

## National Program 301 • Plant Genetic Resources, Genomics, and Genetic Improvement FY 2014 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 speed 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 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 control 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 improvement of 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, bioinformaticists, 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.

This National Program is 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:

- Crop Genetic Improvement (plant breeding, genetic enhancement, molecular marker and trait analyses, nucleotide sequencing, and genetic mapping).
- 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 the large datasets).
- 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 section contains selected NP 301 accomplishments, presented according to the relevant NP 301 Research Components. These are not all of the NP 301 accomplishments for FY 2014, but rather are selected based on impact and level of contribution to meeting the National Program goals.

## **Component 1 – Crop Genetic Improvement**

**Conventionally bred sweet orange-like hybrid and new rootstocks with tolerance to citrus greening released.** Citrus greening or huanglongbing (HLB) is the most serious threat to citrus production worldwide and has reduced Florida citrus production by 50 percent. No inherent genetic protection for citrus trees has been available for U.S. citrus growers. However, in 2014, ARS researchers in Fort Pierce, Florida, released a new hybrid sweet orange with high-quality fruit that displays excellent tolerance to HLB disease. These trees have been propagated at a commercial nursery and in 2015, will be placed in replicated plantings on

six grower sites with other advanced sweet orange-like selections. Nine new citrus rootstocks have also been developed that display much higher sweet orange fruit productivity and tree health in field trials in areas that have been severely affected by HLB. These rootstocks have been entered into the Florida clean budwood program and are being propagated for entry into large-scale grower trials in 2015. Release of the tolerant hybrid and rootstocks offers a new option for citrus growers for production management in the presence of citrus greening.

**Effect of climate change on crop nutritional quality.** Producers and nutritionists are concerned about how climate change might affect the nutritional qualities of food crops. ARS researchers in Aberdeen, Idaho, and in Urbana, Illinois, and multinational collaborators determined how climate change could affect the nutritional qualities of several staple crops, including wheat, rice, maize, sorghum, and soybean. They grew these crops to maturity under varying levels of atmospheric carbon dioxide, which are expected to become elevated because of climate change. In the first assessment of its kind, seed nutrient content of zinc, iron, and protein nutrition was evaluated. Scientists also measured seed phytic acid content, which is critically important for determining iron and zinc bioavailability. Study results indicated that although seed phytic acid was not largely altered by elevated carbon dioxide levels, seed zinc, iron, and protein levels declined. Iron and zinc deficiencies are significant global public health challenges that impair the health of an estimated two billion people worldwide. These findings, which were published in the journal, *Nature*, provide important new information for understanding how climate change could affect the nutritional quality of crops.

**Release of new apple rootstock with tolerance to apple replant disease.** Diseases affecting U.S. apple crops have been affecting yields and profits. ARS and Cornell University researchers in Geneva, New York, have developed and released a new apple rootstock, named G.814, a dwarfing, productive, early bearing, and highly yield-efficient tree. It is the most recent product from a series of disease-resistant and productive apple rootstocks developed by the Geneva breeding program. This rootstock is resistant to fire blight and crown rot, two serious diseases that infect apple trees with serious economic consequences. Most importantly, G.814 has shown tolerance to the apple replant disease complex. This rootstock was tested for 15 years to evaluate rootstock productivity levels and compared with standard cultivars. On the basis of preliminary trials in the United States, G.814 will increase production of larger, high-quality fruit in marginal replanted orchard land, which will help apple producers increase yields and profits.

**New yield genes from a soybean wild relative found in the USDA soybean collection.** The narrow genetic base of the soybean crop limits progress in developing higher yielding varieties. ARS scientists in Urbana, Illinois, discovered and transferred unique yield genes from *Glycine tomentella* (a very distant, perennial relative of soybean) into cultivated soybean. These two species are so genetically different that direct progeny from these crosses are sterile, and special procedures, including several backcrosses to the soybean parent, were needed to produce fertile progeny. Each new plant from these crosses is likely to have a different complement of *G. tomentella* chromosomes and could be genetically quite different. In tests at seven locations across four states, 10 lines were identified that yielded significantly more than the commercial soybean parent—as much as by 7 bushels/acre. This is the first report of soybean lines derived from perennial *G. tomentella*. Increasing yield is the most important objective for soybean breeders, and the genes to increase yield that were transferred from *G. tomentella* are now available to soybean breeders for the first time.

**Genetic inheritance of cooking time in beans.** Dry beans are a nutrient-dense, low-cost food and an excellent cost-effective food choice for consumers. In spite of this value, bean consumption is limited—especially in developing countries—because of their long cooking times and the high amount of fuel needed for cooking. To develop bean varieties that cook more quickly, plant breeders need information about how genetic traits affect cooking time and how metabolic activity affects those traits. ARS scientists in East

Lansing, Michigan, evaluated a group of 240 Andean bean lines for genetic differences in cooking time. The average cooking time was 38 minutes, ranging from 19 to 87 minutes. Genetic elements associated with cooking time were detected on chromosomes 2 and 10, with evidence suggesting that enzymes coded on chromosome 2 (pectin methyltransferases) may influence cooking time. In each of the four market classes evaluated (yellow, cranberry, light red kidney, and red mottled), the genotypes that required the shortest cooking time also retained a higher percentage of protein and iron, indicating that these bean varieties might potentially provide the most benefit to consumers in terms of convenience and added nutrition.

**Genes for better frost tolerance.** It is known that variation in the ability of winter wheat to survive the winter months in the field is associated with differences in the vernalization 1 (VRN1) and frost resistance 2 (FR2) genes, but knowledge of how specific forms of the genes influence winter hardiness and possible interactions among them is lacking. ARS researchers in Pullman, Washington, assayed variation in the composition of the genes and the number of copies at the FR2 and VRN1 loci in a large set of winter and spring wheat genotypes from around the world representing a broad range of freezing tolerance. Results indicate that selection of wheat varieties with a specific form of the FR2 gene (the FR-A2-T allele) and three copies of the recessive *vrn-A1* allele would be a good strategy for improving frost tolerance in winter wheat. These findings provide wheat breeders with valuable new molecular tools for improving winter survival in wheat.

**Saving energy and reducing ginning costs by improving ginning efficiency.** Cotton cultivars differ in how strongly fibers are attached to the seed, and cultivars with less fiber-seed attachment force can be ginned faster with less energy and fiber damage. ARS cotton breeders and engineers in Stoneville, Mississippi, determined that percent fuzz was correlated with ginning efficiency and that selecting for genotypes with low fuzz percentage resulted in genotypes with better ginning efficiency. This finding will help cotton breeders develop cotton cultivars that gin faster with lower ginning energy requirements and high fiber quality.

**A new common bean with tolerance to low soil fertility.** Inadequate soil fertility, high costs of fertilizers, and root rots are common crop production constraints worldwide. TARS-LFR1, a multiple disease-resistant common bean with superior performance in low-nitrogen soils and with root rot resistance was developed via collaboration among researchers with ARS in Mayagüez, Puerto Rico, the University of Puerto Rico, and Cornell University. In addition to root rot, this germplasm has resistance to common bacterial blight and Bean common mosaic virus, and it yields well in association with rhizobia through biological nitrogen fixation. This combination of traits will be valuable for plant breeders who seek to target low-input and organic production systems, in which little to no fertilizer is applied.

**Sorghum multi-seeded mutants increase seed yield.** ARS researchers in Lubbock, Texas, and in Ithaca, New York, identified multi-seeded mutants and related genes with more primary and secondary flowering branches. These have been incorporated into higher yielding sorghum germplasm lines. These discoveries are now enabling public and private sector sorghum breeders to exploit the germplasm lines and related molecular markers to develop new varieties with substantially increased sorghum yields.

**New Hessian fly resistance gene identified in wheat.** Hessian fly populations have become virulent to most resistant wheat varieties grown in the southeastern United States. ARS researchers in West Lafayette, Indiana, worked with collaborators at Purdue University to identify a new resistance gene called H33 and moved it from a wheat relative into cultivated bread wheat. The H33 gene was shown to provide effective protection of wheat against Hessian fly attack in the southeastern United States. Molecular markers were identified to aid in moving this resistance gene into wheat cultivars through marker-assisted selection. Knowledge from this study will help wheat breeders prevent yield loss due to Hessian fly attack.

**Next-generation sequencing of organellar genomes in cranberry to enhance breeding efficiency.** ARS scientists in Madison, Wisconsin, used molecular methods and computer-based approaches to reconstruct the cranberry plastid and mitochondrial genetic codes. These cellular organelles are involved in energy formation (photosynthesis) and utilization (respiration). This organelle sequence enables the study of photosynthesis and respiration in cranberry, key processes in the formation of fruit and ultimately cranberry yield. The genetic codes of cranberry organelles deciphered through this research are the first and only codes available in the entire cranberry family, which comprise thousands of species without previous information. Ultimately, the genetic information about energy production/utilization systems in cranberry can be used by plant breeders to breed more energy-efficient cranberries and sister species such as blueberry and lingonberry.

**Identifying cacao varieties from a sample of only one bean.** Cacao, the source of cocoa, is grown primarily on small farms primarily in West Africa. Production and marketing of specialty, high-value cocoa can provide economic opportunities for growers in the developing world and greater profits for the cocoa/chocolate industry. But to realize those benefits, the varietal identity for high-value cacao, some of which is rather rare, must be authenticated. ARS researchers in Beltsville, Maryland, developed a new method of DNA testing that can identify a cacao variety from a single bean. This new testing method can more efficiently identify high-value cacao for on-farm protection and propagation, and also can authenticate commercial sources for this increasingly high-value product.

**Plumbing systems identified as a common source for fungi that infect humans.** Life-threatening infections caused by *Fusarium* fungi have increased dramatically during the last 30 years. ARS researchers in Peoria, Illinois, and their collaborators applied genetic analyses to examine the occurrence of a *Fusarium* species that is often a primary cause of those infections. They found that plumbing systems are a common source for that species. This finding can help minimize the risks from such fungal infections by contributing to more effective infection-control programs in hospitals and other settings that house individuals at risk for fungal infections.

**New software tool developed to analyze the genetic diversity and relationships in maize.** The vast volumes of genetic data now available for major crops such as maize are highly valuable for accelerating progress in crop research and breeding; however, distilling those data into applicable knowledge requires novel analytical approaches. ARS researchers in Ames, Iowa; Ithaca, New York; and their collaborators developed the software tool TypSimSelector, accessible on the web via the ARS Maize Genome Database, which enables genebank managers, researchers, and breeders to rapidly retrieve highly accurate genetic comparisons of maize lines. Knowledge of the lines' genetic make-up will enable curators to better manage the U.S. national maize genebank collection and requestors to choose the best genetic materials for advancing their research or breeding programs.

**Drought tolerance traits identified in wild relatives of watermelon.** Drought strongly affects the yield and quality of watermelons in the southeastern United States. ARS researchers in Griffin, Georgia, evaluated the morphology, anatomy, and physiology of drought-tolerant wild relatives of watermelon from the ARS genebank in Griffin. They found that greater leaf thickness characterized a drought-tolerant wild relative, a correlation that could facilitate the incorporation of drought tolerance into watermelons.

**New genetic sources of grain mold resistance identified in sorghum.** Grain mold, a disease caused by a combination of different fungi, severely affects sorghum grain yield worldwide. ARS researchers in Mayagüez, Puerto Rico, evaluated more than 800 germplasm samples from the ARS genebank in Mayagüez and identified several with host-plant resistance to grain mold. Two samples that originated from Africa also had commercially-acceptable traits that could facilitate their immediate incorporation into sorghum breeding programs for combating this virulent disease.

**Conventional high oleic acid soybean without yield drag.** To meet market demands for healthier cooking oils, research is ongoing to develop and commercialize soybean varieties with the high oleic acid seed oil trait. A major impediment to commercial success of new soybean varieties with improved seed composition traits is the threat of inferior yields associated with the trait. ARS researchers in Columbia, Missouri, crossed the high oleic acid trait with a commercial soybean variety and compared the yields of the resulting new high oleic lines with control varieties, and results from two years of field trials demonstrated high oleic acid soybean lines produced yields similar to the high yielding control varieties. The high oleic lines averaged 80 percent oleic acid in the seed oil compared to 30 percent oleic acid for the control varieties. These results demonstrated that yield potential for high oleic acid soybean varieties was not negatively impacted by the high oleic trait itself. Breeders are referencing this discovery as they continue to breed new high oleic cultivars. Continued development of high yield/high oleic soybean varieties will provide U.S. producers with expanded opportunities to meet market demands.

**Release of eight new high quality cotton germplasm lines.** The cotton industry critically needs new genetic resources that possess high quality and broad adaptation. In 2014, ARS researchers in Florence, South Carolina, released eight high quality cotton germplasm lines with broad adaptation across the U.S. cotton growing area. In coordination with their release, these cotton germplasm lines are being made available to public and private cultivar development programs to be used for developing the next generation of high quality, commercial cotton cultivars. Ultimately, these high quality germplasm lines will serve as a genetic resource to increase U.S. cotton fiber quality and grower profitability.

**Genes for resistance to Fusarium head blight mapped in new Chinese source of resistance.** Fusarium head blight (FHB) is a devastating disease of wheat worldwide. Growing resistant cultivars is the most effective strategy to control the disease. ARS researchers in Manhattan, Kansas, genetically mapped resistance genes in a population developed from a cross between the highly resistant Chinese landrace, 'Huangcandou,' and 'Jagger,' a moderately susceptible hard red winter wheat from Kansas. Marker analysis identified three genes from 'Huangcandou' and two from 'Jagger' that were associated with scab resistance. Markers associated with the resistance genes were identified and can be used to enhance scab resistance in wheat breeding programs.

**An advanced pedigree linkage map in switchgrass.** Having direct knowledge of which alleles reside on the same strand of DNA is important for genotype-phenotype associations and selection. Previous linkage maps in switchgrass did not include this information, but ARS scientists discovered that by including grandparent genotypes in a linkage analysis, it can be directly assessed. ARS scientists in Albany, California, in collaboration with the Samuel Roberts Noble Foundation, performed a linkage analysis including four grandparents that is now being used for trait association. Population development led to both self-fertilized and hybrid groups of individuals which demonstrated the natural capacity of some switchgrass to tolerate self-pollination. This observation has important implications for breeders attempting to produce more productive switchgrass cultivars.

**Co-regulation of leaf and tassel architecture in maize.** Leaf angle is an important trait that can influence the number of plants that can be grown in a corn-field, and tassel branch number is an important trait that may determine the amount of pollen produced. ARS scientists at the Plant Gene Expression Center in Albany, California, and University of California, Berkeley, collaborators identified two transcription factors which regulate tassel branch number and angle. Understanding transcription factors that regulate plant architecture provides useful information to breed for the ideal plant form.

**Pre-harvest sprouting tolerant white wheat developed.** ARS researchers in Pullman, Washington, have developed Zak ERA8, spring white wheat germplasm with improved pre-harvest sprouting tolerance. This is

a non-GMO technology that was based on selection for increased sensitivity to the seed dormancy hormone abscisic acid during grain germination. Because this line has increased seed dormancy at maturity, it shows reduced sprouting when it rains, but it loses dormancy rapidly after maturity, allowing farmers to replant their winter wheat grain within 6-8 weeks of harvest without negative consequences.

**A low acrylamide-forming potato breeding clone with multiple disease resistance.** The presence of acrylamide in processed food products has become a human health concern over the past decade. French fries contain acrylamide, and the potato processing industry has been proactive in reducing acrylamide levels in processed potato products. French fries made from A02507-2LB, an advanced potato breeding clone developed by ARS researchers in Aberdeen, Idaho, and their university colleagues, have 80 percent less acrylamide on average than fries made from the potato variety Russet Burbank, the industry standard. Seed of A02507-2LB is being rapidly increased to allow large-scale industry evaluation. A02507-2LB is also notable for having resistance against all Potato virus Y strains due to incorporation of the Rysto gene, and additionally has resistance to late blight, Verticillium wilt, early blight, and corky ringspot. The commercial use of A02507-2LB will enhance the sustainability of potato production.

**QTL mapping of downy mildew resistance in cucumber.** Downy mildew of cucumber is an important emerging disease of cucumber, responsible for significant yield losses in the past several years, and is considered to be the primary disease threat to production. ARS scientists in Madison, Wisconsin, identified one major gene, and two minor genes for downy mildew resistance in a Plant Introduction line of cucumber. Results from this study provide new insights into phenotypic and genetic mechanisms of downy mildew resistance in cucumber that will help growers and plant breeders identify cucumber genes that impart disease resistance.

**Highly effective gene for common blight resistance found and characterized in dry bean.** Common bacterial blight is a persistent disease that limits dry edible bean yield in production regions across the United States and worldwide. Clean seed programs and planting cultivars with high levels of resistance provide the best opportunity to control this disease. An ARS scientist in Prosser, Washington, in collaboration with scientists at the University of Idaho, identified a new Quantitative Trait Locus (QTL) with broad resistance against common bacterial blight in dry edible bean and studied its interaction with two existing major QTL. This QTL is the first to be discovered in 20 years, and it represents a major breakthrough because it is the most effective QTL for common bacterial blight resistance described to date. Breeders will use this gene to enhance and broaden the resistance of new dry bean (pinto, black, kidney, etc.) cultivars in the United States and worldwide. These cultivars with the new gene will be widely deployed by breeders to combat this disease.

**Identification of potato germplasm with tolerance to high levels of salinity.** Salinity tolerance is not available in cultivated potato. Increasing human demand for fresh water resources is putting pressure on fresh water resources for agricultural production, i.e., irrigation and soil salinization is increasing. The development of salt tolerant crops would allow agricultural production to continue with marginal resources (irrigation with brackish water or production on saline soils). ARS scientists in Beltsville, Maryland, have identified salinity tolerance in a wild potato species and documented the expression of several genes involved in salinity tolerance. This salt tolerant germplasm will enable development of commercial salt-tolerant potato cultivars and foster improved production sustainability.

**Herbicide-tolerant lettuce varieties.** Weed control for lettuce in the United States largely depends on one herbicide, pronamide (Kerb®), which has an uncertain future because it is a carcinogen and has been found to leach into ground water. ARS researchers in Salinas, California, in collaboration with researchers at University of California, transferred resistance to sulfonylurea herbicide (found by scientists at University of Idaho) into five common commercial lettuce types: butterhead, crisphead, green leaf, red leaf, and romaine.

In field trials conducted over two years, sulfonylurea herbicide effectively controlled weeds but did not damage plants or reduce yield of the herbicide-resistant lettuces. It provides lettuce growers a new tool for weed control and has the potential to establish a novel system of weed management.

## Component 2 – Crop Genetic and Genomic Resources and Information Management

**Successful preservation of oaks under genebank conditions.** Oaks, key tree species for many temperate and arid-land forests, furnish highly valuable wood for construction, furniture, and other uses. Endangered oak species require protection in genebanks, but until now, that has been problematic because acorns did not survive under conventional ultra-cold genebank storage conditions. ARS researchers in Fort Collins, Colorado, and their collaborators developed methods for successfully preserving under ultra-cold conditions embryos dissected from acorns of more than 20 oak species. This breakthrough will enable ARS and other genebanks to effectively protect the gene pool of endangered, highly valuable oak species.

**Crop adaptation to extreme environments.** Acidic soils constitute 40 percent of arable land in the tropics and subtropics. Aluminum (Al) toxicity in acidic soil stunts and damages root growth resulting in significant reductions in crop yields due to nutritional deficiencies and drought stress. Rice is the most Al-tolerant of the major cereal crops. ARS and university scientists in Ithaca, New York, showed that rice tolerance to Al is due in part to a novel transporter gene (OsNRAT1) that promotes Al sequestration into the root cell vacuole. OsNRAT1 is sufficient for promoting Al transport in diverse systems from plants to yeast. This knowledge may allow the growing of target crops with Al tolerance in acidic soils using conventional breeding or transgenic approaches.

**Conserving key plant genetic resources more effectively in genebanks and in the field.** The wild relatives of crops provide critical raw material for genetic improvement that underpins crop productivity, but they can be difficult to conserve effectively in genebanks and to protect in the field. ARS researchers in Pullman, Washington, compared the genetic contents of samples from an endangered U.S. wild clover species conserved for 10 years in an ARS genebank with those of the wild populations where they originated. The genetic changes between the wild-collected and genebank samples were minimal. If collected adequately, genebank samples could effectively conserve the genetic diversity of an endangered crop wild relative, but continued monitoring of protected field populations is needed to detect genetic erosion and determine when additional collections are required to effectively conserve this valuable germplasm.

**High concentrations of seed oil and protein found in seeds of cotton genebank samples.** Cotton not only yields valuable fiber, but cotton seeds (a byproduct of ginning) can be fed to dairy cattle and contain oil valuable for cooking and industrial purposes. Consequently, cotton seeds with more protein and oil could generate additional profits for producers and processors. ARS researchers in College Station, Texas, and their collaborators analyzed more than 2,000 ARS cultivated cotton genebank samples and identified some with seed oil and protein concentrations that exceeded current commercial varieties. The results showed that these high value traits were in genetic backgrounds that would enable rapid incorporation into commercially-competitive lines.

**Identification of historic and novel gene pools within Chinese fringe trees.** Chinese fringe tree (*Chionanthus retusus*) is an increasingly popular flowering tree valued for its wide adaptability across North American landscapes; however, little was known about the diversity and origin of material in the nursery industry. Molecular markers developed by ARS researchers in Poplarville and Stoneville, Mississippi, and in Washington, D.C., were used to determine relationships among cultivated Chinese fringe trees in the United States. Commercially available material originated from three sources, the majority from northeastern China, followed by Taiwan, and Japan. Additional novel material from China and Korea are available in

botanical collections, with the U.S. National Arboretum housing the most diverse and complete collection. For the first time, morphology and performance of cultivated Chinese fringe trees are linked with their geographical origin, which allows researchers to more effectively collect and distribute adaptable material to the nursery industry.

### Component 3 – Crop Biological and Molecular Processes

**EPA amends the registration of USDA’s C5 HoneySweet biotech plum, thus clearing the way for a public release.** Sharka disease, which is caused by the plum pox virus, has devastated stone fruit production (plum, peach, cherry, and almond) in Europe and periodically threatens the United States. There is no known source of natural genetic resistance to Sharka. When outbreaks are discovered in North America, diseased trees are eradicated by removal at great cost. ARS scientists in Kearneysville, West Virginia, have developed a biotech plum called HoneySweet that is resistant to Sharka. In 2014, EPA approved an amendment to the registration of HoneySweet that will require ARS, but not nurserymen or HoneySweet growers, to be responsible for registering, keeping records, and reporting production of HoneySweet to the EPA. This agreement provides a way forward for ARS to officially release C5 HoneySweet plum as an option for plum growers facing a severe outbreak of Sharka disease.

**Soybean genes that retard cyst nematode development.** Soybean cyst nematodes attack the roots of soybean plants and cause approximately \$1–2 billion in damage each year to the U.S. soybean industry. Genetic resistance combined with crop rotations is the most sustainable way to manage this pest, but the pathogen changes so rapidly that this is a challenging strategy. Toward providing a longer-term source of genetic resistance, ARS researchers in Beltsville, Maryland, designed and evaluated multiple DNA constructs to provide resistance to both soybean cyst and root-knot nematodes. The DNA segments successfully decreased galls formed by root-knot nematode and cysts formed by the soybean cyst nematode by approximately 70–90 percent. This new strategy using several gene constructs can now be exploited by soybean breeders to combat nematodes that lower soybean yields, and could be adopted for use with other crop species. The technology has been patented and transferred to industry partners, and products are being developed for commercialization.

**Producing “clean” berry crops free of targeted pathogens.** To be competitive and profitable, berry producers require clean plants (i.e., those with no viruses) that establish quickly and have higher yields and fruit quality than diseased plants. ARS scientists in Corvallis, Oregon, with collaborators at the University of Idaho evaluated strawberry, blackberry, raspberry, elderberry, grape, and blueberry and eliminated viruses from multiple cultivars and advanced selections as part of the National Clean Plant Network with funding from USDA-APHIS. These resulting “clean” plants are the starting material for certification programs that monitor and regulate the large-scale production of these crops. The testing and cleanup that occurred through this effort is also facilitating the export of more than 50 million berry plants for planting in other countries.

**Deciphering soybean rust resistance.** Discovery of soybean genes and proteins that are important for resistance to soybean rust will improve soybean cultivars through conventional breeding or transgenic technology. Proteins previously discovered in the cell nucleus of soybeans resistant to soybean rust were thought to help activate resistance, but this had not been confirmed. ARS scientists in Beltsville, Maryland, discovered that resistant genes function as a network to govern resistance to soybean rust, and disruption of specific genes within this network is necessary to breed resistant plants. They identified two genes that when disrupted by the addition of a specific virus, trigger the production of molecules toxic to fungi, including those that cause soybean rust; thus, soybean rust resistance was attributed, in part, to the production of antimicrobial molecules. Several genes that control the production of these antimicrobial

molecules were discovered. The genes are being tested in soybean plants to determine functionality. This discovery provides novel soybean genes needed to fight rust diseases.

**Discovery of locations of the cotton chromosome controlling cotton fiber quality.** Negative correlation between yield and fiber quality is an obstacle for cotton improvement. Identification of stable cotton fiber quantitative trait loci (QTL) is essential in order to improve cotton cultivars with superior quality using marker-assisted selection (MAS) strategy. ARS scientists in New Orleans, Louisiana, identified 131 fiber QTLs and 37 QTL clusters using a random-mated recombinant inbred population. The fiber QTLs and QTL clusters identified in this research can be readily selected and implemented in a cotton breeding program to improve fiber quality while maintaining yield via MAS strategy using the identified markers.

**Developing trap crops to combat Potato Cyst Nematode (PCN).** PCN is a quarantine pest that threatens the Idaho potato industry and is extremely difficult to eliminate because it can persist in the soil for 30 years without a host. Currently, the only means of eradication is through soil fumigation. ARS scientists in Prosser, Washington, have confirmed that Litchi Tomato is an effective trap crop against PCN. An improved line with less thorns was developed, and large amounts of seed are being increased for use by the Animal and Plant Health Inspection Service in the first field trial in the United States in 2015. ARS scientists identified another potential trap crop in addition to the Litchi Tomato, which is being further characterized. Progress has been made in determining ways to extract compounds from potatoes that have potential to eradicate or control the nematode. These findings have the potential to reduce the threat posed to the U.S. potato industry by PCN without the use of environmentally harmful fumigants.