

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

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

FY 2019 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.

Many of the NP 301 projects include significant domestic and international collaborations including government, industry and academia. These collaborations provide opportunities to leverage funding and scientific expertise for USDA-ARS research and accelerate dissemination of ARS research results, thus enhancing the impact of ARS research programs. During FY 2019, NP 301 scientists participated in research collaborations with scientists from the following 70 countries:

Argentina	Ecuador	Ireland	Oman	Thailand
Australia	Egypt	Israel	Pakistan	Trinidad and Tobago
Austria	England	Italy	Panama	Tunisia
Bangladesh	Ethiopia	Ivory Coast	Peru	Turkey
Belgium	France	Japan	Philippines	Uganda
Brazil	Georgia	Kazakhstan	Poland	United Kingdom
Burkina Faso	Germany	Kenya	Romania	Uruguay
Canada	Ghana	Mexico	Slovakia	Uzbekistan
Central African Republic	Greece	Morocco	South Africa	Vietnam
Chile	Guatemala	Mozambique	South Korea	Zambia
China	Haiti	Netherlands	Spain	Zimbabwe
Colombia	Honduras	New Zealand	Sweden	
Costa Rica	Hong Kong	Nicaragua	Switzerland	
Czech Republic	Hungary	Nigeria	Taiwan	
	India	Norway	Tanzania	

The quality and impact of NP 301 research was evidenced during FY 2019 by the following:

- ✓ 602 refereed journal articles published,
- ✓ 52 cultivars and breeding lines released,
- ✓ 8 new invention disclosures submitted,
- ✓ 7 new patent application filed, and
- ✓ 15 new patents issued.

During fiscal year 2019, this National Program was composed of four 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 – Plant and Microbial Genetic Resource and Information Management*
- *Component 3 – Crop Biological and Molecular Processes*
- *Component 4 – Information Resources and Tools for Crop Genetics, Genomics, and Genetic Improvement*

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 2019, but rather are selected based on impact and level of contribution to meeting the National Program goals.

Component 1 – Crop Genetic Improvement

Key parts of the maize genome responsible for heat stress tolerance and susceptibility are identified.

Maize is one of the most widely grown crops in the world. Like many crops, the primary limiting factors for maize production are drought and high-temperature stress. Although the effects of drought can be mitigated by irrigation, heat stress is often unavoidable and presents significant challenges for crop management. ARS scientists in Lubbock, Texas, and Iowa State University collaborators conducted field trials in Texas and identified maize lines with superior and hypersensitive heat stress responses based on leaf and floral stress responses. These characteristics were chosen because they are the components of yield that are reduced when maize undergoes heat stress. Subsequent genetic mapping studies identified specific regions controlling these responses that have the potential to be used by breeders to improve heat tolerance in maize. Results of these studies of heat stress tolerance in maize and sorghum were published in two professional journals.

Release of winter feed barley cultivar ‘Fortress’ resistant to Russian wheat aphid and greenbug.

Greenbug and Russian wheat aphid are a threat to small grains in the southern U.S. Plains, where small grain producers are seeking an alternative to wheat. Although historically produced in the southern Plains, there has not been a barley variety released for this area since 1980. Barley is a good grazing and grain feed source for animals. Resistant varieties are an environmentally and economically sound solution to aphid attack. ARS scientists in Stillwater, Oklahoma, crossed a Russian wheat aphid-resistant barley with a greenbug-resistant winter feed barley adapted to the southern Plains. Many years of

screening for aphid resistance and repeated crossing followed by many years of field evaluation at several locations in Oklahoma resulted in the selection of 'Fortress', the first U.S. barley variety resistant to both Russian wheat aphid and greenbug. Growers now have a new alternative to wheat for small grain production and the added advantage of reduced economic and environmental expense. There will be no need for seed treatment or field spraying of insecticides with 'Fortress'.

Tough yet flavorful 'Keepsake' strawberry cultivar. Strawberries are a valuable crop in the United States, so loss of a small percentage of the crop to disease or physical degradation in the field or during postharvest storage is costly to growers and consumers. ARS researchers in Beltsville, Maryland, released and patented 'Keepsake', a mid-season, "spring-bearing" strawberry with fewer rotted or physiologically degraded fruits in the field or after refrigerated storage. The fruits are very sweet with outstanding flavor and are firm and tough enough for commercial handling. 'Keepsake' is expected to be of greatest value to growers in the Mid-Atlantic and northeastern States, especially to those who must store harvested fruit for delivery to market. Plants of 'Keepsake' were directed to nine U.S. and Canadian nurseries for propagation and licensing for sale. Nursery and grower demand for 'Keepsake' already exceeds supply.

The genome sequence of pecan. Pecan breeding has fallen behind other major crops because of the lack of genomic and genetic resources. ARS scientists in College Station, Texas, working with university collaborators in the United States and China, developed the first reference genome for pecan. The work focused on the prominent cultivar 'Pawnee', was developed in conjunction with a reference genome for the Chinese hickory (*Carya cathayensis*), and was made available for public use. The genome sequence will allow the identification of important genes that control life-history and productivity/quality traits in pecan. This accomplishment represents a major milestone in the development of pecan genetic resources.

New high-yielding and disease-resistant sugarcane cultivars for commercial production. There is no private-sector breeding program for sugarcane in the United States, thus the industry is founded 100 percent on publicly developed varieties. The biggest challenge Florida sugarcane growers face is orange rust and brown rust diseases. The rusts recently caused considerable yield losses and an increase in input costs of fungicide applications. ARS researchers in Canal Point, Florida, released two new high-yielding sugarcane cultivars (CP 12-1743 for muck soils and CP 11-1640 for sand soils) with disease tolerance. The new cultivars will mitigate negative effects of brown and orange rusts and other stresses on sugar yield and profits in Florida. The Louisiana sugarcane industry is dependent on early maturing varieties. ARS scientists from Houma, Louisiana, in collaboration with the American Sugarcane League of the U.S.A., Inc. and the Louisiana State University Agricultural Center, developed and released a new sugarcane variety called 'Ho 12-615'. The variety is high-yielding year over year, which increases profits because planting costs are the biggest expense to growers. The release of this variety offers growers a well-adapted variety that can increase industry profits and expand the genetic variability contained within the growing region.

Stem rust-resistant wheat germplasm released. Stem rust is a re-emerging disease in East Africa and the Middle East. New highly virulent races threaten wheat production around the world. Three hard winter wheat lines with multigenic adult plant resistance to stem rust were officially released by ARS scientists in Manhattan, Kansas. These lines are now globally available to breeders to use as parents in crosses to

develop winter wheat germplasm that is resistant to stem rust, including the highly virulent east African races of the disease.

Identification of genetic markers for resistance to leaf spot in peanut. Early and late leaf spot, major foliar diseases of peanut, are responsible for severely decreased yield in the absence of intensive fungicide spray and cost the U.S. peanut industry more than \$50 million annually. The development of resistant varieties is a sustainable solution to reduce these costs. Genetic markers linked to resistant genes can be used in marker-assisted selection to speed the development of resistant varieties. To identify genetic markers linked to the resistant genes, ARS researchers in Tifton, Georgia, determined the genetic control of leaf spot resistance disease and uncovered how these genes are expressed in the plants of a segregating population of peanut. They identified multiple resistance genes for early and late leaf spot, determined their locations, and developed genetic markers for selecting plants with the resistance. They determined resistance to early and late leaf spot are genetically independent and found the presence of late leaf spot resistance genes might result in protection from yield loss caused by disease damage. Moreover, the genetic markers for the genes can effectively identify resistance and susceptible breeding lines, confirming the effectiveness of selecting for both early and late leaf spot resistance together using marker-assisted selection to improve host-plant resistance in peanut breeding programs. The information and markers have been made available publicly, and breeders are using them to develop peanut cultivars with resistance to the two diseases.

ARS releases 'Twilight' and 'Hall's Beauty' blackberry. The thornless, semierect 'Twilight' and trailing 'Hall's Beauty' have expanded options for fresh and processed blackberry growers. 'Twilight' thornless blackberry was released by ARS researchers in Corvallis, Oregon, and provides growers with a better option than the current standard, 'Triple Crown'. It is produced in the same season and has excellent fruit quality, especially much better firmness. 'Hall's Beauty' thornless trailing blackberry is best suited to the Pacific Northwest and provides another option for growers. It can be grown for either the machine-harvested processed fruit market or the hand-harvested fresh fruit market.

Sorghum lines resistant to sugarcane aphid and greenbug released. Sugarcane aphid is a new invasive pest of sorghum and causes severe damage to sorghum that results in substantial production losses (i.e., \$742.7 million in 2015). ARS scientists in Stillwater, Oklahoma, screened germplasm resources for resistance to this devastating aphid through evaluation of a large collection of sorghum germplasm, leading to the identification of resistant materials and subsequent incorporation of this genetic resistance through traditional breeding. Two breeding lines have been released: STARS 1801S has genetic resistance to both sugarcane aphid and greenbug, and STARS 1802S has resistance to sugarcane aphid and head smut disease. These new resistant sources are already available to the sorghum community and will directly contribute to genetic improvement of sorghum for crop protection and can successfully help sorghum producers safeguard their crops from this severe aphid pest.

Using exotic landrace germplasm to broaden the genetic base in cotton breeding. New genetic variation is needed to broaden the genetic base and improve the economic competitiveness of U.S. cotton. ARS scientists in Florence, South Carolina, and College Station, Texas, evaluated the potential of using an exotic upland landrace accession from the National Plant Germplasm System in cotton breeding. These exotic accessions do not require a short daylength to flower as many exotic cotton accessions do, and represent an untapped, rich diversity for cotton breeding programs. The scientists demonstrated that

using these exotic accessions generated offspring with broadened genetic diversity and good fiber quality. However, offspring also suffer from a negative relationship between yield potential and fiber quality. These results provide guidance that public and private breeding programs can use when considering using exotic landrace accessions as new sources of genetic diversity.

Improved soybean cultivar with diverse exotic parentage. Current U.S. soybean cultivars are derived from a small and narrow set of ancestral parents, resulting in a potential genetic bottleneck for yield, and exposes soybean to vulnerabilities to new or invasive diseases and abiotic stresses. A novel, genetically diverse, high-yielding soybean germplasm line was released by ARS researchers in Stoneville, Mississippi; Urbana, Illinois; and Jackson, Tennessee. LG03-4561-14 was derived from 25 percent exotic parentage and is the first improved soybean germplasm line containing PI 445837 in its pedigree. LG03-4561-14 was registered in the *Journal of Plant Registrations*, with seed deposited for long-term storage in Fort Collins, Colorado, and for maintenance and distribution in Urbana, Illinois. This germplasm is the first Maturity Group III germplasm derived from exotic sources and released for use in the early production system of the southern United States. Seeds of LG03-4561-14 have been requested by soybean breeders in Germany and India and are being used domestically in the United States in multiple public soybean breeding programs.

Component 2 – Plant and Microbial Genetic Resource and Information Management

New tools for breeding dwarf bunt-resistant wheat. Wheat is one of the most important U.S. food crops, with a farmgate value of more than \$9.7 billion in 2018. Dwarf bunt disease can damage wheat yields and quality, especially in organic production systems. Host-plant resistance is the best means for controlling dwarf bunt without the use of fungicides. ARS researchers in Aberdeen, Idaho, and cooperators from the University of Idaho and Utah State University combined genome analysis with replicated field testing to identify samples from the ARS National Small Grains Collection at Aberdeen that were resistant to dwarf bunt. Then they used genetic information to locate resistance factors on the genomes and identified genetic markers associated with resistance to dwarf bunt. The disease-resistant samples and genetic markers identified in this study will help U.S. wheat breeders incorporate dwarf bunt resistance into adapted bread wheat cultivars.

More efficient method for analyzing genetic data for tree breeding. Tree breeding requires long periods of plant growth and significant expenses of land and personnel. Genotyping trees at the seedling stage can increase the efficiency and reduce the costs of tree breeding by identifying the best parents for breeding crosses and the best resulting progeny. ARS researchers in Miami, Florida, and cooperators from Florida International University, University of Florida, and Department of Agriculture and Fisheries in Queensland, Australia, developed a more efficient method of analyzing DNA genotype data for mango and avocado germplasm and hybrids. This method can distinguish specific cultivars of interest from all other cultivars and identify self-pollinated individuals and the possible paternal parents of particular trees. Identifying self-pollinated individuals is particularly important because it can help uncover deleterious traits to eliminate from breeding stocks. With this method, breeders can determine the genetic content of breeding stock early at the seedling stage to optimize breeding efficiency and accelerate genetic gain.

Discovering the genes for slow canopy wilting in soybeans during drought. Drought causes soybean leaf canopies to wilt, but some soybean varieties differ in the time of onset and the severity of canopy wilting. Previous studies identified two exotic soybeans that exhibited reduced and delayed canopy wilting phenotypes, but the genetic mechanisms underlying canopy wilting were unclear. ARS researchers in Beltsville, Maryland, with University of Missouri, University of North Carolina, and Kansas State University colleagues, deciphered the physiological and genetic mechanisms responsible for improving yield under limited water availability in two soybeans and validated major genetic factors protecting soybean yield under drought in the field. The research resulted in a better understanding of the water conservation of the slow-canopy-wilting mechanism and provides genetic resources for improving drought tolerance in soybeans through various approaches such as gene cloning, editing, or gene transferring via traditional breeding.

Powerful new genomic tools for walnut research and breeding. Approximately 90 percent of the walnut crop in the United States is grown in California, and it generated a farmgate value of more than \$1.5 billion in 2017. But breeding walnuts is a lengthy, expensive process because they are grown on large trees. Consequently, genomic tools such as genetic markers would be valuable for accelerating walnut breeding progress. ARS researchers in Davis, California, and their University of California-Davis colleagues applied a novel combination of genome sequencing tools to generate a new, more complete genome sequence for an interspecific walnut hybrid between English walnut and a wild walnut species, a potentially important walnut rootstock, to identify economically important traits. They identified, catalogued, and mapped disease resistance genes in the parental genomes of two walnut species and studied their chromosomal distribution. This information yielded a valuable new tool for guiding walnut breeding.

More effective methods for identifying optimal carrot germplasm for research and breeding. Many crop breeders want to incorporate germplasm from genebank collections into their breeding stock but find it difficult to identify the best germplasm for their purposes. Breeders often try to identify a subset of larger collections, called a core subset, as a start. But current methods for constructing those subsets do not consistently capture genetic diversity tailored to the breeders' needs. With genome sequencing data and horticultural trait data for numerous carrot germplasm samples, ARS researchers in Madison, Wisconsin, and cooperators from the University of Wisconsin tested whether custom core subsets could be constructed for specific breeding purposes. Significantly, genome sequencing data were not effective for devising optimal subsets. But increasing the size of the core subset relative to the total size of the collection did improve the accuracy of predicting the useful samples, suggesting that the utility of custom subsets can be improved by expanding their size to represent the most important genetic diversity present in the overall genebank collection. This finding suggests that approaches for choosing such custom subsets should include a sufficiently large number of samples to adequately represent the genetic diversity in the overall collection.

Soybean wild relatives with unique new genes. Many of the U.S. soybean perennial relatives in the National Plant Germplasm System soybean collection originate from Australia and other locations with warm and drought-prone environments, but their potentially valuable traits for adaptation have been little explored. These accessions are sources of genes that do not exist in currently cultivated U.S. soybean. ARS scientists in Beltsville, Maryland, defined the genetic diversity and phylogenetic relationships of perennial *Glycine* (soybean) species. They found one perennial species, *Glycine*

canescens, had a higher level of genetic diversity, and determined that three accessions from the dry and warm region of western Australia were genetically distinct from the other eight accessions from central and eastern Australia. These three perennial species could be used as donors of useful soybean genes to help improve resistance to heat, drought, and pests.

Goatgrass genes confer disease resistance in wheat. Goatgrass (*Aegilops markgrafii*) is a good source of new genes for resistance to the major diseases of wheat, including stem rust, leaf rust, stripe rust, and powdery mildew. A set of six wheat lines, each carrying a single additional chromosome from *Ae. markgrafii* designated as B through G, was previously produced. ARS researchers in Fargo, North Dakota, studied these lines to determine which of the *Ae. markgrafii* chromosomes carry genes for disease resistance, to determine the relationship of the *Ae. markgrafii* chromosome to the wheat chromosomes, and to discover molecular markers associated with each *Ae. markgrafii* chromosome. The results showed leaf rust resistance was associated with chromosome B; powdery mildew resistance associated with chromosomes D, E, F, and G; and stem rust resistance associated with chromosomes C and D. Thus, each *Ae. markgrafii* chromosome conferred resistance to at least one disease. The disease data, molecular markers, and chromosome groupings will facilitate transfer of the *Ae. markgrafii* genes for resistance to these diseases into wheat.

Component 3 – Crop Biological and Molecular Processes

Innovation in agricultural microbiome utilization. A growing number of bacteria and fungi are found to promote plant growth through mutualistic interactions involving volatile organic compounds (VOCs). Recently, ARS scientists in Kearneysville, West Virginia, identified an environmentally isolated strain of fungus (*Cladosporium sphaerospermum* TC09) that dramatically enhances plant growth upon exposure in the laboratory and under greenhouse conditions. Seedlings exposed to TC09 cultures for 20 days increased stem height and whole plant biomass up to 25- and 15-fold, respectively, over comparable control plants. Moreover, TC09-exposed plants retained higher rates of growth even when transplanted to soil under greenhouse conditions. For example, pepper plants that are pre-exposed to TC09 and planted in a greenhouse flower 20 days earlier and yield up to 213 percent more fruit than untreated controls. Altogether, *C. sphaerospermum* is a powerful new tool for improving crop productivity in protected and field environments, and commercial partners are working on applications.

Susceptibility restored for Bt-resistant rootworm. The western corn rootworm has evolved resistance to nearly all management tactics targeting its mitigation, including Bt corn. Using rootworm strains that are resistant and susceptible to Bt, ARS researchers in Columbia, Missouri, evaluated ribonucleic acid (RNA) produced after corn rootworms were fed Bt corn or non-Bt corn and identified genes associated with resistance. They used this information to synthesize a form of RNA called dsRNA in which the identified resistance genes were “knocked down” (neutralized) and then introduced this dsRNA into new susceptible and resistant rootworms. The dsRNA that contained one of the altered resistance genes restored significant Bt susceptibility to the resistant rootworm strain and susceptible rootworms maintained their full susceptibility to Bt. This is the first time that susceptibility to Bt has been restored after knocking down a resistance gene and could be applied by expressing the dsRNA in corn along with Bt or by better understanding resistance for future management tools.

Innovations in crop bioengineering. The genetic improvement of important crops such as potato is one of the most effective ways to increase agricultural productivity. It has typically been difficult to genetically engineer improvements in complex traits like yield or disease resistance that require the action of multiple genes. ARS researchers in Albany, California, demonstrated that a novel technology called Gene Assembly in *Agrobacterium* by Nucleic acid Transfer using Recombinase Technology (GAENTRY) allows the efficient assembly and introduction of up to 10 genes in potato. The system was shown to efficiently generate high-quality genetically engineered potato plants that carried all the introduced genes and exhibited the desired traits. The technology was transferred via 20 material transfer agreements to industry and university laboratories. This technological breakthrough will enable the use of crop biotechnology to effectively improve complex traits in potato and related crop plants.

Component 4 – Information Resources and Tools for Crop Genetics, Genomics, and Genetic Improvement

Crop genome sequences are key to food security. A crop genome sequence provides a linear array of the genes that determine crop performance in the field, and thereby serves as a genetic roadmap for breeders, geneticists, and plant biologists seeking to improve agricultural productivity, pest and disease resistance, human nutrition, and environmental sustainability. Genome sequences, for example, are the source of markers that are used by breeders to improve traits such as product quality, drought tolerance, freezing tolerance, and water use efficiency. In 2019, ARS scientists and university collaborators sequenced, curated, and released new genome sequences for peanut, New World cotton, wild soybean, cowpea, and plum. These releases were reported in the journals *Nature Genetics*, *Genome Biology and Evolution*, *Nature Communications*, and *Plant Journal*.

New seedling screening method for *Phomopsis* seed decay in soybean. Seed decay in soybeans caused by *Phomopsis* fungi can cause both yield and seed quality losses under some harvest conditions. Qualitative measurements of the disease can be extremely time consuming and expensive. In addition, *Phomopsis* seed decay is a seedborne disease and researchers must wait until after harvest to evaluate symptoms on the seed. A seedling inoculation and evaluation method to rapidly screen soybean for resistance to *Phomopsis* in the seedling stage has been developed by ARS researchers in Stoneville, Mississippi. Results from this innovative cut-seedling inoculation method were comparable to those obtained from tests conducted with mature seeds. This research can facilitate the identification of resistance to *Phomopsis* seed decay without having to wait for an entire growing season to conduct the seed assay. Also, this approach could provide a more uniform distribution of the pathogen on soybean seeds tested, thus reducing the chance of escapes, especially when the environmental conditions are not conducive to disease development. The method has been adopted by public soybean breeders at other laboratories in the United States and in China.

Assembly of a yellow dry bean collection for consumer trait improvement. Dry beans are rich in fiber, protein, and minerals. However, long cooking times deter bean consumption. In addition, although beans are rich in minerals, such as iron, that are important for human nutrition, the bioavailability of iron from beans is generally low. Several yellow bean genotypes have shown short cooking times and high iron bioavailability. Yellow-colored beans are found in the gene pools from the Andes and Middle America, and there are numerous yellow market classes of importance around the world. But it is unknown

whether the fast cooking and high iron bioavailability traits observed in some yellow bean genotypes are based on origin or color. Thus, the Yellow Bean Collection was assembled by ARS researchers in East Lansing, Michigan, working with university collaborators. The panel includes 306 genotypes with yellow seed coat of diverse origin. They identified 52,622 genetic markers associated with cooking time among 296 genotypes. In conjunction with actual cooking time and iron bioavailability data, the genetic marker data will serve as a useful tool for searching the genome to find diversity among many accessions and identifying genetic associations with faster cooking time. Ultimately, as a result of this work, breeders will find it easier to use genomic and marker-assisted breeding to improve yellow beans for consumer-targeted traits.