

National Program 301 • Plant Genetic Resources, Genomics, and Genetic Improvement

FY 2015 Annual Report

The USDA-Agricultural Research Service's (ARS) National Program (NP) 301, Plant Genetic Resources, Genomics, and Genetic Improvement, supports research that maintains, protects, enhances, and expands the United States genetic resource and information base, and increases knowledge of the structure and function of plant genes, genomes, and biological and molecular processes. Through innovative research tools and approaches, this National Program manages, integrates, and delivers vast amounts of genetic, molecular, biological, and phenotypic information to a diverse global clientele. The ultimate goals for the preceding efforts are to improve the production efficiency, yield, sustainability, resilience, health, product quality, and value of U.S. crops. This National Program addresses the need to:

- Ensure the long-term safety and integrity of our agriculturally valuable genetic resource collections and associated information;
- Develop novel approaches for analyzing complex traits, identifying favorable genes underlying those traits, and deploying them in breeding stocks;
- Exploit new technologies that enhance traditional methods of genetic improvement;
- Genetically improve a broad spectrum of major, specialty, and new crops;
- Increase our knowledge of the structure and function of crop genomes and of plant biological and molecular processes; and
- Acquire, analyze, and deliver genetic and information resources to research communities and to the public.

Genetic resources are the foundation of humanity's agricultural future. ARS genebanks contain sources of resistance, tolerance, and adaptation to biotic and abiotic stresses and new genes to improve the quantity, quality, and production efficiency of our food, feed, bioenergy, fiber, and ornamental crops. To ensure those genes are available for research and breeding, ARS must continue to strategically acquire and conserve germplasm that contains them; develop new screening methods for identifying favorable traits; ensure that germplasm is distributed where and when it is needed; and safeguard these collections for future generations.

ARS has taken a leadership role in developing and curating crop genomic and phenotypic databases, which are expanding now and will continue to do so in the future. New tools are needed to efficiently capture phenotypic data and extract useful information, via innovative data-mining strategies, from the ever-increasing flow of data into these databases. Methods to interconnect databases containing diverse types of information are needed to more efficiently and effectively identify important properties of genes and genomes and apply that knowledge to crop improvement. In addition, these interconnected databases will enable researchers to better associate specific genes with agriculturally-important traits and build on genetic advances in one crop to speed genetic gain in others.

For major, specialty, and new crops, ARS, in close cooperation with diverse public and private sector collaborators, will improve and broaden the genetic base of U.S. crops to reduce genetic vulnerability. NP 301 scientists will devise and apply new technologies to develop superior new crop varieties and enhanced germplasm and will accelerate the deployment of high-value traits into breeding populations. New genetic sources of key crop traits will be identified and incorporated into crop breeding lines and gene pools. New breeding theories and strategies that exploit the vast amount of available genotypic data will be developed to effectively capture the intrinsic genetic potential in germplasm. To do so,

innovative tools will be developed for dissecting the architecture of complex crop traits. These tools will be applied to mapping and determining the function of underlying genes so that variation in them, and in linked genomic sequences, can be exploited as more precise genetic markers. This knowledge will also enable molecular and genetic variability to be associated with specific phenotypes to enhance the effectiveness of genomic selection, thereby accelerating and strengthening progress in crop genetic improvement.

Plant breeding has a long history of improving crops through phenotypic or marker-assisted selection, usually in the absence of information regarding underlying genes or gene networks that control key traits, or that control how plants interact with their environment. Understanding the key biochemical pathways and the underlying controls for plant growth, development, and metabolism has been elusive. However, recent advances in plant molecular biology, genetic engineering, and physiology could create opportunities for improvement of crops by more precisely and rapidly manipulating the existing variability in plant properties, or by creating new variability when warranted. Knowledge of how to precisely modify biological mechanisms will contribute not only to advances in fundamental plant biology, but will also help identify potential unintended consequences of that manipulation.

In addition to conducting research, ARS and its university cooperators will continue to mentor and train the next generation of crop breeders, geneticists, bioinformaticians, genome researchers, and genetic and genomic resource and information managers. Developing the next cohort of researchers is particularly important, considering the projected strong demands for these scientific personnel.

This National Program is composed of three Research Components (see below) and their constituent Problem Statements. Notably, these categories do not act as barriers or “stovepipes” that impede research across the National Program. Rather, many of the individual research projects and resources contribute to the goals of several NP 301 Research Components, or even several National Programs:

- **Component 1** – Crop Genetic Improvement (plant breeding, genetic enhancement, molecular marker and trait analyses, nucleotide sequencing, and genetic mapping).
- **Component 2** – Crop Genetic and Genomic Resources and Information Management (conserving a broad spectrum of genetic resources and facilitating their use; maintaining and delivering genetic resource, genomic, and genetic data via databases and information management systems; and devising new analytical tools that compile, dissect, interrelate, manage, and visualize the information contained in the large datasets).
- **Component 3** – Crop Biological and Molecular Processes (fundamental – often high-risk – research to generate an enhanced knowledge base and devise superior research tools that ultimately contribute to greater crop productivity and efficiency; better product quality and safety; improved protection against pests and diseases; enhanced tolerance to abiotic stress; and sustainable practices that maintain or enhance environmental quality).

The following section contains selected NP 301 accomplishments, presented according to the relevant NP 301 Research Components. These are not all of the NP 301 accomplishments for FY 2015, but rather are selected based on impact and level of contribution to meeting the National Program goals.

Component 1 – Crop Genetic Improvement

New potato variety ‘Payette Russet’ with reduced acrylamide. Acrylamide in processed food products has become a human health concern over the past decade. French fries contain acrylamide, and the potato processing industry has been proactive in reducing acrylamide levels in processed potato products. ARS researchers in Aberdeen, Idaho, and their university colleagues in Idaho, Oregon, and Washington, have developed and released a new potato variety, ‘Payette Russet,’ which produces French fries with 75 percent less acrylamide than fries made from the potato variety ‘Russet Burbank,’ which is the industry standard. Payette Russet also has resistance against all Potato Virus Y strains, as well as late blight, Verticillium wilt, early blight, and corky ringspot diseases, all of which are critically limiting diseases in potato production. The adoption of Payette Russet by industry will reduce acrylamide content in processed potato products and enable more sustainable potato production.

‘Goshen Gold’ extends apricot sales season. Apricots are generally the first stone fruit to appear at markets in late spring and the first to disappear from markets once all cultivars have completed maturity. Their season is short, generally with only 8 weeks difference between the earliest and latest maturity cultivars. ARS researchers in Parlier, California, have been breeding apricots since the 1950’s and have recently developed a late-season cultivar that extends the apricot maturity window approximately 10 days beyond the current latest maturing cultivar. Named ‘Goshen Gold,’ the new late-season apricot provides producers with a self-fruitful tree that is both vigorous and productive, can be marketed fresh as well as cut, and is dried to a high-color premium product. When dried, Goshen Gold retains color significantly better than the cultivar ‘Patterson,’ the predominant apricot used as drying stock in California.

Giant, thornless blackberry developed. ARS researchers in Corvallis, Oregon, developed the ‘Columbia Giant’ thornless blackberry for the commercial blackberry industry. ‘Columbia Giant’ produces good yields of tasty, very large blackberries that can be machine-harvested for the processing market but are more likely to be hand-harvested and sold in the fresh market. The berries are very symmetrical, uniform, and long. It is definitely the largest trailing blackberry cultivar and may be the largest of all blackberries.

New blueberry bred for extended harvest season. ARS scientists in Poplarville, Mississippi, bred a productive and high quality mid-late season rabbiteye blueberry cultivar ‘Bluesfest’ that will extend the harvest season for growers in the region and provide insurance against late spring frosts that frequently cause significant crop loss. The midseason ripening rabbiteye blueberry ‘Powderblue’ is among more popular rabbiteye blueberries mostly due to its exceptionally light blue fruit that results from a thick natural waxy coating on berry skins. However, the relatively small berries of ‘Powderblue’ might at times sell for less than larger berries of other cultivars. ‘Bluesfest’ is a productive new rabbiteye blueberry that has a mid-to-late season ripening period, exceptionally light blue color, and berry size exceeding the fruit of ‘Powderblue.’

Superior new apple rootstock developed. Some apple scions like ‘Gala’ have a tough time blooming in low winter chill subtropical regions; therefore, apple growers need yield efficient, disease resistant apple rootstocks when growing apples in low chill environments or when current

environments are affected by climate change. ARS researchers in Geneva, New York, bred a new productive, disease resistant apple rootstock G.213 which improves bud break and productivity in low chill environments. This rootstock, developed over 35 years, seems to be the first in the world that increases bud break in low chill environments of scion cultivars like ‘Gala.’ Therefore it will increase production of high quality fruit in apple growing regions in the United States and worldwide that are affected by low winter chilling hours.

A new high oleic Virginia type peanut with improved shelf life. Virginia peanuts have the largest kernels of all peanut types and account for most of the peanuts roasted in shell. The larger kernels are often sold as gourmet snack peanuts. Virginia peanuts are grown mainly in southeastern Virginia, northeastern North Carolina and South Carolina, but there is an important niche in the Southwestern United States. Higher oleic acid gives peanut oil the notable qualities of staying naturally fresh for longer in the products on the shelves. In the Southwestern U.S. peanut production region (largely Oklahoma and Texas), all cultivated peanut varieties are high-oleic except for Virginia type peanuts, largely due to the lack of available high-oleic Virginia cultivars. Producers, shellers, and manufacturers are in urgent need of high-oleic Virginia cultivars adapted for production in the Southwest. A problem that other high-oleic peanut varieties faced in this region was that their desirable oil quality came with lower yields, often so low that the value of their excellent nutritional quality and longer shelf-life could not compensate. Also, they were more susceptible to fungal diseases, forcing farmers to endure high fungicide cost and still produce lower yields. Therefore, ARS scientists at Stillwater, Oklahoma, released a new high oleic peanut cultivar in 2015 with good yields, enhanced grade, and excellent disease resistance to address these problems. The first high oleic Virginia peanut cultivar developed for the Southwestern United States, “VENUS,” will fill a void in the peanut industry for high oleic Virginia peanut production in this region, which in 2014 was comprised of 45 percent Virginia peanuts. Production of this Virginia cultivar will save producers \$50–\$100/acre in disease control costs and will add \$7–\$10 million, annually, to the economy.

Two genes identified that increase seed number in sorghum. ARS researchers in Lubbock, Texas, identified two genes that can double the seed number and significantly enhance the seed weight per panicle (head) in sorghum. Seed number per panicle is a major determinant of grain yield in sorghum and other cereal crops. From the sorghum experimental lines maintained at the Lubbock site, several multiseeded (msd) mutants that might increase grain yield were isolated, and in collaboration with ARS researchers in Ithaca, New York, two genes underlying the msd trait were identified through next-generation sequencing. The msd mutants have been distributed to other researchers and seed companies to develop high yield sorghum hybrids.

Breeding more nutritious and more widely-adapted tepary beans. Tepary bean is a highly heat- and drought-stress tolerant crop, native to the Southwestern United States and to Mexico. However, there has been limited research on its genetics, nutritional value, and cooking characteristics, key aspects when considering the potential for broader adoption globally. ARS researchers at Mayagüez, Puerto Rico, developed the Tepary Diversity Panel (TDP), composed of 320 tepary bean samples representing all of the publically available tepary germplasm in the Americas. Subsets of the TDP were evaluated for response to bean common mosaic virus (BCMV), biological nitrogen fixation, root rot resistance, and heat tolerance, and several samples were identified with

BCMV resistance. ARS researchers at Mayagüez, Puerto Rico; East Lansing, Michigan; and Houston, Texas, also found that tepary bean had half the fat and double the sucrose concentration as compared to common bean. Several tepary bean lines showed consistently shorter cooking times and higher water uptake than common bean. The variability for seed composition and cooking characteristics in tepary bean can be used for genetically improving this highly nutritious crop. These results have been published, and germplasm is being used for commercialization of tepary bean as a crop in itself, and as a breeding parent for common bean improvement.

New genetic tools to develop strawberries with extended fruiting time. Breeding of strawberry, a fruit with many valuable nutritional properties, is slow in part because seedlings derived from breeders' crosses must be grown to maturity before evaluating many traits, including whether the plant will produce fruit spring through fall, or just a brief period in the spring. The breeding process would be more efficient and greatly accelerated if potential parent plants and the resulting seedlings could be tested in the laboratory to predict which seedlings would have desired traits. ARS scientists in Beltsville, Maryland, in Corvallis, Oregon, and university cooperators discovered genetic markers for selecting strawberry seedlings that, when adult plants, bear fruit from spring through fall. Strawberry breeders worldwide will apply these markers to more efficiently develop improved repeat-fruiting strawberry varieties to avoid the economically damaging effects of weather extremes such as spring frosts and summer heat waves.

High yielding waxy hybrid sorghum for the food and ethanol industries. Genes for the waxy trait alter the starch composition of grain sorghum, which is valuable to the food and ethanol industries. Older lines of waxy sorghum performed poorly compared to normal lines, which has prevented commercialization of the trait. Several new waxy inbred lines were bred and tested by ARS scientists in Lincoln, Nebraska, and the grain yield of waxy hybrids with some of those lines as parents was similar to standard hybrids. These lines are some of the first publically-available sorghum germplasm that can produce high-yielding waxy hybrids.

Genetic diversity in protein and zinc in dry bean seeds. Dry beans are a dietary staple in regions of Africa and Latin America. They are rich in protein and minerals, such as zinc, which are essential to the human diet, but not all bean varieties have the same nutritional profile. ARS scientists in East Lansing, Michigan, characterized the genetic diversity for seed protein and zinc in a panel of over 200 diverse bean lines, including many from Africa. These lines represented nine market classes of beans of economic importance, including kidney, yellow, and red mottled seed types. Genetic variability for seed protein ranged from 16 to 31 percent and for seed zinc from 19 to 54 $\mu\text{g g}^{-1}$. Protein and zinc levels were positively correlated, suggesting that by selecting for one in a breeding program, the other will increase as well. These published findings are being used to breed more nutritious bean varieties adapted to regional bean seed color and market class preferences.

Important insights into the structure and function of the hop genome. Understanding the genetic control of important traits in hops is critical for development of new germplasm and cultivars for the U.S. hop industry. The genetics of disease resistance and important agronomic and chemical properties in hop are currently rudimentary. ARS scientists in Corvallis, Oregon, and university colleagues sequenced the hop genome and identified the genomic locations of approximately 25,000 genes in the USDA hop cultivar 'Teamaker.' This is a significant accomplishment that will

enable the identification and development of genetic markers for traits such as disease resistance, yield, bittering, and essential oil flavoring and storage-ability.

Potato germplasm with high iron content in the tubers. Iron is one of the micronutrients identified as a target for increase for one billion people who are at risk of iron deficiency anemia. Potatoes are an excellent food for increasing iron in human diets, since it is the most widely consumed vegetable. ARS scientists in Prosser, Washington, and visiting colleagues from Mongolia, measured the iron reductase activity in thirty clones. Interestingly, red-skinned potatoes clearly had higher iron reductase than white skinned potatoes. Consumption of potatoes high in iron could reduce the frequency of iron deficiency anemia among the world's poorest people. The clones analyzed in this study are being used to develop iron-rich potatoes for public release.

Genes from wild cotton types broaden the genetic breeding base for cotton. The wild, photoperiodic types of cotton contain many useful genes for broadening the genetic base available for breeding improved cultivars, but these types will not flower in the United States Cotton Belt where cotton breeders are located. Therefore, ARS scientists in Starkville, Mississippi, developed a random-mated cotton breeding population from crosses of derived day neutral lines of 30 wild types and four cultivars. The germplasm population has incorporated genes for agronomic and fiber properties similar to the parent cultivars from the primitive cottons from 10 countries into a population useful to cotton breeders, but also with many genes from the wild types transferred into the population. Thus this population (RMPAP-C4) should be valuable for many years to public and private cotton breeding programs.

Resistant Pima Cotton Germplasm to Combat *Fusarium* Wilt Race 4 in California. Over the past 12 years, race 4 of the fungus causing *Fusarium* wilt disease (FOV race 4) has impacted cotton production in California. Cotton varieties resistant to FOV race 4 can be effective in controlling yield losses, providing an economical approach for dealing with this fungal disease, and breeding efforts over the past several years have identified tolerant cultivars/germplasm. However, using tolerant plants in a pathogen infested field can result in an increase of inoculum levels, or tolerant cultivar/germplasm may become susceptible over time. Thus, new mechanisms of resistance are needed. To continue providing germplasm with good levels of resistance to FOV race 4 to cotton researchers and breeders, ARS researchers at Lubbock, Texas, and University of California colleagues, developed and jointly released five Pima cotton germplasm lines with resistance to FOV race 4, combined with good yield and fiber quality. These lines provide needed alternative sources of FOV race 4 resistance to cotton breeders, and are being used to broaden the genetic base, which is critical to maintaining a healthy, disease-free Pima cotton industry in the San Joaquin Valley of California.

New cotton germplasm resistant to cotton leaf curl virus, listed among the top 20 threats to U.S. agriculture. Although cotton leaf curl virus (CLCuV) disease has not yet been reported in the United States, the USDA has ranked it among the top 20 potential threats to U.S. agriculture and funded a multinational partnership project to proactively develop resistant cotton varieties. The goal is not for immediate use of these new lines, but to be prepared before the disease comes to the United States by screening for CLCuV in Pakistan, where the disease is endemic and causes losses of a million or more bales of cotton each year. Therefore, ARS scientists in Stoneville, Mississippi,

developed cotton lines and screened for resistance to CLCuV for two years in Pakistan. They released two resistant germplasm lines and made them available to breeders who are now actively using them in breeding programs to develop CLCuV resistant varieties.

RNAi-mediated silencing of aflatoxin synthesis genes in peanut. Aflatoxins are powerful carcinogens normally accumulated by two species of fungi in crops and other agricultural products. It is estimated that 25 percent of the food crops in the world are contaminated with aflatoxins, and one hundred million tons of grain, mainly maize, and peanut are diverted from human consumption or discarded each year because of aflatoxin contamination. There are no effective non-chemical methods of controlling the fungi or preventing aflatoxin production. Therefore, ARS scientists in Dawson, Georgia, developed a method to silence the aflatoxin-synthesis genes by RNA interference (RNAi) in peanut plants to control aflatoxin accumulation. Plant-RNAi-mediated control of mycotoxins has never been accomplished before, and no method is available to evaluate new peanut breeding lines for the aflatoxin accumulation trait other than multi-year field testing and analysis of numerous samples. The ARS researchers also developed a method to test the effectiveness of RNAi to prevent accumulation of aflatoxins in peanut seeds and found five RNAi-peanut lines showed statistically significant reduction (74-100 percent) in aflatoxin accumulation when infected by one fungal species. The scientists have publicly released this new technology and are partnering with a Kenyan university to apply the novel technology in countries most severely affected by mycotoxins.

Downy mildew disease promotes the colonization of lettuce leaves by human enteric pathogens. ARS researchers in Salinas and in Albany, California, demonstrated that the plant pathogen that causes downy mildew disease of lettuce changes the plant environment so that human enteric pathogens have higher survival and multiplication rates on lettuce leaves. These published findings show for the first time a significant interaction between downy mildew infection and survival of human enteric pathogens on lettuce. Therefore development of lettuce breeding lines with high resistance to downy mildew is extremely important for both the quality of the final product (less blemishes on lettuce leaves) and the product safety (less likely survival of human pathogens). This highlights the value of ongoing ARS research on downy mildew-resistant lettuce cultivars to provide a continuous and safe supply of commercial lettuce varieties.

Molecular markers linked to crown rust disease resistance in oat. Crown rust is the most damaging disease of oat worldwide. New oat cultivars with crown rust resistance represent an economical tool for managing the disease. ARS researchers in Aberdeen, Idaho, and in St. Paul, Minnesota, with university cooperators, applied newly developed oat molecular markers called ‘single nucleotide polymorphisms’ or SNPs to genetically map resistance in two oat lines. The map locations for resistance were discovered on three oat chromosomes. The SNPs associated with the resistance traits can serve as genetic markers to help plant breeders develop new crown rust resistant oat cultivars more rapidly.

Boxwood cultivars evaluated for resistance to the emerging boxwood blight pathogen. Boxwood is considered the “bread and butter” of the U.S. nursery industry. Each year, more than 13 million boxwood plants are sold in the United States, making boxwood one of the most popular and valuable shrubs in the landscape. A new blight disease, caused by a fungus, significantly threatens

the profitability of nurseries and the quality of landscapes throughout the United States. The U.S. National Arboretum houses the world boxwood collection as a valuable resource for disease resistance. ARS scientists at the U.S. National Arboretum, Washington, DC, developed molecular markers to assess the genetic diversity of boxwood species and hybrids bred for disease resistance. The molecular markers and the information published are a critical first step in cultivar identification and genetic conservation, as well as in guiding breeding strategies to deliver blight resistant cultivars to the industry.

Thrips resistance in onion. The onion thrip is the most important insect pest of onion for both bulb and seed production, requiring frequent insecticide applications. In addition, thrips are responsible for transmission of *Iris yellow spot virus*, which is an increasingly damaging virus of onion crops in the United States and worldwide. ARS researchers in Madison, Wisconsin, published information that revealed two major genetic factors that control amounts and types of leaf surface waxes in onion, which impact both resistance to thrips and the viruses they transmit. Lower amounts of these waxes are associated with resistance to thrips. Deployment of onion cultivars with lower amounts of those waxes should reduce the build-up of thrips populations and virus infection during onion production and reduce the frequency of insecticide sprays, reducing costs for growers and overall environmental impact of pesticide sprays. This provides for the first time an approach to controlling this important pest and respective viruses through plant breeding.

Multiple disease resistant pintos combat emerging strains of established pathogens in the United States. New races of bean anthracnose and bean rust have emerged in North Dakota, in Minnesota, and in other northern U.S. states. Common bacterial blight also continues to cause considerable losses for bean producers, and new sources of resistance are needed to control these diseases. An ARS scientist in Prosser, Washington, in collaboration with university cooperators, applied marker-assisted selection to quickly combine genes for disease resistance into pinto beans adapted to North Dakota and Minnesota. These multiple disease resistant pinto breeding lines will provide breeders with new germplasm lines for developing varieties with improved disease resistance.

Detection of decay in fresh-cut lettuce. ARS researchers in Salinas, California, and Australian colleagues developed the first method for automated detection of decay in salad-cut lettuce held in modified atmosphere plastic bags through the use of hyperspectral analysis and chlorophyll fluorescence imaging. The method was 97 percent accurate when tested on lettuce leaves that ranged in color from light yellow, to green, dark green, to dark red. These are the first reported methods that apply hyperspectral analysis and chlorophyll fluorescence for post-harvest evaluation of fresh-cut lettuce. The non-destructive nature of the methods enables rapid and repeated evaluation of samples over time and presents the opportunity for development of a commercial, high throughput scanner for evaluation of bagged, salad-cut lettuce quality. This technique will facilitate breeding lettuce for longer shelf life and preserve the quality of this popular, high-value vegetable.

Component 2 – Crop Genetic and Genomic Resources and Information Management

The one-day rice genome. Knowledge of the sequence and structure of crop genomes is critical for accelerating progress in crop research and genetic improvement. Such information is particularly

important for exploiting the wild relatives of crops for their rich source of genes for increasing yield, enhancing disease resistance, and accelerating adaptation to weather extremes. But the process of assembling individual pieces of genomic data into a coherent picture of crop genomic structure has been slow and expensive, primarily because of the volume of data and the computationally-intensive data analyses involved. ARS scientists in Ithaca, New York, and university cooperators at the iPlant Collaborative, a national project to facilitate access to high performance computing, software, and DNA sequence analysis tools, developed a computational “pipeline” that, for the first time, will enable a researcher to assemble a rice genome sequence and characterize all of its genes – all in the same day – through the computational resources at iPlant. This new capacity could substantially accelerate genetic improvement initially in rice, and later in other crops.

Cotton genome sequenced. Upland cotton accounts for more than 90 percent of cultivated cotton worldwide and is the primary source of renewable textile fiber. It is a tetraploid species – two genomes in one – and thus was extremely challenging to sequence and analyze. The cotton genome sequence and structure were completed by Chinese and U.S. researchers, including ARS scientists in Stoneville, Mississippi, and U.S. university colleagues. The team developed the first “reference genome” of a tetraploid cotton species – laying the foundation for development of new U.S. cultivars with longer, stronger fiber; increased yield; and enhanced disease resistance.

Genetic structure of wheat ancestor’s genome determined. Tausch’s goatgrass is a modern wild grass species that directly descended from one of the three ancestors of modern bread wheat. As such, it contains many genes that could improve the baking quality, disease resistance, and growth characteristics of current bread wheat varieties. An international consortium of scientists, including ARS researchers in Albany, California, has completed an initial version of the *tauschii* goatgrass genome sequence. The DNA sequence is available online to researchers everywhere and can immediately be applied by wheat breeders to develop molecular markers and to map and isolate individual wheat genes. This resource will accelerate genetic improvements in wheat productivity and utilization.

New interactive genome browser enables plant breeders to exploit “Big Data.” Advances in sequencing, imaging, chemical analysis, and robotics are making it easier to assess thousands or millions of sites across the plant genome for genetic diversity, through genome-wide association studies or “GWAS.” However, analyzing the mass of data for meaningful associations between a particular phenotype (trait) and specific genes is complicated. ARS researchers in St. Louis, Missouri, have developed with open source software an interactive browser that enables researchers to analyze GWAS data for multiple crop agronomic traits or experiments in the same computer screen “window.” This browser can be customized by researchers and breeders for soybean, corn, rice, sorghum, and other crops to find genes for specific traits for their own research data or by accessing freely available source code. This browser will greatly facilitate the transformation of genome and genomic derived data (“Big Data”) to practical tools for plant breeding.

New sources of traits for sweet potato breeding are identified. U.S. sweet potato production, currently valued at more than \$500 million/year, is increasing steadily as the health-promoting qualities of this crop are recognized. Furthermore, sweet potato is a key source of calories and vitamins throughout developing nations. Safeguarding and expanding crop production

consequently are high priorities, and require a sweet potato plant with better tolerance to extreme temperatures, rainfall, and soil conditions. Access to such traits from the genetically-rich crop wild relatives of sweet potato has been problematic. Therefore, ARS researchers in Griffin, Georgia, and their university cooperators identified new geographical locations for sweet potato crop wild relatives and characterized their genetic relationships. Those findings yielded information, valuable for guiding sweet potato breeding, about the best new sources for the horticultural traits needed to meet the U.S. domestic and international demands for higher yielding sweet potatoes tolerant of environmental extremes.

New, more effective methods for predicting seed longevity in genebanks. By preserving seeds, genebanks can efficiently safeguard genetic diversity of thousands of species valuable to agriculture. But seed survival in genebanks varies considerably, creating challenges for effective genebank management as well as additional costs for implementing customized, idiosyncratic preservation treatments and monitoring changes in seed viability. To develop genebank management tools that are more effective and that also reduce costs, an ARS researcher in Ft. Collins, Colorado, applied materials sciences approaches, more commonly used to evaluate plastics, to explain why some seeds die rapidly and others succumb at different rates during storage. This new, unified explanation provides a rational framework to optimize seed storage practices and to predict how long seeds can survive in genebank storage. The new approach will substantially increase the number of species that can be preserved as seeds as well as reduce expenditures on germination tests that detect seed aging during long-term storage.

New sources of nitrogen fixing bacteria for chickpea production. The ability of legumes to produce their own nitrogen fertilizer through interactions with beneficial nitrogen fixing bacteria is one of the primary factors for legumes being essential crops for rotations with cereals, especially in nutrient-poor soils. Despite the importance of biological nitrogen fixation to sustainable crop production, there are considerable gaps in the understanding of how legumes and these bacteria interact with each other and the surrounding environment. ARS scientists in Pullman, Washington, in collaboration with Washington State University, identified chickpea breeding lines and varieties that supported significantly more beneficial bacteria than several chickpea varieties that are currently grown commercially. A collection of more than 100 strains of root-colonizing bacteria isolated from field grown chickpea, has been developed. Genetic data for 150 of the strains show that many that were collected from chickpea roots are genetically distinct from 'commercial' isolates. These bacterial strains are being screened for their ability to function at low pH (below pH 6.0), as acidification of agricultural lands is a growing problem in the Pacific Northwest.

Component 3 – Crop Biological and Molecular Processes

Global warming decreases corn photosynthesis and yield. Research on major crops' responses to a warmer, CO₂-rich environment has been limited to artificial growth environment experiments or to historical analysis of agricultural outputs. ARS researchers in Urbana, Illinois, developed the means to analyze corn growth in elevated CO₂ and higher temperature through field-based equipment. This enabled plants to be grown under typical agronomic conditions, while simultaneously modifying their growth environment in a controlled manner. Corn photosynthetic rates decreased when grown in warmer temperatures, reducing harvestable yields. The sensitivity of corn to warmer

temperature was not influenced by growth in higher CO₂. This research shows that the sensitivity of corn growth to higher temperatures warrants further investigation of whether corn can be successfully adapted to the changing global climate.

Optimizing tree shape for improved crop productivity and sustainability. The large size and spreading growth habit of trees are limiting factors for orchard planting density and crop yield. Genetically improving tree shapes to enable high density orchard production and to limit chemical inputs is hampered by lack of knowledge about the underlying genetic controls of tree architecture. ARS researchers in Kearneysville, West Virginia, applied a new technology that combines knowledge from conventional plant breeding with new DNA sequencing information to identify several genes responsible for naturally occurring architectural traits in peach trees including dwarf, weeping, and pillar (columnar) growth forms. Molecular markers were developed to facilitate breeding these novel tree forms. The genes functioned similarly in diverse plant species; therefore, the technology has potentially broad applications to optimizing plant form in a wide range of tree crops, forest species, and woody ornamentals.

Mystery of 'Ōhi'a Death Solved. 'Ōhi'a, Hawaii's most common and widespread native tree, grows from sea level to a 2,500 meter elevation in both dry and wet forests and diverse soils. It is the most ecologically important native Hawaiian tree, defining native forest succession and ecosystem function over broad areas, providing critical habitat for rare and endangered native bird and insect species, and exemplifying the strong links between native Hawaiian culture and the islands' environment. A newly detected disease has been killing many mature 'Ōhi'a trees in forests and residential areas of the Big Island of Hawaii. ARS scientists in Hilo, Hawaii, partnered with the U.S. Forest Service and university cooperators to identify the causal agent as a vascular wilt fungus. This pathogen poses a serious threat to Hawaii's flagship native tree species whose loss would be catastrophic for the diversity, structure, and function of Hawaii's remaining native forests and the services they provide. New molecular diagnostic tests have been developed for this pathogen, and fungicides are being screened for effectiveness in controlling the disease.

Preventing post-harvest disease losses in sugarbeet. Rhizoctonia root and crown rot (RRCR) is a soilborne fungal disease of sugarbeet that is found in most, if not all, sugarbeet production areas in the United States, and the severity of RRCR symptoms affects the suitability of sugarbeet roots for storage. ARS scientists in Fargo, North Dakota, evaluated the effect of RRCR disease severity on sugar and quality losses during storage and root storageability and determined that roots with mild RRCR symptoms stored nearly as well as undiseased roots, but those with moderate to severe symptoms stored poorly. The research provides guidance to the sugarbeet industry for managing the storage of sugarbeet roots with RRCR. The research also provides information that assists in determining the severity of RRCR disease symptoms that preclude storage or require segregation of roots for early processing, and helps growers whose roots are refused for storage to justify their insurance claims.