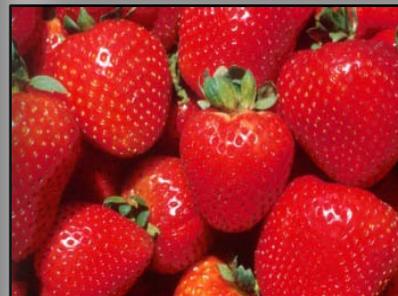


USDA
AGRICULTURAL RESEARCH SERVICE

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

ANNUAL REPORT FY 2008



National Program 301
PLANT GENETIC RESOURCES, GENOMICS, AND GENETICS IMPROVEMENT
FY 2008 Annual Report

Introduction

National Program 301 – Plant Genetic Resources, Genomics, and Genetic Improvement – addresses the need to ensure the long-term safety, value, and integrity of our 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 technologies that can enhance traditional methods of genetic improvement; to genetically improve a broad spectrum of major, specialty, and new crops; to increase our knowledge of crop genome structure and function; and to acquire, analyze, and deliver genetic, genomic, and informatics resources to the public.

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 for future generations.

Under 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 new sources of important genetic traits 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 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, to a limited extent, functional genomics; 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 gene 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) 2008 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 500,000 samples of crop genetic diversity conserved and distributed to researchers.* During fiscal year (FY) 2008, the 20-plus genebanks in the USDA/ARS National Plant Germplasm System (NPGS) added more than 25,000 new samples, so that a total of more than 510,000 samples of more than 13,100 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 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.
- *New Genetic Markers for Sugarbeet and Allied Crops.* There are few publicly-available genetic markers for sugarbeet, table (red) beet, fodder beet, and chard, despite their importance in modern genetic analyses and potential for marker-assisted breeding of these important crops. ARS scientists in East Lansing, Michigan, analyzed existing public genetic sequences, identified more than 2,500 potential markers, and tested for their utility. More than 100 markers were mapped to a specific chromosomal location in the beet genome, increasing by an order of magnitude the number of genetic markers available for beet germplasm characterization and genetic analyses.
- *Improved understanding for the key genetic determinants of apple fruit abscission.* Controlling the timing for abscission or retention of ripening fruit is vital for consistent and high-quality apple harvests, but the genetic bases for abscission-related traits remain mostly unknown. ARS researchers in Geneva, New York, and colleagues from Michigan State University found that seasonal timing of fruit

abscission in wild apple species and hybrids showed a broad distribution resembling that of domestic cultivars, and that internal ethylene concentration at the time of fruit abscission was highly variable. These results suggested important roles in abscission for physiological genetic mechanisms independent of apple fruit ethylene production. This information may aid apple breeding and production management research which is focused on assuring that future annual apple yields are more reliable and that apples can be harvested at an optimal quality stage, without risking premature fruit drop.

- *DNA markers from lowbush blueberry.* About two-thirds of commercial blueberry production is from improved cultivars of highbush blueberry, whereas about one-third is from managed, wild stands of lowbush blueberry, grown primarily in Maine. A reliable DNA genetic marker system is needed for lowbush blueberry, therefore ARS scientists at Beltsville, Maryland, and collaborators from the University of Maine identified “EST-PCR” DNA markers from highbush DNA sequences that also can effectively distinguish individual lowbush blueberry plants, called clones, even when the clones are closely related. These markers can also accurately estimate their degree of genetic relatedness among lowbush clones, and will enable more extensive genetic studies of lowbush blueberry in the future.
- *Genetic regions that control several critical apple rootstock traits identified.* One of the major challenges for apple rootstock breeders is the lengthy evaluation period required for selecting superior lines. ARS scientists at Geneva, New York, discovered four genomic regions that partially control fire blight resistance, three regions that for powdery mildew resistance, four regions for number of internodes produced each season (a component of dwarfing) and three regions for fine root formation – a trait that may be connected to replant disease tolerance. This information is helping to accelerate breeding programs through marker-assisted breeding – which is particularly important for selecting traits that are difficult to evaluate (e.g. root morphology) or that take a long time to develop (e.g. dwarfing). These markers will enable breeding programs to select superior traits early before rootstocks are planted in the field, thereby increasing the efficiency of the breeding program
- *New, radically different type of cacao found in Bolivia.* The genetic constitution of cacao (a highly valuable agricultural commodity that is the source of chocolate) from the tropical lowlands of Bolivia was previously unknown. ARS researchers from Beltsville, Maryland and collaborators from the Tropical Agricultural Research and Higher Education Center (CATIE) in Costa Rica analyzed the genetic content of semi-wild and cultivated cacao from lowland Bolivia and found that it was completely different from that of other types of cacao from South America. These findings provide valuable information about the diversity gaps that must be filled in international cacao collections, and also furnish a source of new genetic variation potentially valuable for cacao breeding.

Component 2: Crop Informatics, Genomics, and Genetic Analyses

- *New leading-edge version of GRIN under development for the world's genebanks.* Supported by ARS funding and by a \$1.4 million, 3-year grant from the Global Crop Diversity Trust, ARS researchers in Ames, Iowa, and Beltsville, Maryland, in cooperation with Bioversity International, are developing a new, leading-edge version of the Germplasm Resources Information Network (GRIN), which currently manages information for the U. S. and Canadian national plant germplasm systems. When complete, the new scalable and modular “GRIN-Global” database system can be readily implemented by any genebank – even in the developing world. The source code will be freely distributed, so that key documentation for the world’s plant germplasm collections will be more secure, and germplasm will be more readily accessible to crop breeders and researchers world-wide.
- *DNA Markers for Beet Curly Top Disease Resistance Identified.* Curly top is a devastating viral disease that almost eliminated the sugarbeet industry in the western United States until resistant cultivars became available. ARS scientists in Kimberly, Idaho, identified genetic markers for genes that confer resistance to this disease in sugarbeets which may accelerate the breeding of new, superior sugarbeet cultivars resistant to curly top.
- *High resolution mapping of the sorghum photoperiod-sensitivity gene.* Sorghum, an important grain crop internationally and in the United States, required additional molecular tools to accelerate its genetic improvement. Much potentially valuable sorghum germplasm materials are of tropical origin and do not successfully flower and produce seed in the United States where day-length is much longer during the growing season. Through high resolution mapping, ARS scientists at College Station, Texas, in cooperation with scientists at Texas A&M University; MMR Genetics, LLC; and the Department of Private Industries and Fisheries, Queensland, Australia, identified candidates for the photoperiod sensitivity gene, *ma1*. This accomplishment is important because it will enable more rapid exploitation of a wealth of previously unusable sorghum germplasm to develop higher-producing sorghum varieties for U.S. farmers.
- *Genome of commercial transgenic papaya sequenced.* The genome of the transgenic papaya cultivar, ‘Sunup’, was sequenced by ARS scientists at Hilo, Hawaii, and their collaborators, so as to better understand the genetic control for key papaya traits such as flowering and to provide information needed by Japan to consider deregulation of transgenic papaya fruit, which could expand Hawaii’s export papaya market. The resulting genomic information might also elucidate the genetic control for other key papaya traits.
- *Anchoring the soybean physical map to the genetic map.* Before physical maps can be fully exploited to isolate and clone agronomically-important genes, they must be integrated with genetic maps. ARS scientists at Ames, Iowa, succeeded in integrating the soybean physical map with the genetic map by identifying nearly 3,300 genetic

markers for Bacterial Artificial Chromosome (BAC) clones comprising the physical map. Two-hundred sixty-five were polymorphic and were genetically mapped so as to further integrate the physical and genetic maps of soybean. The integrated physical map is aiding in a high-quality assembly of the whole-genome shotgun sequence of soybean, which will speed the completion of the project, and might ensure the success of future research relying on the assembly.

- *Identification of candidate genes and discovery of new genes for Asian soybean rust resistance.* Outbreaks of Asian soybean rust have now occurred in all major soybean-producing countries and can cause yield losses up to 75 percent. Thus far, only four resistance genes to Asian soybean rust have been identified. ARS scientists in Ames, Iowa, located and sequenced the chromosomal regions that include two of the resistance genes, finding that the regions contained 23 and 3 candidate resistance genes, respectively. Researchers are rapidly developing markers for those genes to enable more precise use by breeders. Significantly, those regions also confer resistance to other important soybean pathogens. Therefore, the markers developed for Asian soybean rust may also benefit research with other important soybean diseases. Furthermore, ARS scientists in Peoria, Illinois, discovered a new genetic source for soybean rust resistance, confirmed that it is at the same chromosomal location as a currently known resistance gene, but found that it is a different form, or allele, of that gene. This new allele should increase the diversity of types of rust resistance in soybean varieties and, via closely linked DNA markers, the new resistance sources can be readily transferred to new varieties.
- *Providing new genetic resources to protect rice from disease and pests.* Genome sequencing of rice has identified thousands of genes, most of which with unknown functions. ARS researchers at Davis, California, working with scientists at the University of California, Davis, and with USDA Cooperative State Research, Education, and Extension Service support, have generated a large population of rice mutants with altered DNA sequences. Using this resource, rice mutants can be selected for any gene sequence of interest and characterized in the laboratory or field. The rice mutants, called “tilling” mutants, were added to the ARS rice genetics stock collection at Stuttgart, Arkansas, to be shared with interested researchers. These new genetic resources enable researchers to evaluate and exploit the effects of altering any rice gene and may serve as the basis for new strategies to protect rice from disease and pests.
- *Genetic mapping of photo-periodic induction of dormancy in a hybrid grape population.* Grapevines grown in many regions of the eastern United States are poorly adapted to low-temperature 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 initiate dormancy in response to shortening day-length in early fall. To understand the genetic control of day-length sensitivity, ARS scientists in Geneva, New York, identified genes controlling photo-periodic induction of dormancy and mapped through analyses of offspring of parents that differ in their sensitivity to day-

length. One genomic region accounted for more than 40 percent of the variation observed for photo-periodic induction of dormancy. These results will help with developing an assay for more efficiently selecting this trait and generating improved cultivars of grape for cold climates.

- *Characterization of a short-leaf sorghum mutant aimed at more effective use of solar radiation.* Grain yield and biomass production can be increased by more effective capture of solar radiation. ARS scientists at Lubbock, Texas, have characterized a sorghum mutant with steeper leaf angles, advantageous for capturing solar energy. The mutant also has shorter leaves, which can increase drought tolerance. The mutant is now being exploited to map, identify and characterize the gene(s) responsible for the short-leaf trait. This new genetic resource can now be exploited by sorghum breeders to genetically-improve both biomass production and drought tolerance.
- *Discovery and mapping of a new soybean aphid resistant gene and development of new soybean lines with aphid resistance.* ARS researchers at Wooster, Ohio, discovered a new biotype of the soybean aphid that can defeat the previously-known source of host-plant resistance, and also quickly identified several soybean accessions from Asia with resistance to this new soybean aphid biotype. A new gene from a resistant sample in the USDA soybean germplasm collection was characterized and named Rag2. This resistant sample was crossed to an elite cultivar from Ohio to develop mapping populations and backcross lines. This new gene was mapped to soybean molecular linkage group F. Resistant germplasm derived from this newly discovered source is under rapid development.
- *The effect of leaching and boiling on mineral levels in potato tubers.* ARS scientists in Madison, Wisconsin, found that the mineral content of potatoes was drastically reduced by cubing or shredding them, then boiling. In contrast, leaching had little effect on mineral levels. Leaching alone was ineffective for reducing potassium content, and therefore would not benefit renal failure patients trying to reduce potassium consumption. Those with compromised kidney function can decrease their mineral intake, while still taking advantage of the other nutritional qualities of potatoes, by boiling them, thinly sliced, which will remove most minerals, including potassium. This research highlights the significance of understanding the effect of cooking on nutrient levels of potato, both for breeders attempting to improve the mineral content of potatoes and for health science professionals providing advice about potatoes in the human diet.
- *New sunflower cytoplasmic male sterility and fertility restorer genes discovered.* ARS scientists in Fargo, North Dakota, discovered a new type of cytoplasmic male sterility (CMS) from a cross between a wild sunflower accession and cultivated sunflower. This new CMS gene is different from all previously reported CMS types. A corresponding male fertility restoration gene for this CMS gene was also identified from a different wild sunflower accession. The CMS gene and its corresponding fertility restoration gene were introduced into a cultivated sunflower (HA 89)

background through backcrossing and selection. Genetic analysis revealed that this fertility restoration system is controlled by a completely dominant gene, which mapped to linkage group 3. The CMS-Restorer system tagged by molecular markers provides an effective alternative genetic source for hybrid breeding in sunflower, thereby potentially broadening this crop's genetic diversity.

- *Protecting sorghum from disease and pests.* Sorghum insect and fungal pathogens cause major economic losses in yield and seed quality each year worldwide. ARS scientists at Stillwater, Oklahoma, completed a 5-year project to systematically screen the U.S. sorghum collection of 40,000 accessions for greenbug (aphid) resistance. All available U.S. germplasm was screened, resulting in the identification of 32 sorghum lines with varying levels of greenbug resistance, and eight lines with strong resistance to greenbug biotype I that is the predominant greenbug pest in the United States. Also, ARS researchers in College Station, Texas, and Mayaguez, Puerto Rico evaluated, with pathogen-colonized grain inoculation methods, hundreds of U.S. commercial hybrids, and sorghum accessions from Ethiopia, Mali, Sudan, and Uganda for resistance to the fungal pathogen, anthracnose. Many accessions highly resistant to the disease were identified, thereby furnishing sorghum breeders with critical new germplasm for initiating new breeding projects to develop anthracnose-resistant sorghum varieties.
- *Nursery tree scion architecture modification by apple rootstocks.* Choosing a rootstock that can generate a good quality tree with high early production is problematic for finished tree nurseries and apple growers. ARS scientists at Geneva, New York, found that many of the Geneva apple rootstocks have flatter branches and more "feathers" than similar commercial rootstocks, which would be advantageous for high density production systems, such as the Tall Spindle, because less labor would be required to tie down feathers or branches after planting. This trait is valuable when pairing rootstocks with upright growth-habit scion varieties to decrease vigor and increase productivity. Rootstocks can confer traits that change the architecture of the orchard, facilitating mechanized pruning, and enabling apple growers and nurseries to pair specific scions with these rootstocks to obtain better tree quality and orchard architecture.

Component 3. Genetic Improvement of Crops

- *Slow wilting trait discovered in soybean; drought-tolerant germplasm developed.* ARS scientists at Raleigh, North Carolina, developed a new generation of soybean breeding lines with extremely valuable drought tolerance. In regional and local testing, two lines, N04-9646 and N01-11771, were slow wilting, with a substantial yield benefit when grown under dry conditions. Uncharacteristically, they also yielded reasonably well in environments with minimal plant stress. These long-awaited genetic materials, now available to and being used by commercial breeders as parental stock, are likely the most drought-tolerant soybean materials in the world. Their impact on soybean production will be fully realized as commercial breeding programs release new cultivars derived from this ARS stock.

- *Identification of the major gene that determines the level of provitamin A in corn.* Dietary vitamin A deficiency causes eye problems in 40 million children throughout the world each year, and puts an additional 140-250 million children at risk for related vitamin A deficiency disorders and increased mortality. Breeding to increase levels of provitamin A (biofortification) using existing natural genetic variation in corn is an economical and helpful approach to address this challenge, particularly where children subsist on largely corn-based diets. In collaboration with Cornell and University of Illinois researchers, ARS scientists at Ithaca, New York, have identified a major gene that determines the levels of provitamin A in corn. Natural genetic variants of this gene can increase provitamin A content five-fold. Inexpensive markers for the gene were developed that enable crop breeders to genetically select for higher provitamin A content; the markers are now being applied in corn genetic improvement programs in developing countries.
- *A new strawberry for Pacific Northwest production systems.* The strawberry industry in the Pacific Northwest has been dominated for more than 30 years by a single variety ('Totem') with excellent fruit quality, but which is becoming less economical to produce due to increasing disease problems, moderate yields, and medium fruit size that leads to high picking costs. ARS researchers in Corvallis, Oregon, developed new cultivars with excellent processed fruit quality and which are more efficient to harvest. The ARS strawberry cultivar 'Tillamook' became the number one cultivar purchased by the commercial industry in the Pacific Northwest, the first time in over 3 decades that 'Totem' was not the number one cultivar sold. Another strawberry cultivar, 'Stolo', developed and released in cooperation with Agriculture and Agri-Foods Canada, is resistant to root weevils and may enable growers to produce strawberries with reduced inputs of insecticides.
- *Reintroduction of heritage potato variety.* Development of specialty potato varieties with enhanced culinary traits and nutritional profiles has attracted commercial interest, especially of small producers, who can market smaller quantities of potatoes in markets that pay considerably more per pound than the traditional markets. ARS researchers in the Pacific Northwest have identified and collected potatoes grown for hundreds of years by Native Americans and Native Alaskans, introduced these cultivars into tissue culture, eradicated viruses, and re-introduced them to the Native groups. This has helped to preserve their place in the cultures of the tribes and increased enthusiasm for science education focused on their own heritage food items.
- *Stripe-rust resistance protects U.S. wheat and barley.* Wheat and barley stripe rust has caused major yield reductions and economic losses for grain producers in the Pacific Northwest, Midwest, and eastern United States since 2000. ARS scientists at Pullman, Washington; Manhattan, Kansas; and Raleigh, North Carolina, partnered with regional wheat and barley breeders to identify new sources of stripe rust resistance and develop DNA markers linked to resistance genes. ARS genotyping scientists and variety trial coordinators facilitated genetic selection and field disease trials. In 2008, ARS and university geneticists, through the Wheat and Barley Stripe

Rust Initiative, released new wheat and barley varieties with significantly improved stripe rust resistance in all affected regions of the United States.

- *Genetic resistance to Fusarium Root Rot in Pea.* Legume production, especially of dry pea, has increased dramatically in the north central United States. Fusarium root rot is a devastating disease of both vegetable and dry peas in the United States, especially in summer rainfall areas. ARS scientists in Pullman, Washington, released three new pea germplasm lines (W6 26740, W6 26743 and W6 26745) with improved agronomic qualities and high levels of resistance to Fusarium root rot for immediate use by breeders for cultivar improvement. These materials might accelerate development of commercial peas with innate resistance to Fusarium root rot, thereby enhancing yield and reducing the need for chemical application.
- *New Peach Varieties.* Performance of Scarletprince and Julyprince, new peach varieties developed by ARS scientists at Byron, Georgia, was outstanding in the first year of substantial commercial production. Both yielded well in a year when many peaches were damaged by sequential frosts. New moderate chill releases, Gulfking and Gulfcrest, produced their first commercial crops. Despite late frosts which heavily damaged standard cultivars, both of the new selections yielded well and were well-received by growers. Demand was high for budwood of three new peach varieties released last year, Gulfcrimson, Augustprince, and Early Augustprince, which are quickly replacing the existing varieties in that season in the Southeast, due to their superior characteristics. As the new varieties begin to bear fruit in 2-3 years, consumers will have superior peaches available from southeastern growers.
- *Validating phenotypic markers for combining multiple rust resistance genes in beans.* Several rust resistance genes must be combined in bean varieties to effectively manage under field conditions the many different strains of the bean rust pathogen. Phenotypic or molecular markers may facilitate this, but effective molecular markers for most rust resistance genes are currently lacking. ARS scientists in Beltsville, Maryland, have identified excellent, very reliable phenotypic markers that accelerate the combination of two, three, and four rust resistance genes in the same variety. The interactions between the different rust strains with each individual rust resistance gene, which are well-defined and repeatable, were exploited as phenotypic markers to develop snap beans with two rust resistance genes, as well as dry beans (of the pinto, great northern, and small red market class) with two, three, and four rust resistance genes. Bean cultivars with multiple genes for resistance to rust will provide greater protection to the U.S. bean crop, leading to enhanced crop productivity and profitability. This research has already yielded a new great northern bean germplasm line resistant to multiple disease pathogens.
- *Resistance of hemlock to woolly adelgid.* Hemlock woolly adelgid is a devastating introduced insect pest of native eastern hemlock species which are important forest and landscape trees. Controlled inoculations of interspecific hemlock hybrids were conducted to investigate maternal and paternal effects on susceptibility to hemlock woolly adelgid. Multiple sources of resistance to hemlock woolly adelgid were

identified which will guide future crossing experiments. Significant tolerance to the adelgid was noted in F1 interspecific crosses that might yield effective resistance in landscape plantings and ultimately generate several novel hemlock hybrids.

- *Genetic inheritance of powdery mildew resistance in grapes.* Powdery mildew is the most devastating fungal disease of grapes with over 17 million pounds of sulfur applied, as a control measure, to table grapes alone in 2004. Natural resistance exists in wild grape species, and might serve as an alternative to chemical control of powdery mildew. A Chinese grape species was hybridized, by ARS scientists at Parlier, California, with raisin germplasm. Analyses of the preceding hybrid showed that host-plant resistance was inherited as a single dominant gene through the third backcross generation, and demonstrated that mildew resistance can be transferred, via modified backcrossing, to raisin, table or wine grapes while improving fruit quality. The potential impact is the development of powdery mildew-resistant grape varieties.
- *Chloroplast Markers for Pecan.* Pecan rootstocks influence performance of trees in orchards, but few tools are available to analyze the effects on performance of different open-pollinated seedstocks. ARS scientists at College Station, Texas, and their Texas A&M University cooperators tested five prospective universal chloroplast primers, two of which effectively detected genetic differences in pecan varieties. This research has yielded simple methods for analyzing the genomic variation in interspecific hybridizations as well as the distribution of pecan genetic diversity in relation to geography. It will also enhance the understanding of rootstock adaptations and might yield superior recommendations for pecan cultivar deployment. Ultimately, application of these and other markers to pecan development will yield improved cultivars for producers.
- *Fairy ring disease of cranberry impacts host genotype.* Fairy ring is a fungal disease that kills plants in an expanding circle. ARS scientists at Chatsworth, New Jersey, demonstrated through DNA fingerprinting that as fairy ring disease sweeps through an infected cranberry bed, the primary cultivar, which is typically clonal, is largely killed. This allows seedlings with other genetic backgrounds to establish, and over time the cultivar that was originally planted is lost in areas devastated by the disease. This dramatically reduces yield potential in the affected cranberry beds, because surviving seedlings, although not the original productive cultivar, are likely to be more resistant to the disease, thus providing a potential source of genetic resistance. This information suggests that growers may wish to replant areas affected by the disease to insure continued productivity, but also suggests that recolonizing plants may be useful for resistance breeding
- *Relationship of yield, berry weight, and pollination effectiveness in highbush blueberry.* Growers often wonder whether small berry size in blueberries means that pollination was less than optimal. ARS scientists at Beltsville, Maryland, documented the relationship between yield, berry weight, and pollination effectiveness, as measured by seed number, in two major highbush blueberry cultivars. In a 10-year period there was no correlation between yield and berry

weight, but seed per gram of fresh weight was correlated to total yield. The research showed that although berry weight has been shown to be correlated to seed number, for the cultivar 'Duke', berries with similar seed numbers varied in weight by as much 86 percent between years. This research aids in understanding the parameters that affect and may contribute to improvement of total marketable yield by enabling growers to concentrate on critical yield-related factors.

- *Fungal pathogen evaluated for its ability to cause disease on chickpea.* Using genetic transformation techniques on a highly destructive fungal pathogen, *Ascochyta rabiei*, ARS scientists in Pullman, Washington, identified the genetic regions that are responsible for the pathogen's ability to cause disease. These genetic domains are currently being examined by DNA sequence analysis. The identification of genes responsible for the ability of the fungus to cause disease will provide critical basic knowledge on mechanisms of pathogenicity and can also serve as DNA probes for identifying genes controlling pathogenicity in other fungal pathogens of plants.