National Program 301

USDA

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Plant Genetic Resources, Genomics, and Genetic Improvement

Action Plan 2023 – 2027



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National Program 301

Plant Genetic Resources, Genomics and Genetic Improvement

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Vision

The vision of the ARS Plant Genetic Resources, Genomics, and Genetic Improvement National Program (NP 301) is to be a global leader for research in plant genetic resources, genomics, and genetic improvement by providing knowledge, technologies, and products that deliver crops with climate resilience, reliably high yields, superior product quality, and decreased vulnerability to destructive diseases, pests, and environmental extremes, to attain the overall goal of reducing global food insecurity.

Mission

The mission of this national program is to harness the genetic potential of plants to transform U.S. agriculture.

Relationship of this National Program to the USDA Strategic Plan

This Action Plan outlines research that supports primarily the following objective in the <u>USDA Strategic Plan for</u> <u>FY 2018 – 2022</u>:

- Goal 2 Maximize the ability of American agricultural producers to prosper by feeding and clothing the world.
 - Objective 2.1 Provide an effective financial safety net for farmers and ranchers to sustain economically viable agricultural production and support rural jobs and economic growth.
 - Objective 2.3 Protect agricultural health by preventing and mitigating the spread of agricultural pests and disease.

Research outlined in this Action Plan also supports the following USDA Strategic Plan objectives:

- Goal 1 Ensure USDA programs are delivered efficiently, effectively, and with integrity and a focus on customer service.
 - Objective 1.4 Improve stewardship of resources and utilize data-driven analyses to maximize the return on investment.
- Goal 5 Strengthen the stewardship of private lands through technology and research.
 - Objective 5.2 Promote productive working lands.
 - Objective 5.3 Enhance productive agricultural landscapes.

Relationship of this National Program to the USDA Science Blueprint

This Action Plan outlines research that supports Theme 1 of the 2020-2025 <u>USDA Science Blueprint</u> – Sustainable Ag Intensification.

Relationship of this National Program to the USDA Resource, Education, and Economics (REE)

Action Plan - 2014 REE Action Plan

This NP 301 Action Plan will outline research that supports:

- Goal 1 Sustainable Intensification of Agricultural Production: Subgoal 1A. Crop and Animal Production; Subgoal 1C. Crop and Animal Genetics, Genomics, Genetic Resources, and Biotechnology.
- Goal 2 Responding to Climate and Energy Needs: Subgoal 2A. Responding to Climate Variability; Subgoal 2B. Bioenergy/Biofuels and Biobased Products.

Relationship of this National Program to the ARS Strategic Plan

This Action Plan outlines NP 301 research that supports several goals listed in the <u>2018 – 2020 ARS Strategic</u> <u>Plan</u> (see chart).

NP 301 Action Plan Support of the 2018-2020 ARS Strategic Plan				
Strategic Goal Area 1 Nutrition, Food Safety and Quality	Strategic Goal Area 2 Natural Resources and Sustainable Agricultural Systems	Strategic Goal Area 3 Crop Production and Protection	Strategic Goal Area 4 Animal Production and Protection	
Goal 1.1 – Define the Role of Food and Its Components in Optimizing Health Throughout the Life-Cycle for All Americans	Goal 2.1 – Effectively and Safely Manage Water Resources to Sustain and Increase Agricultural Production and Water Use Efficiency While Protecting the Environment and Human and Animal Health	Goal 3.1 – Harness the Genetic Potential of Plants to Transform U.S. Agriculture (NP 301)	Goal 4.1 – Improve Food Animal Production Efficiency, Industry Sustainability, Animal Welfare, Product Quality, and Nutritional Value While Safeguarding Animal Genetic Resources	
Goal 1.2 – Protect Food from Pathogens, Toxins, and Chemical Contamination During Production, Processing, and Preparation	Goal 2.2 – Improve Management of Soil Resources, Reduce Impact on Air Resources, Efficiently Use Inputs, and Contribute to Ecosystem Services	Goal 3.2 – Enhance U.S. Agricultural Crop Productivity, Efficiency, and Sustainability, and Ensure a High Quality and Safe Supply of Food, Fiber, Feed, Ornamental, and Industrial Crops ARS National Program for Crop Production (NP 305)	Goal 4.2 – Improve Domestic Aquaculture Production Efficiency and Product Quality While Minimizing Impacts on Natural Resources	
Goal 1.3 – Improve Postharvest Quality and Develop New Uses of Agricultural Products	Goal 2.3 – Improve Management Decisions and Enhance the Function and Performance of Rangelands, Pastures, Forage, and Turf Agroecosystems While Enhancing Ecosystem Service Goal 2.4 – Integrated Solutions for Agriculture Enabling Greater Productivity, Profitability, and Natural Resource Enhancement	Goal 3.3 – Improve and Expand Our Knowledge of Existing and Emerging Plant Diseases and Develop Effective, Safe, and Sustainable Disease Management Strategies ARS National Program for Plant Diseases (NP 303) Goal 3.4 – Provide Technology to Manage Pest Populations Through the Integration of Environmentally Compatible Strategies ARS National Program for Crop Protection and Quarantine (NP 304)		

This includes support of Strategic Goal Area 3 – Crop Production and Protection, Goal 3.1 – Harness the Genetic Potential of Plants to Transform U.S. Agriculture. In addition, NP 301 research and outreach efforts supporting Goal 3.1 require close linkages with ARS research supporting Goal 3.2 – Enhance U.S. Agricultural Crop Productivity, Efficiency, and Sustainability, and Ensure A High Quality and Safe Supply of Food, Fiber, Feed, Ornamental, and Industrial Crops for the Nation, which is conducted by scientists in the ARS Crop Production National Program (NP 305). With increased global movement of plant material, NP 301 research conducted supporting Goal 3.1 must be coordinated with ARS research supporting Goal 3.3 to combat emerging threats and protect markets for U.S. plants and plant products. This work is conducted by ARS scientists in the ARS Plant Diseases National Program (NP 303), and Goal 3.4 (Pest and Weed Mitigation).

NP 301 researchers must also work closely with those working on Goal 1.1 – Human Nutrition, Goal 1.2 – Food Safety, and Goal 1.3 – Product Utilization to Enhance Consumer Acceptance, Food Safety, and Producer Profitability.

Research conducted in NP 301 must also be conducted in collaboration with research in Goal Area 2 – Natural Resources and Sustainable Agricultural Systems, especially Goal 2.1 – Effectively and Safely Manage Water Resources to Sustain and Increase Agricultural Production and Water Use Efficiency While Protecting the Environment and Human and Animal Health; Goal 2.2 – Improve Management of Soil Resources, Reduce Impact on Air Resources, Efficiently Use Inputs, and Contribute to Ecosystem Services; and Goal 2.3 – Improve Management Decisions and Enhance the Function and Performance of Rangelands, Pastures, Forage, and Turf Agroecosystems While Enhancing Ecosystem Service. NP 301 researchers working on Goal 3.1 must also collaborate with those working on Goal 2.4 – Integrated Solutions for Agriculture Enabling Greater Productivity, Profitability, and Natural Resource Enhancement to develop integrated solutions to solve challenges related to agricultural system productivity, profitability, energy efficiency, and natural resource stewardship.

NP 301 researchers contributing to Goal 3.1 must also collaborate with scientists in Goal 4.1 – Improve Food Animal Production Efficiency, Industry Sustainability, Animal Welfare, Product Quality, And Nutritional Value While Safeguarding Animal Genetic Resources and in Goal 4.2 – Improve Domestic Aquaculture Production Efficiency and Product Quality While Minimizing Impacts on Natural Resources.

PERFORMANCE MEASURES FOR GOALS 3.1 AND 3.2. Develop knowledge, strategies, systems, and technologies that maximize the production efficiency of our annual, perennial, nursery, orchard, and greenhouse cropping systems. Develop new technologies and tools that improve these systems to meet current and future crop production needs of diversified consumers while ensuring economic and environmental sustainability and production efficiency, health, and value of our Nation's crops.

Relationship of this National Program to the ARS Grand Challenge-Synergy Initiative

The NP 301 Action Plan will be a key contributor to the ARS Grand Challenge – to "Transform agriculture to deliver a 20% increase in quality food availability at 20% lower environmental impact by 2025." Achieving this Grand Challenge will require coordination and collaboration among NP 301 scientists across Research Units, as well as with scientists in other National Programs. This coordination may involve common objectives shared across multiple NP 301 Project Plans that will serve to solve critical problems outlined in this Action Plan and tackle the broader target goals of the ARS Grand Challenge.

Introduction

Crop plants underpin U.S. agriculture and food security. Increased crop yield, product quality, and production efficiency are required to safeguard the Nation's agricultural economy and food supply. This national program addresses the critical needs for increased crop productivity by providing crop plants with superior genetic potential, requiring continuous crop genetic improvement through more effective plant breeding. The process exploits sources of new genes and traits from the Nation's genebanks, combined with innovative breeding methods, data mining, bioinformatic tools, and incisive knowledge of crop molecular and biological processes. ARS breeders, plant genetic resource managers, plant scientists, computational biologists, programmers, and many others are engaged in this global quest to transform and accelerate the pace of innovation in plant breeding and crop production. New noteworthy additions to the 2023-2027 Action Plan include cropmicrobiome interaction analysis, genome editing for crop improvement and gene function analysis, and artificial intelligence/machine learning for field and laboratory studies.

ARS places a high priority on realizing the products and accomplishments described in this NP 301 Plant Genetic Resources, Genomics, and Genetic Improvement Action Plan 2023 – 2027. NP 301 will execute a key part of the overall USDA goals to maximize the ability of U.S. agricultural producers to prosper by feeding and clothing the world, and attain the major ARS goals to protect, expand, and enhance the crop genetic resource base of the United States; increase scientific knowledge of crop genes, genomes, biological processes and systems; and deliver economically and environmentally sound technologies that improve the production efficiency, quality, health, and value of the Nation's crops. At its core, ARS research in NP 301 will harness the genetic potential of plants and beneficial microbes to translate that potential into products that generate economic gain and consumer benefits. This national program will significantly contribute to meeting the anticipated global demands for food, feed, fiber, and renewable energy, and to meeting the USDA-ARS Grand Challenge to "Transform agriculture to deliver a 20% increase in quality food availability at 20% lower environmental impact by 2025."

Partnerships are vital to the success of the NP301 2023-2027 Action Plan. NP 301 scientists, together with university and industry cooperators, will develop and effectively apply new knowledge of crop genes, genomes, and the control and expression of genes to accelerate the rate of genetic improvement and product quality improvement through traditional and breakthrough plant breeding methods. Through innovative research tools and approaches, this National Program will generate, manage, integrate, and deliver vast amounts of raw genetic materials (genetic resources); superior cultivars; and genetic, molecular, biological, and phenotypic information to a diverse global clientele. The ultimate goals for these efforts are to improve the production efficiency, yield, sustainability, resilience, nutritional and product quality, and value of U.S. crops. This Action Plan represents a nationally-coordinated, stakeholder-driven, and outcome-oriented effort to address a diverse portfolio of customer/stakeholder needs. Targeted research focus areas are outlined under each component to address those needs.

The USDA National Plant Germplasm System, a major component of NP 301, safeguards and delivers 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. Conserved genetic resources, including crop wild relatives and critical microbial species, play a critical role in crop genetic improvement and genomic research by contributing to the long-term safety and assurance that genetic diversity exists for future needs, especially considering the threats to genetic diversity, coupled with the uncertainty of future environmental extremes, and changing climates. To ensure access to those genes for future research and breeding, NP 301 must continue to strategically acquire and conserve crop and microbial germplasm that can be exploited when needed. NP 301 must also strive to develop efficient methods for

identifying favorable traits, ensure that high quality plant and microbial germplasm are distributed where and when needed, and safeguard these collections for future generations.

The long-term plant breeding goals of NP 301 research are to develop and release improved germplasm that includes breeding and pre-breeding materials or superior cultivars for incorporation into commercial breeding programs, or directly into commercial production, as the crop species and specific commercial requirements might dictate. In many instances, trait-specific considerations will be important and will include high yields, disease and pest resistance, improved processing, and nutritional quality. NP 301 scientists will pay special attention to potential nutritional trade-offs as they consider selection for priority end-product traits such as processing and shelf life.

To attain higher crop genetic gain over the long-term, and to achieve other relatively short-term goals, breeding programs will incorporate new technologies and innovative methods to modify genomes and devise new ways to incorporate novel genetic elements to develop higher yielding crop plants with priority traits such as enhanced water and input use efficiency, and durable protection against diseases, pests, and environmental extremes. NP 301 scientists will devise and apply technologies such as biotechnology and genome editing to develop superior new cultivars and enhanced germplasm, and to accelerate the deployment of high-value traits into breeding populations. High-resolution, sequence-based genomic maps will be developed to leverage knowledge of regulatory pathways and to help identify genetic markers for enabling population enhancement and understanding the functions of desired alleles so that their effects can be more efficiently measured and influenced.

Enabled by the NP 301 research that generates new fundamental understanding of the genetic and physiological bases for plant growth and development, plant breeders will apply the leading-edge tools developed by NP 301 scientists and collaborators, such as machine learning and artificial intelligence, to devise powerful new methods to achieve sustainable yield increases despite environmental extremes and changes in climate, and to better understand the role of microbiomes in determining phenotypic expression of priority traits. Also, knowledge of how various phenotypic responses are manifested at the physiologic, biochemical, and molecular levels will generate new insights to identify and characterize the genetic control of superior traits for breeding programs. NP 301 research will develop groundbreaking tools that foster new breeding strategies for designing crop plants with optimal architecture and efficient response to numerous environmental stresses present above and below ground.

As biotechnological advances continue, NP 301 research will deliver scientific assessments and technical leadership to support the coexistence of classical and biotechnologically engineered crops. Evaluation of potential unintended consequences from biotechnology approaches, on behalf of U.S. biotechnology regulatory agencies (APHIS BRS, EPA, FDA), that focus on effects on crop plant biology, crop performance, and the environment, will be coupled with development of coexistence strategies. NP 301 scientists will devise new tools and methods to increase the accuracy of genetic engineering through precision genome editing, epigenetics, and conventional biotechnology.

NP 301 research will continue to lead the development and curation of crop genomic and phenotypic databases, and to devise ways to ensure the interoperability needed to manage complex data types, along with intuitive interfaces to enable efficient access that makes the information more widely accessible to users. Those efforts will be strengthened by this new Action Plan. NP 301 research will expand data management and exchange protocols to improve efficiency of access, analysis, and integration of data from diverse sources. NP 301 scientists will develop bioinformatic solutions supporting research and breeding for the broad range of U.S. crops, including specialty crops. Robust infrastructure and access to high-performance computing resources will support informatics, big data and image analysis, artificial intelligence/machine learning, and

cloud computing to provide value-added downstream analysis and support stewardship goals. NP 301 database curators will formulate efficient strategies to assure continued maintenance of the databases, with strengthened infrastructure for storage, computation, and data transmission. Standards will be developed for data collection and storage, and for data management processes, such as preservation and archiving.

New tools will be constructed to efficiently capture phenotypic data and to extract information, via leadingedge data-mining strategies, from the ever-increasing flow of data into databases managed by NP 301. New approaches for interconnecting databases containing diverse types of information will more efficiently and effectively identify important properties of genes and genomes and apply that knowledge to crop improvement. Furthermore, NP 301 scientists will further improve database interconnections that link the Germplasm Resource Information Network (GRIN)-Global with crop genome databases, enable users to better associate specific genes with agriculturally important traits, and build on genetic advances in one crop to speed genetic gains in others.

Mentorship is critically important to the continued success of public research as a whole, and a refreshed workforce must be constantly maintained. But to be successful, the entire research community, including ARS and universities, must participate in the training effort. Therefore, in addition to conducting research, NP 301 scientists and university cooperators will continue to mentor and train the next generation of crop breeders, geneticists, bioinformaticists, genome researchers, and genetic and genomic resource and information managers. Developing the next cohort of those scientists is particularly important, considering the projected strong demands for such personnel.

NP 301 comprises four research Components, as shown in Figure 1.

- 1. Crop Genetic Improvement
- 2. Plant and Microbial Genetic Resource and Information Management
- 3. Crop Biological and Molecular Processes
- 4. Information Resources and Tools for Crop Genetics, Genomics, and Genetic Improvement



Figure 1. The four research components interact to accomplish National Program 301 goals [2023-2027 Action Plan]. The four research components interact and interconnect to attain the overall goals of NP 301. In this interactive web, the Anticipated Products and Accomplishments for each of the NP 301 Components are often critical for the success of research conducted under other Components. However, for organizational and administrative purposes, each NP 301 research objective within a research project is usually assigned membership to only one of the four NP 301 Research Components. Overall, many individual research projects and resources contribute to the goals of multiple NP 301 Research Components, and even other National Programs.

Component 1. Crop Genetic Improvement

U.S. agriculture requires crops that are higher yielding, durably disease and pest resistant, efficient in resource use, and resilient to environmental extremes and changes in climate. Improved plant varieties are the products of innovative use of genetic resources and efficient plant breeding strategies. Strategically coordinated research programs must expand the knowledge and tools of plant breeding and develop improved germplasm to meet the challenges of supplying the United States with food, fiber, fuel, feed, and ornamentals. Effective genetic improvement of crops requires access to a broad base of well-characterized genetic resources. Plant breeding approaches that integrate the most effective new methods and technologies with time-tested techniques will accelerate progress. A solid theoretical foundation of modern principles and methods underpins effective identification and evaluation of genetic variability for key traits, choice of breeding stocks, and incorporation of traits into new cultivars. In addition, genetically and phenotypically characterized cultivated and wild germplasm, experimental populations, and breeding stock are required to understand gene function and to develop superior cultivars.

High throughput genotyping and phenotyping methods are required to analyze complex traits in diverse crop species. High-resolution genetic maps and sequenced genomes enable genetic markers to be identified and mapped and will lead to more effective genetic selection through knowledge of the genetic structure of traits with complicated modes of inheritance. Functional analysis of genes affecting traits must be conducted. New methods of genomic selection and prediction enable genomic-assisted crop breeding approaches to address genetic complexities such as epistasis, polyploidy, crossing barriers, differential heritability, and associations of genotypes with phenotypes. Application of genomic information from model plants and superior methods for the identification and introgressive hybridization of exotic alleles into adapted genetic backgrounds will improve the efficiency of plant breeding. Improved and wider application of genome editing, mutagenic screens, and other genetic modification technologies will facilitate the creation of genetic variability and stocks to test research hypotheses and accelerate cultivar improvement.

Problem Statement 1A. Trait discovery, analysis, and superior breeding methods.

ARS conducts genetic and breeding research on a wide spectrum of crops, many of which require customtailored approaches. To meet the challenges posed by climate change and population growth, crop geneticists and breeders require not only the toolbox currently available from crop genetics and breeding, but also amalgamations of current knowledge with a suite of new basic and applied tools and approaches. Methods, techniques, and knowledge gained from advances in genetic and genomic research must include improved genotyping and phenotyping approaches which, at least for specialty crops, may be enhanced by the Breeding Insight initiative over the next 5 years. These methods will reduce costs and increase throughput and scale by leveraging leading edge sequencing, sensor, and robotics technologies, leading to improved analytical capacity from novel predictive computational tools. Together, these will accelerate plant breeding and increase the specificity of breeding targets.

The best way to design superior cultivars and improved breeding populations for crops grown under extreme environments is to extensively test them in the field. The ability to analyze and ascertain how

genes ultimately determine traits in the field is limited by the national capacity to phenotype plants in the field. ARS scientists are key partners in the development of new automated field systems for measuring and analyzing phenotypes across many different crops, as well as methods for predicting and determining which combinations of genetic, environmental, and management factors should be enlisted for efficient cultivar development.

Building on these advances, ARS researchers under this Problem Statement 1A and Problem Statements 1B and 2A will exploit crop genetic resources (older varieties, landraces, crop wild relatives, elite and experimental breeding stocks, and genetic mapping populations) to identify and understand the genetic bases for key traits. They will elucidate the genetic diversity and population structure of crops and crop wild relatives to reveal their potential for crop improvement. New research populations will also be generated, including mapping populations, mutant lines, genome edited lines, and introgression populations. These materials will be characterized genetic tools and insights will lead to testable hypotheses for assessing the merits of inventive plant breeding methods that maximize rates of genetic gain, and result in genetically enhanced populations improved for valuable agricultural traits, many of which with complicated modes of inheritance. These traits will be analyzed and catalogued with unprecedented levels of detail, and the range of effects and frequencies of relevant genes will be functionally characterized in both improved and pre-breeding populations.

A thorough understanding of genome structure and genetic variation will enable more extensive trait analyses. Genetic and physical maps will be integrated, and comparative analyses of related genomes and shared genomic sequences will improve the accurate assembly of physical maps. Once advantageous alleles for specific traits are identified, genetic maps and reference genomes—highly saturated with genetic markers—will facilitate marker-assisted introgression to improve the traits. Introgression of existing variation from well characterized genetic resources and creation of new sequence variation will ensure a sufficiently deep breeding pool to reduce genetic vulnerability and enable future genetic gain from selection. To exploit this new variation most effectively, new crossing and selection schemes will be developed to recombine genomes effectively and achieve the introgression of useful alleles into new varieties.

Research Focus

Crop improvement and genetic/genomic research both require knowledge of the genetic basis for the wide range of phenotypic variation maintained in breeding stocks, landraces, crop wild relatives, and other source populations. This knowledge will be provided by sequencing and annotating plant genomes, as well as localizing and functionally characterizing genes affecting priority traits. Understanding the genetic architecture of complex traits and the function of individual genes requires a diversity of experimental populations. Existing germplasm and breeding materials can serve as primary research materials, but in many cases, they must be supplemented by new genetic stocks to enable functional genetic analysis. High throughput genotyping and efficient quantitative phenotyping technologies must be applied to analyze these populations. In addition to current germplasm resources, new genetic variation needs to be generated. Doing this will require developing and applying mutagenic techniques, biotechnology, and genome editing.

High-resolution, sequence-based genomic maps must be assembled to leverage knowledge of genetic regulatory pathways gained from model species and to identify genetic markers that enable populations to be enhanced for desired alleles. The function of these alleles must be understood so that their effects can be more efficiently measured and influenced.

Innovative high throughput, quantitative phenotyping methods are needed because trait measurement is now often the critical bottleneck to genetic analysis and breeding progress. This must entail improving efficiency, precision, and cost-effectiveness of trait analyses through automation, increased throughput, or parallelization and use of new sensors and platforms (images, radiation wavelengths, chemistries, barcoding systems, radio frequency identification, unoccupied ground and aerial vehicles, satellites, robotics, and more). Managing and extracting useful information from this data will require the application and development of new approaches including machine learning models and tools.

Phenotypic, genetic, and other "-omic level" data from large populations must be combined in a coordinated effort to predict the performance of untested genetic resources and breeding stocks. The effects of the environment and management strategies on the expression and phenotypes of each trait must be considered. To better account for these variables, new statistical, mechanistic, and machine learning methods must be developed. As research capacity and accumulated knowledge permit, genomic selection and related breeding by prediction methods must be extended and evaluated empirically for more complex genetic architectures (e.g., many interacting loci, especially in polyploids), different breeding system constraints, and a wide range of specialty and other crops, which until now lacked these genetic tools. Species such as specialty crops can now rely on the Breeding Insight initiative for the necessary capacities required to meet these needs.

Anticipated Products

- High-throughput genotyping and phenotyping approaches, such as machine learning, designed for efficiently discovering and predicting the function of genes governing important traits in diverse crops.
- Well-characterized genetic mapping populations, mutant lines, other germplasm, and associated molecular markers designed for trait discovery, analysis, and breeding diverse crops.
- Priority genomes sequenced, and genes functionally characterized.
- New variation in agriculturally important traits discovered and/or created through mutagenesis, biotechnology, genome editing, and/or other means.
- Pipelines for accelerated trait discovery through functional genomic analysis and for gene identification via genetic mapping.
- Improved plant breeding techniques that apply knowledge from genetic interaction with environment and management factors and interactions with economically important pests of crops.
- New or improved methods to recombine genomes and introgress alleles and novel diversity more rapidly.
- Improved methods for discovering useful nutritional, post-harvest and climate adaptation traits and translating them into breeder-friendly breeding stocks.

Potential Benefits

- New tools, methods, and approaches for attaining crop breeding goals more rapidly and costeffectively.
- More efficient and effective genotyping and phenotyping methods, superior functional genetic analyses, and the capacity to combine disparate large data sets to accelerate gene discovery and translate that knowledge into cost-effective breeding tools.
- More comprehensive characterization of genetic stocks and other crop genetic resources to enable their judicious incorporation into cultivar improvement and gene discovery programs.

- Improved application of genome editing, mutagenic screens, and other genetic modification technologies to facilitate the creation of genetic variability and stocks to test hypotheses and accelerate cultivar improvement.
- Improved nutritional quality of food crops and capacity to identify additional variation for nutrition.

Problem Statement 1B. Develop new crops, cultivars, and germplasm with improved traits.

U.S. agriculture requires new crops, new cultivars, and adapted germplasm with improved traits that provide food security for a growing population, remain productive amidst rapid climate change, meet shifting consumer demands, and enhance sustainability and efficiency, thereby protecting consumer health, agricultural jobs, and the environment. The traits needed for new cultivars, crops, and improved genetic resources include higher and sustainable yields; resistance or tolerance to biotic and abiotic stresses; resilience to environmental extremes; improved agronomic or horticultural characteristics; and superior processing, nutritional, and product quality properties. Researchers in Problem Statement 1B must work in tandem with those in Problem Statement 1A to effectively apply new traits and superior breeding methods. Well-characterized genotypes, aided by the work accomplished in Problem Statement 1A and Breeding Insight, will also provide breeders seamless access to materials needed for improving priority traits. Additionally, breeders will utilize the efficient breeding strategies crafted in partnership with Problem Statement 1A to efficiently make use of available diversity, especially with landraces and crop wild relatives, to develop new crop plants. New technologies, such as high-throughput genotyping and phenotyping, are required to enhance traditional methods of genetic improvement and breeding for a broad spectrum of major, specialty, and new crops, including crops for alternative production systems that reduce their environmental impact. Genotyping and phenotyping germplasm and breeding lines for biotic resistance and abiotic tolerance traits will continue in breeding programs, but increased collaboration with scientists in Component 1A is needed for implementation of higher throughput technologies to improve traits underlying consumer quality and nutrition to balance the needs of the industry and the consumer more adequately.

Although the past accomplishments of this National Program in breeding are widely recognized, more effective breeding methods to mine genetic resource collections for novel traits, developed in Component 1A, will allow breeders to take advantage of recent rapid advances in technology to make breeding more efficient. Also, high-throughput genotyping and phenotyping technologies should be adopted to enhance breeding efforts. Improved cultivars must be adapted to a wide variety of cropping systems, and to the rapid changes of global consumer demands. The increased need for improved germplasm will require breeders to apply novel genotyping, phenotyping, and analytical approaches that rely on accurate genetic and physical maps from work in Component 1A, to facilitate superior selection methods. Faced with a shrinking supply of land, labor, water, and inputs, new cultivars and new crops developed by Component 1B scientists must have improved plant architectures, improved resource-use efficiencies, and optimal production and harvest efficiencies. New crops, such as hemp, are needed to meet the needs for bioenergy and bio-based products, while current crops, such as cotton and guayule, must be bred for new uses and to meet changing global market demands. In addition, a more concerted effort is needed during the next 5 years to breed crops adapted to biotic and abiotic stresses and other environmental extremes.

Research Focus

Improved, well-characterized, and genetically diverse germplasm, breeding lines, and cultivars are needed to produce crops that yield abundantly and reliably with value added traits that are productive in a changing environment and agricultural production systems. More effective methods to mine germplasm collections for important traits are needed, such as adoption of high-throughput genotyping and phenotyping technologies. New cultivars must exhibit more durable resistance and

tolerance to multiple diseases and stresses. Cultivars are needed that are more efficient in their use of water and fertilizers. Cultivars with modified architectures are needed to maximize production efficiency and quality. Seeds and other propagules of new cultivars must produce a uniform plant stand with adequate vigor under commercial production systems.

U.S. producers and consumers need improved crop product quality, such as more flavorful and attractive fruits, vegetables, and ornamentals, more nutritious food and feed crops, prolonged product storage life and quality, and reduced energy requirements for production and processing. New crops and crop plants with new traits are needed for new uses and new production systems, including protected environments such as greenhouses and tunnel systems, organic systems, small farms, home gardens, and cityscapes. Non-food crops capable of growth on underutilized agricultural lands must be bred as feedstocks for bioenergy production. There is a need to improve yield and product quality of crops with bio-based products, such as for bioenergy applications. Crop plants are needed that incorporate new value-added traits that improve end-use quality and broaden product utilization.

Anticipated Products

- Sustainable, higher yielding crop plants with stable performance across a wide range of environments.
- Crop plants with tolerance to biotic and abiotic stresses, including resilience to climate or environmental extremes.
- Crop plants with enhanced nutritional or product quality to address the needs of producers, processors, and consumers.
- Crops with traits that maintain postharvest quality and reduce losses.
- Crop plants with traits optimized for production and harvesting efficiency, including plant architecture.
- Crop plants with improved traits (e.g., fiber, protein, oil, or biomass) for novel products or production technologies, such as bioenergy and plant-based protein.
- Crops that reduce environmental impact by sequestering carbon, promoting soil health and the microbiome, or supporting biodiversity.
- Enhanced germplasm that broadens genetic diversity by incorporating superior traits from wild relatives, landraces, and underutilized species.

Potential Benefits

- Supplies of safe, plentiful, high-quality food, feed, fiber, fuel, and ornamental products with price stability and affordability that enable a stronger, more secure agricultural economy.
- Crops with higher profit margins for growers to help stabilize rural economies, promote the efficient use of arable lands, and increase farm-gate value.
- Reduced use of pesticide and fewer negative environmental impacts.
- Improved competitiveness of U.S. agriculture in both conventional and organic farming sectors.
- Expanded markets for reduced pesticide or pesticide-free agricultural products.
- Reduction in pre- and postharvest losses and lower production costs.
- Reduced risk of catastrophic losses for growers, and improved food security.
- Enhanced economic viability of both small producers and large-scale commercial production agriculture.
- Improved product quality and nutrition leading to reduced food waste and improved human health.
- Increased demand for high-quality U.S. crop products in a global market.

- New opportunities for producers to use crops and non-food crops adapted to marginal environments.
- Bioenergy crops that ensure agricultural price stability, foster U.S. energy independence, and reduce environmental degradation and the carbon footprint associated with fossil fuel production and use.
- New crops that provide alternative markets for farmers and a variety of novel products for domestic and international consumers.
- Increase in quality and quantity of fresh produce to urban customers from cultivars suitable to novel production technologies.

Component 2. Plant and microbial genetic resource and information management

Continued strong increases in agricultural productivity are needed to meet the growing demands for agricultural products and for future food security of the world's expanding population. One way to meet the challenge of improving crop output and nutrition is to leverage the inherent genetic diversity conserved in both plant and microbial genetic resource collections. Access to and utilization of genetic resources in these collections continues to provide sources of traits and/or aid in scientific inventions that improve yields, nutrition, abiotic stress resistance, and resilience to environmental extremes in agricultural production systems. Large and genetically diverse plant and microbial collections are managed by dedicated NP 301 personnel in genebanks and other service and research facilities. These comprehensive collections represent crop plant species and many of their wild relatives, as well as important microorganisms (e.g., bacteria, fungi, and oomycetes) that have significant positive and negative impacts on crop production. Managing these extensive collections involves the development of innovative, effective, and efficient tools for long-term preservation, characterization, evaluation, distribution, and facilitated use. Priorities continue to be the long-term preservation of these collections in modern, secure genebank facilities while maintaining genetic integrity of the collections and their associated information.

Significant numbers of samples are distributed annually from both the plant and microbial collections, demonstrating their value and impact to the U.S. and world crop production, agricultural research, and educational communities. Added value could be gained and collections used more extensively if detailed characterization and evaluation data were gathered and associated with collections. As novel genotyping and phenotyping approaches are developed, adopting them to describing collections would aid genetic resource management. This additional information associated with collections could provide stakeholders with knowledge for choosing optimal genetic resources for their needs and for refining and targeting requests for genetic resources. Although current plant and microbial genetic resource holdings are comprehensive, and opportunities for expansion are limited, genetic resource acquisitions should proceed strategically. Additions would target filling gaps in collection coverage, focusing on crop wild relatives or vulnerable plant and microbial collections. Significant stakeholder priorities such as new agricultural uses, adaptation and resilience to climate change, nutritional traits, and biotic and abiotic stressors will influence acquisition decisions. As collections have expanded, so has the information associated with these genetic resources. Data systems and software must be developed or continually optimized to effectively manage collections and provide public access to information. GRIN-Global is a frequently accessed, advanced information management system developed by the NPGS and international collaborators to specifically manage genetic resource information. Similar platforms are required for managing information associated with microbial collections.

Current and future service and research objectives are addressed by this Component through extensive collaborations. Genetic resource managers rely on longstanding and new partnerships, across ARS programs, with academic institutions (e.g., land-grant universities), and non-profit and private organizations. These

collaborations stimulate innovations and exchange of ideas and information for devising superior genebank management approaches, acquisitions, characterizations, evaluations, and training. Specialized skills and knowledge are required to manage these agriculturally diverse plant and microbial collections and should incorporate expertise from diverse biological disciplines. Therefore, the development of training resources and instruction of the next generation of genetic resource managers will be vital, especially during the current and forecast trend of retirements and new hires.

Problem Statement 2A. Plant genetic resource and information management.

The National Plant Germplasm System (NPGS), within NP 301, provides plant genetic resources, associated information, research technologies, and knowledge that contribute to achieving crops with higher yields, increased nutritional quality, new uses, abiotic and biotic stress resistance, and tolerance to environmental extremes, thereby contributing to resilient food and agricultural production systems. The NPGS maintains one of the most comprehensive plant genetic resource collections in the world with more than 600,000 accessions representing more than 13,000 agriculturally important plant species. It is a priority for NP 301 to ensure that these *ex situ* plant genebank collections have high levels of genetic integrity, health, and viability and are maintained in secure modern facilities. The positive impacts of the NPGS are demonstrated in part through the distribution to stakeholders of an average of 250,000 plant samples per year.

Plant genetic resource management teams are challenged with not only meeting the needs of current customers and stakeholders, but also anticipating the genetic resource needs of the future. This requires creativity and foresight to maintain and further develop plant collections to strategically include crop wild relatives, landraces, and cultivars of historical importance. Strengthening stakeholder relationships will ensure that plant genetic resource characterization and evaluation facilitate efficient acquisition, curation, and identification of optimal germplasm for research, education, and breeding. National and international collaborations are essential for successful genebank management and distribution, conducting significant research and strengthening collections according to the standards of access and benefit sharing established by both domestic legislation and international agreements. Future agricultural advances depend on maintaining and strengthening open and free data access. Information associated with NPGS collections is stored, curated, and made publicly available via GRIN-Global, an advanced information management system that is accessed by 200,000+ users annually. GRIN-Global will become even more valuable as interoperability develops with other public databases that maintain additional environmental, geospatial, pedigree, phenotypic, and genomic information.

Research Focus

Agricultural systems throughout the world have many needs for NP 301's plant genetic resources and associated information. High quality plant genetic resources must be actively maintained and safeguarded in state-of-the-art genebanks. Plant genetic resource management includes germplasm acquisition, maintenance, documentation, distribution, characterization (descriptors, genotyping), and evaluation (phenotyping) over an extended timeframe. As leaders in the field of genetic resource management, the NPGS must work to meet and inform international standards (e.g., FAO Genebank Standards for Plant Genetic Resources for Food and Agriculture). Substantial research is needed to devise more effective methods for regeneration, particularly for crop wild relatives. Best management practices for NPGS collections must be developed, updated, or improved, and applied to ensure the efficient, effective, long-term, and safe preservation of plant genetic resources.

Plant genetic resource conservation standards require safety duplications of plant genebank collections. In the NPGS, these back-up collections are maintained as seeds, embryos, vegetative propagules, or pollen at the National Laboratory for Genetic Resources Preservation (NLGRP) in Fort

Collins, Colorado. Research is needed to identify widely applicable methods to ensure long-term, high quality collection back-up samples chosen according to the optimal conservation targets for each crop. Necessary research includes the development of tissue culture and cryopreservation technologies to ensure that regenerable plants can be successfully retrieved from long-term storage. In addition, seed testing programs require non- or minimally invasive methods with optimized testing intervals to ensure sample genetic integrity is maintained during storage. Collaborations among other NPGS genebanks and NLGRP will develop preservation priorities and implement processes based on feasibility, vulnerability, and resources available.

Technologies to efficiently genotype numerous accessions or entire crop genetic resource collections are becoming increasingly available and cost-effective. Genebanks could leverage the data generated by those genotyping methods to inform plant genetic resource management by measuring diversity within crops, identifying gaps, ensuring identity preservation, and unambiguously identifying duplicated/redundant accessions. Research conducted by NPGS researchers, collaborators, and through other NP 301 Research Components is needed to develop new reference genomes sequences for some curated species to identify informative single nucleotide polymorphisms (SNPs) from resequencing technologies, and to effectively employ genomic data to manage the genetic diversity within each collection. Collaborations between curators and stakeholders, especially Crop Germplasm Committees (CGC) and Breeding Insight, will ensure that the reference genome sequences and genomic profiles can be exploited by genebank customers.

Phenotypic data collection must balance the critical needs of stakeholders and the challenges of acquiring high quality, useful information appropriate for the improvement status of accessions (e.g., wild vs. cultivar). Digital documentation of seed, plant, and propagules is an important first step. Collaborations are critical to ensure data meet current (and future) stakeholder priorities including resilience to climate change, nutritional traits such as protein quantity and quality, and resistance to biotic stress and abiotic stress tolerance. To this end, phenotypic evaluations might need to be conducted across multiple environments and management approaches, following published procedures. Use of high-throughput phenotyping should be conducted where efficiency gains can be realized, and where resources and expertise permit. Collaborations with other ARS National Programs, as well as collaborations with external groups such as Breeding Insight, public universities, and other stakeholders, will be at the forefront of the adoption of such methods by NPGS sites.

Because the capacities for plant genetic resource management are limited, it is imperative to balance the strategic expansion and rationalizing of the germplasm collections. NPGS scientists need to consider stakeholder needs, taxonomy, geospatial distribution, as well as genotypic and phenotypic assessments to identify gaps and redundancies in germplasm collections and efficiently prioritize accessions for inactivation, regeneration, and maintenance. Best management practices need to be developed with university partners and other stakeholders for potential acquisition and subsequent maintenance of valuable mapping populations, genetic stocks, and their associated information.

The NPGS must continue to supply genetic resources to domestic and international scientific and educational communities according to national policies and international obligations. Plant genetic resources must be high quality, healthy, viable, true-to-type, well-documented, and distributed to customers in a timely manner. To maintain genetic integrity within seed crop collections, research is needed to appropriately scale routine viability, germination, or longevity testing protocols to identify when genetic resources deteriorate below predefined critical thresholds. Further research is also required to develop and adapt interventions for crop/pathogen complexes, including pathogen cleanup, found in potentially contaminated germplasm to support global germplasm exchange.

Detailed best management practices will need to be followed for managing accessions of crops with deregulated genetically engineered traits to prevent adventitious presence and regulatory barriers to distributions. NPGS must continue to cultivate strong relationships with international regulatory, import, and export agencies to coordinate phytosanitary exchanges of crop genetic resources.

The GRIN-Global information system must continue to improve access and delivery of passport, phenotypic, and genotypic data to customers and stakeholders. It will require improvements to ensure user-friendly interfaces to support genebank management and efficient distribution of plant materials and associated information. Standard practices will facilitate the development of interoperability with environmental, geospatial, pedigree, phenotypic, and genomic databases. Capacities to request and incorporate data from genebank customers (e.g., accession performance reports, results from external evaluations) need to be developed and implemented.

Genetic resource management capabilities must be strengthened by continuing to develop collaborations with domestic and international partners in private, non-profit, and academic settings. These partnerships expand the capacity of NPGS by supporting regeneration, characterization, evaluation, pre-breeding and crop improvement, and germplasm exchange activities. Often these collaborations are formed through the close relationship between NPGS locations and land-grant universities, and existing stakeholder collaboration structures such as the Crop Germplasm Committees (CGC)s and the Regional Technical Advisory Committees. CGCs communicate knowledge from experts in crop communities, and plant genetic resource managers must actively seek the involvement of CGCs when developing and updating Crop Vulnerability Statements and other management tools to ensure collections continue to be valued and effectively used by customers. Ongoing and new collaborations with land management agencies and public gardens will support the collection and conservation of North American crop wild relatives. International collaborations foster exchange of material and assist in the development of management tools that can be deployed in developing countries. National and international research, breeding, and educational partnerships must be strengthened to promote the long-term technology transfer, innovation, and conservation of germplasm.

NPGS collections are irreplaceable resources, and highly skilled personnel are needed to ensure that genetic integrity and quality of collections are maintained, particularly during retirement/new-hire transitions. In addition, the science of genetic resource management is increasingly complex, integrating disciplines that include agronomy/horticulture, genetics/genomics, physiology, policy/regulations, pathology, and plant breeding. Widely available online training materials are needed to provide critical information to current and future generations of those who manage and use plant genebank collections in national and international programs. Freely available training resources can be incorporated into on-the-job and university courses, which will expand the diversity and quality of future applicant pools.

Anticipated Products

- High-quality plant genetic resources and associated information safeguarded in state-of-the-art genebanks and information management systems.
- Research conducted to develop more efficient and effective genetic resource regeneration, documentation, and information management approaches and practices.
- Gaps in genetic resource collections identified, and priority genetic resources (especially crop wild relatives) acquired to fill those gaps or safeguarded in reserves where possible.

- Plant genetic resource genotypic characterizations and key phenotypic evaluations conducted with established and innovative approaches, and resulting data incorporated into information management systems.
- High quality genetic resources and associated information delivered to customers.
- Plant genetic resource, information management, and training capacities strengthened through partnerships.

Potential Benefits

- Continued and improved access to collections of high-quality, well-documented, and diverse plant genetic resources with excellent vigor, viability, and health.
- Collections will be secured through safety duplication and back-up within the NPGS, international collaborations, and, where possible, in situ reserves.
- Improved efficiencies will be achieved as new genetic resource management approaches and best management practices are updated, developed, and implemented.
- Collections will be strategically expanded through explorations and exchanges to fill gaps. As appropriate, duplicate and nonviable accessions in crop collections will be identified and inactivated.
- Crop Vulnerability Statements and other collection assessments will ensure that the NPGS continues to safeguard critical genetic resources and meet the needs of customers as resources allow.
- Strengthened partnerships with national and international organizations will enhance the ability of NPGS to effectively carry out its mission.
- Expanded and standardized genotypic and phenotypic diversity data will facilitate comparisons within and among crops and provide information for priority agricultural traits (nutrition, climate adaptation) to researchers, breeders, and producers.
- Expanded interoperability of GRIN-Global with external public databases will broaden its utility and allow curators to make increasingly tailored recommendations to customers.
- Collaborative phenotyping and regeneration networks between public and private cooperators will be developed to expand capacity in attaining the NPGS mission.
- Educational resources will provide training opportunities to current and next generation genebank managers and staff.

Problem Statement 2B. Microbial genetic resource and information management.

National Program 301 is responsible for conserving and actively managing more than 100,000 unique living cultures and one million preserved specimens of beneficial or pathogenic microbes that are important to crop production, industrial processes, food safety, and human health. Scientists throughout the world rely upon NP 301's microbial collections and associated information for research in fields such as plant pathology, agronomy, microbial genomics, taxonomy, systematics, diagnostics, and bioprocessing. Each year, more than 5,000 of these bacterial and fungal strains are distributed across the United States and worldwide to numerous research and education institutions, private companies, and non-profit organizations.

Research and Service Focus

Microbial collections play a critical role in supporting research and product development at ARS and other institutions throughout the world. However, active and ongoing management and curation efforts are required to ensure the continued health, genetic integrity, and viability of these biological resources. Microbial collections require specialized controlled environment storage and laboratory facilities that support activities such as culturing, viability testing, and phenotypic characterizations

and genotypic evaluations. Facilities containing pathogenic microorganisms operate under strict containment and biohazard handling protocols and must comply with local and federal regulations to ensure these organisms are handled safely and are not inadvertently released into the environment. Routine inspections are essential to ensure that collection materials are properly preserved and not subject to deterioration. Collections must be backed up at a second geographically-separate facility to safeguard against loss due to unpredictable catastrophes (e.g., natural- or human-caused).

The growth of microbial collections often outpaces budgets and available space. Priorities for new acquisitions and management of existing collections should focus on maintaining genetic integrity and limiting genetic drift and/or mutation of microbial strains by implementing strategies that limit the time between and number of regeneration events. Research and threatened microbial collections with rare or important strains that are held by academic researchers will be given extra consideration for strategic addition and conservation of ARS collections. The collections must also be able to accommodate a breadth of eukaryotic and prokaryotic diversity that spans multiple biological kingdoms that vary in their ability to be preserved with standard methods. This requires microbial genetic resource managers to conduct research and partner with user groups to identify and develop efficient and effective methods to conserve diverse genetic resources.

DNA sequencing and genotyping technologies have led to major reorganizations and advancements in bacterial and fungal taxonomy in the last 20 years. Notably, many of the resources housed in NP 301 microbial collections were deposited prior to the advent of DNA sequence-based identification and taxonomy. Distribution of microbial strains with accurate and current taxonomic identification is paramount to the user community. Genotyping of strains for which these data do not exist should be a focus. Microbial genetic resources should be characterized by the most cost-effective technologies and include taxonomic information from DNA barcodes where management capacities permit. In addition, stakeholders accessing this information could apply it to refine and target requests for the most taxonomically and functionally relevant genetic resources. Characterization of these resources can be further strengthened by prioritized descriptor and standardized trait/ontology lists for both genotypic and phenotypic evaluation and use of uniform methods for genotypic characterization where applicable. Cross-referencing ARS culture databases with core external databases such as those maintained by NCBI would enable access to genetic data in an interface familiar to researchers without requiring the development of additional bioinformatic infrastructure.

Close interactions with stakeholders will ensure that the characterization of genetic resources generate data that enable effective acquisition and use of microbial culture collection materials. The process of genetically and phenotypically characterizing culture collections can also be incorporated into microbial genetic resource management decisions regarding increased collection genetic diversity, reduced redundancy, and identification of isolates better adapted to survival under abiotic or biotic threats associated with climate change.

Anticipated Products and Accomplishments

- Microbial genetic resources, comprising both living and preserved reference collections, safeguarded.
- Innovative, efficient, and effective tools and approaches developed to conserve, classify, and characterize microbial genetic resources.
- New sources of microbial genetic resources strategically identified, including vulnerable collections, and when possible, acquired and preserved in genebanks or reference collections.
- Genotypic characterization and phenotypic evaluation of key microbial collections.

- Passport information, digital images, and characterization data associated with microbial collections made available in integrated, public data management systems.
- High quality microbial genetic resources and associated information delivered to customers.
- Microbial genetic resource and information management capacities strengthened through partnerships.

Potential benefits

- High quality, well documented collections of agriculturally important microbial genetic resources and reference materials will be readily accessible to customers and stakeholders.
- Valuable microbial genetic resources will be preserved and safeguarded through off-site back-ups of collections.
- Collection management practices will be improved and standardized by implementing novel, effective tools and practices developed to conserve, classify, and characterize microbial genetic resources.
- Expanded characterization data, accurate nomenclature, and taxonomic literature resources will support priority research and development needs of scientists, breeders, and producers.
- Strengthened partnerships with national and international institutions and organizations will enhance the impact and contributions of microbial collections.

Component 3. Crop Biological and Molecular Processes

Fundamental research, often long-term and high-risk, generates the knowledge base to drive scientific advances that ultimately improve crop productivity and sustainable production, nutrient and water use efficiency, pest and disease resistance, product quality, and adaptation to and mitigation of climate change. Research conducted in this component elucidates key genetic, biochemical, physiological, biotic, and abiotic processes underlying crop productivity and quality, and additionally develops plant genetic engineering and gene editing solutions along with associated risk assessment and potential environmental impact. This component emphasizes understanding the function of genes and gene networks in both model and crop species to devise biotechnology-based strategies and systems biology approaches to manipulate plant gene expression and function. Research will also examine the potential environmental impact of such genetic manipulations.

Modern biological tools offer new avenues for genetically improving plants by exploiting existing variability in plant properties and by creating new variability when warranted. Increased understanding of plant biological mechanisms and knowledge of how they can be precisely modified will lead to new and more effective approaches to crop breeding and enable more rapid response times for deploying genetic solutions to address emerging threats. As the biological mechanisms that link molecular and genetic properties to phenotype are increasingly understood, the rate of genetic gain for crop breeding will be accelerated, its potential risks will be reduced, and its efficiency enhanced.

Translating research at the molecular level into information that can solve agricultural problems demands an integrated approach that exploits knowledge of how variability in crop traits stem from changes in gene expression and activity of gene networks. This approach must provide the means to coordinate and integrate fundamental investigations with more applied methods to develop focused research strategies for solving crop-specific problems. Specific areas for research emphasis include understanding how plants interact with the abiotic and biotic environments, at the phenotypic, molecular, whole genome, and systems levels; the control of plant growth and development at the genetic and epigenetic levels; the control of plant metabolism

and biochemical pathways influencing nutrition and quality of crop plants; improving crop resilience to environmental change; and mitigating climate change through agricultural system manipulation.

Crop genetic manipulation through genetic engineering and gene editing constitutes a major emphasis for ARS' fundamental plant research. It includes not only discovery research, but also improving biotechnology by developing superior new public domain genetic tools that enhance the efficiency of genetic engineering, gene editing and conventional plant breeding as well as assess potential unintended impacts of genetically engineered/gene edited crops on agricultural production and the environment.

Problem Statement 3A. Fundamental knowledge of plant biological and molecular processes.

Crop plants provide the fundamental agricultural products of food, feed, fiber, fuel, ornamentals, and carbon sinks, as well as metabolites that are beneficial to health, nutrition, flavor, and industrial applications. Agricultural production must continue to increase to meet the demands of an ever-growing global human population with reduced land, water, and nutrient inputs in order to be sustainable. Disease, pests, climate variability and additional abiotic stresses will further constrain agricultural production. Traditional plant breeding approaches alone will be insufficient to meet these challenges. Understanding the fundamental molecular, physiological, and genetic bases of agronomic and horticultural performance must be improved for effective application of biotechnology to crop improvement, and optimal effectiveness of marker-assisted and whole genome-based selection strategies.

To be successful, crop plants must efficiently convert light, water, and nutrients into high-quality and highvalue organs and tissues in the context of reduced amounts of those preceding inputs. Plant architecture, development and biochemistry must be optimal for crops to thrive in a specific environment. At the same time, crop plants continually sense and actively respond to numerous and varied environmental cues. These include changes in light and air quality, temperature, nutrient and water availability, and the presence or colonization of beneficial and pathogenic microbes above and below ground. The effectiveness of plant responses to challenges varies greatly throughout development, among cultivars, and across geographical regions. The capacity to improve valuable traits is limited by gaps in understanding of the fundamental underlying molecular and physiological mechanisms regulating plant metabolism, growth, development, and environmental responses.

To meet the needs of consumers and producers, ARS research will exploit the genetic diversity in plant and microbial genetic resource collections to identify new beneficial traits, and the underlying genes and gene networks that govern those traits, to produce crops with improved performance across diverse environments. This will require highly coordinated and integrated research in the field, laboratory, and across cyber infrastructure. ARS research will apply expertise in plant phenotyping, genetics, genomics, proteomics, metabolomics, epigenetics, metagenomics, and bioinformatics to identify the basic mechanisms regulating the phenotypes of agriculturally important traits. Improving our understanding of these processes will enable NP 301 to breed crops with improved productivity, quality, resilience, and sustainability more effectively.

Research Focus

To better understand the molecular, genetic, and physiological processes underpinning important crop traits, the capacity to characterize and measure complex plant traits and collect, share, compare, and store data describing the attributes of diverse crop species must be expanded. Technologies such as gene-editing, next-generation sequencing, and a suite of whole genome-based techniques must be applied according to rigorous scientific principles to generate comprehensive datasets for crop genetic diversity, gene expression and regulation, proteins, and metabolites that enable systems-level comparisons both within and across crop species. Molecular, biochemical, and physiological

phenotypes must be linked with genetic variation within and across crop and model plant species to enable the dissection and identification of the genetic determinants underlying traits with complex modes of inheritance that are priorities for crop breeding. These approaches must generate new tools to test gene function and develop new algorithms and computational methods for data analysis, integration, sharing, and utilization.

A more complete and detailed understanding of plant growth and developmental regulatory processes affecting agricultural product quantity, quality, postharvest shelf life, and processing characteristics is necessary for enhancing plant breeding and biotechnology-based solutions to maintain and increase crop productivity while reducing waste products. To adapt crops successfully to a changing climate, the genes and networks underlying resistance or tolerance to biotic and abiotic stress must be identified. The molecular mechanisms for plant resilience and ability to mitigate stress must be elucidated. Genetic networks must be explored and exploited across the diversity present within our germplasm collections and other sources through focused expansion of said collections. The potential for both identification of superior alleles and targeted gene modification must be assessed for its role in altering the fundamental biological processes underlying improved crop productivity, superior quality, enhanced resource use efficiency, and adaptation to environmental change.

In addition, developing a broader understanding of plant-microbiome synergy and its contribution to crop health will be key for meeting future yield demands in an agriculturally sustainable manner. This understanding must include plant-microbiome interactions and multi-species interactions within microbiomes; characterization of the role of microorganisms in modulating host crop fitness at the molecular, biochemical, and physiological level; and a refined knowledge of the environmental and host-mediated factors that influence microbial community recruitment and development.

Anticipated Products

- Enhanced knowledge of crop plant interactions with abiotic and biotic environmental factors at the molecular, whole genome, and systems levels.
- Comprehensive knowledge at the genetic, molecular, and physiological levels of how plant microbiomes positively and negatively influence crop performance and utility.
- Expanded knowledge of how growth and development of crop plants are controlled at the genetic, molecular, and physiological levels.
- Increased understanding of the biochemical pathways and metabolic processes that underpin crop traits and improvement.
- Enhanced biological understanding of agricultural adaptation to and mitigation of climate change.
- Enhanced knowledge of food (seed, fruit, tubers, etc.) quality, nutritional value, as well as storage and processing characteristics at the genetic, molecular, and physiological levels.
- New tools for applying fundamental genetic and biological knowledge to crop improvement.

Potential Benefits

- Increased knowledge of the molecular mechanisms underlying crop adaptation and plantenvironment interactions will lead to breeding new cultivars with greater productivity in unfavorable growth environments and improve the resilience of agriculture to a changing climate.
- Understanding the complex regulation of plant growth and metabolism will enable scientists to improve crops for increased carbon sequestration and optimized synthesis of value-added products.

- More effective breeding for pest and pathogen resistance will result from identifying and characterizing new sources of resistance integrated with a thorough understanding of how host-plant resistance functions at the molecular, cellular, and whole plant levels.
- Knowledge of the plant microbiome will improve crop productivity and tolerance of environmental stress through identification of beneficial microorganisms with the ability to increase nutrient availability, improve defense responses, compete with pathogenic microbes, and modulate crop growth and development.
- Knowledge of the mechanisms controlling both plant architecture above and below ground will enable development of crop cultivars more amenable to mechanical production and harvest.
- Understanding the molecular mechanisms controlling key developmental transitions in plants will enable selection of genotypes for optimal timing of seedling emergence, flowering, pollination, seed, and fruit maturation.
- Knowledge of plant metabolism combined with understanding of plant growth and developmental processes will enable selection of genotypes with optimal biochemical pathways for producing valuable plant-based chemical products, improved nutritional profiles, enhanced stress tolerance, and superior yield.

Problem Statement 3B. Crop biotechnology development, implementation, and evaluation.

Crop biotechnology offers tremendous promise for improving crops by increasing product quality and sustainability and reducing the environmental footprint of production systems. The products derived from these technologies include foods with improved quality and nutritional properties; crop plants with enhanced abiotic stress tolerance, disease, and pest resistance; plants with improved agronomic traits; and tools for accelerated precision crop breeding. Research that integrates the improvements in biotechnological methods and the knowledge of potential effects on agricultural production and the environment can enable these technologies to be applied successfully. Although genetic engineering and gene editing approaches have been successfully applied to numerous crop species, relatively few crops have an easy and efficient means of implementing biotechnology-based genetic improvements, making this a bottleneck restricting research progress as well as agricultural deployment. Thus, additional techniques are required for broadly and efficiently applying these technologies to a wide range of crops and elite cultivars. Crop genetic engineering includes the production of plants with precise genome edits and the addition of gene sequences from diverse sources to create novel genomes. It is best implemented with the precise introduction of only the sequences of interest and when the expression of the introduced traits occurs only in the desired tissue and when they are needed/desired. Currently, the capability to accomplish these tasks is quite limited.

Although biotechnology offers great promise for crop improvement, a careful evaluation of the intended and potential unintended consequences of these products is necessary to facilitate the coexistence of conventional and biotech crops in global agriculture. In addition, this research will provide critical support to regulatory agencies charged with ensuring the safe utilization of biotech crops and the new technologies under development. The intersection of genetic engineering, genomics, and plant breeding approaches has yielded, and will continue to yield, novel technologies for modifying plant genomes and genetically improving crops. Research is required to provide a technical foundation for addressing the potential concerns about the impacts of crop genetic engineering and for removing barriers to coexistence of different crop production systems.

Research Focus

New techniques and approaches are needed for biotechnological improvement of crop plants and evaluation and mitigation of potential unintended consequences of these improvements to crop plant

performance, agricultural production systems, and the environment. Such approaches include methods and molecular tools for the precise genetic modification of crops to enable increased specificity and limit off-target effects, for post-transformation removal of unnecessary DNA sequences, and for the characterization of off-target modifications. Techniques are needed to accelerate the breeding process and enable "pyramiding" of multiple transgenes and/or gene edits to incorporate multigenic traits. Methods that take advantage of epigenetic gene control may lead to more reliable control of gene expression. Also, improved biotechnology methods with broader applications are needed to benefit a wider array of crop species, both of major commodities as well as specialty crops.

It is important to emphasize that, although genetic engineering technologies revolutionized the production of a few crops, the lack of specific enabling technologies slowed or prevented its application to most crops, particularly within elite crop germplasm. New and innovative approaches must be developed for the biotechnological improvement of diverse crop species and cultivars. These genetic improvement tools include improved transformation procedures, tissue culture, and culture-free methods to enable routine, rapid and efficient deployment of biotechnology in improved cultivars. As more crops become genetically engineered, associated methods must be refined to evaluate their potential consequences and to meet regulatory requirements.

Anticipated Products

- Improved and new public domain tools for producing genome edited and/or genetically engineered crops.
- Improved methods for the application of genome editing and biotechnology to a broader selection of crop species/cultivars.
- Genetic engineering technologies that improve the efficiency of conventional crop breeding.
- Assessment of the impacts of biotechnology.

Potential Benefits

- Improved public domain biotechnological tools and strategies for generating and characterizing genetically engineered and gene edited crops will help keep pace with increased consumer demand for higher quality and more nutritious food and better response to emerging threats to crop production including new diseases and climate change.
- Efficient utilization of these technologies in a wider array of crop species and cultivars will advance research as well as enable the more rapid deployment of genetically- engineered cultivars.
- More precise biotechnological improvements will help protect the environment, facilitate the coexistence of agricultural markets, and promote science-based regulation of crop cultivars produced with biotechnology.
- Integration of genetic engineering, gene editing, molecular breeding, and crop biological knowledge.
- Novel research tools that accelerate breeding and germplasm enhancement of long generation cycle crops (such as woody tree species) as well as technologies to develop crops better suited for novel growing systems such as indoor and urban farming and off-planet agriculture.

In total, these efforts will enhance the capacity to generate and deliver crops that can address the needs of U.S. and global agricultural production, including improving crop resilience to environmental change, nutritional value, and introduction of new/emerging crop plants.

Component 4. Information resources and tools for crop genetics, genomics, and genetic improvement

The discovery of knowledge which could have broad impacts for reducing food insecurity and crop vulnerability increasingly relies on access to well-curated data delivered through the versatile and multifaceted informatics services upon which the researchers in the other components, such as Component 1, rely. Cyberinfrastructure; data stewardship; outreach efforts; and resources to manage breeding, genetics, and genomics data are needed to strengthen breeding and genetic enhancement efforts, annotate gene function, and translate those findings into products that increase crop quality and production. In addition, advances in bioinformatics, artificial intelligence, predictive modeling, and high-throughput functional genomics can produce new opportunities to develop frameworks to associate genomic, genetic, and trait information (with increased emphasis on susceptibility and resistance traits). These frameworks must represent pan-genomic relationships between cultivars and support data interoperability across species as the genomes of crops are sequenced. Collectively, these information resources will facilitate germplasm development by demonstrating how crop diversity contributes to breeding and other critical agricultural programs, as outlined in Component 1.

Problem Statement 4A. Information resources and tools for crop genetics, genomics, and genetic improvement.

Innovative approaches and analytical capacities to manage breeding, genetics, genomics, and genetic resource data (see Components 1, 2, and 3 of this Action Plan) produced a catalog of resources documenting our crops' genetic and molecular diversity. To better meet rapidly evolving demands for food, feed, fuel, and fiber from crops subjected to new or worsening biotic and abiotic stresses, digital data must be transformed into knowledge applicable to breeding, genetics, genetic resource management, and genome function. Improved bioinformatics tools, services, and outreach built on a robust computational infrastructure are needed to handle changing data types that continue to increase in volume, complexity, variety, and velocity. In addition, these resources need to adapt to technological advances and inventions in genomics, image analysis, sensor technologies, modeling, and functional annotation. Successfully applying these resources to crop genetic improvement presents tremendous challenges, as well as opportunities.

Genomics-assisted breeding, which integrates data generated by genomic analyses with trait data for more rapid selection of superior breeding lines, is a standard procedure in public and private-sector breeding programs. In recent years, the scale, scope, and acceleration of data generation have far exceeded what has previously been available. For example, dozens of high-quality genomes have been sequenced, assembled, and annotated in a fraction of the time and cost, compared to the single-genome reference approach of just a few years ago. Various current and emerging technologies have provided major opportunities to advance to the next level of crop improvement, in which both natural genetic variation and variation generated by precise genome editing can be fully leveraged. Such enabling technologies include multiple reference genomes per crop, pan-genomic and comparative data resources, multi-omic data sets, comprehensive gene expression atlases, and high-throughput phenotyping. In addition, artificial intelligence/machine learning, modeling, and image analysis provide high-throughput methods to annotate and discover functional insights from existing and new datasets. Increased capacities are needed for data stewardship and expanded informatics resources to make these data accessible and enable "biology-assisted breeding", especially to improve crop product quality, yield, and resilience. Designing our next generation of crops will require genomic and phenomic information integrated with information from genetics, physiology, molecular biology, biochemistry, environmental interactions, and evolutionary diversity. Multi-disciplinary collaborations with partners skilled in computer science, statistics, engineering, and image analysis will be essential to exploit fully information contained within these diverse data types. NP 301 research will continue to lead the integration of these disparate data streams to support more efficient crop genetic improvement and the long-term sustainability of our crop production systems.

As the scale and diversity of plant genetics and genomics information grow, crop breeding will require cyberinfrastructure that is expanded in terms of computational capabilities, improved storage capacities, and more effective and efficient analytical methods. The expanded resources will make "biology-assisted" breeding, now common in the major crops, more accessible to specialty crops and forages. Working across ARS National Programs and with international partners, NP 301 will provide stewardship of important biological data and resources to enable crop improvement. NP 301 will spearhead the development of data exchange protocols, standards, training, and outreach that promote FAIR (Findability, Accessibility, Interoperability, and Reuse of digital data) principles for data management. NP 301 research will build on these principles and deliver bioinformatics solutions for the full range of crops important to U.S. agriculture.

Research Focus

Crop improvement has traditionally depended on superior varieties selected from relatively small populations by farmers or breeders. This process was remarkably successful for realizing dramatic initial genetic gains and for selecting phenotypic traits that contain large genetic effects. But it is becoming increasingly difficult to make substantial genetic gains within the current elite crop varietal gene pool. Improving elite cultivars, or making rapid improvements for any crop, requires much more intensive exploitation of information about many factors. These factors include available crop diversity, the performance of genotypes in multiple environments, accurate characterization of agronomic and horticultural traits (phenotypes), genetic markers for priority traits, gene and regulatory functions, and genome sequences to identify genomic features valuable for crop breeding. Targeted curation of information about genes, loci, and genetic maps for phenotypes related to tolerance to abiotic and biotic environmental factors will contribute to the development of climate-resilient cultivars.

The information sources needed to support crop genetic improvement can be categorized according to four, mostly distinct dimensions:

- Germplasm dimension includes information about germplasm and breeding stocks held in a breeding program and/or in the National Plant Germplasm System;
- Genotype dimension contains information about genetic variation across gene pools;
- Genome sequence dimension has positional and functional information for genes, pangenomic data, and other genetic features; and
- Phenotype dimension incorporates information about agricultural traits for any breeding line or germplasm accession.

Managing the preceding multi-dimensional information for crop improvement requires interoperable databases to hold the complicated data types mentioned above, as well as intuitive interfaces to those databases to enable efficient access. Data standards and metadata formats are essential to meet best practices and data sharing principles that enable data curators and plant scientists to efficiently collect, organize, store, access, and use diverse and complicated biological data. Visualization and analytical tools are essential for leveraging this information to accelerate the progress of plant breeding and research.

Robust infrastructure and access to high-performance computing resources will support informatics, big data and image analysis, artificial intelligence/machine learning, and cloud computing. These approaches will provide both value-added downstream analysis (examples include genome annotation, multi-omic analysis, and pan-genome construction) and support stewardship goals, including data storage, maintenance, reusability, integration, standardization, and validation.

Information across multiple dimensions must be integrated to identify optimal elite breeding lines and to locate germplasm accessions that are either genetically identical or genetically distinct from elite lines in targeted genomic regions. This kind of analysis involves querying and visualization tools from several databases and portals to connect information. Such information includes germplasm (via GRIN-Global); traits and quantitative trait loci, protein structures and interaction networks, metabolic pathways, epigenetics and regulatory features, genes and genomic frameworks from species or clade databases (e.g., SoyBase, Gramene, GrainGenes, MaizeGDB, SorghumBase, or the Triticeae Toolbox); and genotypic data from species-specific databases or from a multi-species genotype database and sets of software tools, such as TASSEL or GOBII.

ARS database and information management projects will increasingly require adopting best practices for software development, data management, documentation, and sharing, including reuse and extension of open-source software programs, common database schemas and web application programming interfaces. For efficient data collection, analysis, and sharing, NP 301 scientists must adopt and promote metadata standards suitable for heterogeneous data types; participate in refining common data standards, formats, nomenclature, and protocols for data collection and storage; coordinate with other plant database projects inside and outside ARS; apply curatorial and development expertise from many groups; and provide outreach and training to use these resources. Those approaches are needed to maintain the flexibility to create and test new interconnected, modular, data-driven software tools according to a rapid development cycle.

Across ARS research programs, the rapid growth of information presents opportunities for significant advances in crop production. Nonetheless, those same opportunities represent substantial challenges for data management, including physical data storage, organized file storage, and searchable and retrievable data for future analysis by pertinent databases. An effective ARS data management system is needed for data ingestion standardization, data preservation, and archival standardization to make ARS research operations more efficient. In addition, federal policy requires that scientific data generated by federal funding are retained and accessible.

Anticipated Products

- Curated, interconnected, interoperable, and searchable information resources and tools actively and efficiently stewarded and maintained for crop research and breeding.
- Information tools that connect prioritized traits with molecular markers, specific germplasm accessions, or samples.
- New bioinformatic tools developed for data analysis and mining, and to manage highthroughput genotypic and phenotypic data and knowledge, including the use of artificial intelligence/machine learning approaches.
- Enhanced functional genome annotation through targeted curation and computational analyses using existing biological information, statistical modeling, and artificial intelligence approaches.
- Strategic partnerships, training, and outreach activities with user communities and stakeholders maintained and strengthened.

Potential Benefits

 New and enhanced knowledge about plant phenotype, genotype, gene function and regulation, and genome interrelationships, and their interactions with environmental factors discovered through information available from integrated datasets and bioinformatics tools and resources.

- Expanded access and availability of plant biological data to a broader spectrum of scientists and stakeholders, thus broadening participation in crop research.
- Improved efficiencies in both time and cost that accelerate crop genetic research, breeding, and genetic resource management.
- Enhanced resources and approaches to provide support, stability, maintenance, and valueadded analysis to genomics, genetics, and breeding.
- New techniques to annotate, integrate, and visualize genetic and genomic data.
- Enhanced functional annotation of genes as a result of integrating phenotypic and genomic data.
- Availability of high-quality, high-impact data sets for training, testing, and validating machinelearning and other modeling approaches.
- Enhanced knowledge of the relationships between diverse genotypes, traits, and environments that facilitate the development of climate-resilient plants tolerant to abiotic and biotic environmental factors.

NP 301 Resources

Arizona

Maricopa, AZ - U.S. Arid Land Agricultural Research Center, Plant Physiology and Genetics Research Unit

Arkansas

Stuttgart, AR - Dale Bumpers National Rice Research Center

California

Albany, CA - Plant Gene Expression Center Albany, CA - Western Regional Research Center, Crop Improvement and Genetics Research Unit Davis, CA - Crops Pathology and Genetics Research Unit Davis, CA - National Clonal Germplasm Repository - Tree Fruit & Nut Crops & Grapes Parlier, CA - San Joaquin Valley Agricultural Sciences Center - Crop Diseases, Pests and Genetics Research Unit Riverside, CA - National Clonal Germplasm Repository for Citrus Riverside, CA - Agricultural Water Efficiency and Salinity Research Unit Salinas, CA - Crop Improvement and Protection Research Unit

Colorado

Fort Collins, CO - Center for Agricultural Resources Research, National Laboratory for Genetic Resources Preservation, Agricultural Genetic Resources Preservation Research Unit Fort Collins, CO - Center for Agricultural Resources Research, Soil Management and Sugarbeet Research Unit

District of Columbia

Washington, DC - U.S. National Arboretum, Floral and Nursery Plants Research Unit Washington, DC - U.S. National Arboretum, Gardens Unit

Florida

Canal Point, FL - Sugarcane Production Research Station Fort Pierce, FL - U.S. Horticultural Research Laboratory, Subtropical Insects and Horticulture Research Unit Gainesville, FL - Center for Medical, Agricultural and Veterinary Entomology Chemistry Research Unit Miami, FL - Subtropical Horticulture Research Unit

Georgia

Byron, GA - Fruit and Nut Research Unit Dawson, GA - Peanut Research Unit Griffin, GA - Plant Genetic Resources Conservation Research Unit Tifton, GA - Crop Genetics and Breeding Research Unit

Hawaii

Hilo, HI - Daniel K. Inouye U.S. Pacific Basin Agricultural Research Center, Tropical Plant Genetic Resources and Disease Research Unit

Idaho

Aberdeen, ID - Small Grains and Potato Germplasm Research Unit Kimberly, ID - Northwest Irrigation and Soils Research Laboratory

Illinois

Peoria, IL - National Center for Agricultural Utilization Research, Bio-Oils Research Unit Peoria, IL - National Center for Agricultural Utilization Research, Mycotoxin Prevention and Applied Microbiology Research Unit Urbana, IL - Global Change and Photosynthesis Research Unit Urbana, IL - Soybean/Maize Germplasm, Pathology, and Genetics Research Unit

Indiana

West Lafayette, IN - Crop Production and Pest Control Research Unit

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Ames, IA - Corn Insects and Crop Genetics Research Unit Ames, IA - Plant Introduction Research Unit

Kansas

Manhattan, KS - Center for Grain and Animal Health Research, Hard Winter Wheat Genetics Research Unit

Louisiana

Houma, LA - Sugarcane Research Unit New Orleans, LA - Southern Regional Research Center, Cotton Fiber Bioscience Research Unit

Maryland

Beltsville, MD - Beltsville Agricultural Research Center, Genetic Improvement for Fruits & Vegetables Laboratory

Beltsville, MD - Beltsville Agricultural Research Center, Molecular Plant Pathology Laboratory

Beltsville, MD - Beltsville Agricultural Research Center, Mycology and Nematology Genetic Diversity and Biology Laboratory

Beltsville, MD - Beltsville Agricultural Research Center, National Germplasm Resources Laboratory

Beltsville, MD - Beltsville Agricultural Research Center, Soybean Genomics & Improvement Laboratory

Beltsville, MD - Beltsville Agricultural Research Center, Sustainable Agricultural Systems Laboratory

Beltsville, MD - Beltsville Agricultural Research Center, Sustainable Perennial Crops Laboratory

Michigan

East Lansing, MI - Sugarbeet and Bean Research Unit

Minnesota

St. Paul, MN - Plant Science Research Unit

Mississippi

Mississippi State, MS - Crop Science Research Laboratory, Corn Host Plant Resistance Research Unit Mississippi State, MS - Crop Science Research Laboratory, Genetics and Sustainable Agriculture Research Unit Poplarville, MS - Southern Horticultural Research Laboratory Stoneville, MS - Crop Genetics Research Unit Stoneville, MS - Genomics and Bioinformatics Research Unit

Missouri

Columbia, MO - Plant Genetics Research Unit

Nebraska

Lincoln, NE - Wheat, Sorghum and Forage Research Unit

New York

Geneva, NY - Grape Genetics Research Unit Geneva, NY - Plant Genetic Resources Research Unit Ithaca, NY - Robert W. Holley Center for Agriculture & Health - Plant, Soil and Nutrition Research Unit

North Carolina

Raleigh, NC - Plant Science Research Unit Raleigh, NC - Soybean and Nitrogen Fixation Research Unit

North Dakota

Fargo, ND - Red River Valley Agricultural Research Center, Cereal Crops Research Unit Fargo, ND - Red River Valley Agricultural Research Center, Sugarbeet and Potato Research Unit Fargo, ND - Red River Valley Agricultural Research Center, Sunflower and Plant Biology Research Unit

Oklahoma

Stillwater, OK - Wheat, Peanut, and Other Field Crops Research Unit

Oregon

Corvallis, OR - Forage Seed and Cereal Research Unit Corvallis, OR - Horticultural Crops Research Unit Corvallis, OR - National Clonal Germplasm Repository

Puerto Rico

Mayagüez, PR - Tropical Agriculture Research Station, Tropical Crops and Germplasm Research Unit

South Carolina

Charleston, SC - U.S. Vegetable Laboratory Florence, SC - Coastal Plains Soil, Water and Plant Conservation Research Center

Texas

College Station, TX - Southern Plains Agricultural Research Center, Crop Germplasm Research Unit Lubbock, TX - Cropping Systems Research Laboratory, Plant Stress and Germplasm Development Research Unit

Washington

Pullman, WA - Grain Legume Genetics and Physiology Research Unit Pullman, WA - Plant Germplasm Introduction and Testing Research Unit Pullman, WA - Wheat Health, Genetics, and Quality Research Unit Wapato, WA - Temperate Tree Fruit and Vegetable Research Unit

West Virginia

Kearneysville, WV - Appalachian Fruit Research Laboratory - Innovative Fruit Production, Improvement and Protection Unit

Wisconsin

Madison, WI - Cereal Crops Research Unit Madison, WI - Vegetable Crops Research Unit