

USDA  
AGRICULTURAL RESEARCH SERVICE

**NATIONAL PROGRAM 301 –**  
PLANT GENETIC RESOURCES, GENOMICS, AND GENETICS IMPROVEMENT  
**ANNUAL REPORT FY 2010**



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*Introduction*

National Program 301 – Plant Genetic Resources, Genomics, and Genetic Improvement – endeavors to ensure the long-term safety, value, and integrity of agriculturally valuable genetic resource collections; to identify favorable alleles from plant genetic resources and breeding stock and create novel methods to deploy them in crops; to exploit new genomic approaches and technologies to enhance traditional methods of genetic improvement; to genetically improve a broad spectrum of major, specialty, and new crops; to increase our knowledge of the structure and function of crop genes and genomes; and to acquire, maintain, analyze, and deliver genetic, genomic, and informatics tools and resources needed to attain the REE Research Priorities for climate change; food safety; children’s nutrition/health; international food security; and bioenergy.

Genetic resources are the foundation of our agricultural future. The Agricultural Research Service (ARS) genebanks contain the sources of resistance to biotic and abiotic stresses and new alleles to improve the quantity and quality of our food, feed, energy, fiber, and ornamental crops. To ensure that those genes are available for research and breeding, ARS must continue to acquire and conserve germplasm that contains them, to develop new screening methods for identifying favorable traits, to ensure that germplasm is distributed where and when it is needed, and to safeguard these collections and associated data for future generations.

Through this National Program, ARS also assumes a strong leadership role in developing and curating crop genomic and phenotypic databases and information management systems. It develops new tools needed to efficiently extract useful information from the ever-increasing flow of data into these databases. Methods to interconnect diverse databases are constructed to more efficiently and effectively identify important properties of genes and genomes, to apply that knowledge to crop improvement, to associate specific genes with the genetic control of agriculturally important traits, and to build upon genetic advances in one crop so as to accelerate genetic gain in others.

For major, specialty, and new crops, ARS, in close cooperation with many public and private sector collaborators, improves and broadens the genetic base of U. S. crops to reduce genetic vulnerability. As part of this National Program, it devises and applies new technologies to develop superior new crop varieties and enhanced germplasm, and to accelerate the deployment of high-value traits into breeding populations by identifying and incorporating superior new alleles and gene combinations into crop breeding lines and gene pools. It devises new breeding theories and strategies to effectively capture the intrinsic genetic potential in germplasm, especially for key agronomic or horticultural traits. In addition to conducting research, ARS and its university cooperators play a key role in mentoring and training the next generation of crop breeders and geneticists.

This National Program is divided into three research components:

- *Plant and Microbial Genetic Resource Management* (conserving a broad spectrum of genetic resources and facilitating their use in genetic improvement and scientific research);
- *Crop Informatics, Genomics, and Genetic Analyses* (developing and applying new approaches for comparative and functional crop genomics; elucidation the underlying genetic basis for key crop traits; developing new software tools for analyzing and managing genomic and genetic resource information; maintaining and delivering the former via databases and information management systems implemented on up-to-date computer networks); and
- *Genetic Improvement of Crops* (including plant breeding, genetic enhancement, molecular marker analyses, nucleotide sequencing, and genetic mapping).

Together, these research components are yielding breakthroughs in understanding genome composition, manipulating genetic material, and providing genetically diverse gene pools with sustained and enhanced agricultural value. During fiscal year (FY) 2010 this program produced many important discoveries and advances. Some of these are described on the following pages, grouped by research component.

## **Component 1: Plant and Microbial Genetic Resource Management**

*More than 535,000 samples of crop genetic diversity conserved and distributed to researchers.* During fiscal year (FY) 2010, the 20-plus genebanks in the USDA ARS National Plant Germplasm System (NPGS) added more than 5,800 new samples, so that a total of more than 535,000 distinct types of more than 13,400 plant species are now conserved by NPGS genebanks. Scientific interest, especially for germplasm of specialty crops, has increased tangibly during the last few years, with the average number of samples distributed per year by the NPGS now totaling about 150,000 – 50,000 more than the average a decade ago. These materials are keys for continued progress in crop genetics and breeding which is requisite for future food security.

*Key genetic tools for grain and biofuel crop improvement research are safeguarded.* The genomes of the major grains wheat and barley and the biofuel crop switchgrass are so large and complicated that analyzing their genetic function and structure requires special genetic tools. Researchers from the ARS genebank in Pullman, Washington, greatly expanded the collection of genetic lines of Brachypodium (purple false brome), a small, rapidly flowering grass, with a relatively tiny genome which has been completely sequenced. Knowledge gained about the gene content, structure, and arrangement of this “model plant” can be readily extended to gene discovery and functional analyses of related grain and bioenergy crops. Thus, by safeguarding and distributing a large collection of different lines of this key genetic tool, ARS genebanks are catalyzing efforts to map and manipulate key traits for genetically improving major crops.

*New methods developed for safeguarding invaluable citrus plants.* Oranges, grapefruit, lemons, limes, and other citrus trees are highly susceptible to many lethal diseases, damaging pests, and low temperatures. Breeding citrus resistant to the preceding perils is one of the most effective means of protecting this multi-billion dollar crop. Key resistance genes often occur in the invaluable genetic resources comprising unimproved dooryard varieties and wild citrus species. These genetic resources are often reproduced as clones, and are currently maintained in field orchards and screen houses because long-term storage of citrus clonal vegetative tissue has been infeasible. Researchers in ARS’ genebank in Fort Collins, Colorado, developed new “micrografting” recovery methods that enable clonal citrus samples to be stored at the temperature of liquid nitrogen and successfully re-propagated. Storing duplicate clonal samples in secure genebank vaults will safeguard these precious materials from disease, damage, or loss suffered in field orchards and screen houses, and will enable them to be distributed to researchers more efficiently.

*Demonstration that *Ulmus americana* (American elm) consists of at least two chromosomal races.* The American elm (*Ulmus americana*) has been decimated across the United States by the Dutch elm disease, and efforts are ongoing to develop trees that are resistant to this disease. An ARS scientist in Washington, D.C. investigated geographical variation in chromosome number in American elm. Cells from plants throughout the range of the species were examined with flow cytometry, which revealed that both diploid and tetraploid chromosome races are found in the species. The diploid race was previously unknown, suggesting that considerable untapped genetic variation remains in this species, one of the most important tree species for the American nursery industry. This information will be valuable as efforts continue to develop American elms that are resistant to Dutch elm disease.

*Identifying key sorghum lines for bioethanol production.* Sorghum with high sugar content (sweet sorghum) is an important biofuel crop, but its genetic content must be characterized before it can be bred and incorporated into genetic research efficiently. Researchers at ARS' genebank in Griffin, Georgia, analyzed 96 sweet sorghum samples with DNA genetic markers to determine their genetic variability and population structure. This new genetic information for these sweet sorghums will enable breeders to develop superior sweet sorghum cultivars for bioethanol production.

## **Component 2: Crop Informatics, Genomics, and Genetic Analyze**

*The Legume Information System (LIS) interlinks genetic and genomic information across food and forage legumes.* The global production of legume crops, including soybean, common bean, lentils, chickpea, pigeonpea, fava bean, and more, is crucial for global food security and human nutrition. Yet few legume crop research and breeding communities have the full complement of genomic and genetic resources to sustain a modern breeding program. ARS scientists in Ames, Iowa, together with scientists at the National Center for Genome Resources (NCGR), Santa Fe, New Mexico, have addressed this critical need through the Legume Information System (LIS) – a Web site and database that serves as a long-term data repository and a portal interlinking the genetic and genomic resources of a growing number of legume species. The LIS provides powerful new tools to retrieve, analyze, compare, and visualize legume genetic data. It enables domestic and international researchers to apply knowledge collated from legumes with complete genome sequences to develop additional genomic resources for the genetic improvement of other legume crops.

*The corn haplotype map (HapMap) provides new insights into corn breeding at the genome level.* Genetic diversity is the raw material for germplasm improvement by breeders. ARS scientists in Ithaca and Cold Spring Harbor, New York, and Columbia, Missouri, produced a high-resolution haplotype map of DNA sequence differences for the genomes of 25 carefully selected lines of corn. More than 3 million DNA sequence differences between the B73 reference genome sequence and the 25 diverse lines were identified. The data revealed that approximately 130 regions of the corn genome have been selected strongly over the years by breeders and thus contain agriculturally important and valuable genes. The comparison of the DNA sequence variation data and genetic data revealed that 15 percent of corn genes are in regions characterized by low rates of genetic recombination, or chromosome shuffling, indicating that regions of the maize genome have been underexploited by breeders and thus represent potential sources of germplasm improvement.

*Integrating the soybean genome sequence with the soybean genetic map and developing an encyclopedia of soybean gene messages.* The full genome sequence of the soybean was difficult to assemble because of its large size and complexity. ARS researchers in Ames, Iowa, working with the U.S. Department of Energy and ARS collaborators in Beltsville, Maryland, helped to assemble the sequence and to integrate the whole genome sequence with the soybean genetic map. Thus, the sequence is now correlated with soybean traits collected during the last 30 years (~85 distinct mapped traits). Plant breeders can now begin to understand at a molecular level the genes that govern the traits for which they breed. This is an important addition to our knowledge about soybean and, will be an invaluable tool for developing improved varieties. Soybean has nearly 50,000 genes within its genome, but the function for most of these genes is unknown. Knowing when and how much each gene is turned on will help determine the gene's function. ARS scientists at Ames, Iowa, analyzed many millions of gene messages from 14 tissues

or stages of development. This resulted in a “gene Atlas”, which will be critical to the eventual identification of the function for all the genes in the soybean genome.

*Cacao genome sequenced.* Cacao, the source of chocolate, is a multi-billion dollar international commodity grown by several million small farmers in tropical developing nations. Threatened by many virulent diseases and damaging pests, cacao requires new tree types with inherent resistance to pests and diseases, plus high yields and fine cocoa quality. Currently, cacao breeders lack DNA genetic markers required for rapid selection of trees with desired traits at the seedling stage, rather than at maturity. ARS scientists in Miami, Florida, and Stoneville, Mississippi, with collaborators at Mars, Inc., IBM, and several U.S. universities enlisted a novel mixture of traditional and leading-edge techniques to fully sequence the genome of a particular cacao variety that shares ancestry with many of the trees grown world-wide. This genome sequence can now be compared with genetic information from other cacao varieties with different properties to rapidly identify many thousands of genetic markers, and thereby accelerate cacao genetic improvement to benefit farmers and cocoa processors globally.

*Molecular markers for chilling requirement in peach.* Chilling requirement determines where peaches are adapted. In cooperation with Clemson University, ARS scientists in Byron, Georgia, identified molecular markers associated with chilling requirement in peach seedlings from the ARS Byron breeding program. Identifying the associated genes will facilitate breeding for chilling requirement, and enhance understanding of how the chilling process works.

*Discovery of 33,065 new simple sequence repeat DNA markers to enrich scientific understanding of the soybean genome.* With the recent release of the complete DNA sequence for the soybean genome, the task now at hand is identifying large numbers of DNA markers located throughout the 20 soybean chromosomes. ARS scientists in Beltsville, Maryland, collaborating with ARS scientists in Ames, Iowa, screened the DNA sequence of the 20 soybean chromosomes and identified more than 33,000 simple sequence repeat (SSR) DNA markers with a high probability for effectively locating the positions of genes on the soybean chromosomes, information which will enhance DNA marker-assisted soybean breeding. A database was created that contains the information required to effectively apply these markers, including the specific position of each marker on the 20 soybean chromosomes. This information is publicly available on SoyBase (<http://soybase.org>), the USDA ARS Soybean Genome Database. The information will be useful in fine-mapping for genes, a process that involves identification of markers that are very tightly linked to a targeted gene. A genetic fine map for a specific gene locus is one standard route for identifying and locating markers situated as close as possible on both sides of the targeted gene. In soybeans, this process has been hindered by lack of that type of information. Researchers can now identify specific genes for further analyses or for crop improvement by transgenic technology.

*Sugar beet seed germination under high salt concentrations.* High salt concentrations in soils are common in sugarbeet growing areas. Poor seedling establishment is a key limiting factor in sugar beet production, and numerous causes have been suggested, including high salt-soil environments. Poor seedling establishment means that far more seeds are required to ensure optimum production. To identify key breeding lines that enhance seedling vigor and ensure optimum germination and establishment, the response to salt stress on germination and production was determined. Two different responses to saline environments were found – one resulted in a dose-dependent reduction in germination percent, and the other mode was a time-delayed germination rate, but less overall reduction in total germination. As a

result of this study, valuable, new germplasm was identified with tolerance to salt stress during germination that will be available to sugar beet seed companies for further development.

*Development of a low-cost and high-throughput genotyping method for peanut.* Traditionally, peanut cultivars have been developed solely by conventional breeding methods. Combining traditional breeding with marker-assisted selection in plant breeding has significantly increased the rate of genetic gain, compared to conventional breeding alone. Due to the many molecular markers required for genotyping studies and the high cost of developing these markers, laboratories with small budgets and/or limited or no access to expensive equipment cannot afford marker-assisted breeding. ARS researchers in Tifton, Georgia, introduced a low-cost, relatively high-throughput system utilizing silver staining for peanut genotyping applications. This method was successfully applied by ARS researchers to peanut genotyping and linkage map construction, and may also be applicable to other crops.

*Development of “intragenic” potatoes containing a late blight-resistance gene.* The commercial introduction of crop plants improved by biotechnology has been limited by negative public perceptions for the safety of transgenic foods. These negative perceptions are being addressed, in part, by developing novel methods for in vitro genetic modification, referred to as “intragenic” technology. This method of gene introduction results in transgenic lines that contain no foreign DNA. ARS scientists in Albany, California, in cooperation with scientists at the J.R. Simplot Co., in Boise, Idaho, have successfully developed intragenic potatoes that contain a gene from wild potatoes known to confer resistance to the most devastating of potato diseases, late blight – the cause of the Irish potato famine, and which still plagues growers today. These potatoes do not contain any non-potato DNA, and were generated in vitro without selection (i.e. they do not contain antibiotic/herbicide resistance genes as markers). Intragenic lines with late blight-resistance in the greenhouse and under field conditions will represent an important option for preventing losses to late blight.

*New approaches to citrus improvement through “intra-genics”.* Genetically transforming crops with genes derived from that particular crop, termed “intra-genics,” has been advanced as a commercially viable means of developing resistance to the devastating Huanglongbing (HLB) or citrus greening disease. But this approach requires a citrus genome database. The limited amount of publicly accessible citrus genomic DNA sequence has significantly impeded applying this process to citrus improvement. To encourage the application of this technology to citrus breeding, ARS scientists in Albany, California, and Fort Pierce, Florida, partnered to sequence the genome of the citrus rootstock ‘Carrizo’, and made this sequence publically available (<http://citrus.pw.usda.gov/>). Although this database will be useful for a broad array of applications, ARS researchers are applying it to identify citrus DNA sequences containing HLB-resistant genes. For example, these data have identified DNA sequences which enable high-level expression of introduced genes in vascular tissue, where the causal agent of HLB is found. Given that HLB currently represents the most serious threat to citrus production in the United States and no resistance genes have yet been identified, the successful development of resistant trees offers a potential solution crucial in sustaining this crop.

*New molecular breeding tools for heart-healthy oats.* The oat genome is so large and complex that little genetic information and molecular markers have been available to assist oat breeding. This has meant that breeding for sustainable oat production and increased nutritional value has been slowed. In 2010, ARS researchers in Aberdeen, Idaho, and Albany, California, applied innovative DNA sequencing methods to produce 650,000 oat gene DNA sequence fragments. In addition, ARS researchers in

Aberdeen teamed with ARS scientists in Fargo, North Dakota, and Raleigh, North Carolina, to develop the first oat-based single nucleotide polymorphism (SNP) markers. More than 700 SNP markers, which are highly useful to plant breeders, have been developed. The research was supported by ARS with additional funding from General Mills, North American Millers Association, and the USDA National Institute of Food and Agriculture. These major advances in molecular markers are publicly available to all oat breeders. This plethora of new tools will enable oat breeders to use molecular markers for the first time to select and accelerate breeding for agronomic traits, disease resistance, and nutritional quality (high fiber and beta-glucans).

*New method developed to identify drought-tolerant sorghum lines.* Sorghum yield losses to drought are significant, but crop breeding for drought tolerance under practical field conditions is difficult because of variable rainfall patterns. ARS scientists in Lubbock, Texas, have developed a break-through method to screen for drought tolerance in plants that are not even drought stressed. A new method, involving a short-term heat stress of leaf tissue followed by temperature recovery, is effective in identifying “stay-green” lines with drought tolerance. The method has proven effective in identifying more drought tolerant lines at both pre- and post-flowering growth stages and has identified new sources of drought tolerance in sorghum lines from Sudan. This new selection method will greatly reduce the selection time crop breeders need to develop more drought tolerant sorghum.

*Apple rootstock breeding and genetics for improved mineral absorption.* Nutrient and micronutrient absorption and translocation are important apple rootstock traits that have been largely unexploited by breeding programs due to the high cost of testing tissue samples for mineral absorption. Developing a method for discovering, breeding, and selecting efficient absorbers and translocators of mineral nutrients would greatly enhance the overall impact on sustainable apple production worldwide. Furthermore, it could improve the concentration of essential dietary minerals for humans. ARS apple researchers in Geneva, New York, in collaboration with Cornell University, the Lithuanian Institute of Horticulture, and USDA ARS Children's Nutrition Research Center, Houston, Texas, grafted an array of representative apple rootstock genotypes with the same scion (Gala) and tested for genetic influence on the uptake of macro- and micronutrient minerals at different soil pH levels. As a general trend, absorption of molybdenum, calcium, and phosphorous increased with higher pH levels, while absorption of iron, manganese, and nickel decreased with increasing pH. Absorption of potassium, copper, sodium, zinc, magnesium, and sulfur did not seem to be affected by soil pH. The researchers discovered significant differences among rootstocks for leaf concentration for all macro and micronutrients tested. These differences were also transferred to an experimental population so as to discover genes related to nutrient metabolism. This new knowledge will be incorporated into the marker-assisted breeding scheme of the ARS apple rootstock breeding program to improve the efficiency of selecting superior lines.

*Elucidating the genetic control for high-value apple rootstock traits.* Dwarfing and precocity are high-value apple rootstock traits that require lengthy periods (3-9 years) of field testing for breeding and selection of new rootstocks. The discovery of the genetic control of these traits enables ARS scientists in Geneva, New York, to select dwarfing/precocious plant material before it is planted in the field, thus creating substantial efficiencies in the breeding and selection of new rootstocks. The researchers elucidated the inheritance and location in the apple genome of these multi-gene traits, as well as their effect, and are applying this information to implement marker-assisted selection in their breeding program.

*Accelerating introduction of powdery mildew resistant table, raisin, and wine grape cultivars through marker-assisted selection.* New cultivars with powdery mildew resistance are desired by grape growers, but durability of this resistance is critical due to the cost of vineyard establishment and the necessary longevity of grapevines. ARS researchers in Geneva, New York, successfully documented that some resistances in breeding programs could be overcome quickly by common pathogen isolates and communicated a need for breeders to incorporate (or “pyramid”) multiple resistance genes into new cultivars. The researchers applied molecular markers to track these resistance genes and to accelerate the breeding of varieties with durable, multi-gene resistance. They also identified a source of powdery mildew resistance that prevents the pathogen penetration and appears to be durable by itself. They are applying molecular markers to track the introgression of this resistance gene into high quality raisin, table, and wine grapes. Varieties bred with broad spectrum powdery mildew resistance would save growers between \$100 to 400 per acre per year in pesticide costs and reduce direct and indirect effects of pesticide application.

*Localizing genes for cold hardiness in grape.* Grapevines grown in many regions of the eastern United States are poorly adapted to low temperatures and frequently are damaged by severe winters and fluctuating temperature during the spring and fall. There is tremendous variation among cultivated and wild grapes for tolerance to low-temperature stress, including some types that can survive -40° F. To understand the genetic control of freezing tolerance, the genomic locations of grape genes controlling freezing tolerance were identified by ARS researchers in Geneva, New York. Mapping this trait is the first step for developing an assay that will improve the selection efficiency within grape breeding programs for this trait and generating improved cultivars of grape for cold climates.

*Sugarbeet breeding for bacterial root rot resistance.* An important new bacterial species, *Leuconostoc* sp. was identified to cause root rot that can lead to 70 percent or more loss of sugarbeet root mass in the field prior to harvest. In addition, significant losses are incurred post-harvest in sugarbeet storage piles where many varieties are stored together for weeks and months. Bacterial rot caused by *Leuconostoc* sp. contributes even further to losses in the sugar factory, where gums produced by the bacteria interfere with processing. Therefore, reducing bacterial root rot and developing methods to identify resistant sugarbeet varieties will increase processing efficiency along with enhancing yield and profits for sugarbeet growers. A key problem in storage is that sugarbeet varieties associated with the rotted area are mixed, and cannot be identified. ARS researchers in Kimberly, Idaho, with the cooperation of the Amalgamated Sugar Co., identified four DNA markers to differentiate the commercial sugarbeet varieties approved for production in Idaho, Oregon, and Washington. These markers provide a valuable tool for evaluating differences in sugar losses among sugarbeet varieties during storage, and will help in identifying those varieties that are susceptible to bacterial rots. Therefore, developing cultivars with effective host resistance to bacterial root rot and providing a means to identify commercial varieties when combined in piles post-harvest are valuable disease management tools, and important addition to the current breeding program. Introducing resistance to bacterial root rot into commercial sugarbeet cultivars should substantially reduce losses in the field, in storage, and in the sugar processing factory, thus enhancing production and economic returns.

*Molecular mapping of sunflower rust resistance genes.* Rust is a serious fungal disease in the sunflower growing areas worldwide, with increasing importance in North America in recent years. The most profitable and environmentally friendly strategy for farmers to control sunflower rust is to grow genetically resistant hybrids. Several genes conferring resistance to sunflower rust have been identified, but some were not efficient for breeding because they were not genetically mapped. One such rust-

resistant gene, R4 in the germplasm line, HA-R3, confers resistance to 88 percent of 300 rust isolates tested in the United States. ARS scientists in Fargo, North Dakota, mapped this gene within a large gene cluster in the sunflower genome which is often associated with disease defense response. Two molecular DNA markers were identified that flank the R4 gene closely on both sides, a tight linkage advantageous for incorporating (“pyramiding”) genes for rust resistance through molecular marker-assisted selection.

*Genome-wide analysis identifies genes involved in Southern corn leaf blight resistance.* Southern leaf blight causes losses in corn production, but resistance breeding is difficult because of the many genes associated with this complex trait. To identify Southern leaf blight resistance genes, ARS researchers in Raleigh, North Carolina, have exploited new corn genomic information and genetic resources, including the corn genome sequence, the Nested Association Mapping population, and the maize Haplotype Map, with 1.6 million DNA markers. The preceding tools were generated with support from the USDA, National Science Foundation, and the U.S. Department of Energy. ARS researchers applied genome-wide analysis methods to pinpoint specific DNA sequence variations associated with Southern leaf blight resistance throughout the genome. This discovery will enable crop breeders to develop corn with genetic protection to Southern leaf blight.

### **Component 3. Genetic Improvement of Crops**

*ARS scientists develop innovative, genome-wide selection methods to make crop breeding more efficient and faster.* Genome-wide selection methods which incorporate DNA genome sequence information are potentially more effective than breeding methods based on trait selection and molecular markers. However, when ARS scientists in Ithaca, New York, simulated 20 cycles of breeding, they determined that genome-wide selection methods provided short-term gains, but became less effective after multiple cycles of genetic selection. With that insight, the scientists developed an improved breeding method that capitalizes on molecular marker data to make genome-wide predictions, but also maintains genetic diversity and minimizes the loss of favorable traits during genetic selection. Through this method, the researchers demonstrated that genome-wide selection out-performed trait (phenotypic) selection in both the short and long terms. These new breeding tools provide practical methods for plant breeders to adopt genomic selection methods that substantially improve long-term benefit without reducing rapid initial gains.

*Method to enhance propagation of woody plants.* Shoot regeneration from leaves of known fruit varieties is a preferred method of regeneration of transgenic plants, because the transgenic plant is identical to the variety except for the inserted gene. Genetically engineered stone fruit plants are currently made from seedlings, so they are all genetically different from the original variety. The seedlings are preferred, because leaves from varieties of plum and other stone fruits generally will not regenerate plants. ARS researchers in Kearneysville, West Virginia, found that, when plum leaves express an inserted corn gene, KNOX1, they produced shoots in high frequency. This is the first report of plant regeneration from leaves of a woody perennial fruit tree, such as plum, using a regeneration-inducing gene from corn.

*New sorghum germplasm developed with improved value as a bioenergy feedstock.* The value of sorghum as a bioenergy feedstock can be improved by increasing biomass digestibility. ARS scientists in Lincoln, Nebraska, have determined the effects of inserting and combining brown midrib gene mutations into a grain sorghum hybrid. These mutations lowered the content of lignin, a polymer that provides

rigidity to the cell wall and hinders cell wall decomposition. Effects of the genetic changes on sorghum biomass composition and whole-plant physiology were assessed in a 2-year field experiment. Overall, sorghum brown midrib mutants have reduced lignin and increased biomass digestibility, with minor impacts on plant fitness and yield in hybrid backgrounds. This sorghum germplasm with reduced lignin content and increased biomass digestibility provides a new genetic resource to develop sorghum as a bioenergy feedstock.

*Late-flowering blackberries are sweeter and higher in antioxidants.* ARS researchers in Beltsville, Maryland, compared 122 blackberry cultivars and breeding selections for antioxidant levels, flavor, flowering season, and fruiting season to help farmers and blackberry breeders better select blackberry varieties. In addition to finding a tremendous range for all traits observed, late-flowering blackberries tended to be sweeter and higher in antioxidants. This information can be applied by breeders to develop new varieties that extend the growing season.

*New germplasm and genetic resources developed to protect wheat and barley from the Ug99 stem rust.* Wheat and barley germplasm with resistance to the virulent Ug99 stem rust strain is urgently needed to protect the global grain supply. ARS researchers in Raleigh, North Carolina; Aberdeen, Idaho; and St. Paul, Minnesota, evaluated 4,000 wheat and barley varieties and germplasm lines in Njoro, Kenya, for resistance to Ug99 stem rust. Lines were submitted from more than 25 public and private sector U.S. breeding programs. ARS researchers in Raleigh also developed 750 wheat lines with stem rust genes combined in two, three, four, and five gene stacks (or pyramids). These lines also have gene combinations for leaf and stripe (yellow) rusts. The researchers in Raleigh also developed and distributed 30 advanced lines of wheat incorporating multiple-gene resistance to stem rust race Ug99 to wheat breeders in 32 countries in cooperation with the International Wheat and Maize Improvement Center in Mexico. This information will enable breeders in the United States to identify and deploy resistance to Ug99 stem rust in advance of the pathogen ever arriving in the United States. These lines will greatly aid U.S. and international wheat breeders develop better worldwide resistance to stem rust race Ug99.

*Can rice be considered a healthy starch for consumers?* The incidence of diabetes has dramatically increased in recent years in the United States. Starchy foods, like rice, are not recommended for people managing diabetes. ARS scientists in New Orleans, Louisiana, and Beaumont, Texas, evaluated 16 commercial rice cultivars and found that they differed in starch digestibility. Some cultivars had high levels of resistant and slowly digestible starch, indicating that, when consumed, the sugars would be slowly released into the bloodstream, as compared to other rice cultivars. This is important to consumers interested in moderating sugar in their diet. This study demonstrated that rice cultivars differ in the amount of nutritionally important starch fractions and offers the opportunity for developing new cultivars with improved dietary benefits.

*Developing beans adapted to growth under high temperatures.* Common bean (*Phaseolus vulgaris* L.) is a vital part of the diet in many areas of the world. Bean reproductive development is particularly sensitive to high temperature stress, resulting in yield reduction and limited adaptation to warmer climates. ARS scientists in Mayaguez, Puerto Rico, with cooperators at the University of Puerto Rico, Cornell University, and the University of Tennessee, developed two kidney bean varieties that are tolerant to high temperature conditions. One variety is tolerant to high day and night temperature stress, while the second is tolerant to high daytime temperature stress and moderate nighttime temperature stress. These kidney beans yield more grain under hot summer conditions when grown by farmers in regions prone to high

temperature stress. In addition, they can be used for improving heat tolerance in other large-seeded beans through breeding and selection.

*The new soybean genome sequence is linked to 30 years of trait information by SoyBase and the Soybean Breeders Toolbox.* The complete DNA sequence for the soybean genome produced by ARS scientists in Ames, Iowa, and Beltsville, Maryland, together with university and Department of Energy collaborators, was released in 2010. It is one of the largest and most complex genomes sequenced to date. To take full advantage of this important new resource for soybean improvement, ARS scientists incorporated the sequence information into SoyBase and the Soybean Breeders Toolbox, the USDA's soybean genetics and genomics database. SoyBase now includes extensive 'under-the-hood' links to 30 years of data for many high-value traits, including seed yield, seed quality and disease susceptibility, biochemical pathways, and tens of thousands of new DNA marker sequences and genes, as well as powerful, new visualization tools for the soybean genetic and physical maps and the soybean genome sequence. SoyBase now will enable plant breeders to comprehend the genetic control and function of genes that govern critical agronomic traits.

*Progress in lowering barley feed grain phosphorus content.* A valuable strategy to reduce the environmental impact of dairy and beef production and other forms of animal agriculture is to minimize the amount of nutrients in feeds to a level that both maintains productivity and results in reduced waste. This is a key concern for higher than necessary levels of feed grain phosphorus and the resulting high phosphorus level in animal waste. ARS researchers in Aberdeen, Idaho, demonstrated that one function of the barley *lpa1* (low phytate) gene is to generate a signal in the developing seed that regulates the amount of phosphorus transported into it from the mother plant. This provides new information that plant geneticists can apply to reduce total seed phosphorous. In complementary research, ARS researchers in Aberdeen released four new germplasm lines with highly digestible phosphorous in the important commercial categories of barley. All this new information and genetic resources will advance the development of environmentally friendly feeds that lower phosphorous levels in animal waste and manure.

*Antioxidant activity in rabbiteye blueberry.* Extensive variation in antioxidant enzyme activities exists among cultivars of rabbiteye blueberries and rabbiteye-hybrid derivatives, but the range and nature of this variation are not well characterized. ARS scientists in Beltsville, Maryland, found that rabbiteye blueberry cultivars had varying levels of non-enzyme antioxidant components, such as ascorbic acid, and a wide range of levels of antioxidant enzyme activities. Among 42 cultivars, 'Early May' had the highest enzyme activity. This information will be applied by blueberry breeders to develop new blueberry cultivars with enhanced nutritive value.

*ARS scientists discovered natural variation that markedly increases Vitamin A in corn.* Billions of people and livestock use corn (maize) as a major source of subsistence and nutrition. However, corn is generally not a good source of pro-Vitamin A, and vitamin A deficiency can lead to childhood blindness and immune deficiencies. Building on a prior discovery, ARS researchers in Ithaca, New York, and collaborators, discovered that the natural variation at two genes in corn can be exploited to breed corn with a 16-fold higher level of pro-Vitamin A than is contained in standard corn. Crop breeders are already starting to use this discovery to breed more nutritious varieties of corn, particularly where increased pro-Vitamin A is urgently needed.

*Improved efficiency for utilizing the USDA peanut germplasm collection – finding genes for improved fatty acid composition.* Fatty acid composition is an important characteristic for oil seed crops such as peanut. High oleic acid composition is favored in peanuts because it confers health benefits and improved oil stability. The high oleic trait in peanut is controlled by two genes, and peanut has a normal oleic fatty acid composition unless both genes are present. Most current peanut genotypes already contain one of the genes, but it has been very difficult to identify the other mutant gene. Plant breeding efficiency would be improved if the normal oleic peanut genotypes that contained this other gene could be identified. ARS researchers in Tifton, Georgia, not only developed a molecular marker that can do just that, but also applied the marker to survey the U.S. peanut germplasm collection for the frequency and distribution of the mutated gene. They discovered that almost one-third of the collection contained the mutant gene, and found that this mutation was much more prevalent in types of peanuts, but not in others. This information will help plant breeders decide which parents to incorporate into variety development to improve fatty acid composition.

*Providing solutions to a new virus in potato breeding programs.* The ARS potato breeding program depends on diverse wild relatives of potatoes as sources for important traits, such as enhanced nutrition and resistance to frost, pests, or diseases. Commercial potato undergoes extensive tests and clean-up for viruses that are transmitted through seed pieces for planting. Many viruses infect potatoes and closely related species, resulting in substantial economic losses, thus necessitating the potato virus clean-up programs in the United States. One of these potato relatives, *Solanum acaule*, contributed valuable genes to potato breeding programs, but the USDA Animal and Plant Health Inspection Service detected a new virus that had been introduced into the United States in the seed of *S. acaule*. ARS scientists in Prosser, Washington, identified the virus as a new variant of cherry leaf roll virus and alerted personnel in potato breeding programs that the virus posed a threat. The scientists developed new methods for rapid detection and identification of the virus in their breeding programs to limit its spread, and minimize the negative impact on the industry.

*Potato germplasm resistant to cold-induced sweetening and acrylamide development in tubers.* Potato tubers stored at temperatures less than 10°C accumulate glucose and fructose in a process referred to as cold-induced sweetening. Such tubers produce dark colored, bitter tasting chips and fries with unacceptable amounts of acrylamide, a chemical compound that has been identified as detrimental to human health. One way to prevent these problems is to breed new cultivars with resistance to cold-induced sweetening. ARS researchers in Madison, Wisconsin, have conducted an extensive evaluation of wild relatives of cultivated potato to identify species with extreme resistance to cold-induced sweetening. They also quantified sugar composition and asparagine content in tubers of these wild species. Because glucose, fructose, and asparagine are involved in the fried chip off-color and to the formation of acrylamide, these data will be of interest to potato breeders who want to minimize these problems by incorporating germplasm resistant to cold-induced sweetening into cultivated potato, and to food scientists seeking materials that can serve as more effective models for the contribution of each substance to chip color and acrylamide formation.

*Potential new sources of key tomato traits identified.* Tomato, the most heavily-consumed vegetable in the United States, is a critical source of key minerals and vitamins, such as lycopenes, responsible for the tomato's red color, and implicated in reducing the occurrence of cancer and chronic diseases. Consequently, improving the quality and nutritional content of tomato is a high priority for breeding programs. ARS researchers in Geneva, New York, applied new genetic marker analyses to tomatoes

collected throughout the world as an initial step of identifying new genes that determine nutritional and other key traits. Tomatoes from South America were slightly more diverse than tomatoes from other regions for gene diversity per se, and for lycopenes, vitamin C, sugar, and the traits fruit color, size, and shape. Thus, South American tomato genetic resources are a particularly rich source for traits potentially valuable to tomato crop improvement, but no geographical region should be considered as completely lacking such traits.

*Improvement in the nutritional quality of rice grain.* Arsenic is a common, natural element in agricultural soils, and low concentrations do occur in all food crops, including rice. High concentrations, though, are not desirable because of its potential detrimental impact on plant growth and yield and its potential toxicity to humans. ARS scientists in Stuttgart, Arkansas, along with researchers at Texas A&M University and the University of Arkansas, evaluated for arsenic content 25 cultivars selected from the USDA rice germplasm collection. The researchers identified rice cultivars that have 50 percent lower arsenic content compared to other cultivars and developed field management practices that can reduce accumulation of arsenic in rice grain. Breeders and researchers can use the identified cultivars with low arsenic concentrations as parents to develop new cultivars with improved nutritional value. Farmers can use the new cultural management practices to assure high nutritional quality of the rice grain.

*Understanding the genetics behind shelf life in fresh cut lettuce mixes.* Fresh cut, bagged lettuce mixes have become very popular in the marketplace, but some varieties are clearly better suited for this than others. ARS scientists in Salinas, California, tested all advanced lettuce breeding lines for shelf life after adding harvested lettuce leaves into salad mixes. Testing was especially important for romaine-type cultivars with the lettuce dieback resistance gene, which appeared to be susceptible to rapid breakdown of tissues during processing. Resistance to lettuce dieback is essential for the major lettuce growing area of Salinas Valley, California, and resistance is the only means of control. However, the dieback-resistant material frequently produces fresh cut salad mixes with very short shelf life. Testing of lettuce for a rate of decay after processing enabled the researchers to identify two advanced breeding lines with complete resistance to dieback and significantly improved shelf life. The two lines were released and seeds were provided to lettuce-breeding companies.

*New corn genetic resources developed for high-fiber products.* Corn lines with higher levels of slowly digestible starch could provide new sources of high-fiber food products. ARS scientists in Ames, Iowa, in collaboration with Iowa State University researchers, have applied traditional breeding methods to modern and exotic corn germplasm to develop lines with higher levels of slowly digestible starch. Cooking characteristics and the effects of heating on end-product quality have been determined. These new corn lines provide new types of starch for food processing and development of high-fiber products.

*'HoneySweet' plum conditionally registered by EPA.* There are limited sources of Plum pox virus (PPV) resistance in stonefruits. 'HoneySweet', a plum genetically engineered for resistance to PPV, which had previously been deregulated by the USDA Animal and Plant Health Inspection Service and the FDA, is now conditionally registered by EPA. 'HoneySweet' is the result of more than 20 years of research by ARS researchers in Kearneysville, West Virginia, and other ARS and European collaborators. It was resistant to PPV in test plots in Europe over the last 10 or more years. When commercially available, it will be the first genetically engineered disease-resistant temperate fruit tree available to U.S. growers, providing them a high quality, fresh market, PPV-resistant plum. It can also serve as a breeding parent to reliably and efficiently introduce the resistance trait into additional new plum varieties.

*Release of new apple rootstocks.* ARS researchers in Geneva, New York, released four new apple rootstocks:

- G.214, a dwarfing, precocious, productive rootstock resistant to fire blight, with multiple disease resistance (fire blight, phytophthora root rot, and wooly apple aphid) that has performed very well in replant trials under organic management and is tailored to fresh market high density apple production amenable to mechanization.
- G.890, a semi-dwarfing productive tree resistant to fire blight that has performed well in difficult replant soils in Washington State and is tailored to fresh and processing apple production.
- G.210 is semi-dwarfing, has survived the series of inoculations with apple rootstock pathogens (*Erwinia amylovora*, *Phytophthora cactorum*, wooly apple aphid), and is tolerant to the replant disease complex.
- G.969, a semi dwarfing productive plant, is resistant to fire blight and serves as a superior rootstock for weaker or more difficult scion varieties like Honeycrisp.

All these rootstocks were tested in the field for productivity and precocity and performed very well when compared to other rootstocks with similar vigor characteristics. These rootstocks have been transferred to the nursery industry for large scale production and are expected to have a major role in sustainable apple production for years to come.

*New blueberry selections.* New blueberry cultivars are needed to address consumers' desire for improved fruit quality. ARS scientists in Chatsworth, New Jersey, have released the blueberry selection 'Sweetheart' with superior flavor, very good firmness, good productivity, attractive medium- to medium-large-sized fruit, and early season, concentrated ripening. They also have released the blueberry selection 'Razz' with reliable productivity, good yields, midseason ripening, medium-to-large fruit, medium-to-light blue fruit color, and excellent flavor with remarkable raspberry overtones. These superior new varieties have been distributed to commercial blueberry nurseries for national distribution.

*Growers have new rootstock options for stone fruits and almonds.* A successful orchard requires trees with a rootstock that can resist infection by soil-borne diseases and pests as well as providing trees with water and nutrients necessary for a bountiful harvest. When an orchard is replanted with the same rootstock as was previously used, tree vigor can suffer and yields are generally reduced. ARS researchers in Parlier, California, collaborated with University of California-Davis scientists to develop three new clonal rootstocks that are compatible with stone fruits and almonds. The new rootstocks are resistant to the prevalent root knot nematode, and produce trees of slightly smaller stature, but fruit/nut bearing capability is not affected. Growers can expect enhanced growth of young trees when these rootstocks are planted in extant orchard sites. An additional benefit lies in reduced pruning costs throughout the life of the orchard.

*New blackberry cultivars.* New cultivars are needed to sustain the strength of the small fruit industry in the United States. ARS researchers in Corvallis, Oregon, released two new cultivars of blackberry, 'Newberry' and 'Wild Treasure.' 'Newberry' produces a tremendous amount of fruit with outstanding flavor and is ideally suited for the fresh market. 'Wild Treasure' is a thornless, small-fruited cultivar with superb flavor and appearance and is best suited for mechanical harvesting and processing. 'Newberry' is planted in California and throughout the Pacific Northwest and has earned the acceptance of major fresh market wholesale distributors whereas 'Wild Treasure' is planted largely in Oregon and is marketed for its small fruit size that fit better into bags of frozen berry mixes along with raspberries and blueberries. These new cultivars fill important needs of the blackberry industry.

*'Orablue' plum was released to growers.* ARS researchers at Kearneysville, West Virginia, released a superior new plum variety. 'Orablue' provides U.S. growers and gardeners with an exceptionally large, sweet, and highly flavored plum that grows and fruits well in the mid-Atlantic and northeastern United States, and other plum growing areas.

*New hibiscus varieties released.* New woody ornamental cultivars are needed with enhanced pest resistance in combination with improved production traits and superior landscape performance. ARS scientists in Poplarville, Mississippi, recently released two *Hibiscus rosa-sinensis* cultivars and one *Hibiscus acetosella* cultivar. 'USS California', a tropical hibiscus cultivar with superior yellow flowers, has uniform, intermediate growth habit, sets many flowers, and has improved pest tolerance. 'USS Arizona', a tropical hibiscus cultivar with brilliant orange flowers, has uniform, intermediate growth habit, sets many flowers, and has improved pest tolerance. Flowers are a unique phosphorescent brilliant orange. These plants are ideal for landscape use and are adapted to summer heat. Nursery producers will benefit from the superior production traits of this selection including easy propagation and vigorous growth. ARS researchers also released *Hibiscus acetosella* 'Sahara Sunset', an African hibiscus cultivar with variegated foliage. 'Sahara Sunset' is the first stable variegated form of the purple leaf type. The nursery industry will benefit from the unique multicolored foliage that can be grown as a specimen plant in landscapes, a color accent in shrub borders, or a contrast plant in mixed annual planters. Heat tolerance and broad environmental adaptation make 'Sahara Sunset' an important component of low maintenance, low water plantings. It thrives in summer heat and full sun, has a spreading upright growth habit, and is tolerant of common insects and diseases.

*New southern highbush blueberry named 'Pearl'.* U.S. fresh markets favor early ripening blueberry cultivars, which command premium prices. ARS scientists in Poplarville, Mississippi, recently released 'Pearl', a new highbush blueberry cultivar which produces ripe berries earlier than the earliest rabbiteye blueberry cultivars in production today. It has high yield potential and produces large, attractive, light blue, firm berries with excellent flavor and small picking scars. 'Pearl' has low to moderate chilling requirements and will perform well in the Gulf-coast region and in other areas where southern highbush blueberry cultivars are grown successfully. Growers will benefit from the early ripening and can participate in the lucrative early U.S. fresh market where opportunities for marketing rabbiteye blueberries have diminished.

*New rootstock for peaches.* Premature tree death caused by several soilborne diseases adds significantly to production costs of U.S. peach growers. The first interspecific hybrid peach rootstock with broad disease resistance developed by the ARS researchers in Byron, Georgia, rootstock breeding program has been proposed for release. Material has been multiplied for commercial propagation. In research and grower trials conducted on disease infested sites this new rootstock has provided significant improvements in tree performance and longevity compared to current commercial standards.

*A root-knot nematode-resistant, yellow-fruited, Habanero-type pepper breeding line released.* The increasing popularity of hot peppers in the United States has created intense interest in the Habanero, an extremely pungent type of pepper. Root-knot nematodes are major pests of peppers, and the ideal solution to this pest problem is resistant cultivars. ARS researchers in Charleston, South Carolina, transferred a root-knot nematode-resistant gene from a Scotch Bonnet-type pepper into a yellow-fruited Habanero-type pepper line. These efforts resulted in the release of the yellow-fruited, root-knot nematode

resistant, advanced breeding line PA-560, which is recommended as a parental line for pepper breeders interested in developing yellow-fruited, root-knot nematode resistant cultivars of Habanero-type peppers. It is particularly recommended for the organic, specialty crop, and home garden markets because these segments of the pepper industry do not have easy access to alternative production sites or nematicides. Similar breeding efforts also have led to the release of a root-knot nematode resistant, pimento-type line PA-566, which can be used directly as a replacement for pimientos widely grown in the southern United States. It can produce high yields under high temperatures and nematode pressure in soils.

*Release of sunflower and soybean germplasm with resistance to multiple diseases.* The most cost-effective and environmentally friendly methods for controlling plant diseases are disease-resistant cultivars. ARS researchers in Fargo, North Dakota, have released a novel sunflower germplasm with genes for both downy mildew and sunflower rust resistance. These resistance sources have not been defeated by the newest virulent races of either fungus, so they will provide a valuable source of resistance to these two diseases, along with high yield and desired agronomic characteristics. These ARS researchers also released and registered three sunflower genetic stocks in 2010, each contributing a new gene for incorporation of downy mildew resistance into hybrid sunflower seed production. In addition to this disease resistance trait, these three genetic stocks also provide the genes for high oleic acid content and superior agronomic and yield characteristics. In addition, ARS researchers in Stoneville, Mississippi, released a soybean variety with high-yield potential and resistance to soybean cyst nematode, reniform nematode, charcoal rot, stem canker, and sudden death syndrome. This release can directly reduce yield losses and can serve as a parent for breeding new disease-resistant cultivars.