

**United States Department of Agriculture
Agricultural Research Service**

**National Program 301 • Plant Genetic Resources, Genomics, and Genetic Improvement
FY 2016 Annual Report**

The USDA-Agricultural Research Service's (ARS) National Program (NP) 301, Plant Genetic Resources, Genomics, and Genetic Improvement, supports research that maintains, protects, enhances, and expands the United States genetic resource and information base, and increases knowledge of the structure and function of plant genes, genomes, and biological and molecular processes. Through innovative research tools and approaches, this National Program manages, integrates, and delivers vast amounts of genetic, molecular, biological, and phenotypic information to a diverse global clientele. The ultimate goals for the preceding efforts are to improve the production efficiency, yield, sustainability, resilience, health, product quality, and value of U.S. crops. This National Program addresses the need to:

- Ensure the long-term safety and integrity of our agriculturally valuable genetic resource collections and associated information;
- Develop novel approaches for analyzing complex traits, identifying favorable genes underlying those traits, and deploying them in breeding stocks;
- Exploit new technologies that enhance traditional methods of genetic improvement;
- Genetically improve a broad spectrum of major, specialty, and new crops;
- Increase our knowledge of the structure and function of crop genomes and of plant biological and molecular processes; and
- Acquire, analyze, and deliver genetic and information resources to research communities and to the public.

Genetic resources are the foundation of humanity's agricultural future. ARS genebanks contain sources of resistance, tolerance, and adaptation to biotic and abiotic stresses and new genes to improve the quantity, quality, and production efficiency of our food, feed, bioenergy, fiber, and ornamental crops. To ensure those genes are available for research and breeding, ARS must continue to strategically acquire and conserve germplasm that contains them; develop new screening methods for identifying favorable traits; ensure that germplasm is distributed where and when it is needed; and safeguard these collections for future generations.

ARS has taken a leadership role in developing and curating crop genomic and phenotypic databases, which are expanding now and will continue to do so in the future. New tools are needed to efficiently capture phenotypic data and extract useful information, via innovative data-mining strategies, from the ever-increasing flow of data into these databases. Methods to interconnect databases containing diverse types of information are needed to more efficiently and effectively identify important properties of genes and genomes and apply that knowledge to crop improvement. In addition, these interconnected databases will enable researchers to better associate specific genes with agriculturally-important traits and build on genetic advances in one crop to accelerate genetic gain in others.

For major, specialty, and new crops, ARS, in close cooperation with diverse public and private sector collaborators, will improve and broaden the genetic base of U.S. crops to reduce genetic vulnerability.

NP 301 scientists will devise and apply new technologies to develop superior new crop varieties and enhanced germplasm and will accelerate the deployment of high-value traits into breeding populations. New genetic sources of key crop traits will be identified and incorporated into crop breeding lines and gene pools. New breeding theories and strategies that exploit the vast amount of available genotypic data will also be developed to effectively capture the intrinsic genetic potential in germplasm. To do so, innovative tools will be developed for dissecting the architecture of complex crop traits. These tools will be applied to mapping and determining the function of underlying genes so that variation in them, and in linked genomic sequences, can be exploited as more precise genetic markers. This knowledge will also enable molecular and genetic variability to be associated with specific phenotypes to enhance the effectiveness of genomic selection, thereby accelerating and strengthening progress in crop genetic improvement.

Plant breeding has a long history of improving crops through phenotypic or marker-assisted selection, usually in the absence of information regarding underlying genes or gene networks that control key traits, or that determine how plants interact with their environment. Understanding the key biochemical pathways and the underlying controls for plant growth, development, and metabolism has been elusive. However, recent advances in plant molecular biology, genetic engineering, and physiology could create opportunities for improving crops by more precisely and rapidly manipulating the existing variability in plant properties, or by creating new variability when warranted. Knowledge of how to precisely modify biological mechanisms will contribute not only to advances in fundamental plant biology, but will also help identify potential unintended consequences of that manipulation.

In addition to conducting research, ARS and its university cooperators will continue to mentor and train the next generation of crop breeders, geneticists, bioinformaticians, genome researchers, and genetic and genomic resource and information managers. Developing the next cohort of researchers is particularly important, considering the projected strong demands for these scientific personnel.

During fiscal year 2016, this National Program was composed of three Research Components (see below) and their constituent Problem Statements. Notably, these categories do not act as barriers or “stovepipes” that impede research across the National Program. Rather, many of the individual research projects and resources contribute to the goals of several NP 301 Research Components, or even several National Programs:

- **Component 1** – Crop Genetic Improvement (plant breeding, genetic enhancement, molecular marker and trait analyses, nucleotide sequencing, and genetic mapping).
- **Component 2** – Crop Genetic and Genomic Resources and Information Management (conserving a broad spectrum of genetic resources and facilitating their use; maintaining and delivering genetic resource, genomic, and genetic data via databases and information management systems; and devising new analytical tools that compile, dissect, interrelate, manage, and visualize the information contained in large datasets).
- **Component 3** – Crop Biological and Molecular Processes (fundamental – often high-risk – research to generate an enhanced knowledge base and devise superior research tools that ultimately contribute to greater crop productivity and efficiency; better product quality and

safety; improved protection against pests and diseases; enhanced tolerance to abiotic stress; and sustainable practices that maintain or enhance environmental quality).

The following sections contain selected NP 301 accomplishments, presented according to the relevant NP 301 Research Components. These are not all of the NP 301 accomplishments for FY 2016, but rather are selected based on impact and level of contribution to meeting the National Program goals.

Component 1 – Crop Genetic Improvement

High-yielding drought-tolerant soybean cultivar. Drought is a major problem for many crops and has not been thoroughly addressed in soybean research. Drought resistant soybean cultivars are virtually non-existent in the United States, and the first drought-resistant Asian soybean accession from the USDA National Plant Germplasm System (NPGS) was reported only in 1989. ARS researchers in Raleigh, North Carolina, report the incorporation by classical breeding of drought resistance traits into a new high-yielding cultivar ‘USDA-N8002’. This new USDA release traces its ancestry partially to the previously mentioned Asian soybean, and partially to a more recently identified drought-resistant NPGS accession from Nepal. The newly released cultivar exhibits slow, or delayed canopy-wilting, sustained nitrogen fixation during drought stress, and a water-conserving transpiration response when exposed to atmospheric vapor pressure deficit conditions. It has very stable yields over the Southeastern United States in both full season and double cropping production. This new cultivar traces 12% of its pedigree to one NPGS accession and 25% to another, and is thus very diverse and distinct genetically compared to most other cultivars in the southern United States. This new cultivar is not only available for production but also for use as parental stock for commercial breeding programs aimed at breeding native-trait, drought-resistance genes into soybean cultivars. The article describing the germplasm release is being featured in the Crop Science Society of America news magazine, CSA News.

Release of high-phytonutrient potato varieties. Health professionals and consumers are placing increased importance on the nutritional value of foods, and nutrition is also a key component of food security. Potatoes are nutritionally dense crops that are very low in fat while being rich sources of protein, fiber, anti-oxidants, minerals, and calories. ARS scientists in Prosser, Washington, working with collaborators in the TriState Breeding Program, released two new high-phytonutrient potato varieties. “Yukon Nugget” and “Smilin’ Eyes” are yellow flesh potato varieties that have higher yields, improved disease resistance, and greater anti-oxidant concentrations than “Yukon Gold,” which is the standard commercial, yellow flesh potato variety. These new varieties enable growers to produce potatoes that require less applications of chemicals to control disease and meet evolving consumer preferences for nutritional foods, while supporting tens of thousands of potato related jobs in the United States.

Durable sunflower rust and downy mildew resistance. Rust and downy mildew are two of the most devastating diseases of sunflower. In the United States, oilseed sunflower is challenged by a serious foliar leaf rust disease that has been increasingly prevalent in much of the production region, with rapid development of new virulent races. Very few suitable sunflower inbred lines with high levels of rust resistance are available to commercial sunflower breeders. ARS scientists in Fargo, North Dakota, developed and released rust-resistant germplasm derived from the annual crop wild relative

of sunflower that incorporates a single dominant gene with resistance to all known races of North American sunflower rust, with related molecular markers for marker-assisted breeding. In addition, this germplasm also contains a single dominant gene with resistance to all known races of the pathogen causing another devastating sunflower disease, downy mildew, along with molecular markers. Stacking these genes provides the sunflower industry with resistance to multiple pathogens, assuring sustainable sunflower production in the presence of two of the most devastating diseases.

Sequencing the carrot genome. Carrots are nutritionally dense vegetables that are rich sources of fiber, anti-oxidants, and minerals. However, carrot producers in the United States suffer millions of dollars of losses annually due to pathogenic nematodes, and the development of improved carrot varieties has been impeded by a lack of understanding of the carrot genome. ARS scientists in Madison, Wisconsin, led an effort involving 20 scientists from seven countries to sequence the carrot genome. Genes were identified that are involved in nematode resistance, resistance to environmental stresses, and the production and accumulation of phytonutrients. Significant advances were made in understanding the genetic control of orange and yellow pigment development. The improved understanding of the carrot genome and the genetic control of important traits provides breeders with knowledge required to accelerate the development of improved carrot varieties with enhanced disease resistance and improved nutritional qualities, as well as providing genetic tools to identify gaps in the U.S. national carrot germplasm collection that require filling.

New soft white winter club wheat cultivar "Pritchett" released. The club wheat market class represents approximately 8% of the total wheat production in the Pacific Northwest region of the United States, but there are no private or other public sector research programs developing club wheat. Existing cultivars either do not emerge well from deep sowing in dry conditions, are susceptible to preharvest sprouting, or suffer from lower quality at harvest. ARS researchers in Pullman, Washington, in collaboration with wheat breeders from Washington State University, developed and released a new winter club wheat cultivar, "Pritchett." "Pritchett" is resistant to the major diseases of stripe rust and cephalosporium stripe, and moderately resistant to eyespot. The yields from "Pritchett" are significantly better than "Bruehl." In addition, the variety possesses better milling and baking quality than "Bruehl." This release has generated excitement among growers in the drier areas of the club wheat production zone because it has excellent emergence from deep sowing and promises to be a cultivar that can be grown with reduced fungicide inputs, while still producing a high quality, desirable market class of wheat that generates a premium to the grower.

Successful implementation of reverse genetics in soybean. Reverse genetics is the process of discovering the biological function of a gene by modifying or deleting it, then determining what effect the change has on the organism. While gene and RNA sequencing technologies have become routine and inexpensive, there are still many unanswered questions about how the genes function. Simply knowing a gene's function, however, does not translate into useful products, such as improved soybean germplasm, without a way to easily identify usefulness of the genetic variants resulting from the change. Therefore, ARS researchers in West Lafayette, Indiana, and collaborators implemented a method to use high throughput DNA sequencing to identify variants in any gene

from large soybean mutant populations. A non-functional variant of a gene involved in carbohydrate biosynthesis in soybean seeds was discovered. Elimination of this gene resulted in seeds with lower raffinose family oligosaccharide content, which creates a soybean meal from which humans and other monogastric animals (pigs and poultry) can now digest the oligosaccharides. This variant creates a more functional soybean meal for food and feed, is being evaluated in genetic crosses for its impact on carbohydrate composition, and will be useful to soybean breeders for improving soybean meal.

Release of high-yielding and disease resistant sugarcane varieties. The biggest production challenges faced by sugarcane growers in Florida are orange rust and brown rust diseases, which reduce yields and increase production costs because of the need to apply fungicides for disease control. Consequently, the development of new sugarcane varieties with enhanced disease resistance is a priority for increasing crop yields and economic returns. ARS researchers in Canal Point, Florida, collaborated with other researchers and released eight new high-yielding sugarcane varieties that are especially adapted to sandy soils in Florida and have improved resistance to rust diseases. The new cultivars produce high yields while reducing production costs, which results in higher grower profits and supports the economic viability of sugarcane production in Florida.

Identification of lettuce and spinach varieties with tolerance to heat, drought, and salinity. Global warming and climate change pose serious threats to U.S. agriculture and food security. Consequently, the development of crops that can cope with heat, drought, and other environmental stresses may well be the single most important step that can be taken to assure food security under changing environmental conditions. ARS researchers in Salinas, California, screened about 4,000 lettuce and 400 spinach varieties in greenhouse tests and field trials, and identified varieties with tolerance to heat, drought, and salinity. These varieties are useful for growers that produce lettuce and spinach in areas that are prone to these stresses, and for breeders trying to develop new vegetable varieties with enhanced resistance to environmental stresses. These varieties will also help expand the growing seasons for lettuce and spinach in areas where land costs tend to be lower than traditional lettuce and spinach growing areas, such as the San Joaquin, Yuma, and Imperial Valleys of the southwest United States, which will confer hundreds of millions of dollars of economic benefit to these production regions.

“Kardia,” a new food barley cultivar. Increasing the levels of grain beta-glucan in barley is desirable as it is associated with cardiovascular health. Barley bred and grown specifically for food use has therefore received more attention in recent years. The food barley cultivar “Kardia,” developed by researchers in Aberdeen, Idaho, has 40% higher grain beta-glucan and better grain yield than the current industry standard cultivar, “Salute.” This combination of characteristics will increase the efficiency of producing food-grade, high-beta-glucan barley, which will increase producer and processor profitability and increase availability of highly nutritional food for consumers.

Nearly half of maize field genetic variation is determined by the 2% of the genome that regulates genes. Maize is the number one crop grown in the United States. The maize genome is large and complex, so determining what portion of the genome has effects on traits has been challenging. ARS researchers in Ithaca, New York, along with university collaborators, assayed maize to identify the portions of the DNA sequence accessible to proteins that regulate gene expression. Then, using

quantitative genetics, the 2% of the maize genome controlling most field variation was identified. Approximately half of the measured genetic variation could be explained by regions of the genome accessible to gene regulators. This finding and method for identification of functional field variation is a general approach that can be applied to all plants, and it has the potential to accelerate breeding of crops around the world because it reduces the regions of the genome that would have to be examined.

Release of new citrus rootstock with tolerance to Huanglongbing disease (citrus greening).

Huanglongbing disease, also known as citrus greening, is the most economically destructive disease of oranges and other citrus crops in the world. The disease has spread to all citrus production regions of the United States and has reduced orange yields in Florida alone by over 40%. There are no varieties of citrus with resistance to the disease, and no other methods for effectively controlling the disease have been identified. ARS researchers in Ft. Pierce, Florida, identified and released a new citrus rootstock, US-1516, which promotes better tree health and produces higher orange yields than other commercial rootstocks when grown in the Florida central ridge area, which is severely affected by Huanglongbing disease. Rootstock US-1516 provides growers with an important tool to manage Huanglongbing disease that promotes the continued production of citrus fruits in the United States.

A rapid and precise method to identify boxwood plants with resistance to blight disease. Each year, more than 13 million boxwood plants are sold in the United States, making boxwood one of the most popular shrubs in the American landscape. A new blight disease, caused by the fungus *Calonectria pseudonaviculata*, is causing devastating losses to boxwood throughout the northeast and mid-Atlantic United States. Developing disease resistant cultivars of boxwood is the only long-term sustainable solution to this problem, but it has been difficult to rapidly identify disease resistant plants. ARS scientists at the U.S. National Arboretum in Washington, DC, developed a method using detached leaves that can be used to quickly and effectively screen boxwood for blight resistance. The screening method provides plant breeders and pathologists with a means of rapidly identifying disease resistant plants. Resistant plants are used as parents to develop new boxwood varieties with improved blight resistance, which reduces losses to nurseries and the landscape of the eastern United States.

Marker-assisted selection for improving ginning efficiency in cotton. To keep cotton fabrics competitive with synthetic fabrics, the American cotton grower needs to save on production and processing costs wherever possible. It was previously discovered that cotton cultivars differ in how strongly fibers are attached to the seed, and cultivars with reduced fiber-seed attachment force, gin faster, with less energy and fiber damage. ARS researchers in Stoneville, Mississippi, identified cotton cultivars with lower net ginning energy (NGE) requirements and discovered an association between the NGE trait and fuzz percent which estimates the amount of fiber remaining on the seed after ginning. Breeders, being able to quickly and accurately identify cotton lines with lower ginning energy requirements, can develop cultivars that save energy at the gin, as well as provide varieties with fiber that is less prone to damage, as longer, unbroken fiber is highly desired by the textile mills.

Identifying genes in broccoli responsible for heat tolerance. Broccoli is a nutritionally dense food that is a rich source of dietary fiber, protein, minerals, and anti-oxidants. Unfortunately, high temperatures towards the end of the growing season result in reduced yields and lower nutritional quality of the harvested crop. This susceptibility to high temperatures is the primary factor limiting where and when broccoli can be grown, and poor understanding of the genetic control of heat tolerance has impeded the development of improved broccoli varieties. ARS scientists in Charleston, South Carolina, identified four genes that account for up to 60% of the differences between broccoli lines for tolerance to high temperatures. Breeders use this knowledge to search for these genes in other broccoli lines, which accelerates the development of improved broccoli varieties that will extend the growing season, expand production areas, and increase resilience to fluctuating climatic conditions.

Tropical sorghums converted to short stature, early flowering temperate-zone adapted germplasm. Sorghum is an important grain crop in many areas of the United States and other temperate regions worldwide. However, much of the potentially valuable sorghum germplasm is tropical in origin and does not successfully flower and produce seed in temperate environments, making these sources of genetic variability unavailable to many of the world's sorghum producing areas. ARS researchers in College Station, Texas, working with a retired private seed company scientist, used molecular tools in conjunction with classical plant breeding techniques to convert ARS tropical sorghums to short stature, early flowering versions with the objective of making new elite inbreds available to the sorghum industry. Three hundred seventy-five plots of converted germplasm were screened visually by breeders and desirable individuals self-pollinated for the development of higher-producing sorghum inbreds for farmers in the U.S. and worldwide.

Dhurrin, a compound that leads to stay-green sorghum for higher drought tolerance. Post-flowering drought tolerance or stay-green in sorghum is associated with reduced lodging, charcoal rot resistance, increased grain fill, and increased grain yield. Dhurrin is a cyanogenic glucoside produced by sorghum and is generally considered a natural defense compound capable of producing the toxin hydrogen cyanide (HCN) to deter animal herbivory. Recently, ARS scientists from Lubbock, Texas, reported that high levels of leaf dhurrin in grain sorghum genotypes was correlated with post-flowering drought tolerance (stay-green). Additionally, ARS scientists from Lubbock, Texas, discovered that leaf dhurrin level was highly heritable and controlled by the Dhu1 genomic region. Dhu1 is aligned with genes involved in dhurrin biosynthesis. Protein sequence variants found in some of these genes appear to be the cause of the observed differences in leaf dhurrin levels in many sorghum lines that vary in leaf dhurrin content. These discoveries will assist sorghum breeders in the development of more drought tolerant sorghum hybrids.

New genes and enhanced yields from crosses with wild soybean. The wild relatives of soybean are a largely untapped resource for soybean breeding. Some scientists are using wild soybean with limited success, but ARS scientists in Urbana, Illinois, were highly successful breeding with these perennial Glycine species. The ARS team completed two years of testing of the first soybean experimental lines with *G. tomentella* as the female parent, ensuring that the resulting progeny contain the *G. tomentella* cytoplasm. An agronomically improved line was recovered with 22% higher yields than the adapted soybean parent, and was only five days later in maturity. Yield increases of this magnitude over the better parent have not been previously reported in soybean

breeding, even when crossing two adapted parents. To obtain these results with a distant, wild, perennial relative is a remarkable achievement. Additional research is underway to determine the role of *G. tomentella* cytoplasm in this large yield increase. This new discovery provides new yield genes with unique alleles never before used in the North American soybean gene pool.

Genetic analysis of profuse bloom wax leads to identification of genes for wax production in sorghum. An important feature of sorghum that is associated with drought tolerance is the presence of wax compounds that cover and protect the stem and underside of leaves. However, there is lack of genetic information on genes that underlie wax production in sorghum. ARS researchers in Lubbock, Texas, in cooperation with Cold Spring Harbor scientists, identified two genes that underpin profuse wax or bloom of sorghum. This discovery is highlighted in the Journal “The Plant Cell.” Discovery of genes for waxy bloom will allow the manipulation of the trait to improve drought and heat tolerance in sorghum with implications for other cereal crops.

Interspecific sunflower “amphiploid” genetic stocks. Sunflower crop wild relatives include interspecific relatives, containing a large gene pool of 53 different species that possess useful genes needed for maintaining genetic diversity. It is extremely challenging to mine these genes, especially due to incompatibility issues, such as hybridization barriers between cultivated sunflower and the perennial species. Successful hybridization by ARS scientists in Fargo, North Dakota, produced “amphidiploids” containing a full balanced set of chromosomes from both the crop wild relative and the cultivated sunflower, overcoming common fertility problems often encountered when making wide crosses. The team developed six genetic stocks derived from different wild sunflower species. The value of these interspecific amphiploid genetic stocks, is that they can act as a bridge in interspecific gene transfer, allowing for easier backcrossing with the cultivated sunflower to further broaden the genetic diversity of the sunflower crop, as well as to transfer useful target genes for specific traits. The genetic stocks will also allow the development of chromosome addition lines that contain individual wild species chromosomes added to the background of the cultivated sunflower lines, to be used for studying the genetics of the wild species. These amphiploids will give sunflower breeders increased access to more genetic diversity that has been previously extremely difficult to obtain using traditional breeding methods.

New stem rust (Ug99) resistant wheat varieties released in Pakistan. The globally-virulent stem rust race, known as ‘Ug99’ can potentially cause significant yield loss and even crop death. New Ug99 stem rust resistant wheat varieties ‘Borlaug 15’, ‘Insaf 15’, ‘Pakhtunkhwa 15’, ‘Pirsabak 15’, and ‘Ujala 15’ were developed by using Ug99 stem rust resistance genes identified and incorporated by ARS researchers in Raleigh, North Carolina, in collaboration with Pakistani partners. The release of these new Ug99 resistant varieties will aid in achieving national food security.

Release of new sugarbeet breeding line with enhanced resistance to the sugarbeet root maggot. The sugarbeet root maggot (SBRM) is the most destructive insect pest of sugarbeet in the United States. Growers have to make two applications of insecticide to control the pest in highly infested fields, which increases production costs and potentially exposes non-target organisms, including humans, to toxic insecticides. Consequently, the development of new sugarbeet varieties with genetic resistance to the pest is the most desirable method for pest control. ARS scientists in Fargo, North Dakota, released a new sugarbeet breeding line, F1043, which has resistance to the sugarbeet

maggot. Resistance in F1043 is derived from a unique sugarbeet source that is not present in any other breeding lines that are resistant to the sugarbeet maggot. Breeding line F1043 is being used to develop commercially successful varieties of sugarbeet that are resistant to the sugarbeet maggot, which will increase profitability and promote more environmentally sustainable production of sugarbeets in the United States.

Maize landraces (farmer varieties) carry tremendous variation necessary for future adaptation to changing environments. Maize landraces are very diverse and have adapted to many different environments. Identifying the genetic control of this variation, however, has been a slow and tedious process. With new genomic tools and experimental designs, ARS researchers in Ithaca, New York, collaborated with the International Maize and Wheat Improvement Center (CIMMYT) to identify and catalog the genes controlling the large scale adaptation patterns of maize across the Americas. This efficient approach to tap landrace genetic diversity can be applied to numerous other traits and species, and will likely be a model experimental design for rapidly accessing natural diversity. Additionally, it provides the knowledge necessary to move key traits between varieties adapted to different latitudes.

New high-yielding “low phytic acid” barley cultivar “Harriman” released. The problem with grain and legume-based feeds used in non-ruminant animals (poultry, swine and fish) is that nearly 75% of the total phosphorus is in a chemical form called phytic acid, and non-ruminants cannot efficiently digest phytic acid. As a result, if the expensive enzyme additive “phytase” is not used, these livestock excrete most of the seed-derived phosphorus they consume, resulting in high waste phosphorus that contributes to water pollution. Also, excretion of phytic acid phosphorus contributes to poor mineral (iron, zinc, magnesium and calcium) levels which results in reduced overall animal health and productivity. ARS geneticists and breeders in Aberdeen, Idaho, have developed a low-phytic acid barley cultivar called “Harriman,” which has excellent yields. Use of “Harriman” barley as the grain component of a feed would result in healthy and more productive animals, resulting in more “meat per unit of feed,” while at the same time contributing to sustainability via more efficient use of the increasingly expensive feed component phosphorus and via reduced environmental impact of livestock production.

Identification of markers for use in selection for barley stripe rust resistance. Barley stripe rust can cause severe losses in yield and quality of barley, but it does not reliably occur in the breeding nurseries used for selection of new lines. Therefore, breeding progress can more quickly and efficiently happen if molecular selection can be made regardless of whether the disease occurs in any particular year. ARS researchers in Aberdeen, Idaho, and in Pullman, Washington, in collaboration with scientists at the University of California, Davis, California, and Oregon State University, Corvallis, Oregon, made crosses with a resistant landrace held in the National Small Grains Collection, mapped four genetic loci associated with resistance, and identified molecular markers that can be used for selection in the absence of disease. This information will be useful for the development of superior, stripe rust resistant varieties.

Sugarbeet disease resistance genes identified and characterized. The sugarbeet industry in the United States is valued at over \$2 billion annually. Sugarbeet producers suffer millions of dollars of losses annually to a range of diseases and pests, among which the sugarbeet maggot is especially

destructive. ARS scientists in Beltsville, Maryland, discovered and characterized several disease and pest resistant genes in sugarbeet, and also identified genes in the sugarbeet maggot that are responsible for disease development. The DNA sequences of the sugarbeet genes are used by plant breeders and pathologists to identify new sources of disease resistance in sugarbeets and to devise improved strategies for the development of improved sugarbeet varieties that will benefit farmers by increasing sugar yields for human consumption.

Identification of Osmanthus varieties with tolerance to cold. Osmanthus species are flowering, evergreen shrubs or small trees that are popular throughout the southern half of the United States. Little is known about the relative cold tolerance of different Osmanthus species, which leaves nursery growers with limited information for choosing Osmanthus to grow in their areas and results in considerable losses throughout the United States due to cold stress. ARS scientists in McMinnville, Tennessee, evaluated sixteen Osmanthus varieties in the field for cold tolerance and identified both highly tolerant and highly susceptible varieties. This information provides nursery growers with guidance to assist them in making data-driven decisions on what varieties are suitable for specific growing regions. The cold tolerant Osmanthus varieties are also being used as parents to develop new varieties that are extremely tolerant of cold.

Identification of a novel gene for resistance to tan spot in wheat. Tan spot is a devastating fungal disease of wheat in many wheat-growing regions around the world. Previous research has uncovered several genes in wheat that govern low-levels of tan spot resistance, or resistance to only specific strains of the fungus. ARS researchers in Fargo, North Dakota, identified a new tan spot resistance gene in a wild relative of wheat that conditions high-levels of resistance to all known strains of the tan spot fungus. The deployment of this gene into commercial wheat varieties should greatly reduce the economic losses attributed to this disease.

“Cool” sorghums, diverse mapping populations with cold tolerance traits, are now available through the Germplasm Resources Information Network (www.ars-grin.gov/npgs). The United States is the leading sorghum producer in the world, but early season planting and stand establishment is hampered by cool soil and ambient temperature in the U.S. sorghum belt during late March to early April. Planting at early season is needed by farmers to adapt to climatic changes, avail of spring moisture, and aid in realizing higher yield using longer growing season cultivars. ARS researchers in Lubbock, Texas, developed, released, and characterized two recombinant inbred populations that exhibit an overall increased germinability at cooler soil and ambient temperatures between the temperatures of 55-58F (14-16C). The populations offer wide diversity for improvement of cold tolerance, seed quality, and desirable agronomic qualities. The population was distributed to university breeding programs for evaluation and used as a parental resource for breeding for early season cold tolerance.

Corn gene that reduces both insect and corn ear mold growth discovered. Corn ear molds can produce toxins harmful to people and animals, causing hundreds of millions of dollars in losses in the United States alone. Plant resistance is an economical means to reduce corn ear damage caused by ear rots, but there continues to be a need to determine what genes are involved in producing resistance. A gene coding for a small protein from a corn inbred resistant to an ear rot fungus line was evaluated for its resistance role by ARS scientists in Peoria, Illinois. When introduced into maize

cells, cell clumps that had the gene were not colonized as heavily by a representative fungus compared to cell clumps that did not contain the gene. Insects that fed on the cell clumps containing the gene gained less weight than those that fed on cell clumps not containing the gene, which appears to be the first discovery of activity of this gene type against insects. This knowledge can be used to guide breeding for ear rot resistance in crop plants, thereby enhancing yield, quality, and safety.

Spectral reflectance used as a selection tool for drought tolerance by breeders. The use of spectral reflectance indices can assist breeders to conduct selection for drought tolerance in wheat. While selection for productivity in dry environments is a goal of many breeding programs, genetic gain from selection in dry locations is low because of environmental variability and low yields. ARS researchers in Pullman, Washington, collaborated with colleagues at Washington State University to identify hyperspectral indices that can be used to provide additional information about plant response to drought and whether these indices could serve as indirect selection tools for drought tolerance. The positive associations that we detected between regression models using hyperspectral data and grain yield can overcome phenotyping bottlenecks and allow us to characterize larger germplasm collections to identify new sources of resistance to drought.

Sorghum transcription factor that controls lignin synthesis discovered. Lignin is the major structural component of plant cell walls whose presence and composition influences the usability of plant biomass for the production of biofuels and other natural products. ARS scientists in Lincoln, Nebraska, discovered a Myb transcription factor, SbMyb60 that activates synthesis of lignin in sorghum. Experiments showed that overexpression of SbMyb60 activated nine genes in the lignin biosynthesis pathway, and led to increased lignin levels in sorghum biomass. SbMyb60 is the first activator of lignin synthesis to be identified in grasses. SbMyb60 represents a tool to modify plant cell wall composition and the potential to improve biomass for renewable uses in sorghum and other bioenergy grasses.

Development of molecular markers for the stem rust resistance gene Sr47. The wheat gene Sr47, which was previously transferred from goatgrass into durum wheat, is highly effective in conferring resistance to all strains of the fungal pathogen that cause the disease stem rust. ARS researchers in Fargo, North Dakota, and their collaborators at North Dakota State University developed four new molecular markers that are tightly associated with Sr47. These new markers will greatly facilitate the transfer and deployment of Sr47 in durum and bread wheat breeding programs, which will lead to the development of stem rust resistant varieties.

Identification of a novel disease susceptibility gene in wheat. Septoria nodorum blotch (SNB) is a severe fungal disease of wheat worldwide. ARS researchers in Fargo, North Dakota, identified a new gene in wheat that makes it susceptible to SNB. They also developed molecular markers that can be used by wheat breeders to monitor the presence of the gene among their breeding lines, which will help them to eliminate this gene from varieties to be released to wheat growers.

Component 2 – Crop Genetic and Genomic Resources and Information Management

GRIN-Global information system implemented in the U.S. National Plant Germplasm System and international genebanks. Researchers and breeders require access to comprehensive descriptions of plant germplasm's traits to accelerate progress in crop genetic improvement. ARS software developers and plant germplasm curators in Beltsville, Maryland, and Ames, Iowa, completed the first major update in 20 years for the Germplasm Resources Information Network (GRIN), the global standard for managing and delivering information associated with plant germplasm. The new "GRIN-Global" was implemented in late 2015 in the U.S. National Plant Germplasm System, and was also adopted by 6 international genebank systems. During 2015-2016, GRIN-Global provided breeders and researchers with access to key descriptions for plant germplasm via more than 1.5 million individual web page visits, and facilitated distribution of more than 240,000 plant germplasm samples domestically and internationally. Collectively, distribution of germplasm and associated information constituted a technology package that contributed significantly to strengthening crop breeding and research in the U.S. and internationally.

New genomics powered database tools address key breeder needs for maize (corn) and rice. ARS scientists in Ames, Iowa, and Stuttgart, Arkansas, developed three new bioinformatic tools to accelerate maize and rice breeding and research. First, the MaizeGDB Genotype Visualization Tool enables maize researchers to survey the genomes of 17,000 maize lines and display all DNA differences in any region of their respective genomes. The MaizeGDB Pedigree Viewer enables breeders to visualize pedigree relationships between maize germplasm lines and identify the best lines genetically as parents for crossing. Combined with knowledge of maize genome functional variation in MaizeGDB, these tools enable breeders to select maize lines to cross to improve germplasm for researchers and farmers. For rice breeders, ARS scientists in Stuttgart, Arkansas, created Ricebase, a new database that integrates rice genetic variation, pedigrees, and whole-genome-based data, thus accelerating the discovery and design of molecular markers for marker-assisted breeding and selection, and thereby enabling rice breeders to go faster more efficiently. ARS bioinformaticians continue to develop powerful new tools that enable maize and rice researchers to leverage USDA's open germplasm, open data, and open information for crop improvement.

Peanut genomes sequenced. ARS scientists at Stoneville, Mississippi; Ames, Iowa; and Tifton, Georgia, and partners, sequenced the genomes of the two wild relatives of cultivated peanut whose ancestors merged to form a new species, which was then domesticated to become modern cultivated peanut. An important finding of this research is that the unusual hybridization of these two species was likely the direct result of early agriculturalists in South America. The genome sequences from these wild species thus comprise essentially all of the genetic material in the modern cultivated peanut. This research will be used by plant researchers and breeders to more efficiently select improved peanut varieties, and to speed development of varieties that are well suited for growing in various regions of the world. The genome sequence has already been useful in helping identify mechanisms for resistance to root-knot nematodes and rust (a fungal disease), which are serious challenges for many peanut farmers. This knowledge will be used to breed better peanut lines.

Genetic markers for accelerating lentil genetic improvement. U.S. lentil production has increased more than 20% because of high export demand and recognition of its health-promoting qualities. But little information about the genetic diversity in this crop and its association with ecological adaptation has been available to breeders. ARS researchers in Pullman, Washington, and their international cooperators, analyzed more than 300 genebank samples with more than 1,000 genetic markers and identified specific agroecological zones containing much lentil genetic diversity. Those findings yielded information valuable for selecting superior breeding stock and guiding lentil breeding to increase yield and product quality to meet the U.S. domestic and international market demands.

New method for assessing through historical records the loss of crop genetic diversity. The popular press periodically cites as evidence for loss of crop genetic diversity that fewer named crop varieties are available now as compared to the past. ARS researchers in Colorado developed a novel approach to test that claim. They first assessed the importance of historical U.S. apple cultivars based on how frequently they were mentioned in historical records, such as seed catalogs and county fair notices, during 1736-1909. They determined that nearly 70% of the important historic U.S. apple cultivars and their constituent genes are currently available from the ARS National Plant Germplasm System genebank, and an additional 20% are available from other collections. Thus, the first application of this new method demonstrated that most of the key U.S. historic apple cultivars are currently available. This method also provides a valuable tool for identifying specific cultivars to safeguard in genebank collections, making additional genetic diversity available to producers, researchers, and breeders to enhance global food security.

Genetic markers for accelerating pineapple genetic improvement. Pineapple, one of the most valuable crops grown in Hawaii, is also the third most important tropical fruit crop globally. Pineapple production in Hawaii and internationally is continually threatened by diseases, pests, and production inefficiencies. Pineapple breeders require estimates of pineapple genetic diversity and access to new horticultural traits to maintain this crop's economic viability. ARS researchers in Hilo, Hawaii, and in Beltsville, Maryland, developed hundreds of new DNA genetic markers which breeders are applying to evaluate pineapple more efficiently for new horticultural traits, and to identify the genes governing those traits. Furthermore, the genetic markers improve the efficiency of pineapple genetic resource management at the Hilo genebank by identifying undesired duplicate samples and genetic gaps in the collection which are priorities for future germplasm acquisition.

New genetic analysis of an important traditional cacao variety from Peru. Cacao, the source of chocolate, is a multi-billion dollar international commodity grown by several million small farmers in tropical developing nations of Latin America, Asia, and Africa. Furthermore, U.S. cacao production is expanding in Hawaii and Puerto Rico. Threatened by many virulent diseases, damaging pests, and the effects of climate change, cacao farmers require sturdier trees with inherent resistance to pests and diseases, plus high yields and fine cocoa quality. ARS scientists in Beltsville, Maryland, and their Peruvian collaborators analyzed the genetic diversity in "Piura Porcelana," a traditional cacao variety from Peru. They confirmed the genetic uniqueness of this variety, which has a distinct flavor in demand by high-end international cacao markets. Based on this new genetic information, this variety was collected from the field and safeguarded in Peru's germplasm collection, thereby filling a

diversity gap in the cacao germplasm collection and also supporting on-farm conservation and sustainable use of valuable cacao genetic diversity.

Improving the soybean genome map. The DNA sequence of the soybean genome was published in 2010. ARS scientists in Beltsville, Maryland, provided the genetic map that allowed the segments of DNA sequence to be “anchored” to positions along the 20 soybean chromosomes. Because the number of DNA mapping markers were limited at the time, some of the segments of DNA could not be properly oriented along the soybean chromosomes, and some segments did not contain a DNA marker and therefore could not be positioned in the soybean genome sequence. ARS scientists in Beltsville, Maryland, discovered 37 regions in the 2010 version of the soybean genome sequence where the order of the DNA in the genome sequence needed to be corrected. Furthermore, 28 DNA fragments that could not be determined in 2010 were accurately oriented in the newest version of the soybean genome. The new and improved version of the soybean genome sequence will help breeders at universities, government agencies, and private plant breeding companies identify genes controlling seed yield, seed quality, and resistance to biotic or abiotic stresses.

New physical maps of the wheat genome developed. Several characteristics important for wheat grain yield are encoded by genes that are mostly inaccessible to breeders because they are located in genomic regions with low genetic recombination. Mapping technologies that rely on physically breaking chromosomes can provide much better resolution in low recombination regions than those that rely on genetic recombination. ARS scientists in Albany, California, in collaborations with scientists from both ARS and university laboratories, developed three wheat maps from deletion mutants and radiation-treated hybrid cell populations. The utility of these maps was validated by using them to isolate a novel gene that mediates the genetic compatibility between the nucleus and mitochondria in wheat cells. The availability of physical maps that are independent of genetic recombination will accelerate breeder improvements in wheat productivity and utilization.

Movement of genetic information captured in grapevine. Grafting has been widely practiced for centuries for the propagation and production of many vegetable and fruit crops including grapes. However, the underlying mechanism for how two grafted partners communicate to produce a successful graft are largely unknown. ARS researchers in Geneva, New York, identified 3,000 genes whose genetic code is transported across graft junctions via messenger RNAs (mRNA) in the field. While many biological processes and mechanisms involved in such mRNA movement are yet to be elucidated, one obvious benefit from such exchange of mRNAs between two genetically distinct graft partners would be increased diversity of the genetic information accessible to both shoots and roots as a consequence of grafting, which in turn can make the whole plant more productive and adaptive to disease and climate variation; thus, these findings have important practical applications for grape breeding.

Resistance to aphids genetically mapped in black raspberry. Most of the U.S. production of black raspberry (annual farmgate value of \$16.8 million) is centered in the Pacific Northwest. The current standard commercial black raspberry cultivar is highly susceptible to infestation by the North American large raspberry aphid, which is a vector for the Raspberry Mosaic Virus complex that causes rapid declines in plant health, necessitating re-plant of black raspberry fields after only three to four growing seasons. ARS researchers in Corvallis, Oregon, have genetically mapped a region of

the black raspberry genome associated with host-plant resistance to aphids. Mapping this resistance trait has elucidated this trait's genetic control, enabling breeders to more effectively identify and select aphid-resistant black raspberries.

Component 3 – Crop Biological and Molecular Processes

Reduced-allergen wheat. Wheat flour is one of eight foods responsible for 90% of the food allergies in the United States. ARS scientists in Albany, California, created transgenic wheat lines in which the omega-5 gliadins, the major sensitizing allergens in a severe food allergy called wheat-dependent exercise-induced anaphylaxis (WDEIA), were significantly reduced in the flour without adverse effects on flour quality. In collaboration with scientists at the French National Institute for Agricultural Research (INRA), the allergenic potential of these lines was evaluated using sera from a collection of WDEIA patients. Most patients showed strong reactivity to the omega-5 gliadins in flour from the non-transgenic control and little or no reactivity to omega-5 gliadins in the transgenic lines, indicating that the transgenic lines could be considered reduced-allergen. However, low levels of reactivity with other gluten proteins were also observed in the transgenic lines. While flour from the transgenic lines would not be suitable for individuals diagnosed with WDEIA, introduction of wheat lacking omega-5 gliadins could reduce the number of consumers who become sensitized to these proteins and decrease the overall incidence of this food allergy.

“Proxy Selection,” a new approach for altering gene expression in maize. Altering expression of genes allows development of crops with improved agronomic performance and reduced environmental impact. Several approaches using biotechnology to alter gene expression have been developed; however, some of these methods rely only on transgenes. ARS researchers in Ames, Iowa, have developed an approach called Proxy Selection in which traditional breeding methods are used to select for altered expression of a transgene. As a consequence of this selection, the expression of an endogenous gene that is similar to the transgene is altered in a predictable way as well. The changes to endogenous gene expression are maintained in the absence of the transgene. Thus, researchers have demonstrated a new method to produce non-transgenic plants with specific alterations in gene expression. This method uses a combination of biotechnology and traditional breeding and may have utility in developing improved non-transgenic crops.

Unraveling the genetic control of nonhost resistance to wheat stem rust. Global wheat production is threatened by new forms of wheat stem rust that defeat many existing stem rust resistance genes. One promising strategy for protecting wheat from stem rust involves a poorly understood type of resistance called nonhost resistance. Using the model grass, *Brachypodium distachyon*, a wild relative of wheat that is a nonhost for wheat stem rust, the genetic control of nonhost resistance was determined to involve genes located at seven chromosome locations. This finding provides the first step toward isolating nonhost resistance genes in *Brachypodium* for use in constructing a new and durable layer of resistance to stem rust in wheat, and in turn increasing food security by protecting global wheat production.