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 accelerate 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 also 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 determine 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 improving 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.

Many of the NP 301 projects include significant domestic and international collaborations including government, industry and academia. These collaborations provide opportunities to leverage funding and scientific expertise for USDA-ARS research and accelerate dissemination of ARS research results, thus enhancing the impact of ARS research programs. During FY 2020, NP 301 scientists participated in research collaborations with scientists from the following 65 countries:

- Argentina
- Australia
- Austria
- Bangladesh
- Belgium
- Brazil
- Canada
- Chile
- China
- Colombia
- Costa Rica
- Czech Republic
- Denmark
- Dominican Republic
- Ecuador
- Egypt
- England
- Ethiopia
- France
- Georgia
- Germany
- Ghana
- Greece
- Guatemala
- Haiti
- Honduras
- Hungary
- India
- Israel
- Italy
- Ivory Coast
- Japan
- Kazakhstan
- Kenya
- Mexico
- Morocco
- Mozambique
- Netherlands
- New Zealand
- Nicaragua
- Nigeria
- Norway
- Pakistan
- Panama
- Paraguay
- Peru
- Philippines
- Poland
- Portugal
- Romania
- South Africa
- South Korea
- Spain
- Sweden
- Switzerland
- Taiwan
- Tanzania
- Thailand
- Tunisia
- Turkey
- Uganda
- United Kingdom
- Uzbekistan
- Vietnam
- Zambia
The quality and impact of NP 301 research was evidenced during FY 2020 by the following:

- 672 refereed journal articles published,
- 47 cultivars and breeding lines released,
- 7 new invention disclosures submitted,
- 4 new patent applications filed, and
- 6 new patents issued.

During fiscal year 2020, this National Program was composed of four 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**
- **Component 2 – Plant and Microbial Genetic Resource and Information Management**
- **Component 3 – Crop Biological and Molecular Processes**
- **Component 4 – Information Resources and Tools for Crop Genetics, Genomics, and Genetic Improvement**

Research in Component 1 lead to improved plant varieties, which were the products of innovative exploitation of genetic resources and efficient plant breeding strategies. High throughput genotyping and phenotyping methods were developed for quantitative analyses of complex traits in diverse crop species, and high-resolution genetic maps and full or partial genome sequences enabled genetic markers to be identified and mapped. NP 301 scientists in Component 1 devised innovative ways to apply genomic information from model plants for developing superior methods that were used to identify and breed exotic alleles into adapted genetic backgrounds, helping to improve the efficiency of plant breeding.

The strength of Component 2 lies in the National Plant Germplasm System (NPGS), which is comprised of one of the most comprehensive plant genetic resource collections in the world. Genebank curators and NP 301 researchers also conserved, characterized, and distributed cultures of pathogenic or beneficial microbes that are important to crop production, industrial processes, food safety, and human health. Information associated with NPGS collections were stored, curated and made publicly available via GRIN-Global, an advanced information management system that was made more readily accessible, and was accessed by more than 1.5 million unique "visits" annually (as indicated by IP addresses).

Component 3 research sought to understand the functions of crop genes and devise ways to manipulate gene expression. Research conducted under this component elucidated the biological processes underlying crop productivity and quality, and developed new means for assessing the potential effects and risks associated with plant genetic engineering.

Component 4 rendered improved bioinformatic tools and services built on powerful computational infrastructures that are needed to handle changing data types and increased volumes and scales of datasets that present tremendous opportunities for more rapid crop genetic improvement. ARS led in developing data exchange protocols that facilitated access, analysis, and integration of these data sources. Building on these principles, NP 301 research delivered bioinformatic solutions for the full range of crops important to U.S. agriculture.
The following sections contain selected NP 301 accomplishments, presented according to the relevant NP 301 Research Components. These are not all of the NP 301 accomplishments for FY 2020, but rather are selected based on impact and level of contribution to meeting the National Program goals.

Component 1 – Crop Genetic Improvement

Redesigning soybean meal for nonruminant animals. Soybean is the top global source of protein meal for animal feed. Soybean seeds, however, contain carbohydrate compounds called raffinose family oligosaccharides (RFOs) that prevent effective digestion of soybean meal in nonruminant animals. To combat this problem, ARS scientists in West Lafayette, IN, and Columbia, MO, collaborated with university partners to identify and incorporate new genes to reduce or eliminate RFOs in soybean meal. A soybean population treated with an agent to induce mutations was screened to generate desirable genes in the RFO biosynthesis pathway. A new mutant was recovered from this screen that reduced RFOs from 5 to 6 percent of total carbohydrates to below detectable levels when used in combination with other modified RFO soybean genes. Essentially, a “No-RFO” soybean was created. Field studies established the stability of the genes, and feeding trials demonstrated that No-RFO soybean meal improved poultry growth and nutrition. The researchers discovered close associations of the genes controlling the modified RFO plant type with molecular markers that can be used to detect the variant alleles during breeding. These discoveries have been shared with public soybean breeders, along with the modified seeds and marker information that can be used to enable marker-assisted selection for improved soybean meal that can add value to soybean by improving the metabolizable energy of the meal.

Identification of romaine lettuces with reduced browning discoloration for fresh-cut processing. Lettuce is one of the most valuable fresh vegetables and one of the top 10 most valuable crops in the United States, with an annual farm-gate value of more than $2.5 billion. Fresh-cut lettuce is the primary ingredient of the increasingly popular packaged, ready-to-eat salads; however, discoloration (browning) represents a major challenge that limits its quality and shelf life. Processors who lack effective browning control methods are relying on modified atmosphere packaging (MAP) to achieve low oxygen atmospheric conditions and maintain the shelf life. ARS researchers in Salinas, CA, and Beltsville, MD, identified lettuces with limited browning that will be used in breeding programs and to help identify genes associated with limited browning. These findings are of great benefit to the U.S vegetable industry.

New hybrid hemlock ‘Traveler’ is resistant to insect pests. The native hemlock, Tsuga canadensis, plays an essential role in forest ecosystems and cultivated landscapes; however, it is susceptible to feeding damage by the hemlock woolly adelgid, which has caused widespread loss of hemlocks in wild and cultivated settings. ARS scientists at the National Arboretum in Washington, D.C., developed and introduced the first interspecific hybrid hemlock to the trade. ‘Traveler’ is a cross between the Chinese hemlock and the Carolina hemlock. It was explicitly bred for resistance to hemlock woolly adelgid and selected for its regular and slightly pendulous shape and its moderately slow growth rate. It is currently being propagated under license at cooperator nurseries and promises to be a valuable addition to residential, commercial, and forest landscapes.
Genetic mapping of traits associated with pollinator visitation, yield, and seed size in sunflowers. Pollination by wild bees increases yields of both oilseed and confection sunflowers, and bees prefer sunflowers with shorter florets for easier nectar access. In addition, seed size (length and width) is important in the confection sunflower market. ARS scientists in Fargo, ND, and University of Colorado-Boulder colleagues mapped genes associated with both floret depth and seed size to specific chromosomal locations in cultivated sunflowers and designed genetic markers to use in identifying desirable lines carrying both those traits. Floret length and seed length are correlated, but when the team mapped these traits, they discovered that the genetic bases for the two traits are largely independent and can be improved separately. Markers developed for seed and floret length will improve private- and public-sector breeding by allowing effective selection of lines that are attractive to bees and possess desirable seed size and shape for the confection sunflower market. These cultivars will provide ecosystem services for bees and economic value for sunflower producers and consumers.

Galena Russet, a new potato variety with high yield and attractive tubers suitable for multiple uses. U.S. potato production is valued at $4 billion annually. However, the industry needs new potato varieties with high yields and better processing quality. ARS scientists in Aberdeen, ID, along with researchers at experiment stations in Idaho, Oregon, and Washington, released and filed for Plant Variety Protection for ‘Galena Russet’, a new potato variety that produces high yields in both early and full-season harvests, allowing for use over more growing areas. Galena Russet has excellent processing characteristics for fries due to cold sweetening resistance, allowing for lighter colored fries late in the storage season. This is an improvement over other varieties in which conversion of starch to sugar results in a darker product. Galena Russet has an attractive tuber shape and low levels of defects, making this a good fresh market potato. This new potato variety will greatly benefit the potato industry.

New food barley variety with a winter growth habit provides additional options for growers. Winter habit cereal varieties can provide growers with options to manage soil moisture resources and to minimize crop losses to biotic and abiotic stress pressures. A new winter barley cultivar, ‘Upspring’, is the first two-row food barley cultivar that will fill this niche. Upspring is the product of breeding by ARS researchers in Aberdeen, ID. The new cultivar is well balanced in yield, winter hardiness, and quality traits with high beta-glucan content.

Release of two new high yielding spring yellow pea varieties. Approximately one million acres of dry peas are grown each year in the U.S. Pacific Northwest and Northern Plains. More than 70 percent of peas produced annually in the United States are exported, and yellow peas are an especially popular export crop because they are widely used for industrial production of plant-based protein and starch. Commercially grown varieties must be improved to continually produce high yields under evolving disease pressures and expanding areas of production. ARS scientists in Pullman, WA, released two new spring yellow pea varieties, ‘USDA-Kite’ and ‘USDA-Peregrine’. These two varieties were developed through several years of field testing in Idaho, Montana, North Dakota, and Washington. Both varieties produce yield and seed sizes comparable to the popular yellow pea variety ‘Carousel’ and are more resistant than Carousel to powdery mildew disease. A research partner is currently producing certified seed of both varieties in the field for commercial availability in 2021. They are expected to be grown widely and will provide economic value in several different local economies.
Three new blackberry cultivars complete the Celestial blackberry series. ‘Eclipse’, ‘Galaxy’, and ‘Twilight’ are three improved blackberries that are thornless, semi-erect, and produce high-quality fruit. They were released from ARS scientists in Parma, ID, and Corvallis, OR, with Oregon State University and Nigde Omer Halisdemir University (Turkey) collaborators. These three patented cultivars have firm, dark fruit that is well-suited for the fresh market and have lower anthocyanin (red pigment) levels compared to standard commercial trailing blackberries. Plants in the Celestial blackberry series are the first cultivars derived from eastern and western North American blackberry germplasm. These blackberries will further contribute to U.S. blackberry production, valued at $31 million.

Development of a genetic transformation system for sorghum. Sorghum improvement has mainly relied on traditional breeding methods, which were successful in developing genetically improved hybrids and cultivars. However, conventional breeding is often too slow to achieve certain breeding goals or is limited because some genetic traits may not be available in sorghum. ARS scientists in Stillwater, OK, successfully developed a cutting-edge technology for designing and creating new varieties of sorghum with desired traits. This new technology is based on a gene transfer system using early flowers of sorghum as the targets. The transgenic plants that result appear normal in morphology and are fully fertile. This method represents a simple and efficient method for genetic transformation of sorghum that can speed up and facilitate the process of engineering new varieties in sorghum. This technology is an alternative tool for sorghum breeding and can complement conventional plant breeding, thus benefiting crop breeders and sorghum producers.

Dominant male sterility opens new strategies in wheat breeding. Wheat is a self-pollinated crop, so the production of large numbers of hybrid seeds by cross-pollination is technically demanding and labor-intensive. Genetic dominant male sterility (DMS) can be used to facilitate cross-pollination but is not commonly used by breeders due to the inability to sort sterile from fertile plants in a timely manner. An ARS researcher in Manhattan, KS, identified a breeder-friendly and efficient DNA marker for DMS. Wheat breeders can use the marker to identify sterile plants at the seedling stage and then use mass selection, half-sib selection, and recurrent selection breeding strategies that are used in corn. It will also enable large-scale marker-assisted backcrossing and gene pyramiding. This will speed the development of elite new wheat cultivars with stacks of desirable traits.

Economic benefits of the Northwest Potato Variety Development Program. Since 1985, ARS potato researchers in Aberdeen, ID, and Prosser, WA, collaborated with researchers from the University of Idaho, Oregon State University, Washington State University, and the Potato Commissions of Idaho, Oregon, and Washington. This research collaboration is known as the “Northwest Potato Variety Development Program” and to date has resulted in the joint development and commercialization of many new potato varieties. Varieties released by the Northwest Potato Variety Development Program are produced on 160,420 acres in the Pacific Northwest with value to growers estimated at approximately $660 million annually. Program varieties represent 25 percent, 52 percent, and 35 percent of total potato acreage in Idaho, Oregon, and Washington, respectively. On a national basis, the program varieties are produced on 255,000 acres. With the recent acceptance of Clearwater Russet and Blazer Russet for processing by McDonald’s on a regional basis, the acreage of these varieties is projected to increase significantly.

Identification of genes associated with drought tolerance in soybean. Drought is a major limitation to soybean yield, and the frequency of drought stress is likely to increase under future climate scenarios. Water
use efficiency is associated with drought tolerance in plants. ARS scientists in Stoneville, MS, with collaborators from University of Arkansas and University of Missouri, measured water use efficiency in a genetically segregating family of plants they created and genotyped. The 196-member family was screened in 4 field environments. The scientists identified genes associated with water use efficiency in soybean. Water use efficiency was highly heritable, with a total of 16 DNA regions on 7 chromosomes that are putatively associated with genes affecting water use efficiency. Molecular markers closely linked to the identified chromosomal regions were described and made available to soybean breeders, making it easier to combine the multiple desirable genes associated with drought tolerance into high-yielding soybean lines and create improved drought tolerant varieties for farmers.

**A new rootstock released for marginal soils in western San Joaquin Valley.** In the southern San Joaquin Valley of California, there are more than 1.3 million acres of salt-affected and boron-laden soils currently unsuitable for almond production. ARS researchers in Parlier, CA, released a rootstock that may soon render the affected acreage usable for almond culture. The new rootstock, a hybrid of Floradgard and Israeli almond named FXA, performed well in several rootstock trials established on boron-laden or salt-affected soils. Almond scions grown on FXA rootstock accumulate less chloride in vegetative tissues than when alternative rootstocks are used. Similarly, when cultured in boron-laden soils, FXA-grown almonds accumulate lower levels of boron in hull tissue than those grown on alternative rootstocks. These factors lead to healthier and more productive trees under marginal growing conditions. The new rootstock was released for public propagation.

**Early season cold tolerance genetic markers developed.** ARS researchers in Lubbock, TX, in collaboration with Kansas State University, identified DNA variants that contribute to early season cold tolerance in sorghum. DNA markers were developed and confirmed to function in multiple genetic backgrounds. The markers were also used as a selection tool for identifying six advanced backcross lines now being evaluated and used by public and private plant breeding programs. Additionally, genetic markers for cold tolerance are used in the in-house sorghum breeding program for the development of high yielding sorghum with diverse genetic backgrounds.

**Discovery and transfer of a genomic region responsible for cotton fiber strength.** ARS researchers in New Orleans, LA, discovered a DNA region responsible for stronger fiber and demonstrated its transferability, expression, and stability in adapted cotton germplasm. When they crossed cotton lines and generated new populations, 87.5 percent of the new lines contained the DNA region of interest, and the improvement in fiber strength was clearly observed in all the lines, verifying previous successful attempts by the researchers to transfer this genetic region. The researchers also developed DNA markers for identifying this DNA region in the cotton genome that can be used when cotton plants are at seedling stage so cotton breeders can make early assessments before making major resource investments. Molecular markers tagging the specific DNA region responsible for cotton fiber strength were deployed to commercial breeders and are now used by ARS, universities, and private industry.

**Development of high-yielding disease resistant sugarcane cultivars for commercial production in Florida.** The biggest challenges for sugarcane growers in Florida are orange rust and brown rust diseases. The rusts cause considerable yield losses and increase costs due to fungicide applications. Development of new cultivars with disease resistance, high yields, and high profits is a priority of the Canal Point sugarcane
breeding and cultivar development programs. ARS researchers in Canal Point, FL, collaborated with other institutes and released five new high-yielding sugarcane cultivars (CP 13-1223 and CP 13-1954 for muck soils, and CP 12-1753, CP 13-4100, and CPCL 13-4046 for sand soils) with disease resistance or tolerance. The new cultivars will mitigate negative effects of brown and orange rusts and other factors limiting sugar yield and profits in Florida.

**Identification of the first gene controlling grain size in sorghum.** Grain size is an important trait for grain yield and commercial processing. It is a complex trait controlled by many genes, but none of the specific genes have been identified. Large segments of chromosomes, which contain multiple genes, were previously identified. ARS scientists in Lubbock, TX, collaborated with scientists from the Institute of Crop and Nuclear Technology Utilization, Zhejiang Academy of Agricultural Sciences (China) to identify a gene called SbGS3, a key regulator of sorghum grain size. The identification of SbGS3 and its function significantly advances knowledge of regulatory mechanisms of grain size in sorghum. Furthermore, the SbGS3 gene provides a target to manipulate grain size and increase yield through genome editing because elimination of the gene function is associated with large grain size.

**Genetic information from other crops helps identify genes for fruit sweetness in blackberry.** The genetic control for fruit sweetness, an important trait for the $31.1 million U.S. blackberry industry, was unknown. ARS scientists in Corvallis, OR, enlisted genetic information from apple, peach, and strawberry to seek blackberry genes with structures resembling those known to control sugar production in those other related crops. Based on that information, blackberry genes potentially involved in controlling fruit sweetness were identified and applied to targeted genetic sequencing of 40 blackberry varieties obtained from the University of Arkansas and USDA breeding programs and that were characterized by high and low sugar content. Population modeling identified 173 genomic regions linked to sugar content in these 40 varieties. Genetic markers for those genomic regions were developed and then validated in varieties with known sugar content from the same breeding programs. Knowledge of these first “sweetness related” genomic regions identified in blackberry can be applied to breed new blackberry varieties with sweeter fruits.

**Identification of soybean breeding lines with resistance to Phomopsis seed decay and high seed germinability.** *Phomopsis* seed decay is one of the most economically important soybean diseases in the mid-southern United States. Identifying new sources of resistance to use for breeding soybean lines resistant to *Phomopsis* seed decay and with high seed quality is one of the most effective ways to control the disease. ARS scientists in Stoneville, MS, evaluated more than 200 breeding lines derived from parents with 5 sources of resistance and high seed quality for rates of *Phomopsis* seed infection and germination. Twenty-seven *Phomopsis* seed decay-resistant breeding lines with high seed quality were identified and tested in multi-year trials. Seed of seven improved soybean lines were identified and transferred to public and private soybean breeders to develop high-yielding varieties with reduced mature seed damage from *Phomopsis* seed decay. These accomplishments may result in high quality soybean seeds for planting, and less elevator dockage due to damaged seed.

**New methods to measure fruit quality in cranberry.** Due to the lack of methodologies to measure fruit quality in cranberry, ARS researchers in Madison, WI, developed a high-throughput computer-vision method to measure the internal structure of cranberry fruit, which may influence cranberry fruit firmness. They measured internal fruit structure and analyzed fruit firmness of cranberries over the ripening period. The
resulting data allows growers to better select cranberry varieties to grow and helps researchers explore the relationship between firmness and internal fruit characteristics. This new method highlights the potential use of internal structure and firmness data for breeding varieties with superior fruit quality. It can also be used as a decision-making tool for cranberry processing, especially to determine optimal harvesting schedules and to ensure high quality fruit for different cranberry products, including dried fruit products, which are currently the most profitable and high demand cranberry product in the market.

**Release of three new main-season peach cultivars, ‘Rich Joy’, ‘Liberty Joy’, and ‘Crimson Joy’**. The southeastern United States peach industry’s shipping market needs new main-season cultivars that produce large, firm, melting, freestone peaches with yellow flesh, normal acidity, high blush, and pleasant eating quality. Thousands of hybrids are generated annually by ARS researchers in Byron, GA, and used in the breeding pipeline for cultivar selection and evaluation. Three new main-season peach cultivars with desired characteristics were recently released to commercial growers. ‘Crimson Joy’ and ‘Liberty Joy’ provide improved cropping reliability under suboptimal weather conditions, and ‘Rich Joy’ fills a critical gap in the harvest window.

**Cultivars with stable high resistance to low falling number identified in northwestern U.S. winter and spring wheat cultivars**. The falling number test is a standard method to assess end use quality in the grain trade. While ARS researchers performed falling number tests on the multiple wheat varieties over multiple environments since 2013, summarizing these results was difficult because individual varieties were not included in all years or locations. ARS researchers in Pullman, WA, with collaborators at Washington State University, used the factor-analytic statistical model to analyze data collected from 2013 to 2016. This approach compensated for the unbalanced nature of the dataset, allowing identification of varieties with stable falling number over multiple years and locations. These variety rankings were shared through Washington State University extension with farmers and the grain industry to inform their selection and handling of wheat varieties, reduce discounts for poor quality grain, and improve the grain industry’s ability to meet export market specifications.

**New pinto bean cultivar developed for low-input production systems**. Pinto beans are the most widely grown dry bean market class in the United States. ARS researchers in Prosser, WA, released a new pinto bean cultivar, ‘USDA-Rattler’, developed for superior performance under both low and high input production systems. USDA-Rattler exhibits tolerance to drought and low soil fertility that allows it to grow with less water and fertilizer inputs. It also has excellent disease resistance to bean common mosaic virus and bean rust that expands its range of production across the United States. A major seed company expressed interest in licensing this versatile pinto bean cultivar particularly because of its excellent yield potential under less favorable growing conditions.

**Improved commercial sugarcane varieties for temperate production**. There is no private breeding program for sugarcane in the United States, so the industry relies completely on publicly developed varieties. ARS scientists from Houma, LA, in collaboration with the American Sugarcane League of the U.S.A., Inc., and the Louisiana State University Agricultural Center, developed and released three new sugarcane varieties in 2020. The variety ‘Ho 13-739’ is resistant to sugarcane diseases and moderately resistant to sugarcane borer. Its most significant attributes are early maturity and high sugar yields during early harvest. The ability to harvest early in Louisiana is critical because the harvest season is cut short due to late-season freezing.
temperatures. The variety ‘Ho 13-710’ has disease resistance and cane yield that is well-adapted for growers in Texas and can increase industry profits and expand the genetic variability contained within the growing region. The variety ‘Ho 11-573’ has superior cane yield, particularly in plant cane.

**Resistance genes identified in tomato for anthracnose fruit rot.** Anthracnose fruit rot causes major crop losses for tomato and pepper growers. ARS scientists in Beltsville, MD, working in collaboration with scientists at West Virginia State University, used a high-density tomato genetic linkage map to develop breeding lines of tomato resistant to the fungus that causes fruit rot. The scientists identified five genes that offer fruit rot resistance to tomatoes. These new genetic lines will help breeders transfer fruit rot resistance to advanced tomato breeds. The same methods can be used to provide resistance genes in pepper and other related crops, enhancing marketable yield and reducing cost and environmental concerns related to conventional chemical-based crop disease management.

**Reducing cotton fabric impurities through breeding.** A nep is a small knot or cluster of entangled fibers that may consist either entirely of fibers, or foreign matter such as seed-coat fragments entangled with the fibers. Neps reduce yarn quality and cause white flecks in dyed cotton fabrics. Genetic improvement for fewer neps in cotton cultivars via selection is a proven and effective approach to reduce neps, but there is a negative correlation between fiber yield and neps. Since fiber yield is always the top priority for cotton breeding programs, selection for fewer neps should not decrease yield. ARS scientists in Stoneville, MS, developed an approach to breed for fewer neps without lowering yield. This study provided the first evidence that cotton neps could be decreased without a yield reduction. Cultivars with fewer neps will allow the cotton grower to deliver higher quality cotton fiber to the textile mills and result in less subsequent loss due to rejection of fabrics with white undyed flecks.

**Release of high-fiber sugarcane variety 'Ho 06-9002' for U.S. energy independence.** Sugarcane is one of the most efficient producers of biomass of all plant species and can be used as a renewable fuel. ARS scientists in Houma, LA, developed and released a new high-fiber variety of sugarcane, or energycane. The new variety, ‘Ho 06-9002’, has a high fiber content, excellent regrowth ability over 4 to 5 years, is cold tolerant, has a high stalk population, and produces excellent biomass yields. Ho 06-9002 showed no symptoms of brown rust or smut when exposed to high levels of natural inoculum. Mosaic disease, caused by either sugarcane mosaic virus or sorghum mosaic virus, was not observed in the variety under natural field conditions. Its most significant attribute is cold tolerance and the ability to yield high biomass in non-traditional sugarcane growing regions.

**Transgenic wheat with resistance to wheat streak mosaic virus and Triticum mosaic virus.** Wheat streak mosaic disease complex, caused by wheat streak mosaic virus (WSMV), Triticum mosaic virus (TriMV), and High Plains wheat mosaic virus, is the most economically important viral disease of wheat in the U.S. Great Plains and causes about $100 million in annual yield losses. Since all three viruses are transmitted by the wheat curl mite, mixed infections in a combination of any two or all three viruses were reported in growers' fields with reduced yield. WSMV and TriMV synergistically interact in co-infected wheat with increased accumulation of both viruses and with enhanced disease severity. Hence, wheat cultivars with resistance to at least two of the three mite-transmitted viruses would minimize yield loss. ARS researchers in Lincoln, NE, in collaboration with the University of Nebraska-Lincoln scientists, developed RNA-interference-based transgenic wheat lines that provided dual resistance to both WSMV and TriMV at 25°C or above. However,
the transgenic wheat lines were susceptible to WSMV and TriMV at 20°C, although both viruses accumulated at significantly lower levels compared to those in nontransgenic wheat. The availability of transgenic wheat lines in this study will facilitate stacking the low temperature-sensitive transgene with high temperature-sensitive Wsm1 or Wsm2 genes to obtain wheat cultivars with dual resistance at a wide range of temperatures, helping wheat growers manage wheat streak mosaic disease.

**A new common bean variety with broad resistance to bean rust.** Pinto bean is the most important market class of common bean grown and consumed in the United States. North Dakota is the largest producer of dry beans in the United States, and rust is a major disease of common bean that limits dry bean production in North Dakota, Michigan, Nebraska, Colorado, and other states. The bean rust pathogen, a fungus, is constantly evolving, which produces new virulent strains. A new strain, race 20-3, appeared in North Dakota and was virulent on previously resistant pinto bean varieties, exacerbating the need to develop resistant pinto varieties. Research by ARS scientists in Beltsville, MD, and scientists at North Dakota State University showed that the Ur-11 gene conferred resistance to race 20-3. Most importantly, Ur-11 conferred resistance to all known virulent strains of bean rust globally, except for one strain from Honduras. The scientists used this gene to develop a new pinto bean cultivar, ND Falcon, the first dry bean with Ur-11 in North Dakota. ND Falcon has the Ur-11 rust resistance gene, in addition to many other positive agronomic attributes, and scientists anticipate ND Falcon will have a direct positive economic impact on pinto bean acreage, benefit growers and processors, and contribute to the sustainable production of pinto beans in the United States.

**A wheat gene with broad resistance to a fungal pathogen.** Tan spot is a serious fungal disease of wheat. Interactions between wheat plants and the tan spot fungus are usually specific and rely on specific effector proteins in the fungus that, when recognized by specific genes in the plant, cause cell death and disease. ARS researchers in Fargo, ND, conducted genetic analyses of wild emmer, an ancestor of wheat, and evaluated the plant response to multiple strains of the tan spot fungus that are known to produce a variety of effector proteins. The researchers identified an accession of wild emmer wheat that was resistant to all strains of the tan spot pathogen. Detailed molecular genetic analyses indicated the wild emmer plant carried a single gene that conferred broad-spectrum resistance to all strains of the fungus. The researchers transferred the gene to elite wheat lines to render them resistant to tan spot. Identifying and deploying the tan spot resistance gene by wheat and durum breeders will lead to higher yielding wheat varieties requiring fewer fungicide applications.

**Release of a new high-protein soybean germplasm with competitive yield and genetic diversity.** The soybean industry demands soybean varieties with meal protein content of the minimum market standard of 47.5 percent, and to stay competitive in the international market, U.S. soybean growers and processors require high-yielding soybean with at least 48 percent meal protein. The lack of adequate genetic diversity among soybeans available for improving protein concentration while maintaining yield potential has been a serious concern for breeders. ARS researchers in Raleigh, NC, released a new soybean germplasm line, USDA-N6005, combining high meal protein (49 percent) and achieving 100 percent yield of the check cultivar with low protein. The check cultivar has well-known characteristics and is used for comparison. The new release has a 25-percent exotic pedigree derived from a Japanese cultivar in the USDA soybean germplasm collection. This line will be a new resource for both public and private soybean breeders to develop high performing soybean cultivars with acceptable meal protein standards of at least 48 percent.
**New sources of improved cotton fiber.** Recent advances in spinning technologies require longer and stronger cotton fibers to manufacture high-quality textiles with minimal waste from short or immature fibers. Only modest gains in fiber quality were reported over the last few decades of intensive plant breeding, probably due to the overreliance on a relatively few elite and genetically similar cultivars as parents in most cultivar development programs. Sources of parents with unique fiber traits are limited, but modifying cotton using mutation breeding offers new sources of genetic variation. ARS researchers in Stoneville, MS, used chemical mutagenesis of seeds from regionally adapted cultivars and screening and conventional breeding techniques to recover plants with stable heritable fiber traits superior to parental traits, including improved fiber length and/or strength. These lines were released to the cotton community to be used as parents in breeding programs to develop improved cotton cultivars.

**Discovery and mapping of the two new sunflower rust resistance genes.** Sunflower rust is a serious fungal disease in sunflower worldwide, with increasing importance in North America due to frequent emergence of new pathogen races. The emergence of novel pathogen virulence has rendered most commercial sunflower hybrids susceptible to rust, leading to a need to discover novel rust resistance genes for long-term management. ARS scientists in Fargo, ND, identified two sunflower accessions in the USDA National Plant Germplasm System, KP193 and KP199, that were introduced from South Africa and are resistant to rust. Mapping placed the two rust resistance genes, R17 from KP193 and R18 from KP199, on sunflower chromosome 13. Two homozygous resistant lines selected from KP193 and KP199 were developed with resistance to the most common and virulent rust races, providing valuable germplasm to commercial seed companies for breeding programs.

**Component 2 – Plant and Microbial Genetic Resource and Information Management**

**Breeding Insight supports ARS specialty crop and animal breeders.** ARS specialty crop breeders are often the sole source of publicly available new crop varieties for farmers and growers across the United States and elsewhere. Although specialty crops and animals are a large portion of gross U.S. agricultural revenue, individually these small programs have not had access to innovations that benefited major crop and animal breeding programs and thus have lagged. The ARS Breeding Insight Platform is currently in a pilot phase focused on building support services for six ARS breeding programs (blueberry, table grape, sweet potato, alfalfa, rainbow trout, and North American Atlantic salmon), with the future goal of expansion to all ARS specialty crops, animal, and natural resource breeding programs. The project identified the key workflows common to these diverse programs and initiated the development of extensive software and genomics to support these efforts. Genomic support was delivered for all programs. A key early success was integrating the leading field data collection tool with the community’s leading database. Providing powerful information and genomic tools to ARS specialty crop and animal breeders is helping to improve breeding decisions, meet public demands for more nutritious and flavorful foods, and improve food security for the United States and its trade partners.

**A covert killer of macadamia trees discovered in Hawaii.** Currently more than 17,000 acres (approximately 1.2 million trees) of macadamia nut are grown in Hawaii, constituting a $42 million/year industry. Early detection and identification of newly emerging diseases are the critical first steps for protecting this valuable crop. ARS researchers in Hilo, HI, published the first report of *Phytophthora heveae*, a plant pathogen, as the
cause of macadamia quick decline and the first report of this pathogen on any host plant in Hawaii. *P. heveae* has a wide host range, and its presence in Hawaii also poses a potential risk for avocado, mango, and cacao. ARS researchers are working with macadamia growers and researchers to assess the impact of *Phytophthora* diseases and develop improved management practices that minimize tree loss in mature orchards and maintain the economic viability of the macadamia industry. Commercial macadamia production originated in Hawaii, which now produces nuts that are considered the global “gold standard” for quality and flavor.

**Highly accurate “genetic fingerprints” developed for Arabica coffee varieties.** Coffee is a significant contributor to the U.S. economy. In 2015, the U.S. coffee industry estimated coffee’s total economic output in the country at $225.2 billion, equivalent to 1.6 percent of the total U.S. gross domestic product. But the premium Arabica coffee crop worldwide is threatened by a paucity of genetic variation, leaving it susceptible to virulent diseases, pests, and rapid environmental change. Consequently, discovering new genetic variation from accurately identified coffee varieties and germplasm collections will be key for breeding new resistant and more productive coffee varieties. ARS scientists in Beltsville, MD, developed a core set of 96 high quality genetic markers which determined distinct difference in a wide range of Arabica coffee varieties and germplasm accessions provided by collaborators in Hawai’i, Brazil, Costa Rica, Honduras, Puerto Rico, Indonesia, Rwanda, and Côte d’Ivoire—even those that were very similar genetically or mislabeled. The research organization World Coffee Research already applies these markers to certify coffee nurseries in Latin America, Asia, and Africa, which produce healthy true-to-type coffee planting materials for farmers. Coffee breeders, germplasm curators, seed producers, coffee growers, and the coffee industry can now use these markers to improve the globally important coffee crop.

**Novel antibiotic-producing bacteria discovered on squid eggs.** Discovery of new antibiotics is increasingly critical to combat the dramatic rise in multidrug resistant bacteria. Scientists at the University of Connecticut, the University of Texas-San Antonio, and the University of Florida, in collaboration with an ARS scientist in Peoria, IL, characterized several antimicrobial compounds produced by bacteria in the jelly coat of squid eggs. These antimicrobial compounds prevent overgrowth by fungi and other microorganisms on the eggs. Both experimental and analytical approaches revealed that multiple bacteria associated with the eggs, and chemical extracts of those bacteria, inhibited growth of the pathogenic mold *Fusarium keratoplasticum* and yeast *Candida albicans*. The discovery of novel antimicrobials is critical to promoting public health globally because many antibiotics available to clinicians cannot be administered to patients with life-threatening multidrug resistance infections.

**Priorities for conserving invaluable native crop wild relatives in the United States.** Crop breeders rely not only on crops for genetic raw material; they also need genes from the “close cousins” to crops. These “crop wild relatives” incorporate naturally occurring traits key to improving crop yields, drought tolerance, and disease and insect resistance. Many of these crop wild relatives are native to the United States but only recently have become the focus of collection and research. To optimally collect and preserve these species and their valuable traits, ARS scientists in Fort Collins, CO, and their cooperators recently completed a comprehensive analysis of the geographical occurrence and conservation status of 600 crop wild relatives in the United States. This analysis revealed that about 7 percent of crop wild relatives in the United States are critically endangered, 50 percent are endangered, and 28 percent are vulnerable in their natural habitats. Furthermore, 60 percent were categorized as “high priority” for safeguarding in genebanks, botanical
gardens, and natural environments. This research was critical for developing a strategic plan to secure and make these precious genetic resources available.

**Three new reference-quality soybean genome assemblies.** Plant breeders and scientists use plant DNA genome sequences to identify genes important for yield, disease resistance, and plant growth characteristics. For soybean, a genome sequence assembly for the widely used Williams 82 variety has been available for about 10 years, but there were numerous known gaps and errors in the sequence assembly. ARS scientists in Beltsville, MD, collaborated with researchers at the Department of Energy Joint Genome Institute, Hudson-Alpha Institute for Biotechnology, University of Missouri, Iowa State University, University of Minnesota, University of Georgia, University of Australia, Chinese University of Hong Kong, and the International Crops Research Institute for the Semi-Arid Tropics (India) to make major improvements to the original widely-used Williams 82 reference genome sequence, as well as build new genome assemblies for two other soybeans that breeders rely on for diversity information and genes. They sequenced the most important U.S. southern cultivar, 'Lee', and the closest wild relative of soybean, *Glycine soja*. These three genome sequences are available to the public and can be used to identify similarities and differences that underpin important agricultural traits.

**Diagnostic assays for predicting pathogenic races of the hop powdery mildew fungus.** Powdery mildew of hop is one of the most damaging diseases affecting hop crops worldwide. Multiple pathogenic races of the fungus occur, which complicates management because of uncertainty of what races are present and what varieties of hop may be at risk of disease. ARS researchers in Corvallis, OR, and Oregon State University collaborators developed a diagnostic DNA test that accurately confirms pathogen race within hours, which is critical for implementing timely control measures. This accuracy permits growers and others to make precise management decisions. The assay has practical applications in hop breeding, epidemiological studies, and other settings where rapid confirmation of pathogen race is needed.

**Discovering valuable traits from plant germplasm collections through artificial intelligence.** To improve crops, plant breeders require traits that confer disease and pest resistance and tolerance to environmental extremes. Locating such traits within huge collections of plant germplasm is extremely difficult. Traditionally, this process was often time consuming and expensive, requiring extensive multi-location, multi-season field evaluations. To accelerate progress and increase cost-effectiveness of plant breeding, ARS scientists in Fort Collins, CO, developed an artificial intelligence (AI) program that analyzes entire DNA sequences to identify plants with genes that control important agronomic traits. This important advance in AI-assisted next-generation sequencing provides a faster, less-costly approach to identifying the few samples, from the thousands or tens of thousands in a germplasm collection, with genes for the specific traits needed by the breeder. In addition to accelerating breeding programs, this new tool greatly enhances the value of plant germplasm collections worldwide by enabling targeted discovery of these traits from the vast genetic diversity within those collections.

**Early detection of avocado sun blotch viroid.** Avocado is an important U.S. fruit crop, with a national farmgate value of $400 million in 2018; most production occurs in California, Florida, and Hawai‘i. A highly contagious RNA viroid pathogen of avocado, avocado sun blotch viroid (ASBVd) causes bleached craters on the fruit, discolored leaves, loss of yield, and eventually tree death. This viroid spreads easily to trees through cutting and pruning, root grafting, and pollen transport. ARS researchers in Miami, FL, have developed a
highly sensitive detection assay to test for ASBVd. The valuable ARS avocado germplasm collections in Miami and Fort Pierce, FL, are being tested with that assay to ensure the collections are free of the viroid. This rapid early detection method will enable research with and wide distribution of this invaluable genetic material for breeding and further analyses.

**More accurate detection of a damaging pecan disease.** Pecan is an important crop for both large-scale and small-scale producers in the southeast, southwest, and south-central United States, with a national farmgate value of $425 million in 2018. The bacterium *Xylella fastidiosa* causes pecan bacterial leaf scorch disease, which damages pecan production. Access to key genetic material from the ARS pecan germplasm collection in College Station, TX, is restricted due to the pathogen’s potential presence. ARS researchers in College Station, working with university and ARS colleagues in Byron, GA, developed a comprehensive, improved protocol for *Xylella* detection and monitoring, which established that *Xylella* can be transmitted through the seed. This improved protocol efficiently detects *Xylella* disease in pecan production orchards. It also can play a key role in monitoring the pecan germplasm collection for this disease, which should enable eventual access to disease-free germplasm.

**Development of thrips-resistant onion varieties.** Thrips are the main insect pest of onion, causing serious losses to both the seed and bulb crops. Heavy use of insecticides as the sole control measure resulted in pesticide-resistant thrips populations that limit control options for growers. ARS scientists in Madison, WI, identified onions with unique profiles of waxes on foliage that suffer significantly less feeding damage by thrips. These unique profiles were introduced into advanced onion breeding lines to produce a thrips-resistant, elite hybrid. New onion breeding lines and a hybrid are under review for formal release to stakeholders in public institutions and seed companies.

**Discovery of several major genes controlling carrot root color.** The first colors of carrot 1,100 years ago were purple and yellow, and while purple pigments are not common in carrots today, purple carrots are of new interest by carrot growers, breeders, and consumers. In three studies, ARS researchers in Madison, WI, with collaborators from North Carolina State University and the National University of Cuyo (Argentina), used a diverse collection of modern and historic cultivated varieties to identify three major genes controlling anthocyanin pigment content and chemical structure influencing nutritional quality. This study provides support for studies indicating genes for purple carrot color were important in the early stages of carrot domestication and improvement. It is of interest to plant geneticists, molecular biologists, breeders, nutritionists, vegetable growers, and agricultural historians, as it provides additional insights into fundamental mechanisms of anthocyanin accumulation that shape carrot breeding strategies to improve color and nutritional impact.

**Evaluation of blueberry genetic resources identifies fruit fly resistance.** Spotted wing drosophila fruit fly appeared in the United States in 2009 and now causes more than $511 million in damage annually to fruit production in Western states. ARS scientists from Corvallis, OR, and Poplarville, MS, searched blueberry genetic resources for resistance to that fruit fly. Twenty-nine blueberry species were tested with a bioassay for resistance to feeding by the fruit fly larvae and adults. Ten blueberry species were resistant to feeding by the fruit fly; three of those species are indigenous to East Asia, in the fruit fly’s native range. Blueberry species from Central and South America were also resistant. Most highbush blueberry cultivars were susceptible, but rabbiteye and other blueberry cultivars with smaller, firmer fruit types were resistant. These
findings will enable blueberry breeders to identify parental lines to cross and produce new blueberry cultivars resistant to this fruit fly.

**Uncovering genetic diversity of wild cranberry populations and conserving North America’s crop wild relatives.** Most cranberry cultivars share the same genetic background that is based on only a few Eastern wild selections, which limits the breeding pool for selection to support the cranberry industry. ARS researchers in Madison, WI, studied 36 populations of wild cranberries in the Upper Midwest and demonstrated the presence of high diversity that represents untapped and previously undiscovered cranberry variation in natural areas of Wisconsin and Minnesota. These wild relatives, which are the distant cousins of agricultural plants, are valuable for agriculture because breeders can use them to introduce new or improved traits. The challenges faced by growers in Wisconsin are unique, and these populations may possess unique adaptations and traits useful in breeding cultivars for central Wisconsin, which has the largest cranberry production area in the world.

**New diversity available for the D-genome of wheat in the ‘DNAM’ population.** More than 8,000 years ago, hexaploid (bread) wheat evolved via hybridization between tetraploid (AB) wheat and a small set of the wild diploid (D) wheat, *Aegilops tauschii* spp. *strangulata*. The variability of the D-genome of wheat is much less than that of the A and B genomes due to this bottleneck, and the lack of variability makes it difficult to improve wheat for certain traits like pest resistance and grain quality. ARS researchers in Pullman, WA, together with collaborators at Michigan State University and Washington State University, developed and characterized a D-genome nested association mapping (DNAM) panel which combines linkage and association mapping using multiple and diverse *Aegilops tauschii* accessions crossed to an adapted hard white breeding line from the U.S. Great Plains. Novel resistance to stripe rust and to cereal cyst nematodes was discovered in this population, which was released and deposited in the ARS National Small Grains Collection for plant geneticists and breeders to access.

**Markers developed for four Hessian fly resistance genes in wheat.** Hessian fly is a destructive insect pest of wheat that causes stunting of seedlings and lodging of mature tillers. Genetic resistance is the best control method for Hessian fly. Traditional selection techniques for resistance use live colonies of Hessian fly biotypes and are laborious, slow, and expensive. Marker-assisted selection is simpler, faster, and cheaper but requires development of DNA markers for each resistance gene. ARS researchers in Manhattan, KS, developed new breeder-friendly DNA markers for Hessian fly resistance genes h4, H7, H35, and H36. These markers will help select future wheat cultivars with enhanced resistance to the Hessian fly.

**Phenotyping of USDA guayule germplasm collection.** Guayule, a plant native to semi-arid regions of Northern Mexico and Southern Texas deserts, is a potential domestic source of natural rubber. Until now, no research has been conducted to phenotype the global USDA guayule collection, which includes improved germplasm and wild accessions collected from natural habitats. ARS researchers from Maricopa, AZ, evaluated the phenotypic diversity of guayule traits related to rubber and resin production. The research findings were used to summarize the USDA guayule germplasm collection with regards to their response and stability when grown under different irrigation regimes. Water stress increased resin and rubber accumulation, while well-watered conditions increased dry weight biomass. This study provides the foundation for guayule breeding programs to select guayule parental lines for breeding varieties suitable for
various agricultural systems. These findings can also help expand guayule regional production zones to better meet different end-user demands.

Component 3 – Crop Biological and Molecular Processes

Characterization of the changes responsible for increased stalk pathogen- and drought-resistance in brown midrib 12 (bmr12) sorghum. ARS researchers in Lincoln, NE, examined how two brown midrib lines (bmr6 and bmr12) and the corresponding normal sorghum line responded to two stalk diseases (Fusarium stalk rot and charcoal rot) under drought stress and adequate water conditions. Bmr12 plants have impaired lignin synthesis; lignin is a cell wall component that plays a role in plant defenses against drought and pathogen attack. Bmr12 plants had fewer disease symptoms under drought conditions than normal plants or even bmr12 plants under adequate water conditions. Further analyses show that bmr12 had increased defense signals under drought conditions, which suggested these plants were already prepared for a pathogen attack. This research showed that bmr12 sorghum with reduced lignin may improve its ability to serve as a forage and bioenergy crop. The identification of genes and pathways in bmr12 plants that direct lignin synthesis may lead to the development of more climate- and disease-resilient sorghum hybrids.

Under-the-radar dengue virus infections in natural populations of Aedes aegypti mosquitoes. Metagenomics has helped identify dengue virus in Florida prior to any human infection. ARS researchers in Stoneville, MS, have demonstrated the ability to monitor vector-borne diseases ahead of outbreaks using metagenomics. To date, the current U.S. public health system’s response to outbreaks has been largely reactive, but this research shows that by monitoring mosquito populations, it may be possible to identify emerging mosquito-borne diseases in high-risk, high-tourism areas of the United States to enable proactive, targeted vector control before potential outbreaks occur.

Discovery of microbe-dependent hybrid vigor in maize. Hybrid vigor is the superior yield observed in hybrids compared to their inbred parents and is the basis of commercial corn production in the United States. The physiological and genetic mechanisms linking genomic hybridization to phenotypic superiority remain poorly understood. Nearly all research into the subject thus far has focused on molecular and quantitative genetic processes, with mixed success; meanwhile, the influence of the environment on hybrid vigor has mostly been ignored. In collaboration with North Carolina State University scientists, ARS researchers in Raleigh, NC, showed that hybrid vigor of maize is eliminated or greatly weakened when soil microbes are absent or reduced. The scientists demonstrated the generality of this phenomenon in three distinct microbial environments: in the lab using a synthetic community of seven bacterial strains; in a growth chamber using a complex microbial community derived from soil; and in the field using four different methods of soil fumigation. This striking repeatable pattern indicates, for the first time, that hybrid vigor arises in part from interactions with microbial neighbors. This finding will be of outstanding interest to biologists across a wide diversity of fields, including both micro- and macro-biologists. In addition, hybrid vigor is the reason hybrid corn dominates corn production in the United States and was a cornerstone of global food security for decades. ARS findings have high potential for supporting new methods of using hybrid vigor to improve agricultural productivity.
New technology to screen for higher-yielding crop traits. Measuring photosynthesis in the field using traditional methods requires up to 30 minutes per leaf, but scientists need to measure photosynthesis for thousands of plants each day in many fields during the season. ARS researchers in Urbana-Champaign, IL, reduced the time needed to measure photosynthesis to as little as 15 seconds per plant, allowing researchers to capture the photosynthetic capacity of hundreds to thousands of plants in a research plot. The researchers also reviewed data from two hyperspectral cameras; one camera captures spectra from 400 to 900 nanometers, and the other captures spectra from 900 to 1,800 nanometers. While researchers previously believed that both cameras are required to estimate photosynthetic capacity, this research showed that only one camera is required, lowering the cost of the sensor package and improving the data analysis pipeline. Using these techniques, the team determined how to identify seven important leaf traits from the hyperspectral data that are related to photosynthesis, traits that are of interest to many plant scientists. This technique greatly enhances the capacity for photosynthetic phenotyping of diverse crop genotypes, which is a bottleneck for crop improvement.

New technologies to rapidly identify Cercospora and mutations associated with fungicide resistance. Cercospora leaf spot (CLS) is caused by the fungal pathogen Cercospora beticola and is the most destructive disease of sugarbeet worldwide. Although growing CLS-tolerant varieties is helpful, disease management currently requires timely application of fungicides. Overreliance on fungicides has led to fungicide resistance in many C. beticola populations, resulting in multiple epidemics in recent years. ARS scientists in Fargo, ND, developed a fungicide resistance management ‘toolbox’ for early detection of C. beticola in sugarbeet leaves and mutations associated with commonly used fungicides for CLS management. Methods were developed to detect the pathogen as early as 1 day post-inoculation in field settings. This research provides a low-tech methodology that agricultural field staff or growers can use to quickly identify the pathogen in the field, a critically important step for disease management.

Lignin-related enzyme changes lignin composition of sorghum biomass. Sorghum biomass serves as an important forage crop for livestock, and is being developed as a bioenergy crop. The ferulate 5-hydroxylase (F5H) gene encodes an enzyme involved in the synthesis of the biomass component lignin. To understand the role of this enzyme in lignin synthesis and its effect on cell wall composition, ARS researchers in Lincoln, NE, and their collaborators used biotechnology to greatly elevate expression of the F5H gene in sorghum plants. Using a microscope, they observed that F5H alone and in combination with brown midrib 12 (bmr12) changed the lignin composition within cell walls. This work, published in the journal Plant Molecular Biology, was featured on the cover of the June 2020 issue. This research demonstrated new ways to change lignin composition of sorghum biomass, which may lead to production of renewable chemicals that require specific lignin composition.

Breeding low-acidity cranberry fruit. Cranberry fruit contain very little natural sugar and is highly acidic. Although some acidity is required for expressing fruit flavor, the high acidity of cranberry requires considerable amounts of added sugars to make cranberry products palatable. However, such high amounts of sugars are considered unhealthy. ARS scientists in Chatsworth, NJ, together with cooperators at Rutgers University, used a cranberry germplasm screen to identify lines with fruit that is naturally low in citric acid, the main contributor to acidity in cranberry. The team genetically mapped the responsible gene(s), developed corresponding molecular markers, and demonstrated their genetic association with the low acid
fruit production. New low-acid cranberry varieties will save costs and result in cranberry products more desired by consumers.

**Advances in cassava breeding for root traits.** Cassava is an important staple crop in the developing world, favored by farmers for its drought tolerance and high carbohydrate-containing storage roots. However, the lack of uniformity and irregular shape of cassava storage roots pose constraints for cassava mechanical harvesting and postharvest processing. ARS scientists in Ithaca, NY, performed DNA fingerprinting and image analysis of the cassava storage roots of a large breeding population at the International Institute of Tropical Agriculture in Nigeria. They identified regions of cassava chromosomes that determine key aspects of cassava root size and root shape, including the genetic variation that breeders will now use to enhance root shape. This proof-of-concept project showed that image-based phenotyping and genome sequence-based selection can improve these traits.

**Discovery of a mechanistic link between potato greening and glycoalkaloid production.** Greening of potatoes can cause various issues related to health, grower profitability, increased waste, and trade issues. Tuber greening is caused by an increase in chlorophyll, but the issue comes from a concomitant increase in unrelated toxic compounds called glycoalkaloids. Using a molecular approach, ARS scientists in Prosser, WA, and Washington State University researchers have for the first time identified a mechanism linking greening and glycoalkaloid biosynthesis. Manipulating the general isoprenoid pathway altered chlorophyll and glycoalkaloid biosynthesis, influenced the number of health-promoting carotenoids, and increased biomass. These findings create new approaches for developing potatoes resistant to greening and increasing crop productivity.

**Identification of resistance genes and development of DNA markers for Fusarium wilt and papaya ringspot virus in watermelon.** *Fusarium* wilt race 2 and papaya ring spot virus cause serious damage to watermelon, and there is a need to develop cultivars resistant to these two major diseases. ARS researchers in Charleston, SC, and scientists at Cornell University developed genetic populations segregating for disease resistance and evaluated the populations for response to inoculation by the causal agents of the two diseases. Using genomic data developed through the efforts of the Specialty Crops Research Initiative project “Leveraging Applied Genomics to Increase Disease Resistance in Cucurbit Crops”, the team successfully identified two gene loci and their respective DNA sequences. One locus confers resistance to *Fusarium* wilt race 2 and the other confers resistance to papaya ring spot virus. The data generated by this study are used by seed companies to improve disease resistance in elite watermelon cultivars.

**Identification of candidate genes controlling fatty acids profiles in rapeseed seeds.** Finding environmentally responsible solutions for producing renewable fuels is an alternative path for carbon-based energy production. To meet market and user demands, current bioenergy feedstocks, such as rapeseed oil, must be optimized with respect to end-product composition and quality before these biofuels are used for large-scale energy production. ARS scientists in Maricopa, AZ; Peoria, IL; Morris, MN; Sidney, MT; Mandan, ND; Temple, TX; Ames, IA; Akron, CO; and Pendleton, OR, collaborated with scientists from Idaho State University, University of Arizona, and Cornell University and identified candidate genes controlling rapeseed fatty acid synthesis. These candidate genes could serve as precise targets for genomics-assisted breeding to directly alter seed oil composition and quality to meet market criteria. This research provided new genomics tools.
that plant breeders can use to enhance the speed and effectiveness of rapeseed cultivar development for biofuel production.

**Diverse new annotated corn genomes released at MaizeGDB.** Over the past decade the corn research community relied on a single genome sequence as the reference genome for all corn research. However, corn researchers and breeders depend upon the tremendous genetic diversity within corn as a key resource for improving agriculturally important traits in this important crop. That diversity is not adequately represented by a single reference genome. ARS researchers in Ames, IA, worked closely with the University of Georgia, Cold Spring Harbor Laboratory, and Iowa State University to access 26 new high-quality corn genome sequences and supporting data sets through MaizeGDB, the genetics and genomics database for the maize research community. These reference genomes are notable for their completeness (low number of gaps), accuracy, and a high percentage of sequences assembled into chromosomes. This release includes 26 genome pages, more than 1 million gene pages, 206 downloadable data sets, and 134 sets of sequences that are searchable based on homology. In addition, the MaizeGDB genome browser allows researchers to easily navigate within and across this set of genomes and visualize more than 1,000 data sets corresponding to functional regions within the maize genome. The data includes more than 200 agriculturally important traits associated with tens of thousands of locations across the 10 maize chromosomes. These new resources will lead to improved crop performance, helping researchers better understand the relationship between the genes in a plant and the traits observed in farmers’ fields.

**Novel nematode-based bioinsecticide released.** Wisconsin cranberries perennially endure significant damage from a diversity of arthropod pests, the single greatest threat to berry production. Because certain soil-dwelling species such as cranberry flea beetle are poorly controlled by any registered insecticide, effective control measures are needed. Given issues with excessive pesticide residues in cranberries, the demand for effective biological control agents increased markedly in recent years. ARS researchers in Madison, WI, developed a highly virulent nematode-based bioinsecticide. This two-species nematode blend proved as effective for cranberry flea beetle control as two insecticide sprays. This new bioinsecticide is comprised of native Wisconsin nematodes, and it was field-tested using grower equipment. The nematodes were also shown to effectively attack pests within fruit. The capacity of the nematodes to kill pests while they are ensconced within fruit represents a major new tool for dealing with fruit pests.

**Cloning and introgression of a gene for resistance to Fusarium head blight.** Fusarium head blight (FHB), a disease caused by fungal pathogens that produce food toxins, currently devastates wheat production worldwide, yet few resistance resources have been discovered in wheat germplasm. ARS researchers in Fargo, ND, and Manhattan, KS, participated in an international team to clone the Fhb7 functional gene for FHB resistance based on assembling the genome of a wild wheatgrass species. The results revealed that Fhb7 confers broad resistance to the fungal pathogens causing FHB via detoxification of food toxins. The wheatgrass gained Fhb7 via gene transfer from a fungal species that colonizes temperate grasses. When transferred into wheat, Fhb7 confers FHB resistance in diverse wheat backgrounds without reducing yields, providing a solution for FHB resistance breeding in wheat. Moreover, the assembled wheatgrass genome and molecular and biochemical characterization of the cloned Fhb7 gene provide new knowledge and tools to assist scientists across a wide range of communities, including those working on plant-pathogen interactions and genetic modification of plants. The wheat lines carrying Fhb7 are useful germplasm for developing new FHB-resistant varieties for wheat growers.
Identification of candidate genes controlling soybean canopy greenness. Nitrogen (N) plays a key role in plants because it is a major component of chlorophyll and dark and light reactions of photosynthesis. Genotypic variation in canopy greenness provides insights into the variation of N and chlorophyll concentration, photosynthesis rates, and N fixation in legumes. Researchers from ARS in Maricopa, AZ; Colombia, MO; and Stoneville, MS, and researchers from the University of Arkansas and the University of Missouri were the first to map soybean canopy greenness using unmanned aerial imaging and dark green color index (DGCI) measurements. The researchers discovered genomic regions associated with the intensity of greenness of the soybean canopy and identified genotypes with extreme DGCI values within the USDA soybean germplasm collection. Those genomic regions are important resources for pyramiding favorable genes for improved N and chlorophyll concentrations, photosynthesis rates, and N fixation ability in soybean breeding programs.

Genomic insight into the developmental history of southern highbush blueberry populations. Southern highbush blueberry (SHB) is a cultivar group that was bred by multiple interspecific crosses between northern highbush blueberry (NHB) and low-chill blueberry species to expand the geographic limits of highbush blueberry production. Despite years of research, little is known about the genetic diversity and population structure of SHB. ARS researchers in Poplarville, MS, working with collaborators from Japan, used a DNA sequencing technique to genotype a diverse set of SHB, NHB, and blueberry rabbiteye accessions. Sequence data indicated that rabbiteye accessions were genetically distinct from SHB and NHB cultivars, whereas NHB and SHB were genetically indistinguishable. The population structure results reflect the differences in the gene selection strategies breeders used for developing germplasm adapted to local climates. The genotype data implied there are no, or very few, genomic segments that were commonly introgressed from low-chill blueberry species to the SHB genome. These findings will enable genetic variability to be associated with specific phenotypes and enhance germplasm selection based on DNA sequences.

Functional characterization of a major wheat domestication gene. Wheat domestication occurred about 10,000 years ago in the Fertile Crescent of the Middle East and involved specific genetic mutations that made wheat more amenable to harvesting and processing by early farmers. One of these mutations occurred in the wheat Q gene and rendered the seed free threshing, essentially allowing wheat to be harvested on a massive scale and leading to the rise of modern western civilization. Genetic characterization of the Q gene is important to understanding the genetic networks and processes controlled by the Q gene that may be refined to optimize wheat production. ARS researchers in Fargo, ND, conducted a wide range of genetic, physiologic, and molecular experiments to identify genetic pathways and processes controlled by the Q gene. The results revealed the Q gene is a master regulator controlling numerous traits, including plant architecture, cell wall thickness, photosynthesis, pollen fertility, and seed production, and yield. These discoveries provide insights into the significance of the genetic mutation that gave rise to the Q gene, and provide information necessary to wheat breeders to develop more productive and resilient wheat varieties that will have increased tolerance to harsh environments and reduced yield losses under a changing global climate.
Component 4 – Information Resources and Tools for Crop Genetics, Genomics, and Genetic Improvement

Understanding the genome sequence of pecan. Understanding the detailed genetic makeup of pecan is critical to advancing breeding efforts. The whole genomes of the pecan cultivars 87MX3-2.11, ‘Lakota’, ‘Elliott’, and ‘Pawnee’ were sequenced by ARS researchers in College Station, TX. This also includes sequencing the pecan chloroplast, a small, extra-nuclear genome that is critical for photosynthesis and that is generally passed from the mother to the offspring. Because of this unique inheritance pattern, chloroplast genomes can be used to trace maternal origin over many generations. Sequence data provide the genetic blueprint of gene location and function, thus establishing foundational information to support pecan genetic research for years to come. This accomplishment is critical for future work to establish the origin of pecan in North America, to define evolution of the species, and to guide ongoing efforts to improve pecan trees through breeding.

Fungal volatiles for accelerated plant growth. The profitability of indoor or urban farming is limited by the high costs of energy required to control temperature and lighting. Using technologies that work in controlled environmental production systems can offset these costs and increase crop productivity. ARS researchers in Kearneysville, WV, found a common harmless fungus that promotes fast plant growth in indoor environments through the production of beneficial gaseous compounds. The fungus showed no evidence of being pathogenic to plants but produced extreme increases in plant biomass upon exposure while reducing responses associated with photosynthesis and stress.

High-throughput quantification of resin and rubber in guayule. Natural rubber (NR) is a critical industrial natural resource. However, the current production of NR, mainly harvested from Hevea rubber trees, is faced with many obstacles, including the shortage of supply due to increased demands and the risks of fatal diseases in rubber-producing regions. Guayule is a domestic source for NR in U.S. semi-arid and arid regions. ARS researchers in Maricopa, AZ, successfully adapted reliable high-throughput prediction models to determine presence of resin and rubber in guayule using near-infrared spectroscopy. The models are useful to develop a simple, low-cost, and efficient pipeline to maximize the rubber/resin phenotyping efficiency in guayule. The established models will enable guayule breeders and researchers to rapidly and efficiently screen large populations of genotypes much more quickly than the wet chemistry protocols currently being used.

Computer vision data acquisition and measurement workflow of potato tubers. Effective tools are needed to quantify the size, shape, and colorimetric characteristics of potato tubers. Tuber size, shape, skin, and flesh quality are a few of many factors assessed by the food processing industry when considering the acceptance of a new potato variety. Reproducible and accurate measurement of these characteristics on thousands of tubers generated in each breeding and evaluation cycle is needed to apply statistical genetics models and marker-assisted selection on these traits within a potato breeding program. ARS scientists in Prosser, WA, and in Aberdeen, ID, developed a semi-automated data acquisition workflow to measure these features using a microcomputer, consumer grade digital single-lens reflex camera (DSLR), and flatbed scanner. Tuber size, shape, and colorimetric features of tuber skin and flesh were extracted from digital images and were determined to be highly correlated with manual measurements of tuber length and width acquired using digital calipers. The capability to inexpensively and reliably quantify many tuber traits simultaneously in thousands of breeding population samples every year provides increased value to our...
stakeholders. These tools and datasets collected using these techniques can be easily stored, shared with collaborators, and reused for different purposes, such as the development of machine learning models to classify and quantify tuber defects.

**Friendship Garden redesign and interpretation.** The replanting of the Friendship Garden was completed at the U.S. National Arboretum. The design is based on an ecological planting scheme that reduces maintenance inputs and enhances environmental benefits. Interpretive panels that highlight the garden’s positive impact on pollinators and water resources are completed. The National Capital Area Garden Clubs funded the design, part of a multi-year project to improve the environmental footprint and safety of the Friendship Garden.