National Program 301
PLANT GENETIC RESOURCES, GENOMICS, AND GENETIC IMPROVEMENT
FY 2006 Annual Report

Introduction
National Program 301 – Plant Genetic Resources, Genomics, and Genetic Improvement – addresses the need to ensure the long-term safety and integrity of our agriculturally valuable genetic resource collections; to identify favorable alleles 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 and microbial genomes; and to acquire, analyze, and deliver genetic 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.

This National Program is divided into three 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 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 molecular marker analyses, nucleotide sequencing, gene mapping, comparative and, to a limited extent, functional genomics, plant breeding, and genetic enhancement).

Together, these 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) 2006 this program produced several important discoveries and advances. Some of these are described below, grouped by program component.

Component I – Plant and Microbial Genetic Resource Management

During FY 2006, the 20-plus genebanks in the ARS National Plant Germplasm System (NPGS) added more than 9,000 separate samples of more than 500 plant species to their collections, bringing to a total of more than 474,000 samples of more than 11,800 plant species conserved by NPGS genebanks. Scientific interest in this germplasm has increased tangibly during the last few years, with the average number of samples distributed per year now (as of FY 2006) totaling

more than 130,000, which is 30,000 more than the average a decade ago. These materials are keys for continued progress in crop genetics and breeding requisite for future food security.

<u>Component II – Crop Informatics, Genomics, and Genetic Analyses</u>

One of the most critical elements in the establishment of a new orchard is the quality and the architecture (size, number of branches and branch angle) of the trees that are being planted since good quality trees enable early productivity of the orchard and a faster track to the profit phase. ARS scientists at Geneva, New York, in collaboration with Washington State University scientists and a private nursery, discovered and described how a diverse group of apple rooststocks can predictably modify the branch angle and branch number of finished trees, thereby increasing the quality of the finished tree. This work also has implications on future mechanization technologies where specific tree architecture is required.

A genetically anchored physical map of chromosomes is essential for the isolation of genes underlying agronomically important quantitative trait loci (QTL). ARS scientists at Ames, Iowa, have built a relational database to hold all of the physical and genetic map data for soybean. This database is able to display the physical map overlayed onto the genetic map and is populated with agronomically important QTL. In addition, an online tutorial for the Web-based map displays and databases also was developed. This database will be useful for the interpretation of whole-genome sequence data being generated by Department of Energy.

The mischaracterization of cocoa materials in existing collections and the absence of new accessions of properly characterized wild materials is the single most important factor hampering proper curation and traditional breeding in producing countries. ARS scientists made great strides in identifying wild and previously unknown cocoa varieties by publishing the proper molecular-based labels for 1,124 key accessions of wild Upper Amazonian cocoa and depositing the data in the international molecular database (CocoaGenDB) in Montpellier, France. Also, analysis and publication of wild populations of cocoa in French Guiana established that they form a very separate and heretofore relatively unknown source of genetic diversity. A substantial number of clones maintained in the two international collections at Costa Rica and Trinidad were profiled (2,047 in total) and submitted to the international phenotypic database in Reading, United Kingdom, and CocoaGenDB.

ARS researchers at NPGS genebanks and their university collaborators developed and/or applied powerful molecular diagnostic tools for ensuring that germplasm is free of key diseases. Examples include molecular diagnostic tests for: seedborne Stewart's wilt in maize and bacterial fruit blotch of melons (ARS Ames, Iowa, genebank); Citrus leprosis virus (ARS Riverside, California, genebank); phytoplasmas in hazelnut, strawberry, pear, and blueberry (ARS Corvallis, Oregon, genebank); alfalfa mosaic virus in crotolaria (ARS Griffin, Georgia, genebank); and cucumber mosaic, banana streak, and banana mild mosaic viruses (ARS Mayagüez, Puerto Rico, genebank). These molecular diagnostic tests enable rapid, inexpensive, and accurate detection of key pathogens, which is critical for maintaining germplasm health and permitting international and domestic germplasm exchange. Ready access to vigorous and health plant germplasm is integral to accelerating progress in crop genetic resource conservation and breeding.

Component III – Genetic Improvement of Crops

Researchers, producers, and seed companies depend upon ARS for new and useful germplasm as the basis for creating new commercial varieties. In 2006, ARS released more than 90 germplasm varieties with desirable traits, such as disease resistance, improved quality, and better adaptation to environmental conditions. These traits were identified by stakeholders and producers as being among their priorities for improving the quality of their crops. Germplasm for crops that were released in 2006 included lettuce, soybean, ryegrass, white kidney dry bean, wheat, sugarbeet, southern pea, peppers, rice, pear, sunflower, broccoli, grape, and others.

ARS scientists at Beltsville, Maryland; Urbana, Illinois; Ft. Detrick, Maryland; and the Monsanto Company have identified a simple sequence repeat (SSR) genetic marker (BARC_Sat_187) that is 99.2 percent accurate in predicting soybean breeding lines that carry resistance to Asian soybean rust at the Rpp1 resistance locus. Asian soybean rust caused by Phakopsora pachyrhizi was first found in the continental United States in 2004 and poses a major threat to the U.S. soybean crop. Four genes in soybean confer resistance to Asian soybean rust (Rpp1, Rpp2, Rpp3 and Rpp4), but the utility of these genes in crop improvement has been impeded by a lack of genetic markers. The BARC_Sat_187 SSR marker will be useful for integrating Rpp1 resistance into modern cultivars.

Improving agricultural traits using standard genetic mapping approaches and many molecular markers can be a slow process. ARS researchers at Ithaca, New York, and Cornell University researchers, have developed a new statistical genetic design for dissecting complex traits in corn at the gene level. This new approach is called Nested Association Mapping. Standard mapping approaches result in low resolution of complex traits. This new approach combines high-throughput DNA sequencing with new statistical approaches that provide very high resolution mapping. These new genetic analysis methods can be extended beyond corn and will be useful for manipulating traits in many types of crops.

A newly released pear variety – 'Sunrise' – fills the need for an early-season pear cultivar with excellent fruit quality and appearance and with resistance to the devastating disease known as fire blight. Evaluations by ARS scientists at Kearneysville, West Virginia, and cooperators documented excellent overall consumer acceptance in comparison with existing commercial varieties. It is anticipated that 'Sunrise' will reduce grower losses and provide good economic return to fruit orchards, especially in regions where the annual risk of fire blight disease limits pear production.

With a growing interest in development of sugarcane varieties that provide cold hardiness (to increase the range of cane production in temperate climates), increased sugar, and potential use for biofuels, ARS scientists in New Orleans, Louisiana, have developed several new germplasm lines that incorporate Saccharum spontaneum, a weedy species of sugarcane better adapted to sub-tropical environments, as the female parent. Several of these lines have sucrose contents that match those of current commercially grown varieties, which trace their ancestry to one female parent incapable of surviving most winters in Louisiana and points north. These lines will be used as parents during the 2006 crossing season to develop sugarcane varieties with improved cane and sugar yields over a range of environments.

Four new restorer germplasm lines (RHA 461 to RHA 464) were released by ARS and the North Dakota Agricultural Experiment Station. These germplasm have been selected for their tolerance to Sclerotinia head rot, a major sunflower disease, and provide diversity for agronomic characteristics. RHA 462 provides tolerance to Phomopsis stem canker, and RHA 464 has resistance to the most virulent North American races of rust and downy mildew. These germplasms are available for use by industry and public researchers to create hybrids, parental lines, or germplasms with increased tolerance to Sclerotinia head rot.