

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

National Program 301 • Plant Genetic Resources, Genomics, and Genetic Improvement

FY 2018 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 2018, 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*
- *Component 2 – Crop Genetic and Genomic Resources and Information Management*
- *Component 3 – Crop Biological and Molecular Processes*

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 2018, but rather are selected based on impact and level of contribution to meeting the National Program goals.

Component 1 – Crop Genetic Improvement

Deciphering the genetics of fast cooking dry beans. Cooking time is an important consumer trait in dry bean, and long cooking times discourage greater utilization of beans. ARS scientists in East Lansing, Michigan, previously discovered germplasm that significantly reduces cooking time, but the genetic control of the trait was unknown. The scientists developed a population from a cross between a slow cooking bean and a fast cooking bean. The cooking times for individuals in that population ranged from 21 - 135 minutes. The beans were grown in Tanzania under temperate and hot humid tropical climate for two field seasons, and scientists observed that beans grown in the hot humid zone took 15 minutes longer to cook than those grown in the temperate zone. They determined cooking time was strongly influenced by genetic factors that were controlled by interactions of four different regions of the genome. After tagging those four regions with DNA markers, the researchers identified several bean lines containing genes from all four regions, which made them cook 16 minutes faster. This work demonstrated the potential value of integrating cooking time into

breeding programs and the value of using molecular markers to help select for fast cooking beans. Breeders are now using these lines and markers to develop fast cooking beans.

Novel hard-white waxy winter wheat. Waxy wheats can be used for novel whole grain products and are a promising substrate for ethanol production. Hard-red winter wheat and hard-white winter wheat are both waxy wheats grown in the Great Plains region. White wheats do not contain the condensed tannins that confer the red grain color and have some potential advantages over red wheats, including wider application in non-pasta noodles and steamed wheat products, and the production of higher extraction flours. The lack of condensed tannins imparts a slightly sweeter, less bitter taste to whole grain products; in addition, white wheat products can be significantly brighter in color and have greater appeal to consumers than products made with red wheats. To fill potential demand for a hard-white waxy wheat adapted to Great Plains production, ARS scientists in Lincoln, Nebraska, in cooperation with the University of Nebraska, developed and released ‘Matterhorn’, the first U.S. hard-white waxy high yielding winter wheat.

Reducing Tree Fruit Production Costs Through Architectural Design. The major cost of fruit tree production for growers is managing the shape and size of trees through grafting, training, and/or pruning. The ability to breed trees with simpler and more easily-managed shapes would lead to substantial savings to growers and consumers, but more information is needed about how tree branches adopt specific growth orientations. ARS researchers in Kearnesville, West Virginia, discovered a gene responsible for branch orientation in peach. A mutation in a gene they dubbed WEEP changed the way the peach branches respond to gravity and resulted in branches growing down instead of up. The researchers also determined a set of previously-discovered related genes that control branch growth direction is influenced by gravity, light, and photosynthesis. Collectively, this information and the associated technologies (U.S. Patent 9,371,536) offer new strategies for developing plants and trees with shapes that are easier to manage; the advances have the potential to ultimately boost crop yields and reduce labor costs and chemical spray use.

Analyzing Genome Sequence Architecture by Machine Learning. There are more than two billion base pairs in a genome; they are a complex mixture of “readily accessible” regions that can interact with a wide range of proteins and regions that are not highly “accessible” for protein interactions. The interactions between these regions control how and when genes are turned on and regulated. ARS researchers in Ithaca, New York, and their collaborators constructed machine learning models for understanding natural written language and applied them to understand the language of DNA. These language-based models can predict DNA structure accurately between 95 and 99 percent of the time. This general approach can be applied to learning how aspects of the genome function and help identify single DNA changes that contribute to crop yield losses.

New ‘Contender’ high oleic peanut cultivar increases profits for southwest U.S. producers. Virginia-type peanuts are grown on approximately 35 percent of peanut acres in Oklahoma and in Texas for the export market, which, unlike domestic markets, require larger pods, kernels, and seeds. The high oleic cultivar ‘VENUS,’ which was released by ARS in Stillwater, Oklahoma, in 2016, is produced and marketed domestically, but it does not consistently meet export market preferences for extra-large kernels, pods, and seeds. In 2018, ARS scientists developed and released the peanut cultivar ‘Contender’ for the U.S. export market. ‘Contender’ is unique among cultivars developed for southwestern U.S. production because of its enhanced market characteristics, including large and bright pods (averaging 9 pods per ounce) and large seed size (averaging 104 g/100 seed). ‘Contender’ was developed for optimal performance in Oklahoma and Texas, and its production and export is expected to contribute \$20 million annually to the U.S. economy.

Novel double haploid method produces fertile plants from interspecific sunflower crosses. Sunflower, an important oilseed crop, produces oil that is high in nutritional value for human consumption. Wild sunflower species are known to possess many unique genes for sunflower improvement, but transferring genes from wild species into cultivated sunflower is restricted by cross incompatibility and hybrid sterility, and some crosses between species are sterile and cannot produce seed. ARS scientists in Fargo, North Dakota, developed a tissue culture method of directly producing plants from the tubular flowers of a cross between cultivated sunflower and wild relatives. Plants generated from this tissue culture system produced the same chromosome number and phenotype as their parents. This discovery provides a new method to produce large numbers of fertile sunflower plants derived from crosses with wild species and is helping scientists and breeders overcome incompatibility barriers for transferring useful traits from wild relatives into cultivated sunflowers.

Transfer of a major gene for scab resistance from bread wheat into durum wheat. U.S. durum wheat production has been seriously jeopardized by wheat scab since the early 1990s. However, durum cultivars with high levels of scab resistance have not been available due to limited sources of scab resistance in durum germplasm. ARS researchers in Fargo, North Dakota, successfully transferred a major gene for scab resistance from bread wheat into durum wheat using multiple backcrosses and selections. The durum line carrying the scab resistance gene is being used by U.S. durum wheat breeding programs to develop new durum varieties and adapted germplasm with scab resistance.

New barley varieties for food and craft brewing. Producers need new opportunities to increase the value of commodity grains such as barley. ARS researchers in Aberdeen, Idaho, and University of Idaho collaborators developed 'Goldenhart,' a new two-rowed, spring hull-less food barley with high beta-glucan content, and 'Gemcraft,' a two-rowed, spring malting barley. 'Goldenhart' has shown better yield under irrigated conditions compared to other high beta-glucan barley varieties. Additionally, 'Gemcraft,' which was developed using a novel collaborative model with craft brewers who only use premium barley malt, has similar or higher yields than other malt barley varieties. 'Goldenhart' and 'Gemcraft' will contribute to producer and brewer profitability by providing an in-demand commodity crop option.

Release of TifNV-High O/L, a new peanut cultivar for the southeastern U.S. region. Tifguard, developed by ARS scientists in Tifton, Georgia, and released in 2008 was the first peanut variety with resistance to both the peanut root-knot nematode (PRK) and tomato spotted wilt virus (TSWV), but it did not contain the high oleic trait, which the industry now desires. ARS researchers in Tifton, Georgia, developed TifNV-High O/L, a new peanut cultivar that was released in 2018. TifNV-High O/L has a high level of resistance to peanut root-knot nematode (PRK) and tomato spotted wilt virus (TSWV) and contains a high ratio of oleic acid to linoleic acid, which is highly desirable to the peanut industry. TifNV-High O/L will be valuable for growers who have problems with nematodes and TSWV, and to peanut product manufacturers who prefer high oleic varieties. The cultivar's resistance to TSWV is estimated to save growers approximately \$25 million annually, and its PRK resistance is estimated to save growers \$44 million; additional savings of up to \$100 per acre will result from reductions in fungicide treatments.

Two new sugarcane aphid resistant sorghum lines released. Sugarcane aphids (SCA) have recently become a major pest of sorghum and threaten all U.S. sorghum production, so new SCA-tolerant sorghum breeding lines are urgently needed. ARS scientists in Lubbock, Texas, bred and publicly released two SCA resistant sorghum breeding lines with high grain yields and other favorable agronomic traits. The two lines have been transferred to five seed companies and are currently being evaluated for breeding hybrids in Texas and Kansas grain sorghum performance trials.

Designing soybeans for aquaculture. The most valuable component of soybean seed is its high protein meal, but its use as a feed in aquaculture is limited because it also has components that reduce efficient digestion. ARS researchers in Columbia, Missouri, collaborated with a commercial partner and found genetic processes in seed composition traits that reduce the digestibility of soybean meal by fish. They identified a specific combination of two genes that nearly eliminates a group of anti-nutritional traits typically present in soybean meal, which significantly improves options for using soybean meal as fish food in aquaculture systems. The ARS scientists then developed molecular markers to efficiently select for this trait in soybean breeding programs, and this technology was used by a private soybean seed company to develop and release soybean varieties with the improved seed trait. This collaboration resulted in a joint U.S. patent and the ultimate commercialization of new higher value soybean varieties by the seed company. More than 7,000 50-pound units of seed have been sold during the first two years of commercialization. This research created a high value soybean meal especially for aquaculture, but it can also be used by other livestock industries where soybean meal is incorporated into feed formulations to help ensure a sustainable food supply.

Release of high-antioxidant ‘Scarlett’ rice. The outer bran layer of the rice grain contains most of the nutritional value of the grain, while the interior endosperm is primarily composed of starch. Generally, rice varieties with purple or red brans have compounds that offer more nutritional benefits than brown rice. ARS researchers at Stuttgart, Arkansas, and Cornell University developed ‘Scarlett’ rice, a variety that contains high levels of lipophilic antioxidants and polyphenols in its red bran. ‘Scarlett’ rice will benefit rice growers because of its high yield potential when grown in the southern United States; its nutritionally superior red bran will also be appealing to consumers in high-value markets.

Completion of hop draft genome with gene annotations. Hop breeding is hindered by a lack of information on gene families, promoters, and transcription factors associated with economically important traits. Previously published hop genomes were incomplete and missing up to 33 percent of the estimated hop genome and the genes in these missing regions. ARS scientists in Corvallis, Oregon, along with collaborators at Oregon State University, Hopsteiner Inc., and Pacific Bioscience Inc., completed sequencing and assembly of the complete (2.8 Gigabase) genome. Researchers also identified the location and plausible function of genes that were added to the genome. Scientists now have the capability of determining and identifying which genes or gene families are expressed during pathogen attack, hop cone formation, and plant growth, with new gene expression studies currently underway. These new research abilities enable hop breeders to more quickly develop improved cultivars that address industry needs.

Master regulators of powdery mildew resistance. Understanding how plant pathogens manipulate their hosts will enable geneticists and breeders to promote more stable and more efficient crop production. ARS researchers in Ames, Iowa, partnered with bioinformatics scientists at Iowa State University to discover master regulators of plant disease resistance. Two of these regulators control the output of 961 and 3,296 “worker” genes, respectively. Moreover, of the 961 genes regulated during the early stages of attack, more than 30 percent of these are repurposed as infection progresses. Thus, these genes are part of an immune complex that is activated by multiple signals and encodes proteins functioning together to achieve immunity in response to different pathogen isolates or infection stages. This discovery of a conserved core of genes that can be activated by known molecular signals offers new mechanisms to deploy in crop protection.

Release of Cotton Breeding Information Management System. The cotton breeding and research community has lacked a secure and comprehensive online accessible breeding data management and analysis system. ARS scientists in College Station, Texas, in collaboration with Cotton Incorporated and Washington

State University, developed a Breeding Information Management System (BIMS) in the CottonGen database. The newly developed module enables cotton breeders to create and manage access to their private breeding programs; upload phenotypic data from the Field Book App or Excel templates; generate input files for Field Book; archive their entire data in the BIMS; search and filter accessions/lines by name, trial, location, cross, parent, and traits; and perform basic statistical analysis. With the release of BIMS, cotton breeders can now manage their own breeding data and analyze them with CottonGen's publicly available genomic, genetic, and breeding datasets much more effectively and efficiently, thus expediting development of new and improved cotton types for profitable use by U.S. farmers.

Tomato nutritional improvement. Tomatoes are among the most widely consumed fruit in the United States and are central components of many home gardens. They are important sources of dietary carotenoids including the antioxidant lycopene (which give tomatoes their characteristic red color) and beta-carotene, which our bodies convert to the necessary nutrient vitamin A. ARS researchers in Ithaca, New York, demonstrated that a protein from tomato originally identified in orange colored cauliflower provides a crucial regulatory step in limiting the synthesis of carotenoids in tomatoes. Expression of this protein during early fruit development resulted in accumulation of carotenoids (lycopene and beta-carotene) prior to ripening initiation and resulted in higher ripe fruit carotenoid levels. No changes in other ripening parameters were observed. These results suggest that the gene encoding this protein can be manipulated via traditional breeding or targeted genetic engineering to improve nutrient and visual quality in tomato and additional fruit crops.

Mapping genes that govern sunflower defense against insect pests. Glandular trichomes are a type of plant hair that often contain chemicals that repel or kill insects. Previous research shows larvae of the sunflower moth, a flower- and seed-feeding pest, are repelled or stunted by chemicals extracted from sunflower glandular trichomes. Sunflower lines vary greatly in the number of glandular hairs they produce, which indicates these traits are genetically diverse. ARS scientists in Fargo, North Dakota, developed a mixed sunflower parental population that contained plants with a variety of glandular trichomes to find the genes that determine glandular trichome number. They identified two significant genetic markers for those traits and found that genes located close to both markers resembled the genes known to contribute to trichome development in other plant species. Identifying these markers provides a way for breeders to quickly and easily incorporate genetic traits that enhance glandular trichome levels into any sunflower line and improve insect resistance in sunflower hybrids.

Discovery of genes involved in crop thermotolerance. Rising air temperatures could threaten plant chloroplast thermostability and photosynthetic function, both of which are critical for high crop productivity. ARS scientists in Lubbock, Texas, used the experimental plant *Arabidopsis* to describe how the protein FtsH11 maintains photosynthetic efficiency at elevated temperatures. This same protein was then studied in a sorghum mutant library to identify a similar mutant protein, sbFtsH11, which was found to have similar functions conveying thermotolerance. This work establishes a new functional mechanism that directly impacts crop thermotolerance and could enable direct manipulation or improvement of thermotolerance by breeding or engineering this trait into crop plants.

Estimating fiber quality from hand-harvested bolls during cotton breeding. Cotton, the source of the most valuable "natural" fiber, is a key U.S. crop with a production value of \$7 billion in 2017. The quality of the cotton fiber determines its value, but its fiber quality varies more than synthetic fibers precisely engineered to meet consumer textile demands. To breed cotton with more uniform fiber quality, improved methods are needed for measuring that quality from breeding plots. ARS scientists in College Station, Texas, and Texas

A&M AgriLife Research collaborators identified the method for selecting hand-harvested bolls that most accurately represents the fiber quality in bolls picked by mechanical harvesters. Cotton bolls harvested from the top half of the plant generally have lower fiber quality than bolls harvested from the bottom half of the plants, so obtaining samples that combine bolls from all positions on the plant provides the most accurate estimates of fiber quality for cotton breeding. These improvements in sampling will help producers and breeders streamline the estimation of fiber quality.

Low phytic acid (LPA) wheat germplasm released. Phytate reduces the bioavailability of minerals in wheat for livestock and humans, but low-phytic acid (LPA) varieties of wheat can reduce phytate concentrations by one-third. ARS scientists in Lincoln, Nebraska, used wheat lines carrying an LPA trait and Nebraska winter wheats to develop novel wheat breeding stock. Multi-location grain yield testing and selection for the LPA trait resulted in the identification of eight LPA breeding lines suitable for production in the U.S. Great Plains. There were no significant overall differences in grain yield, grain volume weight, and grain protein concentration between the LPA lines and the control lines, and the LPA lines averaged 18 percent more zinc than the controls. These results indicate LPA wheat lines could potentially be developed as high-yield cultivars with high mineral and low antinutritional compound concentrations. Eight LPA germplasm lines were released and deposited in the USDA-ARS National Small Grains collection for use by wheat breeding programs across the globe.

Impact of ARS dry bean breeding program at Prosser WA. Pinto bean is the most important market class of bean in North America with 2015 U.S. production valued at \$280 million. U.S. bean growers want cultivars with early maturity and disease resistance, and 31 enhanced dry bean germplasm lines released by ARS researchers in Prosser, Washington, provided public and private breeders with exceptional parental material for developing new and improved cultivars. Several releases from public and private bean breeding programs in 2016-2018 have been documented. Three pinto bean cultivars—'Blackfoot,' 'Nez Perce,' and 'Twin Falls'—were released in 2017 by the University of Idaho to provide growers with higher yields, early maturity, and exceptional drought tolerance; all three lines contain in their pedigree the USDA line USPT-CBB-1, released by ARS in Prosser. The cultivar 'Twin Falls' also contains in its pedigree the USDA release USPT-ANT-1. The cultivars 'Red Cedar,' a red kidney bean, and 'Cayenne,' a small red kidney bean, released in 2018 from Michigan State University, provide higher yields with improved disease resistance, and contain in their pedigree USDA K-CBB-15 and USDA SR9-5, respectively, from Prosser. Archer Daniels Midland 'Vero' cranberry bean contains USDA H9678-1, a breeding line from the Prosser program. The addition of these five new cultivars, which all derived at least one parent in their pedigree from USDA germplasm releases, have greatly supported sustainable production in the nearly \$1 billion annual U.S. dry bean industry.

Component 2 – Crop Genetic and Genomic Resources and Information Management

Identifying teas by their DNA fingerprint. The global market for tea (*Camellia sinensis*) is valued at \$40 billion/year, \$12 billion of which is from the U.S. market, but it is difficult to identify or classify cultivated tea plants or their harvested leaves. ARS scientists in Beltsville, Maryland, collaborated with Asian scientists to analyze the DNA "fingerprints" of 760 different kinds of tea that originated from China, India, Vietnam, Laos, Myanmar, Thailand, Korea, and Japan. They discovered these teas belonged to one of four groups of genetically-similar teas, either a small-leaved China type or three broad-leaved Assam types (Indian, Chinese, and Cambodian). Each of the four genetic groups appears to have been domesticated from wild plants independently in different regions, but plants in different groups all can easily interbreed, resulting in a wide array of hybrids in teas. This DNA grouping method has already been applied to help tea researchers in

California and Mississippi identify unknown tea cultivars. The method can also enable U.S. tea growers and the U.S. tea industry to conduct quality assurance of imported and domestic-grown teas, and ensure “trueness-to-type” of materials marketed as premium tea products.

Safeguarding valuable genetic resources for grape. Grape is the most valuable fruit crop in the United States, with an annual market value of approximately \$6 billion per year. New genes are continually needed by breeders to improve grape’s quality, productivity, and resistance to environmental extremes, pests, and diseases. Those genes are contained in grape genetic resources collections managed by the USDA/ARS National Plant Germplasm System, primarily in the form of field plantings that are constantly vulnerable to environmental extremes and biological threats. ARS scientists in Fort Collins, Colorado, developed new methods to “cryopreserve” (store under ultra-cold conditions) samples of grape tissues from the growing points of vine stems. The procedure is applicable to genetically diverse grape plants, is highly flexible, and saves labor. These discoveries will ensure that vital grape genetic resources required by grape producers and breeders are safeguarded in secure storage conditions and available indefinitely.

Rootstock variety released for controlling scion vigor in grafted vines. VR O39-16 is a grapevine rootstock that provides protection against the dagger nematode and fanleaf degeneration disease. However, the VR O39-16 rootstock is not favored by growers because scions that are grafted onto it grow vigorously and produce large vines that need substantial pruning, form dense canopies, and produce low-quality fruit. ARS researchers in Geneva, New York, doubled the chromosome numbers of a VR O39-16 rootstock vine and developed ‘A4,’ a low vigor grapevine rootstock variety. This new rootstock provides grapevine growers with a valuable option for controlling scion vigor and protecting against damage from the dagger nematode and fanleaf degeneration disease.

DNA fingerprints identify impostors for ‘Boysen’ blackberry. The ‘Boysen’ blackberry cultivar made up a significant component of U.S. blackberry production in 2016, which was valued at around \$26.4 million. However, multiple variants of the ‘Boysen’ blackberry have been identified since the cultivar was introduced in 1938, complicating efforts to verify the genetic lineage (and market value) of blackberry cultivars. ARS scientists in Corvallis, Oregon, applied DNA fingerprinting to numerous plants labeled as ‘Boysen’ from public collections, plant nurseries, and private farms and compared the results between the plants and their suspected parents. Five ‘Boysen’ variants were identified. In addition a ‘Boysen’ type that is likely a replicate of the original ‘Boysen,’ and the pedigree for this ‘Boysen’ was confirmed as a ‘Logan’ x ‘Austin Mayes’ hybrid. Misidentified ‘Boysen’ plants were discovered in the nursery trade, so confirming the authenticity of plants marketed as ‘Boysen’ with DNA fingerprints is recommended prior to purchase. Fruit traits will be evaluated next in these ‘Boysen’ variants to identify genotypes with superior fruit quality traits.

Novel tools for identifying fungi that rot grain in storage. Significant post-harvest grain losses result from improper storage conditions that favor pest infestation and microbial growth. A group of species within *Aspergillus* fungal molds specializes in rotting harvested crops with low water content, such as stored grains. ARS scientists in Peoria, Illinois, and an international team of colleagues scientifically described all the storage rot fungi in this *Aspergillus* group and developed methods for their quick and accurate identification. Fourteen previously undescribed species were identified in addition to the seven easily identified species, and genetic “fingerprinting” methods were devised to identify all of them. This research generated the first available information about optimal temperatures and water content levels that support fungal growth, and this data can be applied for devising more effective control methods. Recognizing this novel species diversity will advance research on microbial diversity overall, and potentially generate numerous agricultural and industrial applications.

Improving breeding efficiency with modeling. Genomic prediction models need to be trained with individual phenotypes as closely related to the selection candidates as possible, so newly generated breeding lines with few propagules (seed or vegetative) need to be evaluated in field experiments. ARS researchers in Ithaca, New York, improved statistical methods to account for spatial variation in field experiments and developed methods to account for competition between breeding lines in adjacent plots. They showed that the accuracy of genomic prediction from models trained with the new statistical methods was higher than the accuracy from models trained using standard statistical methods. A direct correspondence exists between genomic prediction accuracy and realized gain from selection, so these modeling enhancements should enable more rapid crop improvement.

Component 3 – Crop Biological and Molecular Processes

A high-throughput automatic platform for root growth phenotyping. Drought threatens crop production in the United States and around the world. Drought tolerance is influenced by genetic, physiological, and environmental factors, including root traits, but more information is needed about the relationship between roots and drought tolerance in agronomic crops. ARS researchers in Columbia, Missouri, have developed a low-cost robotic system to directly observe roots in soil and measure the growth rate response under both optimal and water-deficit conditions. The robot, referred to as “RootBot,” was designed for use in a controlled environment and to enable roots to develop normally in the dark and in soil. This technology has broad applications for use in multiple crops and with varying soil treatments, including water deficit stress. The platform facilitates the rapid assessment of root traits, which will support breeding efforts to improve drought tolerance in all major crops.

New System for Engineering Novel Traits into Crop Genomes. The genetic improvement of crops is one of the most effective ways to increase their productivity in agriculture. Until now, it has been difficult to genetically engineer improvements in complex traits like yield or disease resistance that require the action of multiple genes. An ARS scientist in Albany, California, developed a novel technology called Gene Assembly in *Agrobacterium* by Nucleic Acid Transfer using Recombinase technology (GAANTRY), that enables the efficient assembly and introduction of multiple genes into plants. The system can interlink multiple genes in a simple, reliable and highly effective process, and then generate transformed plants that frequently produce all the introduced traits as desired. This technological breakthrough enables the use of crop biotechnology to effectively improve complex traits in a wide array of crop plants.

Discovery of a new protein that controls oil content in plants. Oilseed crops synthesize and store large amounts of oil (up to 40 percent dry weight) in their seeds. This oil provides carbon and energy reserves for germinated seedlings and is an important nutritional resource for humans and animals. While the enzymes for oil synthesis in plants are generally well understood, the processes involved in the “packaging” of oil into subcellular structures called “lipid droplets” are poorly known. In research collaborations with the University of North Texas and the University of Guelph, ARS researchers in Maricopa, Arizona, discovered a new protein called Lipid-Droplet Associated Protein – Interacting Protein (LDIP) that plays a key role in the formation of lipid droplets in plant cells. Disrupting the LDIP gene resulted in much larger lipid droplets and up to 10 percent more oil in the leaves and seeds of plants. These results open new avenues for using non-transgenic mutation breeding strategies to develop agriculturally-important plants with enhanced oil concentrations. Scientists studying the basic mechanisms of oil formation in plants and plant breeders developing new oilseed cultivars with increased oil content will benefit from this breakthrough.

Pollinator behavior and managing geneflow between genetically engineered (GE) and conventional crops.

Approximately 35 percent of the crops grown for human consumption benefit from insect pollinators, including honey bees, bumble bees, and leaf cutting bees. ARS scientists in Madison, Wisconsin, used miniaturized radio frequency identification (RFID) to study how field size and field isolation affect bee behavior and subsequent gene flow. All the bees in the study visited more flowers in large patches and would travel as far as needed to visit flowers, despite the distances involved. These findings suggest carefully planning the configuration of genetically-modified and conventional alfalfa plots in close proximity could help restrict gene flow resulting from pollinator activities. This information is useful to farmers, the alfalfa seed industry, and the regulatory agencies concerned about adventitious presence in alfalfa seed-production fields.