be difficult to control once they infest a field. Tall fescue is widely used as a forage grass and turfgrass, and for stabilizing soil and preventing erosion. A fungus growing within tall fescue improves plant vigor in drought and poor soil conditions, confers pathogen resistance, and produces compounds that are toxic to insects and other animals. Research conducted in Beltsville, Maryland, with collaborators in Byron, Georgia, led to the finding that planting tall fescue cultivar Jesup (Max-Q) prior to the establishment of peach tree orchards suppresses several species of

nematodes. Additionally, root and shoot extracts and root exudates were found to be nematotoxic to root-knot nematodes. This research will lead to the identification of chemical compounds that contribute to the suppression of root-knot nematode species and provide alternatives to synthetic pesticides that are currently used for suppressing nematode populations.

Galls on corn caused by *Ustilago maydis* may be contaminated with mycotoxins. People in some cultures consume corn smut, which is a fungal reproductive structure caused by an *Ustilago maydis* infection of corn. ARS scientists in Stoneville, Mississippi, examined field and commercial samples of these galls and developed a simple analytical procedure to test for the presence of mycotoxins. Fumonisin was the major mycotoxin found in these samples, followed by aflatoxin and zearalenone. The discovery of mycotoxins in these food products has health implications for people who eat these products; this research will lead to improved human health through improved nutritional knowledge, and it will be used to develop strategies and methodology to reduce mycotoxin contamination in this food product.

Bt insect protection reduces mycotoxin contamination of corn. Insect damage of corn may expose the grain to toxin producing fungi. ARS scientists in Stoneville, Mississippi, conducted experiments to measure the amount of insect damage in Bt corn hybrids and the relationship between the insect damage and mycotoxin contamination of corn. The most effective forms of Bt protection also provided some protection against contamination by the mycotoxin fumonisin. These results provide plant breeders and researchers with new knowledge of mycotoxin contamination that will lead to the reduction of mycotoxins in corn and improve food security.

New sources of resistance to zonate leaf spot and rough leaf spot in sorghum. Global climate change is likely to alter the frequency and/or severity of fungal diseases such as zonate leaf spot and rough leaf spot, which under humid weather conditions can cause significant losses in sorghum. Development of new disease-resistant sorghum varieties to major sorghum diseases is a major priority for sorghum improvement programs. ARS scientists in College Station, Texas, and Mayagüez, Puerto Rico, working with collaborators from Texas A&M University and Kansas State University, evaluated numerous sorghum lines for resistance to zonate leaf spot and rough leaf spot. Several lines were found to be highly resistant to both diseases. This work provides sorghum breeders and other researchers with critical new germplasm for developing new, disease-resistant sorghum varieties for productive use in world agriculture.

Identification and characterization of a gene sequence that regulates grapevine responses to cold and ultraviolet radiation stresses. Productivity of grapevines is regulated by plant hormones, including jasmonic acid, a hormone that controls plant growth and development as well as plant responses to abiotic and biotic stresses. Methyltransferase is an enzyme that mediates production of jasmonic acid in plants. ARS researchers in Parlier, California, identified a gene sequence responsible for the production of methyltransferase in grapevines and demonstrated that gene activity was affected by cold and ultraviolet radiation stresses, but was not affected by heat stress. Findings from this study benefit grape growers by providing knowledge required for understanding grapevine physiological responses to stress, which will lead to improved grape production practices and the development of stress-resistant cultivars.

Wheat gene contributing to *Fusarium* head blight resistance identified. *Fusarium* head blight (FHB) is a major disease threat for production of wheat and barley. FHB is caused by the fungus, *Fusarium graminearum*, which produces the mycotoxin, deoxynivalenol (DON), and the disease is found throughout the spikes and kernels of wheat and barley. ARS researchers in West Lafayette, Indiana, and international collaborators demonstrated that a specific gene is critical for tolerance to DON in wheat. The overexpression of this gene in transgenic wheat results in increased FHB resistance. This work will aid in developing wheat and barley with enhanced FHB resistance.

Nutritional components of xylem sap correlated with glassy-winged sharpshooter egg maturation. The glassy-winged sharpshooter is an important insect vector of *Xylella fastidiosa*. Glassy-winged sharpshooter fecundity is highly variable and dependent on the adult diet, but little is known about the sources of variability in fecundity or nutritional requirements for egg maturation. ARS researchers in Parlier, California, analyzed the chemical profile of xylem sap of glassy-winged sharpshooter host plants and correlated xylem sap composition with rates of female egg maturation. Sets of co-varying amino acids related to female egg production were identified. Knowledge of nutritional requirements for sharpshooter egg maturation will benefit grape growers by enabling the identification and breeding of crop cultivars with suboptimal xylem sap chemistries that are unable to support sharpshooter population growth.

Wheat genes for resistance to stripe rust mapped. Growing resistant wheat varieties is the most effective, economical and environmentally friendly approach for controlling stripe rust. New genes for resistance are needed to diversify the resistance sources used in breeding programs and improve the durability of resistance in commercial varieties. In 2016, ARS scientists in Pullman, Washington, completed stripe rust resistance mapping studies of three genes in spring wheat germplasm 'W18', one gene in the spring wheat germplasm 'PI 184597', and one gene in the winter wheat variety 'Tres'. These genes and their molecular markers will be used for breeding wheat varieties with resistance to stripe rust and to better characterize the races of this fungal pathogen.

Blueberry cultivars with resistance to *Phytophthora cinnamomi*. *Phytophthora cinnamomi* is an important soilborne pathogen of blueberry worldwide, as it causes root rot and limits establishment of new blueberry fields. ARS scientists in Corvallis, Oregon, with collaborators at Oregon State University, evaluated 18 blueberry cultivars for resistance to *P. cinnamomi*. They identified six cultivars with resistance to the pathogen. Results are significant because they provide an alternative disease control method for growers with soil populations of *P. cinnamomi* and for organic growers who cannot apply fungicides to manage root rot disease.

Canine disease detection research is highly successful at identifying citrus diseases. Fifteen years of canine disease detection research has culminated in the training of 10 dogs to detect Huanglongbing (HLB-citrus greening) and three dogs to detect citrus canker at a 99.17% accuracy. Ten more dogs will be fully trained to detect HLB for a total of 20 dogs by end of 2016. Dogs will be commercially deployed over the next two years to various affected states, especially Texas and California. Commercialization plans by detector dog training companies are nearly complete. These highly accurate canine inspectors will help detect and reduce the spread of these economically important citrus diseases.