

Plant, Microbial, and Insect Genetic Resources, Genomics,
and Genetic Improvement
FY 2002 National Program Annual Report

- Introduction
- Component I. Genetic Resource Management
- Component II. Genomic Characterization and Genetic Improvement
- Component III. Genome Databases and Bioinformatics

Introduction

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 2002, this program produced many important discoveries and advances. Some of these are described below, grouped by program component.

Selected Accomplishments by Component

Component I. Genetic Resource Management

The USDA/ARS collections of genetic resources represent the largest and highest quality source of raw genetic material for ensuring continued worldwide progress in genomic research and genetic improvement of agricultural commodities. One component of National Program 301 is the USDA/ARS plant, microbial, and insect genetic resource management program, which is conducted with a variety of university and corporate partners and with other national and international genetic resource programs, especially those at international agricultural research centers. There are very few publicly accessible germplasm collections maintained by the private sector, so all segments of worldwide agricultural research and genetic improvement rely on the USDA/ARS public collections of genetic resources.

New acquisitions of plant germplasm. The National Plant Germplasm System maintains one of the world's largest collection of plant samples important for crop improvement. Access to diverse genetic material is key to ensuring continual progress in crop genetic improvement. ARS scientists in Beltsville, Maryland, coordinated successful plant exploration trips in seven nations that added many new

accessions of peanuts, potatoes, chiles, butternuts, ornamentals, breadfruit, cotton, soybean, common bean, forage legumes and grasses, sunflowers, and amaranths to the National Plant Germplasm System. The wide diversity of genetic material collected by these explorations will be available on request to researchers and breeders worldwide.

Successful processing of genetic resources through quarantine. Federal law requires that germplasm of many vegetatively-propagated crops be introduced through the quarantine process. More than 400 samples of fruit crops, grasses, potatoes, and rice were successfully processed through the specialized quarantine facilities of the Plant Germplasm Quarantine Office in Beltsville, Maryland. This material was successfully incorporated into the National Plant Germplasm System genebanks for preservation and distribution worldwide.

Genetic characterization of the nation's plant genetic resources. Genebanks in the National Plant Germplasm System maintain 450,000 accessions of over 10,000 plant species. Leading-edge genetic resource management technologies are needed to both increase the efficiency and effectiveness of genetic resource management efforts and to make these key data available to germplasm users. ARS scientists at over 20 genebanks "fingerprinted" thousands of accessions with advanced DNA marker technology or tested for pathogens with new molecular diagnostic methods. Digital images of thousands of samples were captured and made accessible via the Internet. Geographical Information Systems were mobilized to detect potential "genetic gaps" in the holdings of the germplasm collections to enable more precise planning of future plant explorations to secure genetic materials needed to close such gaps, and concurrently make available new, high-quality information to germplasm users worldwide.

New genebank for ornamental germplasm. The Ornamental Plant Germplasm Center at the Ohio State University, Columbus, Ohio became fully operative during 2002. Supported by the ARS Plant Germplasm and Information Management Unit in Ames, Iowa, the OPGC will preserve and manage a wide diversity of germplasm from herbaceous ornamental species. This effort will ensure that invaluable breeding stock for these ornamentals is preserved and made available for genetic improvement.

Component II. Genomic Characterization and Genetic Improvement

USDA/ARS researchers apply traditional and contemporary technologies to assess the inherent genetic potential of germplasm. To harness this genetic potential most effectively, novel, rapid, and more efficient methods for identifying useful properties of genes and genomes, for determining the function of genomic segments and for manipulating genetic material and genomic information, must be developed. Through genomic characterization, the structural and functional features of genomic segments or of entire genomes can be elucidated nearly simultaneously--providing knowledge that will help create new agricultural products, ensure food safety and security, and furnish new ways of boosting agricultural productivity. Consequently,

sequencing genomes or genomic components of agriculturally important organisms and determining their function via structural genomic analyses are priorities for this component of National Program 301. Furthermore, the information generated by this National Program component, when combined with more effective breeding strategies, will help ARS scientists more rapidly attain high-priority genetic improvement objectives. All of the preceding tools and information furnish the bases for more effective genetic diversity assessments, diagnostic and varietal/strain identification tests, and superior methods of genetic improvement. Optimal progress in genetic improvement will result from the marriage of the preceding technologies with genetic resources, bioinformatics technology, and genomic/genetic information that are reported below. The ultimate result will be superior, genetically improved organisms for agriculture and additional genetic stocks to enable future research.

Genetic resistance to the first viral disease of U.S. sunflowers. An emerging viral disease, discovered in southern Texas, attacks all commercial sunflower hybrids grown in the United States. ARS scientists in Fargo, North Dakota, have discovered populations of wild sunflower that have resistance to the virus, and also resistance to other devastating plant diseases like rust and downy mildew. Genes governing these disease resistance traits were bred into cultivated sunflower germplasm. This new sunflower germplasm is the only breeding material that combines resistance genes for all three of these severe diseases.

Genetic protection of peanuts from multiple disease attack. Tomato spotted wilt virus and the peanut root-knot nematode are economically significant diseases of peanut. Currently, no peanut cultivars have resistance to both pathogens. ARS scientists in Tifton, Georgia, in collaboration with the University of Georgia, have used genes from wild peanut to develop modern breeding lines with resistance to both diseases. These new genetic resources should reduce input costs while increasing yield for U.S. peanut producers. New varieties with these protection traits should be available for commercial production in 5 years.

New cocoa varieties improve production of chocolate. Cocoa (*Theobroma cacao*) is the principal source of ingredients for manufacture of high-quality chocolate. Industries and governments in Central and South America are concerned about low productivity and poor quality of seeds produced by older cocoa trees. ARS scientists in Mayaguez, Puerto Rico, developed several new varieties with superior quality, productivity, and flavor characteristics. Clonal selections will be released to CATIE, Costa Rica, Corporica, Colombia and other germplasm conservation centers in the Americas for distribution to small farmers and cooperatives.

New disease resistant 'Spuds'. ARS scientists in cooperation with the Tri-State Potato Variety Program, released four new potato cultivars: Summit Russet, Wallowa Russet, Willamette Russet and Modoc. These varieties are resistant to corky ringspot, late blight and potato leafroll virus. Two other releases include the variety Alturas, which produces exceptionally high yields with greatly reduced production inputs, and Ivory Crisp, an excellent chipping variety which accumulates low levels

of sugar during long-term storage. These new varieties will increase the competitiveness of the Pacific Northwest potato industry through enhanced disease and pest resistance, reduced production cost, reduced pesticide usage, enhanced quality, and more efficient recovery of processed product.

New rice varieties with qualities desired by consumers developed. Ensuring an adequate domestic supply of rice is a high priority for many food companies. ARS scientists in Beaumont, Texas, have developed a new rice variety with superior parboiling and canning properties, for use in convenience and quick-cooking products, and enhanced resistance to rice blast disease, which is needed for southern U.S. rice production. In addition, ARS researchers in Stuttgart, Arkansas developed new rice lines with aromatic traits. These early maturing varieties help rice growers conserve water use and enhance production efficiency. Developing new rice varieties with consumer appeal will strengthen the U.S. rice industry by increasing revenue streams for farmers, millers, and processors.

Using genetic diversity to enhance weed control in sunflowers. Broadleaf weed control in sunflower is impeded by a lack of effective, registered herbicides. To overcome this serious deficiency, ARS scientists in Fargo, North Dakota, identified wild sunflower germplasm with resistance to the sulfonyleurea class herbicide 'Express' and have transferred this trait to cultivated sunflower hybrids. These new breeding lines will provide the sunflower seed industry with a means to develop commercial hybrids that enable effective and lower-cost control of broad-leaf weeds.

Progress in developing a malting barley with scab resistance. Scab (*Fusarium* head blight) causes economic losses of over \$2 billion annually to the U.S. wheat and barley industry. ARS scientists in Fargo, North Dakota, have developed a two-row barley variety with improved resistance to scab. The new barley cultivar, 'Conlon', has elevated levels of a transgene that reduces buildup of the toxin produced by the scab disease organism in the grain. Field and greenhouse tests have shown that the new cultivar exhibits reduced scab infection compared to other barley cultivars. Development of this scab-resistant barley offers a promising new strategy to develop new barley cultivars with both excellent malting quality and scab resistance.

More nutritious oat variety for the equine community. ARS scientists in Aberdeen, Idaho, and Raleigh, North Carolina, in collaboration with researchers at North Carolina State University, have developed a new winter oat variety for the Southeast that is more digestible and nutritious for horses. This new variety lacks hulls, so that it is more digestible and has a higher content of nutrients per unit mass. This new oat provides a new production option for Southeastern U.S. oat growers and meets special nutritional needs of the equine industry.

Using microbial genetic resources to improve nitrogen nutrition for non-legume plants. Legumes may acquire nitrogen from fertilizer or from atmospheric nitrogen through the symbiotic association with microorganisms. Fertilizer is the only source of nitrogen nutrition for non-legume crops like corn. However, ARS scientists in

Raleigh, North Carolina, in collaboration with researchers at the University of North Carolina, discovered a bacterium that has an unusual nitrogen fixing system. This bacterium strain binds tightly to tomato roots and confers non-symbiotically fixed nitrogen to the plant. This discovery may provide an important alternative source of nitrogen nutrition for other non-legume plant species, and could help to significantly reduce application of nitrogen fertilizers on farm land.

Development of sunflower oil with lower saturated fat content. In response to consumer demand for more healthful food products, ARS scientists in Fargo, North Dakota, identified sources of wild sunflower that cut in-half the amount of saturated fat of sunflower oil. The genes that control this low-saturated fat trait were transferred to modern cultivated sunflower germplasm and agronomic lines. This material will be a valuable resource for public and private seed company commercialization of sunflower varieties that are more attractive to consumers and more competitive in the marketplace.

New strawberry germplasm is resistant to serious disease. No control exists for the bacterial angular leafspot disease of strawberry, which is a serious disease in Florida, California and the north central United States. ARS scientists in Beltsville, Maryland, identified wild strawberries with resistance to angular leaf spot and determined the mode of inheritance of resistance to the disease. Two native strawberry clones were identified that are highly resistant to angular leafspot and these clones have been released to other breeders around the country to be used as parents to develop resistant varieties in their regions.

Maintaining high standards for more healthful sunflower oil. Companies, such as McDonalds, Frito-Lay and Procter & Gamble are using oil from a new ARS-developed type of sunflower called 'NuSun' which has high-oleic acid content. This oil is used to manufacture more healthful foods with lower 'trans' fatty acid content. At the request of the oil processing industry, ARS scientists in Fargo, North Dakota, also developed an early-detection method to keep NuSun seeds separated from conventional sunflower cultivars in commercial production systems. This method will help the industry meet quality standards and better manage crushing operations to capitalize on the valuable characteristics of NuSun oil.

Identifying host-plant resistance genes for enhancement of small grains. Disease and pest resistant, higher-quality, and more productive small grain varieties are needed to increase producer profitability. ARS scientists in Aberdeen, Idaho, in collaboration with university researchers, evaluated more than 22,000 different samples of wheat and barley for host-plant resistance to diseases and pests, grain quality traits, and agronomic merit. Genes identified in this large-scale screening program may provide genes for better grain quality, and high levels of resistance to diseases and pests, thereby serving as sources of resistance genes for further breeding.

New high-quality peanut variety developed. ARS scientists in Phoenix, Arizona, in cooperation with the Virginia Agricultural Experiment Station, developed the new

peanut cultivar, 'Wilson'. The variety yields 4.7 percent to 12.0 percent higher than currently grown cultivars, and will help ensure a stable and plentiful supply of U.S. produced peanuts.

New high-oil lesquerella germplasm. Reduced cost of lesquerella oil is needed to stimulate industrial commercialization of the crop. ARS scientists in Phoenix, Arizona, bred lines with higher oil content and twice the seed yield of conventional varieties. These hybrid lines will help reduce production costs for this domestic source of hydroxy fatty acids and provide a economically viable alternative to imported castor oil.

Discovery of genes that mediate drought tolerance in soybean. Drought is the greatest single limitation to soybean yield in the United States and no drought tolerant cultivars are available for commercial production. ARS scientists Raleigh, North Carolina, in cooperation with public and private sector researchers in six states, coordinated a national program to develop drought tolerant varieties for U.S. soybean production. Using DNA marker analysis, the first genes were discovered in soybean germplasm, which control plant response to drought. These new genetic resources yield up to 20 percent more than standard varieties, and are now being used extensively by public and private breeders.

New genetic markers for disease resistance in cocoa. The diseases, frosty pod and witches broom have caused up to 80 percent losses in the cocoa crop in South America. ARS scientists in Miami, Florida, identified six areas of the cocoa genome (quantitative trait loci) that harbor genes that confer resistance to these diseases. One hundred molecular markers for these genes, obtained from Brazil, are being positioned on the cocoa genetic map. These genetic tools are being used to develop improved cocoa varieties in Ecuador, Brazil, Costa Rica and Puerto Rico.

Markers developed to greatly speed onion breeding. Onion breeding has been advanced significantly by the use of male-sterility genes to replace labor intensive manual pollination methods for the production of improved hybrids. However, it is still extremely expensive and time consuming to score plants for genetic variation in male-sterility genes. ARS scientists in Madison, Wisconsin, developed special genetic markers for male-sterility genes of onion that help breeders screen plants quickly. Use of these genetic tools has reduced the time required to score breeding populations from years to days. These markers have been released to commercial and public onion breeders and will be widely used to select specific onion plants for hybrid development.

Resistance genes for white mold identified in beans. Integrated disease management strategies are needed for control of Sclerotinia white mold in bean, and other agronomic crops. Genetic resistance, an important component of these strategies, is generally lacking because of the complex inheritance of this trait. ARS scientists in Prosser, Washington, in collaboration with the University of California and Syngenta, Inc. identified, characterized and mapped three genes from two exotic sources that

combat white mold disease of common bean. This enables a better understanding of this serious disease and marker assisted selection methods for the three genes could greatly expedite development of dry bean and snap bean cultivars with improved resistance to white mold.

Wheat leaf rust gene cloned. Leaf rust is one of the most important diseases of wheat in the Great Plains causing significant annual economic losses. ARS scientists in Manhattan, Kansas, in collaboration with Kansas State University, cloned a leaf rust resistance gene from a wild relative of wheat that controls the forms of wheat rust that are prevalent in the Great Plains. The cloning of this gene will accelerate breeding of rust resistant wheat and provide a better understanding of disease resistance mechanisms in cereals.

Identification of genes that affect nutritional quality of grain crops. Phytic acid contributes to poor mineral nutrition in humans and in excess excretion of phosphorus into water supplies from livestock wastes. ARS scientists in Aberdeen, Idaho, in collaboration with researchers at the University of Saskatchewan Canada, identified additional genes that reduce the indigestible organic form of phosphorous (phytic acid) in grains. Identifying the genes that determine phytic acid levels in barley and other cereals represents a valuable new tool to develop low phytate crops.

Increasing genetic diversity in U.S. soybean cultivars. Genetic variation is necessary for improving the productivity and quality of soybean cultivars. ARS scientists in Urbana, Illinois, analyzed DNA sequences among modern North American soybean cultivars, their ancestral parents, unimproved Asian germplasm, and wild soybean accessions. Comparison of these data revealed that modern North American cultivars have 30 percent less genetic variability than their direct ancestors and 50 percent less variation than their distant ancestors. This evidence underscores the importance of maintaining genetic variation in current U.S. cultivars, and provides a way to identify soybean accessions that will be particularly useful for enhancing genetic variability of cultivated soybean.

Soybean gene markers released for public use. A total 200 new gene markers developed by ARS scientists in Beltsville, Maryland, in collaboration with the Monsanto Corporation, were released to public and private sector soybean researchers with "no strings attached." New soybean varieties, developed with the assistance of these genetic markers are now being field tested in preparation for release to soybean producers.

Release of a novel soybean variety. Lodging of traditional soybean varieties can significantly reduce yield potential. This problem may be overcome with semidwarf varieties with specific adaptation to high yield environments. A unique breeding program in Wooster, Ohio, developed the semidwarf variety 'Apex' for Midwestern production. This variety also has multiple race resistance to Phytophthora root rot and produces yields up to 90 bushels per acre.

Development of sunflowers with disease resistance to new types of Broomrape. All cultivated sunflowers are susceptible to new races of broomrape, a plant disease that is threatening sunflower production in Europe. ARS scientists in Fargo, North Dakota, in collaboration with researchers in Spain, discovered wild perennial sunflower species that are immune to all races of broomrape. These genetic resources have been used to produce hybrid cultivated sunflower breeding lines that are resistant to a new form broomrape which has become the most virulent disease in Spain. These breeding lines are a first-line of defense for U.S. producers in the event broomrape is introduced into this country.

Gene-markers to detect downy mildew resistance in sunflower. The fungus that causes the seedling disease downy mildew has developed resistance to the only effective fungicide that is available to farmers. ARS scientists in Fargo, North Dakota, created new gene-markers to identify sources of plant resistance to this devastating disease in sunflower and other plants. These markers will expedite the discovery and selection of resistant cultivars.

Development of new soyfood varieties. Expanding soyfoods markets in the United States and Japan are profit centers for soybean producers who grow value-added specialty varieties. ARS scientists in Raleigh, North Carolina bred four new cultivars that can be grown in North Carolina and the southern United States. These new soyfood cultivars were licensed for production and test marketed in Japan. Commercial production of these lines has the potential to increase U.S. participation in the profitable soyfoods export market.

New pear variety is resistant to fire blight. Fire blight is the single most devastating disease of pear, resulting in significant crop and tree loss. A new pear variety, 'Blakes Pride', was developed by ARS scientists in Kearneysville, West Virginia, which combines a high degree of resistance and excellent fruit quality in a late maturing pear with long storage life. This release provides the pear industry and consumers with a fruit of high quality that is resistant to fire blight thus requiring less pesticide use and has the potential of expanding areas of pear production nationally.

New variety extends fresh-fruit apricot season. The fruit ripening season of apricots is extremely short in comparison to peaches, nectarines and plums. ARS scientists in Parlier, California, developed the new early ripening variety 'Apache' that will extend the duration of the fresh market season of the U.S. apricot industry by 10 days in advance of current cultivars.

New blueberry variety provides new marketing opportunities. 'Alapaha' a new rabbiteye blueberry variety for the Southeastern United States was released by ARS scientists in Poplarville, Mississippi, in collaboration with the University of Georgia. This variety flowers later than other varieties to prevent excessive crop losses due to hard freezes, but still ripens early enough to command higher early market prices for premium, handpicked fruit. 'Alapaha' fruit are also firm enough to machine harvest, making this variety an exceptionally versatile new addition for blueberry production

in milder portions of the country which rely on rabbiteye type cultivars.

Late blight resistance gene identified. Late blight is one of the most serious and costly diseases in potato production worldwide. Using molecular markers, ARS scientists in Madison, Wisconsin, in collaboration with the University of Wisconsin, determined the location of the late blight resistance gene in the potato genome. Cloning this gene enables a better understanding of disease resistance and its eventual transfer into susceptible potato varieties, making the plant resistant and eliminating the need for spraying with fungicides.

An improved method for discovery of genes that confer resistance to Sclerotinia. Sclerotinia is a devastating disease that affects many important crops including sunflower, but weather conditions often impede the search for tolerant germplasm. ARS scientists in Fargo, North Dakota, in cooperation with the National Sunflower Association and the North Dakota Agricultural Experiment Station, developed a system that ensures Sclerotinia disease development in research populations and enables effective selection of genetic resources in sunflower with genes for resistance. This system has facilitated the production of sunflower breeding lines and hybrids with excellent resistance to Sclerotinia head rot.

Genetic diversity of the corn starch pathway assessed. ARS scientists in Raleigh, North Carolina, determined the level of molecular genetic diversity in the corn starch pathway. Genetic variability enables breeders to enhance traits in plants. Using molecular strategies these ARS scientists showed that two-thirds of the genes in the corn starch pathway have very little genetic diversity in contrast to the rest of the corn genome. These findings indicate that further breeding improvement in corn starch quality and yield will require incorporation of genes from more diverse sources, such as the wild relative of corn.

Gene that stimulates stem elongation and plant height cloned. ARS scientists in Pullman, Washington, cloned a hormone response gene, “sleepy”, that affects germination and stem elongation. This gene is a critical part of the biological processes mediated by the plant hormone (gibberellic acid) that affects plant height and yield. ‘Sleepy’ was found to encode a subunit of an enzyme called ubiquitin ligase. Semi-dwarf wheat and other crop plants that have modified hormone response genes have proved to be highly productive. Discovery of this new hormone-response gene provides a significant new tool to improve seed germination and crop stand establishment, particularly under drought conditions.

New corn lines with naturally-occurring starch modifications. ARS scientists in Ames, Iowa, in collaboration with Iowa State University, identified genes that affect the structure and size of corn starch granules in tropical corn germplasm. These genes were bred into corn lines adapted for the Corn Belt for development of speciality hybrids for new food uses, particularly for products with all natural ingredients.

New source of plant resistance to nematodes in Kenaf. The economic threshold for U.S. kenaf production is about 5 to 6 tons per acre. However, most kenaf varieties are susceptible to attack by nematodes, which may reduce yields by 50 to 85 percent. ARS scientists in Stoneville, Mississippi, identified kenaf germplasm from Kenya and Indonesia that are essentially immune to nematodes. These new genetic resources will be used to develop agronomically superior varieties that will help maintain kenaf yields, increase production acreage, and enhance the opportunity for economically sustainable kenaf production.

Component III. Genome Databases and Bioinformatics

USDA/ARS researchers and their public-sector cooperators are developing new software tools for rapidly and readily analyzing and processing the torrent of genome sequence and map data issuing from various large projects which are analyzing crop and model plant genomes. The processed data are managed in the USDA/ARS genome databases, bioinformatics focal points for the collection and dissemination of information relating to genomes, genetic improvement, genetic diversity, and their study. The databases are accessible through the World Wide Web and contain research contacts, the sequences of genes and expressed sequence-tags (ESTs), genetic maps, description of defined genes and DNA markers, genetic control and other genetic information about economically important traits, metabolic pathways and associated enzymes, links between separate model species and agricultural species databases, and links to relevant genetic resource databases and their extensive data on accession traits. The high-quality databases and software tools provided by this National Program component are optimizing access to genetic/genomic information for research, breeding, and genetic resource management.

Development of the largest soybean gene library in the world. Application of biotechnology tools requires knowledge of the structure (sequence) of genes. ARS scientists in Ames, Iowa, in collaboration with the Universities of Illinois, Northern Arizona, Minnesota and Washington, generated 260,000 ESTs from numerous cDNA libraries. This represents the largest collection of partially sequenced genes from any plant. This resource of cloned and partially annotated genes will be used by public and private scientists as the foundation for developing a physical map of the soybean genome.

Deciphering the complex organization of the soybean genome. Soybean has 20 chromosomes that have been duplicated during its evolution. However, the position of genes in each set of chromosomes is not identical. This makes it difficult to determine the exact sequence of genes in the soybean genome. ARS scientists in Ames, Iowa, compared genomic sequences of soybean, common bean, mung bean and Arabidopsis to begin to resolve this problem. This work demonstrated that genomic sequences from model-species can be used to improve understanding of the

evolution and organization of the soybean genome.

International genetic mapping initiative for cocoa. ARS scientist in Miami, Florida, in cooperation with France and the United Kingdom, developed the first international effort to map the cocoa genome. This project will combine genetic assets held separately by cooperating institutions, and will develop and make a comprehensive bioinformatic database system available to scientists and researchers in an internet-accessible format that can be downloaded to CD formats.

Developing improved bioinformatic tools and crop genome databases. Databases and bioinformatic programs are needed to effectively manage, analyze, and deliver the vast volume of DNA sequence, protein sequence, and functional genomic data that are produced by large scale genome projects. The ARS Center for Agricultural Bioinformatics at Cornell University, and its cooperators at Cold Spring Harbor Laboratories, completed and released a highly configurable web-based genome browser that is already in use at more than a dozen public-sector and commercial sites, and also a web-based comparative map viewer (see <http://www.gmod.org>). This novel computational biology approach facilitated the discovery of many new “virulence factors” (genes) and candidate proteins that may be integral to pathogenicity or non-virulence in the plant pathogenic bacterium Pseudomonas syringae. These valuable analytical tools will accelerate the progress of genetic research and crop improvement.

Using genetic diversity to improve bread quality. The characteristics of high-molecular weight glutenin proteins largely determine wheat flour’s unique and valuable properties for dough and for other food uses. ARS scientists in Albany, California, sequenced chromosomal segments of three genomic regions in wheat that encode high-molecular weight glutenins. Similar analyses were conducted in barley. These results provided the first complete description of these critical regions of the wheat genome, identified several other adjacent genes not previously associated with glutenin genes, and furnished information important to understanding wheat and barley evolution.