

Plant, Microbial, and Insect Genetic Resources, Genomics,  
and Genetic Improvement  
FY 2004 National Program Annual Report

National Program 301, Plant, Microbial, and Insect Genetic Resources, Genomics, and Genetic Improvement, is divided into three components: **Genetic Resource Management** (conserving a broad spectrum of genetic resources and facilitating their use in genetic improvement and scientific research); **Genomic Characterization and Genetic Improvement** (including molecular marker analyses, nucleotide sequencing, gene mapping, comparative and, to a limited extent, functional genomics, plant breeding, and genetic enhancement); and **Genome Databases and Bioinformatics** (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). 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 FY 2004 this program produced many important discoveries and advances. Some of these are described below, grouped by program component.

### Component 1. Genetic Resource Management

Crop genetic diversity conserved and distributed to researchers. The 20+ genebanks in the USDA/ARS National Plant Germplasm System (NPGS) now conserve 460,000 separate samples of over 10,700 plant species. During the last few years, scientific interest in this germplasm has increased tangibly, with more than 130,000 samples distributed last year to requesters worldwide. These materials are key to enabling continued progress in crop genetics and breeding requisite for food security.

Adding to the USDA wild sunflower collection. ARS scientists at Fargo, North Dakota, made two explorations for eight rare, endangered, or threatened wild *Helianthus* species. Thirteen populations of *H. californicus* were collected in California. The perennial sunflowers *H. schweinitzii* (endangered), *H. eggertii* (threatened), *H. verticillatus* (rare), and the annual sunflower *H. porteri* (a species recently transferred to the genus *Helianthus*) were collected in the southeastern United States. Seeds of three other species (*H. angustifolius*, *H. atrorubens*, and *H. smithii*) were also collected. All of these materials were incorporated into the National Plant Germplasm System for conservation and distribution. The availability of seed of these eight species will allow researchers around the world the opportunity to investigate the potential of these wild *Helianthus* species for useful traits for incorporation into cultivated sunflower.

Innovative dynamic conservation and genetic improvement site for pecan. ARS scientists at College Station, Texas, established in Louisiana an innovative plantation of pecan seedstocks selected for their combined horticultural and forestry merit. This creates the first long-term pecan test system focused both on pecan genetic improvement in a major U.S. production area, and on the development of large-scale pecan production systems that simultaneously improve wildlife habitat and harvest yield.

Valuable new genetic markers for multiple crops developed. Scientists at ARS genebanks developed and/or applied new genetic markers, called Simple-Sequence Repeat (SSRs), to a broad spectrum of crops, such as peanuts, citrus, grapes, tropical legumes, mango, paspalum, tropical ornamental bulbs, blueberries, and hazelnuts. This technology provides a rapid and inexpensive means for assaying genetic variability in DNA, and thereby provides critical information for designing efficient and effective genetic resource management strategies.

Capitalizing on genes from exotic soybean germplasm. ARS scientists at Urbana, Illinois, demonstrated the value of ‘untapped’ genes in soybean. Four quantitative trait loci (QTL) associated with high protein concentration were mapped in populations derived from three exotic sources of high protein. In near isogenic populations the yield increases per QTL ranged from 2.9 to 4.5 bushels per acre. A new germplasm release with 87% exotic germplasm in its pedigree, LG00-3372, was the highest yielding entry in Uniform Preliminary Test IIIB in 2003.

Adding value to sorghum. ARS scientists at Lubbock, Texas, developed a new assay to identify sorghum lines with high water use efficiency. ARS scientists at College Station, Texas, in cooperation with Texas A&M scientists cloned the pollen fertility restorer gene, important for genetic improvement of sorghum. ARS scientists at Lincoln, Nebraska, screened over 4000 U.S. sorghum accessions for starch, protein, and oil content. This work provides valuable new information for selecting sorghum with improved nutritional values and for improved ethanol production.

Public release of quantitative trait loci (QTL) mapping population. The soybean mapping population NC113 was developed by ARS scientists at Raleigh, North Carolina, as a classroom teaching tool. This genetic resource includes 116 breeding lines, phenotypic data and corresponding DNA marker information for six traits. Identification of QTLs associated with these traits was accomplished in collaboration with scientists at the University of Georgia. This QTL population is the most heavily studied DNA marker population in soybean and QTL mapping in soybean breeding has significantly accelerated the pace of genetic improvement.

## [Component 2. Genomic Characterization and Genetic Improvement](#)

Solving the puzzle of soybean genome structure. Assembling the soybean genome from fragments of DNA is like solving two jigsaw puzzles at the same time, because soybean has two duplicated sets of chromosomes. ARS scientists at Ames, Iowa, developed techniques and bioinformatic software that helps direct the location of gene families onto the correct chromosome with locus-defining markers and also to identify duplicate copies of alleles (genes) for the same trait. Statistical modeling of the soybean genome predicts that most soybean genes will be found in approximately 25% of the genome space. This knowledge provides clues to the strategy that will save many millions of dollars in sequencing costs.

Sunflower genetic map for oleic acid composition developed. ARS scientists at Fargo, North Dakota, constructed a gene linkage map from a set of 129 recombinant inbred lines derived from the cross of 83HR4 x RHA345. The linkage map consisted of 160 markers in 17 linkage groups (chromosomes) plus four pairs of linked markers that spans much of the genome with dense packing between markers. This map will help define the genes affecting oleic acid composition, which is associated with good health, in the oil from sunflower seed.

A high density DNA linkage map of papaya produced. ARS scientists at Hilo, Hawaii, in collaboration with researchers at the Hawaii Agriculture Research Center and University of Georgia, produced a high density DNA linkage map that revealed a primitive sex chromosome that resembles the ancestor of the human Y chromosome. Sequencing of this chromosome may reveal genes and their regulatory elements that can be managed to attain proper sex expression for high yield in seed and fruit crops.

DNA marker for sunflower downy mildew identified. ARS scientists at Fargo, North Dakota identified a DNA marker associated with downy mildew resistance in PI 468435, which is resistant to all known downy mildew races. Downy mildew is one of the most important diseases of sunflower in North America and this marker will be used to accelerate breeding progress toward downy mildew resistant elite sunflower lines.

#### Germplasm Releases:

- ARS cotton geneticists at Stoneville, Mississippi, released a new germplasm line, MD 52ne, with 10% greater fiber strength
- ARS geneticists at Mississippi State in cooperation with Texas A&M University released 17 important lines of upland cotton, each with a different single chromosome from extra-long staple cotton.
- ARS scientists at Corvallis, Oregon, and at Oregon State University released ‘Chinook’ a primocane raspberry for late-season production; ‘Pinnacle’ and ‘Tillamook’ June bearing strawberries; and the early ripening blackberry cultivars, ‘Obsidian’ and ‘Metolius’.
- ARS scientists at Prosser, Washington, and at Aberdeen, Idaho, in collaboration with scientists in Oregon, Idaho, and Washington released ‘Defender’ a cultivar with resistance to late blight in the foliage and tubers.
- ARS scientists at Beaumont, Texas, released the cultivar “Neches” as dessert rice with novel starch and flour properties.
- ARS researchers at Lincoln, Nebraska, in cooperation with the University of Nebraska released two new hard white winter wheat varieties with flour characteristics that are ideal for Asian noodles.
- ARS scientists at Canal Point, Florida, in collaboration with researchers at the University of Florida, Belle Glade, Florida, and the Florida Sugar Cane League, Inc., Clewiston, Florida, released sugarcane cultivars CP 97-1944 and CP 97-1989. These two new cultivars add genetic variability for disease and insect resistance while producing at sustained levels of profitability in Florida.

- ARS scientists at Charleston, South Carolina, released the sweet potato cultivar ‘Liberty’ a significant improvement in dry-fleshed cultivars with resistance to insects and root knot nematodes, and greatly improved storability.
- ARS scientists at Prosser, Washington and Mayaguez, Puerto Rico in collaboration with scientists at the University of Puerto Rico, developed three dry edible bean germplasm with resistance to bean golden yellow mosaic virus, the major viral disease problem in Latin American and Florida.
- ARS scientists at Phoenix, Arizona, released lesquerella germplasm with improved seed oil content to provide an alternative domestic source of hydroxy fatty acids to replace imported castor bean oil.
- ARS scientists at Fargo, North Dakota, released seven cytoplasmic male sterility sources that complement the sole cms source (cmsPET1) currently used in sunflower hybrid seed production.
- ARS scientists at Stoneville, Mississippi, released DT97-4290, a high-yielding charcoal rot-tolerant MG IV soybean germplasm line that is well adapted to the Early Soybean Production System in the lower Mississippi River Valley.
- ARS scientists in Stillwater, Oklahoma, discovered new sources of genetic resistance to the bird cherry-oat aphid, a perennial pest of wheat.
- Purdue scientists and ARS researchers at W. Lafayette, Indiana, developed wheat lines that are resistant to barley and cereal yellow dwarf virus.
- ARS scientists at Aberdeen, Idaho and Stillwater, Oklahoma, developed the barley variety “Burton” that is resistant to Russian wheat aphid.

Researchers, producers and seed companies depend upon USDA-ARS for new and useful germplasm as the basis for creating new commercial varieties.

### [Component 3: Genome Databases and Bioinformatics](#)

New user-friendly web site provides vital genetic and genomics resource for wheat, barley and oats researchers. ARS scientists at Albany, California, and Ithaca, New York, developed a new relational database website “GrainGenes 2.0”. Genomics and genetic data are provided to cereal researchers from this website along with new bioinformatics software tools and genetic mapping information. This central site insures that the most recent genetics and genomics discoveries are rapidly deployed in U.S. wheat, barley, and oats genetic improvement programs.

Successful application of a new “gene-finding” technique. ARS scientists at Ithaca, New York, applied a new statistical genetic approach, termed “association mapping,” to characterizing the genetic control of starch and protein quality in corn. This successful proof-of-concept for a new method for accelerating genetic improvement also identified new genes potentially valuable for breeding corn tailored to meeting specific agronomic and industrial needs.

Powerful new bioinformatic tools developed for understanding grain genomes. ARS scientists located at the Cold Spring Harbor Laboratory in New York, improved bioinformatic tools for comparing the genomic structure of corn and rice. Sorghum and

wheat “physical maps” were incorporated into the grain genome database Gramene. These advances furnish new, more powerful bioinformatic/database tools for accelerating progress in understanding the detailed genetic structure of grain genomes.

New methods for discovering genes in soybean. ARS scientists at Beltsville, Maryland, showed that the loss of genetic diversity in the modern soybean genome was much less rapid than in maize or even *Arabidopsis*, but the decline in genetic diversity was significantly more rapid in wild soybean vs. unimproved cultivated soybean germplasm typical of that in the USDA Soybean Germplasm Collection. This unexpected discovery suggests that genetic association analysis, using whole genome scans, may be feasible for gene or QTL discovery based on the first application of ‘linkage disequilibrium’ theory in a self-fertilized crop species.