

USDA  
AGRICULTURAL RESEARCH SERVICE

**NATIONAL PROGRAM 301 –  
PLANT GENETIC RESOURCES, GENOMICS, AND GENETIC  
IMPROVEMENT**

**ANNUAL REPORT FY 2009**



# National Program 301

## PLANT GENETIC RESOURCES, GENOMICS, AND GENETICS IMPROVEMENT

### FY 2009 Annual Report

#### *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; 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, 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. 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; and delivering the former via databases 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) 2009 this program produced many important discoveries and advances. Some of these are described below, grouped by research component.

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

- *More than 530,000 samples of crop genetic diversity conserved and distributed to researchers.* During FY 2009, the 20-plus genebanks in the USDA-ARS National Plant Germplasm System (NPGS) added more than 20,000 new samples for a total of more than 530,000 distinct types of more than 13,200 plant species that are now being 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 140,000 – 40,000 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.
- *An invaluable collection of black raspberry (*Rubus occidentalis*) germplasm.* Previous research conducted by ARS scientists in Corvallis, Oregon, had identified lack of variability as a critical roadblock to developing new improved black raspberry cultivars. Black raspberry necrosis virus (BRNV) was identified by as a critical problem challenging the long term viability of the black raspberry industry. ARS scientists solicited wild black raspberry seed from friends, colleagues, native plant societies, and other enthusiasts by mail, and then collected black raspberry from along the southern and western edge of its range in eastern North America. Between these two collections, more than 150 populations from many states and several provinces are represented in a common garden in Corvallis. This collection of germplasm has the potential to give researchers new sources of variability, and perhaps resistance to BRNV or its aphid vector, that will aid in the development of critically needed cultivars for the commercial industry.
- *Long-term survival of cryopreserved sugarbeet pollen.* In a heterozygous crop such as sugarbeet, it is difficult to preserve superior, individual genotypes developed in plant breeding programs, and to collect wild relatives of cultivated plants when there is insufficient seed to fully represent the total genetic diversity present. ARS scientists at Fort Collins, Colorado, demonstrated that pollen stored for 17 years in liquid nitrogen was still able to pollinate sugarbeet and produce viable seed. In plant breeding, stored pollen could be used as a long term tester population or, from an individual genotype,

as the parent in a recurrent breeding scheme for genetic analysis. Collection and storage of pollen might furnish a more representative sample of the genetic diversity in wild populations. Additionally, with restrictions on the international transport of seed becoming increasingly stringent, pollen could be an alternate way to distribute sugarbeet (Beta) germplasm.

- *Limits to the utility of “DNA-barcoding” for identifying highly diverse plant species.* “DNA-barcoding” seeks to develop simple, inexpensive, and rapid DNA assays that can be applied by non-experts to identify unknown species. ARS researchers at Madison, Wisconsin, tested the ability of three different DNA “bar-coding” marker genes to determine accurately the species identity for a diverse set of 72 wild potato species. None of the three genes were very accurate at distinguishing or serving as markers for species boundaries for these wild potatoes. Consequently, these results serve as a warning against relying solely on DNA-barcoding genes to identify highly diverse plant species successfully.
- *New, more effective approaches for conserving genetic resources of wild relatives of apples.* Conserving genetic resources of tree crops in field plantings is expensive and subjects the invaluable genetic materials to the constant threats of diseases, pests, and environmental extremes. ARS researchers at Fort Collins, Colorado, and Geneva, New York, applied statistical genetic models to identify a “core subset” of about 100 trees that captures most of the genetic diversity contained in a total of more than 1,000 wild apple trees. Similarly, for another species of wild apple, a core subset of about 30 trees encompassed most of the genetic diversity in 700 trees. These results will enable apple curators to reduce the number of wild apple trees required for field plantings without significantly diminishing the total amount of genetic diversity conserved. They will also enable apple breeders to more rapidly identify new sources of genetic variability for horticultural traits key to apple genetic improvement.
- *Discovery of novel root morphologies in apple rootstocks.* Very little is known about how the morphology of a root system affects field performance of a rootstock. By imaging hundreds of root systems of young trees and subsequent analysis of those images with specialized software, ARS scientists at Geneva, New York, have discovered root morphological characters that may enable apple rootstocks to penetrate, anchor, and explore the soil profile more efficiently than do current commercial rootstocks. This research will aid in the selection and development of improved apple rootstock cultivars.
- *A superior new classification for cacao (cocoa).* Many of the individual samples from genebank collections of cacao (cocoa) have been misidentified. The genetic diversity within this economically-important tropical species generally has been analyzed piece-meal, rather than comprehensively across cacao’s native geographical range. The identification errors and the incomplete understanding of these diverse materials’ relationship to cultivars have long impeded cacao breeding and genebank management. ARS researchers and collaborators from M & M Mars Co., France, Brazil, and Ecuador analyzed the genetic diversity in more than 1,200 geographically-diverse samples of Latin American cacao with more than 100 powerful new genetic markers. The researchers found that cacao actually includes 10 genetically distinct subgroups, rather than the two to four subgroups of traditional classifications. They also measured the amount of inter-group genetic differentiation. This refined knowledge of cacao genetic relationships will improve the value of cacao genebank collections, and

accelerate the ability of cacao breeders to identify genetically distinct materials with desirable traits for genetic improvement.

- *Where did coconut originate, and what are its closest wild relatives?* Knowing the identity of a crop's relatives, its geographical origin, and the relationships among different crop varieties can accelerate the progress of identifying new genes for key crop traits and incorporating them into breeding programs. To date, the geographical origin(s) and closest wild relatives of coconut, a tree vital for tropical subsistence farmers and vegetable oil producers, have been unknown. After analyzing various coconut genes, ARS researchers in Miami, Florida, determined that coconut most likely originated in South America and its closest relative is the palm *Syagrus* — itself an important tropical ornamental. Analyzing other genetic markers, the researchers determined that, because of methodological flaws, previous hypotheses about the genetic relationships among coconut varieties were inaccurate. These findings are valuable for guiding the direction of coconut gene discovery and breeding efforts.

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

- *New Web-based tools accelerate the genetic improvement of soybean.* The soybean genome contains 46,000 predicted genes, and associating specific genes with high-value traits is an important challenge. ARS scientists at Ames, Iowa, released a greatly improved version of SoyBase and the Soybean Breeder's Toolbox (SBT), a powerful suite of Web-based applications, that enable breeders and researchers to more fully exploit knowledge of the soybean genome structure to accelerate crop improvement. SoyBase and the Soybean Breeder's Toolbox is an integrated repository for information on soybean genetic maps, physical maps, genetic markers, gene sequences, disease and stress resistance, and trait ontology. SoyBase, together with the soybean genome sequence, is expected to dramatically speed progress in breeding and identifying the genetic and molecular basis for many important soybean traits.
- *Valuable new genetic analysis software developed.* Until now, there have been no methods to automatically combine genome sequence data with information about the actual location of the sequences within the genome. Such methods would substantially accelerate the rate of discovering genes vital for corn genetic improvement. ARS researchers in Ames, Iowa, invented a new software program, named "Locus Lookup Tool", that enables geneticists and breeders to more rapidly locate regions of the corn genome that most likely include genes controlling specific valuable traits. This tool will enable researchers to exploit more extensively the intrinsic value of the recently completed genome sequences for key corn varieties.
- *New genetic markers for cotton identified and partial sequencing of the cotton genome.* Molecular markers are sophisticated tools for locating and "marking" useful genes controlling important biological functions in living organisms. In cotton, the molecular markers known as simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) can greatly improve the speed and efficiency of cotton improvement by aiding in locating genes associated with traits such as fiber quality, yield, disease resistance, etc. ARS scientists in College Station, Texas, with industry and university scientists, released more than 3,000 SSR and SNP markers for cotton, which will accelerate the sequencing of the cotton genome. With that information, and in collaboration with U.S. and international scientists, ARS scientists in College Station, also sequenced portions of two

chromosomes of the cotton genome. This accomplishment provides foundational data and direction for sequencing all the chromosomes of the cotton genome. Knowledge of the sequence will greatly facilitate development of new cotton varieties.

- *Drought-stress genes in corn and resistance to aflatoxin contamination.* Throughout the world, aflatoxin contamination is one of the most serious food safety issues. Chronic problems with pre-harvest aflatoxin contamination occur in the southern United States, and drought stress is a major factor contributing to the condition. Recent studies have demonstrated that higher concentrations of defense or stress-related proteins were produced in corn kernels of resistant genotypes, suggesting that pre-harvest field condition related to drought stress influenced gene expression for pre-harvest aflatoxin contamination. ARS scientists in Tifton, Georgia, applying proteomic comparisons between resistant and susceptible corn kernel proteins, have identified stress-related proteins, along with antifungal proteins associated with corn kernel resistance. Gene expression analyses of developing corn kernels and the proteomic studies that suggest defense-related genes are up- or down-regulated by abiotic stresses, and this is correlated with post-harvest aflatoxin contamination.
- *ARS scientists and colleagues complete the sequence of the corn genome.* ARS researchers at Ithaca, New York, along with collaborators at Washington University, Iowa State University, the University of Arizona, and the Cold Spring Harbor Laboratory in Cold Spring Harbor, New York, compiled the comprehensive sequence of the corn genome with support of the National Science Foundation, Department of Energy, and USDA National Institute of Food and Agriculture. The researchers also used advanced DNA sequencing data to assemble a haplotype genetic map of the corn genome that detail portions of the genome shared by 27 diverse inbred lines of corn. The map is designed to make it easier to link genes and genetic patterns to significant traits. The corn genome sequence and new genetic map will significantly accelerate breeding of corn and other crops to meet the challenge of increasing productivity and the challenges of climate change.
- *Development and verification of a universal soybean DNA marker set.* Single nucleotide polymorphisms (SNPs) are the DNA markers of choice for most soybean breeders due to their abundance and the rapid high-throughput methods available for the characterization of many markers in a single analysis. ARS scientists at Beltsville, Maryland, with collaborators from universities and other ARS laboratories, developed a set of 1,536 SNP DNA markers for analyzing soybean DNA samples very rapidly. This set of SNP markers, known as the Universal Soy Linkage Panel 1.0 (USLP 1.0), was selected from a larger set of more than 3,000 markers, each of which was genetically mapped across each of the 20 soybean chromosome pairs. The markers in USLP 1.0 will enable rapid genetic analysis and selection in soybean populations. More than 6,000 soybean DNA samples from populations developed by soybean breeders in 12 states have already been analyzed with these markers. Genotype data from those samples are defining the genome positions of genes controlling resistance to soybean rust, soybean cyst nematode, iron deficiency chlorosis, level of oleic and linolenic acid, and seed protein concentration in soybean oil.
- *New genes identified to protect wheat from the Ug99 wheat stem rust threat.* More than 80 percent of the world's wheat varieties are vulnerable to the virulent new wheat stem rust strain, Ug99, which has appeared in Eastern Africa. New sources of Ug99 resistance are urgently needed. In 2009, ARS researchers identified new sources of Ug99 genetic resistance in wild and weed relatives of wheat, and have made initial progress in incorporating those genes into bread wheat. ARS researchers in

Manhattan, Kansas, mapped and transferred a Ug99 resistance gene from the wild wheat *Triticum timopheevii*. ARS researchers in Fargo, North Dakota, identified resistance genes from goatgrass and perennial wheatgrass species and are now advancing genetic resources to facilitate the use of these new resistance genes. ARS researchers in Raleigh, North Carolina, identified 30 breeding lines with Ug99 resistance and are assessing those lines for agronomic traits in partnership with the International Wheat and Maize Agricultural Research Center (CIMMYT) in Mexico for distribution globally. These new sources of genetic resistance to Ug99 are keys for breeding wheat with more durable resistance to Ug99 to protect the global grain supply.

- *Identification of a resistance gene for Rpp4-mediated resistance to Asian soybean rust.* Outbreaks of Asian soybean rust, which can cause yield losses up to 75 percent, have now occurred in all major soybean-producing countries. Thus far, only four genetic locations (loci) in the soybean genome (Rpp1, Rpp2, Rpp3, and Rpp4) have been identified as conferring resistance to Asian soybean rust. Cloning of Rpp4 and the development of markers linked to the gene will aid in breeding resistance to soybean rust and other important soybean pathogens. ARS scientists at Ames, Iowa, in cooperation with scientists from Embrapa (Brazil) and Iowa State University decoded a region of the soybean genome corresponding to the Rpp4 locus and identified three candidate resistance genes. By combining genetic mapping, gene silencing and sequencing, and other cutting-edge methods, the researchers identified a single candidate gene that controls resistance at the Rpp4 locus, a key accomplishment for developing genetic resistance against soybean rust.
- *Apple rootstock map completed.* Genetic maps are an important tool for locating genomic regions that affect apple rootstock traits. ARS scientists at Geneva, New York, completed a genetic map of apple rootstocks that encompasses all 17 linkage groups (chromosomes) of the apple genome and identified the location of 16 genes expressed in roots only and 13 disease resistance homologues, some of which co-locate to known disease resistance regions. This accomplishment has enabled the discovery of markers linked to important apple rootstock traits which will enable marker-assisted breeding.
- *Genetic mapping of day-length sensitivity in grape.* Grapevines grown throughout 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 are capable of initiating dormancy in response to shortening day-length in early fall. To understand the genetic control of day-length sensitivity, ARS scientists at Geneva, New York, identified in the grape genome the locations of genes controlling photo-periodic induction of dormancy. One region of the genome accounted for over 40 percent of the variation observed for photo-periodic induction of dormancy. The mapping of this trait is the first step in developing an assay that will improve the selection efficiency for this trait and generating improved cultivars of grape for cold climates.
- *DNA fingerprint database for hydrangea cultivar identification.* Hydrangeas are the fourth most popular flowering shrub and are sold as landscape shrubs, patio plants, greenhouse floral crops, and cut-flowers. Once mislabeled or lost from trade, it is difficult to re-establish cultivar identity based solely on botanical descriptions. There are numerous suspected cases of mislabeling, renaming, and re-discovery of ‘new’ hydrangeas. ARS researchers at Poplarville, Mississippi, established a DNA fingerprint database for more than 250 hydrangea cultivars and demonstrated real-world application of this biotechnology at 13 nurseries to resolve questions about hydrangea cultivars in the United States,

Belgium, and New Zealand. Applications include detecting mislabeled plants during production and in the marketplace, confirming parentage of self-sown and open-pollinated hybrids, and verifying genetic uniqueness for plant patent protection of select cultivars. Recently a large shipment of exclusive breeding material was mixed upon arrival in the Netherlands. DNA fingerprinting technology allowed trading partners to unambiguously sort the genetic material and varieties, keeping the European release on time and saving the multi-year build-up efforts that would otherwise have been delayed.

- *New biotech wheat method developed and a biotech wheat shown to be more heat tolerant.* Current methods for wheat genetic transformation involve tissue culture, which is time-consuming, expensive, and sometimes includes undesirable somaclonal variation. ARS scientists at Pullman, Washington, developed a new method for genetically engineering wheat that involves transforming opened flowers or spikelets in *Agrobacterium* media. Successful transformation has been demonstrated with a marker for red color. ARS researchers at Manhattan, Kansas, transformed wheat with a corn gene for a chloroplast protein called EF-Tu. The transformed wheat exhibited an enhanced rate of photosynthesis after exposure to heat stress. These discoveries provide the basis for the development of new biotech wheat varieties with enhanced tolerance to extreme temperature and other types of resilience to climate change.
- *New genome discovery identifies thousands of new wheat molecular markers.* Corn and soybean genomes were recently fully sequenced, but the complexity of the hexaploid bread wheat genome continues to impede genetic analysis and sequencing. Bread wheat has a more genetically simple diploid relative that can be more easily sequenced and assessed. ARS scientists in Albany, California, have exploited unique transposable element insertion junction regions from diploid wheat to develop genome-specific markers for hexaploid wheat. A large percentage of the molecular markers previously identified for the diploid wheat genome can be directly applied to hexaploid wheat genetic improvement.
- *Sorghum lignin synthesis gene with bioenergy applications.* Development of new cellulosic biofuels from sorghum and switch grass is restricted by technical barriers in breaking down the lignin in plant cell walls. To overcome that barrier, ARS researchers at Lincoln, Nebraska, have characterized a key gene that controls lignin structure and content. They characterized a low lignin (brown rib) sorghum mutant and sequenced the *bmr-6* gene that causes the mutation. A single amino acid change causes the mutation, which reduces the level of a lignin synthesis enzyme, resulting in reduced lignin content. The mutant sorghum lines have higher ethanol yields and higher ethanol conversion efficiency than do wild type sorghum lines. Characterization of this lignin gene mutation strengthens strategies needed to develop bioenergy feedstocks from sorghum and other grass crops.
- *New genetic methods for increasing the value of sorghum as bioenergy feedstock with increased climate change resilience.* Most sorghum germplasm is of tropical origin and does not flower and produce seed in the United States where the day-length is longer during the growing season. Photoperiod response genes must be incorporated to convert tropical sorghum lines to day-length neutrality for production in temperate environments. ARS researchers at College Station, Texas, have developed molecular markers to facilitate genetic selection of photoperiod-response genes along with genomic methods to accelerate the breeding process. Better water-use efficiency and drought tolerance are also desired. Post-flowering drought tolerance, known as "staygreen", increases

sorghum yield under limited- or no-irrigation conditions. Conventional field testing for this trait requires multiple location and year trials. ARS scientists at Lubbock, Texas, have developed a method to evaluate the “staygreen” trait based on chlorophyll fluorescence in sorghum grown under well-watered conditions. The method has been validated and shown to work as well as conventional field screening under drought conditions. These new sorghum screening methods will accelerate the use of diverse sorghum germplasm to increase bioenergy value and resilience of sorghum to drought stress.

- *Corn circadian clock governs adaptation to environmental change.* The circadian clock serves to synchronize the internal biology of an organism with its environment, and thus plays an important role in plant adaptation to environmental change. ARS scientists at Albany, California, showed that at least 10 percent of all genes in corn, including those involved in photosynthesis, starch utilization, hormone synthesis, and plant growth, are governed by the clock. These processes, in turn, affect key agronomic traits like flowering, biomass, yield, and stress tolerance. The scientists tested five corn genes and confirmed that they affect clock functions, thereby establishing a foundation for manipulating clock genes for improving the adaptability of maize.
- *Inheritance of sunflower downy mildew resistance.* Downy mildew, a serious disease of sunflower, often strikes early in the growing season, especially under cool, damp environments. Sunflower line HA-R5 confers resistance to nine races of the pathogen that causes the disease and is a promising source of downy mildew resistance for commercial sunflower hybrids. It is difficult to transfer the resistance genes without knowing the genetic control or inheritance. ARS scientists at Fargo, North Dakota, determined the inheritance of the downy mildew resistance gene in HA-R5 and genetically mapped it to a genomic location near two DNA SSR markers. These DNA markers closely linked to the resistance gene will enable marker-assisted selection for developing downy mildew resistant lines.
- *Discovery of a secondary gene for powdery mildew resistance.* Resistance to powdery mildew in apple rootstocks is a desirable nursery trait. ARS scientists at Geneva, New York, have discovered the genomic location of a secondary gene that affects disease resistance to powdery mildew. This accomplishment has highlighted the need for an additional genetic marker for marker-assisted breeding for powdery mildew resistance and explains the inconsistencies of earlier reports based on a one-gene model for the resistance.

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

- *New genomic selection methods that are transforming plant breeding.* Marker-assisted selection methods in plant breeding have failed to improve the effectiveness whereby breeders can manipulate many complex traits. ARS researchers at Ithaca, New York, have developed an approach that exploits many markers and statistical methods for the simultaneous estimation of all marker effects. This new genomic selection method is very accurate in predicting breeding values for complex traits, and helps to accelerate breeding through more accurate predictions and by reducing the required breeding cycle time. Plant breeders are already applying the new genomic selection method to more crops including barley, wheat, oat, maize, rice, and sugarcane.
- *Rice sheath blight disease resistance gene discovered.* Sheath blight disease causes yield losses in rice production areas around the world. It has been difficult to develop sheath blight-resistant

cultivars because there are no known sources of complete resistance, and resistance is conditioned by many genes whose expression are modulated by the growing environment. ARS scientists at Stuttgart, Arkansas, identified DNA markers associated with major sheath blight disease resistance quantitative trait loci (QTLs) in a project partially funded by the USDA-NIFA-NRI RiceCAP grant. A total of 10 QTLs distributed on several rice chromosomes were identified, including a major QTL for sheath blight resistance found on chromosome 9. The markers linked to the major sheath blight-resistant QTL will enable breeders to accelerate the introduction of genetic resistance into new rice cultivars.

- *Using molecular biology to develop better pecans.* Pecan is an important nut crop in the United States, and there is need to better understand the genetic make-up of the species to develop improved pecan varieties. ARS scientists at College Station, Texas, applied modern and sophisticated molecular biology techniques to examine in great detail the genetic make-up of more than 150 different pecan types. The work developed and utilized tools known as plastid primers for these genetic analyses, which showed great genetic variety of different pecan types, and identified both those that were very similar if not almost identical, and those that were quite different. Pecan types from Asia and from Mexico were very different genetically from U.S. types, indicating a very long history of isolation and genetic divergence. This accomplishment is important because it provides foundational genetic information that will effectively guide ongoing genetic and breeding efforts aimed at developing more productive, pest/disease resistant, and nutritious pecans that will benefit both producers and the consumer.
- *Corn research unlocks basis of natural diversity and reveals the genetic control of flowering and hybrid vigor.* Corn is the most diverse crop in the world, but much of that useful genetic variation is found in types which are unadapted to U.S. agriculture. ARS researchers at Ithaca, New York; Columbia, Missouri; and Raleigh, North Carolina, with support from the National Science Foundation, have developed and characterized the largest set of mapping lines for complex trait dissection in any species. The scientists found that most natural genetic variation in corn is the product of numerous genes working together, each with a small effect that could be manipulated by breeders. Corn flowering time is controlled by numerous genes each with a small predictable effect. Their work also provided major insights into hybrid vigor, a key element of modern high-yielding crops. Hybrid vigor results from limited reshuffling of genetic diversity in certain regions of the genome. These new genetic resources and discoveries will accelerate progress in crop genetics and breeding which is required for future food security and resilience to climate change.
- *Fresh market apricot Robada is ready for plum pox virus in California.* Plum pox virus (PPV) has been identified in North America, and has been a devastating tree disease affecting apricots in many other growing regions around the world. Growers in California and other regions need varieties that offer protection from PPV. ARS scientists at Parlier, California, throughout the last decade have determined that the Robada apricot, a variety developed and released by ARS, resists attack by PPV. Robada provides growers with a protective option should PPV become established in California orchards.
- *Rice cultivars and molecular markers for straighthead resistance.* Straighthead is a physiological disorder in rice resulting in poor seed set and yield loss, and the cultural management methods required to control this problem add significant costs to farmers in water and energy use. ARS

scientists at Stuttgart, Arkansas, identified 42 rice cultivars from 15 countries in the USDA world rice collection that were resistant to straighthead and developed DNA markers linked with this trait. The resistant cultivars and the associated genetic markers will be valuable to breeders for developing improved cultivars for effective control of this disorder and to reducing rice production costs.

- *New rice blast resistance genes identified.* Rice blast disease is a serious threat to rice production in the United States and worldwide due to constant development of more virulent races of the pathogen. ARS scientists at Stuttgart, Arkansas, analyzed a total of 1,800 rice accessions in the U.S. rice germplasm collection for the presence of blast resistance genes using DNA markers and disease evaluation. Diverse accessions contained the Pi-ta resistance gene. Others appear to possess new genes for blast resistance. These accessions will be important to breeding programs for blast resistance.
- *Molecular marker developed for seedlessness and disease resistance in grape.* New cultivars of seedless table grapes require embryo rescue by tissue culture and several years of growth to evaluate seedlessness. A new molecular marker developed by ARS scientists at Geneva, New York, predicts seedlessness, enabling breeders to select seedless types soon after embryo rescue, and discard seeded grapevines without investing resources in their maintenance and evaluation. In addition, a marker for a broad spectrum powdery mildew resistance was discovered in the same breeding material. Beyond the scientific progress toward isolating and characterizing these genes, the molecular markers will accelerate the selection of seedless grapes with disease resistance, which will enable growers of these future cultivars to drastically reduce pesticide applications. Varieties with the broad spectrum powdery mildew resistance would save growers from \$100 to \$400 per acre annually in pesticide costs and reduce direct and indirect effects of pesticide application.
- *New USDA raisin cultivars dry quicker, and are more suitable to efficient cultural procedures.* Traditional hand harvest of raisin grapes and drying fruit on trays are expensive and subject to damage by early fall rains. Cutting canes to dry raisins on the trellis requires special trellises and trained pruners. Slower drying raisins like Thompson Seedless may not dry completely and require supplemental drying, adding to expense and energy consumption. Six USDA-developed raisin cultivars were evaluated by ARS scientists in Parlier, California, for their drying rates in three consecutive seasons. Summer Muscat, Diamond Muscat, and Primus dried the fastest, whereas Thompson Seedless consistently dried the slowest. Growers' use of the new ARS developed raisin grapes will lead to a reduction in energy consumption for supplemental drying of weather damaged raisins.
- *Valuable new genetic markers for ornamental tree breeding.* Because of the long delay between planting a seedling and its first flowering, breeding ornamental trees is expensive and slow. Genetic markers accelerate progress by enabling breeders to select superior seedlings and cull undesirable types before trees reach reproductive maturity. ARS researchers in Washington, D.C., and Stoneville, Mississippi, developed more than 250 such markers for the Chinese fringe tree, a valuable spring-flowering ornamental. In addition to facilitating progress with breeding this species, these genetic markers will enable accurate species identification, and generate critical information about the genetic variability in wild populations of this tree.

- *Release of high-yielding, high seed protein soybean germplasm.* All high protein soybean releases in the South suffer from the problem of low yield associated with the high protein genes. ARS scientists at Raleigh, North Carolina, developed a new breeding line with the desirable combination of high-yield and high-seed protein. This new diverse release has 50 percent exotic germplasm, a feature that normally lowers yield potential. The release of this new germplasm adds diversity to the narrow genetic range of soybean breeding materials in the southern United States. This germplasm is serving as a parent for a genetic analysis of uncoupling of high protein with low yield.
- *Early flowering genes identified that accelerate fruit tree breeding.* Fruit tree breeding is a slow and expensive process because of the long delay between planting a seedling and its first flowering. Years of breeding and testing can be saved if that time is shortened. ARS scientists at Kearneysville, West Virginia, have identified and incorporated into breeding stock a gene that promotes early flowering and fruiting, shortening the juvenile stage in plum from 4 years to less than 1 year. Once breeding results are achieved, the genetically engineered early flowering trait can be removed before varietal release, resulting in a tree that can be categorized as non-genetically engineered. Early flowering and fruiting will enable the rapid development of new and improved varieties of plum and other fruits, as well as forest and woody ornamental species.
- *Development of high folate potatoes.* Folate deficiency, one of the world's most severe nutritional deficiencies, is a leading cause of major birth defects and is implicated in some heart attacks and strokes. ARS scientists at Prosser, Washington, have developed transgenic potatoes with as much as an eight-fold increase in folate content and could contain over 60 percent of the folate recommended daily allowance for a 6-ounce serving. This research demonstrates a high-folate potato is feasible, so that the potato could play a key role in combating global folate deficiency.
- *High-yielding new variety of lentil.* Lentil is a highly nutritious legume key to global food security, and a lucrative export crop for U. S. producers. An integral component of the Pacific Northwest's small grain production system, lentils help break disease cycles, improve weed control, and fix soil nitrogen for subsequent grain crop production. ARS researchers at Pullman, Washington, bred and released a new lentil variety 'Essex' which out-yields the industry standard by an average of more than 20 percent. Essex provides a new, highly productive lentil that will increase the profitability of lentil producers in the Northern Plains.
- *Release of two new exceptional peach varieties – 'Flavrburst' and 'SummerFest'.* Peach growers are facing increased costs for orchard operations (pruning, thinning, and harvesting). ARS scientists at Kearneysville, West Virginia, and Byron, Georgia, released two new peach varieties that are less expensive to produce while maintaining excellent quality. 'Flavrburst' peach was developed with an exceptional sweet and only mildly acidic flavor, providing a highly desirable flavored peach for the consumer. 'SummerFest' peach is an upright growth habit that is more productive and easier to manage than are standard growth habit peaches. 'SummerFest' provides growers a high quality peach that will reduce the costs of production.
- *Development of common bean germplasm lines with multiple disease resistance.* Diseases are one of the principal constraints to common bean production. ARS scientists at Beltsville, Maryland and collaborators at the University of Nebraska developed common bean lines with resistance to bean rust and other major diseases of dry beans in the United States. Bean lines from Beltsville with several

rust resistance genes, bean common mosaic, and bean common mosaic necrosis potyvirus resistance were hybridized with beans from University of Nebraska with resistance to common blight, halo bacterial blight, and white mold. Traditional selection and molecular marker analysis identified lines with resistance to as many as five different diseases. A total of 34 advanced lines – 14 great northern and 20 pinto market classes – have been developed, each carrying three or four rust resistance genes. These unique resistance gene combinations provide resistance to all known strains of the bean rust, bean common mosaic, and common mosaic necrosis viruses.

- *Rootstocks with tolerance to apple replant disease.* Yield loss caused by apple replant disease is a very important problem for apple growers. ARS scientists at Geneva, New York, have identified Geneva apple rootstocks G.41, G.935, and G.4214 as the best rootstocks for to be used in conventional and organic orchards suffering from replant disease, and also identified rootstocks to be avoided for replant situations. The discovery of new rootstocks for apple replant-prone soils will enable growers and the apple industry to maintain production on good orchard land that has been marginalized because of apple replant disease. These rootstocks provide a viable alternative to soil fumigants, such as methyl bromide, for the management of apple replant disease.
- *New strawberry, ‘Valley Red’, developed.* ‘Valley Red’, a strawberry variety developed by ARS scientists in Corvallis, Oregon, bears fruit with outstanding processing characteristics including deep red internal and external color, good flavor, easy capping, and with excellent quality after freezing. Valley Red is expected to complement the highly successful ARS strawberry release, Tillamook. This variety, which combines excellent yields of uniform fruit on vigorous virus-tolerant plants will give growers another strawberry cultivar for the Pacific Northwest.
- *New pecan cultivars for small farmers.* Pecan is an economically-important U. S. tree nut grown primarily by small producers in orchards smaller than 20 acres. Profit margins are narrow, so producers require new, superior varieties that will enhance their profits. ARS researchers in College Station, Texas, have bred two new varieties for these small producers and home growers. Nuts of ‘Mandan’ mature earlier than those of any other variety, furnishing marketing advantages to growers. ‘Apalachee’ yields a very high proportion of perfect, high-quality pecan halves which are highly desirable for baked goods and other products. Collectively, these two varieties represent new opportunities for U.S. pecan producers to increase their profits.
- *New malting barley varieties.* ARS researchers at Aberdeen, Idaho, developed new malting barley cultivars with high productivity and end-product quality. A two-rowed winter malting cultivar, ‘Endeavor’, was publicly released and is being evaluated in plant-scale tests for malting and brewing trials. ‘Charles’, a winter two-rowed malting cultivar, was officially approved and added to the recommended list by the American Malting Barley Association. Approximately 11,000 acres were grown in Idaho in 2009 with other evaluations by growers in Washington, Oregon, Montana, Colorado, South Dakota, Minnesota, and North Dakota. These new promising varieties provide growers with added flexibility in crop management, reduced water use and increased yield potential.
- *New wheat varieties with disease protection increase food security and provide new markets.* ARS researchers at Raleigh, North Carolina, developed a white and a red wheat variety that produce high protein flour. Both varieties have wheat stem rust resistance and provide the first hard wheat varieties as a new market opportunity for southeastern producers. ARS scientists in Pullman, Washington,

applied DNA marker selection to develop new club and soft winter white wheat varieties with stripe rust and eyespot resistance along with high yields. The three new varieties meet the highest quality standards for western wheat varieties. All the new ARS varieties incorporate genetic protection to disease, reducing the need for chemical fungicides and providing more production stability for growers and consumers.

- *Corn germplasm lines with resistance to mycotoxins.* Contamination of corn grain with mycotoxins – aflatoxin and fumonisin – reduces crop value for producers, lowers grain quality, and endangers human health. ARS researchers at Starkville, Mississippi, have developed and released two corn germplasm lines, Mp715 and Mp717, with resistance to microbial infection by *A. flavus* and aflatoxin accumulation. The new germplasm lines also have resistance to microbial infection by *F. verticillioides* and fumonisin accumulation. The positive impact of these germplasm lines will be realized as the lines are incorporated into new commercial corn hybrids.
- *Accurately estimating levels of fungal disease resistance.* ARS scientists in Beltsville, Maryland, demonstrated that a minimum of 6 years, and possibly as many as 9 years, are needed to derive accurate estimates of blueberry resistance to the fungal infections, mummy berry, shoot blight, and mummy berry fruit infection. This research aids in understanding resistance in cultivars and the process needed for accurate estimation of resistance.
- *Pre-release increase of apple rootstock for commercial production.* The transition from an improved apple rootstock research line to a commercial cultivar may take several years because of the inherent high establishment costs of new propagation beds and the slow propagation cycles. In preparation for the pending release of three new yield-efficient, dwarfing and semi-dwarfing disease-resistant apple rootstocks well adapted to Washington State and New York apple growing regions, ARS scientists in Geneva, New York, have initiated micropropagation and pre-commercial production of 5,000 plants per rootstock of four new apple rootstock varieties. Making more plants available to the nursery industry faster will result in a larger impact on the apple industry much sooner than would be the case through the increase of plant material using conventional methods.
- *The gene for the stoneless trait in plum is identified.* Pits (seed and the hard surrounding woody "stone") reduce the convenience of eating stone fruits (peaches, cherries, apricots, and plums). Pit removal for processed fruit represents a major cost of production, and generates polluting waste. ARS scientists at Kearneysville, West Virginia, found that partially stoneless fruits developed in the early 1900's, although having the gene for forming the woody stone tissue, have fewer cells that express the stone-producing genes than do normal stone fruits. This information can be used by plant molecular biologists and breeders to develop fruit completely without the stone and seed. Pitless plums would be more convenient to eat and easier to process increasing the consumption of healthy fruits.
- *European pear sawfly resistance identified in pear.* The European pear sawfly has emerged as a new, significant pest of pear in the eastern United States, and current cultivars are all very susceptible. ARS researchers in Kearneysville, West Virginia, identified resistance to European pear sawfly in pear germplasm with either *Pyrus ussuriensis* or *Pyrus pyrifolia* pedigrees. Early flowering data was identified as a factor in the escape from infestation. The highly resistant germplasm will be available to breeders to develop new cultivars resistant to this new pest.

- *Viral symptoms tied to damage of the photosynthetic system in plants.* Viruses cause destructive symptoms in crop plants, the most serious being leaf and fruit yellowing and death. ARS scientists at Kearneysville, West Virginia, found that impairment of chloroplast function leads to increased virus susceptibility, suggesting that viruses disable chloroplast function to defeat plant defenses. This finding provides critical insight into the process of plant virus infections and provides a new foundation for developing new virus control strategies.
- *More precise genetic engineering to improve the quality of plants.* Improvement of multiple traits through genetic engineering often requires the co-introduction of multiple genes controlled by different promoters. However, multiple gene promoters can cause unexpected problems with transgene expression. ARS scientists at Kearneysville, West Virginia, found gene “insulator” sequences that prevent the interactions of the multiple gene promoters. The gene “insulator” sequences will be instrumental for transgenic research especially for co-expressing or precisely engineering multiple genes or traits.
- *Unique new high-yielding soybean line released.* The U. S. soybean crop might be vulnerable to unforeseen diseases, pests, and environmental extremes because its genetic base is relatively narrow. ARS researchers in Urbana, Illinois, released a new soybean line with nearly 40 percent of its genetic ancestry differing substantially from currently widely-grown varieties. In addition to providing unique genes to diversify the U. S. crop and reduce such vulnerability, this line is also high yielding, and could be incorporated readily into soybean breeding programs for the southern United States without decreasing the yield potential of current breeding stock.
- *Release of cotton germplasm lines with improved lint yield and fiber quality.* High-yielding cotton varieties in the mid-south and southeast United States lack fibers with sufficient strength and length. In 2009, ARS scientists at Stoneville, Mississippi; College Station, Texas; and Florence, South Carolina, have released cotton germplasm with improved fiber quality. The scientists co-released two sets of Upland cotton lines with excellent high-yield potential and superior fiber quality. These lines, which are now available for public access, will broaden the genetic base of cotton to facilitate long-term genetic improvement. In addition, ARS scientists at Stoneville developed four germplasm lines from an exotic germplasm population originally derived from crosses among several diverse lines. These new releases provide cotton breeders with opportunities to improve fiber quality while maintaining yield in commercial cultivars.
- *Non-destructive method developed for determining oleic and linoleic acid concentration from individual seed.* Gas chromatography, the conventional method for determining oil content of peanut seed, requires that the seed be destroyed in the process. ARS scientists in Stillwater, Oklahoma, developed a new technique, incorporating capillary electrophoresis, to determine the concentration of oleic and linoleic acid in a single peanut seed without destroying the seed. This enables a peanut breeder to plant the seed for breeding purposes if it contains the desired traits. This method also will enable rapid screening for value-added genetic traits in early generation breeding lines for the desired high oleic acid trait, and enable researchers to avoid spending the time and resources to grow the plants in the greenhouse or field first or the costs of sending numerous samples to quality laboratories for testing.