USDA
AGRICULTURAL RESEARCH SERVICE

NATIONAL PROGRAM 301

PLANT GENETIC RESOURCES, GENOMICS, and GENETICS IMPROVEMENT

ACTION PLAN 2006-2011

United States Department of Agriculture
Research, Education, and Economics
AGRICULTURAL RESEARCH SERVICE

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Action Plan
National Program 301
Plant Genetic Resources, Genomics, and Genetics Improvement

Goal: National Program (NP) 301, *Plant Genetic Resources, Genomics, and Genetic Improvement*, supports research that expands, maintains, and protects our genetic resource base, increases our knowledge of genes and genomes, and, through novel tools and approaches, manages and delivers vast amounts of genetic and phenotypic information. The ultimate goals for the preceding efforts are to improve the production efficiency and the health and value of our nation's crops.

This National Program addresses the need to ensure the long-term safety and integrity of our agriculturally valuable genetic resource collections; to identify favorable alleles and create novel methods to deploy them; to exploit new technologies that can enhance traditional methods of genetic improvement; to genetically improve a broad spectrum of major, specialty, and new crops; to increase our knowledge of crop and microbial genomes; and to acquire, analyze, and deliver genetic and informatics resources to the public.

Genetic resources are the foundation of our agricultural future. The Agricultural Research Service (ARS) genebanks contain the sources of resistance to biotic and abiotic stresses and new alleles to improve the quantity and quality of our food, feed, energy, fiber, and ornamental crops. To ensure that those genes are available for research and breeding, ARS must continue to acquire and conserve germplasm that contains them, to develop new screening methods for identifying favorable traits, to ensure that germplasm is distributed where and when it is needed, and to safeguard these collections for future generations.

ARS has taken a leadership role in developing and curating crop genomic and phenotypic databases. New tools are needed to efficiently extract useful information from the ever-increasing flow of data into these databases. Methods to interconnect diverse databases are needed to more efficiently and effectively identify important properties of genes and genomes, to apply those properties to crop improvement, to associate specific genes with agriculturally important traits, and to build upon genetic advances in one crop so as to speed genetic gain in others.

For major, specialty, and new crops, ARS, in close cooperation with a variety of public and private sector collaborators, will improve and broaden the genetic base of U. S. crops to reduce genetic vulnerability. NP 301 will devise and apply new technologies to develop superior new crop varieties and enhanced germplasm, and to accelerate the deployment of high-value traits into breeding populations. To do so, sources of important genetic traits will be identified and incorporated into crop breeding lines and genepools. New breeding theories and strategies will be developed to effectively capture the intrinsic genetic potential in germplasm, especially for key agronomic traits. In addition to conducting research, ARS and its university cooperators are in a key position to mentor and train the next generation of breeders and geneticists.

The Plant Genetic Resources, Genomics, and Genetics Improvement National Program (NP 301) is comprised of three components:

- Plant and Microbial Genetic Resource Management;
- Crop Informatics, Genomics, and Genetic Analyses; and
- Genetic Improvement of Crops.

Relationship of This National Program to the ARS Strategic Plan: Outputs of NP 301 research support the "Actionable Strategies" associated with the performance measures shown below from the *ARS Strategic Plan for 2003- 2007*, Objective 1.2: *Contribute to the Efficiency of Agricultural Production Systems*.

> **Performance Measure 1.2.5:** <u>*Provide producers with scientific information and technology that increase production efficiency, safeguard the environment, and reduce production risks and product losses.*</u> **Target**: Cultivars will be developed that are adapted for management practices that optimize soil microbial, carbon, nitrogen, and water resources for sustainable production; production systems and technologies will be developed that harness genetic potential to maximize profits and provide secure supply and market competitiveness; and user-friendly models and decision aids will be enhanced to determine cost-effective inputs for specific enterprises or the whole operation.
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> **Performance Measure 1.2.7:** <u>Identify genes responsible for plant product quality and resistance to disease, pests, and weather losses.</u> **Target:** Have a more complete understanding of the structure and function of genes responsible for quality, growth, and health of crops and how those individual genes are regulated in the context of gene systems or networks.
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> **Performance Measure 1.2.8:** <u>Maintain, characterize, and utilize genetic resources to optimize, safeguard, and enhance genetic diversity and promote viable and vigorous plant production systems.</u> **Target:** The diversity of the germplasm collections will be expanded by acquisition of new accessions, and genetic resources from these collections will be used to produce new and improved food, agricultural, and industrial applications for agricultural products.

<u>Component 1: Plant and Microbial Genetic Resource Management</u>

The continued support and strategic expansion of *ex situ* genebank collections and *in situ* dynamic genetic resource management programs are priority needs for ARS. Genetic Resource Management includes the identification, acquisition, conservation, secure maintenance, genetic assessment, evaluation, documentation, and distribution of plant and microbial genetic resources and associated information. To ensure efficient and cost-effective security of diverse gene pools, ARS will expand efforts to identify, acquire, and secure unprotected genetic resources currently existing *in situ*. The management capabilities of existing genebank facilities will be maintained and their existing infrastructure continually upgraded so as to ensure long-term genetic resource preservation capabilities. The information management capabilities of the Germplasm Resources Information Network (GRIN) and/or associated linked databases will be significantly enhanced so as to better manage the dynamic phenotypic and genotypic data which underpins ARS's genetic resource management program. To attain these goals successfully, new system-wide assessments by consultative groups will help identify and rank by priority critical crop genetic resource needs and challenges.

Problem Statement 1A: Efficiently and Effectively Manage Plant and Microbial Genetic Resources.

Some of ARS's microbial and National Plant Germplasm System (NPGS) collections do not adequately represent the existing genetic diversity of agricultural importance. Wild relatives of crop species, as well as existing land race populations, within and outside of the centers of crop diversity are in danger of being lost. Those genetic resources will be strategically acquired through collection and exchange, and conserved in ARS *ex situ* collections. Protocols for germplasm regeneration and preservation will be continually developed and refined so as to more effectively maintain the genetic diversity contained in the original sample. Microbial collections are largely decentralized and have not been fully cataloged or developed. These collections, vital to national security, will be secured in both primary and back-up sites. To facilitate the frequent and effective use of plant and microbial genetic resources in research and crop improvement, the germplasm, as well as associated information, will be readily accessible and distributed rapidly and reliably to a wide clientele.

***Research Needs*:**

Crop-specific or microbe-specific managerial priorities and strategic plans to enhance existing collections will be developed by ARS curators in close consultation with Crop Germplasm Committees and other consultative groups. The number of ARS-sponsored plant explorations focused on wild relatives, land races, and important native species should increase, together with international germplasm exchanges in general. ARS genebanks will expand their role in developing, storing, and distributing crop genetic stocks and key microbial genetic resources. Collections will be safely stored and backed-up in appropriate and secure facilities, and regenerated/propagated reliably to provide sufficient viable propagules. Plant and microbial germplasm distributed by ARS will be clean, healthy (pathogen-negative), and true-to-type. Reliable and ready access to information about plant and microbial genetic resources will be sought to efficiently curate these materials. The Germplasm Resources Information Network (GRIN), currently an important source of information about germplasm, will be linked more effectively to other genetic resource databases worldwide, and will be transformed so that it more efficiently and effectively delivers the wide variety of information required for successful germplasm curation and use.

***Anticipated Products*:**

- Strategic genetic resource management plans and priorities, aligned with ARS's agency goals, are developed by genebank curators, in close consultation with Crop Germplasm Committees and new system-wide consultative group(s).
- Genebank collections of agriculturally important organisms, especially microbes, specialty crops, and genetic/genomic stocks, are expanded strategically.
- Timely infrastructure maintenance and facility upgrades ensure the secure, long-term, *ex situ* genetic resource maintenance.
- Expanded international germplasm exchanges and linkages fill critical gaps in collection coverage.

- New regeneration protocols and techniques increase collection quality, ensure genetic integrity, and enhance genetic resource management efficiency.
- More effective methods and strategies for long-term maintenance protect genetic resource vigor, viability, and health, especially from seed-borne diseases.
- A broad spectrum of genetic diversity in the form of viable and well-documented germplasm is conserved.
- Efficient and timely distribution increases the frequency and use of germplasm in research and in crop genetic improvement.
- High-quality, comprehensive characterization, evaluation, and genebank curatorial data are readily accessible, either from a transformed, upgraded, well-maintained GRIN, from databases housed at GRIN as the primary site, or at sites linked to GRIN.

Potential Benefits:
Careful strategic planning for and successful implementation of genetic resource management projects will provide users with a more dependable and more diverse source of high-quality plant and microbial genetic resources. In particular, vulnerable or threatened genetic resources will be better preserved and more secure. Health and genetic integrity of genetic resources will be ensured especially in cross-pollinated species. Capacity for maintaining pathogen collections and reference microbial collections important to agriculture and/or biotechnology will be expanded. Newly developed genetic resource management techniques and methodologies will be available and applied worldwide. Use of genetic resources will be more targeted, efficient, and frequent in terms of number of users served, and frequency and volume of germplasm distributed, leading to subsequent increased development of advanced germplasm and cultivars. This will contribute increasingly to progress in other National Programs, which will rely even more strongly on those genetic resources.

Problem Statement 1B: Assess the Systematic Relationships and Genetic Diversity of Crop Genetic Resources.
Knowledge of the genetic diversity, genetic structure, correct identification, and systematic relationships of some crops (especially specialty crops), wild relatives of crops, and ARS genebank accessions of the preceding, may range from extensive to minimal. Without such knowledge, genetic resource management programs are handicapped, and potential users are less likely to request samples for research and crop improvement.

Research Needs:
More extensive phenotypic and genotypic descriptions of the intrinsic genetic profiles and diversity of crop taxa and genebank accessions are essential for guiding curatorial efforts. Newly acquired and conserved accessions and taxa will be thoroughly assessed via genetic marker analyses so as to measure genetic diversity and divergence. That information will help enhance sampling strategies for germplasm acquisition, circumscribe optimal core subsets, and maximize the genetic diversity and minimize genetic redundancy within genebank collections, thereby reducing the cost of genetic resource management. Effective means for monitoring accessions' genetic integrity, especially for outcrossers, will be developed, so that samples can be maintained true-to-

type. New statistical genetic approaches and strategies are required for addressing the preceding needs more effectively.

***Anticipated Products*:**

- Poorly known crop genetic resources are accurately identified, phenotyped, and classified.
- Knowledge of the genetic variation within and between crop accessions, species, and genera is expanded.
- Genetic marker systems are developed for efficiently assessing genetic diversity and genotyping genebank accessions, especially for poorly understood specialty crops.
- New marker genotype and genetic profile databases for germplasm collections serve as tools for genetic resource management.
- Duplicate accessions, as well as novel genetic variability in collections, are identified.
- Genetic gaps in collections are detected, thereby aiding in setting acquisition priorities.
- New statistical genetic approaches for optimizing the efficiency and effectiveness of germplasm sampling, maintenance, and regeneration are developed.

Potential Benefits:

Complete and accurate genetic assessments will gauge the extent to which collections are taxonomically and genetically representative, will identify redundant accessions, and will determine whether a collection encompasses a full range of genetic diversity. The preceding information will help identify specific acquisition and other genetic resource management needs, and help potential users to more efficiently choose accessions for further research and breeding.

Component 1 Resources:

Thirty nine (39) ARS projects that are coded to NP 301 address the research needs identified under Component 1. ARS scientists who are assigned to these projects include:

Location:	Scientists:
Washington, D.C.	Whittemore, Alan T.; Roh, Mark S.; Aker, Scott M.; Luria, Nancy S.
Beltsville, Maryland	Garvey, Edward J.; Williams, Karen A.; Kirkbride, Joseph H.; Meinhardt, Lyndel; Van Berkum, Peter B.; Mowder, Jimmie D.; Farr, David F.
Geneva, New York	Forsline, Phillip L.; Robertson, Larry D.
Urbana, Illinois	Sachs, Martin. M.; Clough, Steven
Peoria, Illinois	Labeda, David P.
Ames, Iowa	Gardner, Candice A.
Madison, Wisconsin	Spooner, David M.; Bamberg, John B.
Parlier, California	Jenderek, Maria M.
Davis, California	Stover, Eddie W.
Riverside, California	Lee, Richard F.
Hilo, Hawaii	Zee, Francis T.
Fairbanks, Alaska	Pantoja, Alberto
Pullman, Washington	Greene, Stephanie L.; Hannan, Richard M.
Corvallis, Oregon	Hummer, Kim E.

Aberdeen, Idaho	Bockelman, Harold E.
Fort Collins, Colorado	Ellis, David D.; Walters, Christina T.
College Station, Texas	Grauke, Larry J.; Kohel, Russell J.
Griffin, Georgia	Pederson, Gary A.
Miami, Florida	Meerow, Alan W.; Schnell, Raymond J.
Mayaguez, Puerto Rico	Goenaga, Ricardo J.; Erpelding, John E.; Irish, Brian M.

Component 2: Crop Informatics, Genomics, and Genetic Analyses

Plant geneticists face the significant challenge of identifying and describing the genes and alleles that control complex genetic traits and biological pathways. Identifying useful variants of key agronomic genes involved in product quality, protection, and productivity is of particular importance in cultivar development. Informatics, genomics, and genetic analysis are tools needed to dissect these complex traits. Bioinformatics provides the infrastructure necessary to share and analyze data produced by numerous research projects. Genomic approaches apply the techniques of genetics and molecular biology towards the characterization of select genes as well as complete genomes. Genetic mapping is a first step toward identifying genes and alleles that control important traits.

Problem Statement 2A: Genome Database Stewardship and Informatics Tool Development

Data repositories that organize and store large-scale genomic, phenotypic, and germplasm datasets have been developed within the research community with funding by different governmental agencies. However, effective integration of datasets and linkages between data repositories often are lacking, making it difficult for researchers to access and leverage emerging information for breeding and development of genetic markers and genetic and physical genomic maps. The software tools required to enable such connections are either poorly utilized or altogether nonexistent. ARS will assess the merit of current database technologies and informatics tools, develop new technologies and tools where needed, create integrated datasets, and facilitate interoperability among databases that store divergent types of data.

Research Needs:

A coordinated effort guided by the Interagency Working Group on Plant Genomes is needed to standardize data formats and develop an integrated network system among existing genomic databases. Ontologies and shared data types will be standardized to facilitate database interoperability. Web services will be employed to create single access points to data stored at various databases. Crop genome datasets will be expanded, curated, and implemented to enable access to divergent databases by a standardized set of protocols. Where appropriate, molecular data will be added to the GRIN database to enable connections by way of the shared data type between phenotypic accession descriptions and genetic/genomic datasets stored in other databases. Database interfaces and stand-alone informatics tools will be developed via a coordinated approach to address the research needs.

Anticipated Products:

- Interconnected and interoperable databases.
- Single points of access (portals) to multiple databases.

- Long-term maintenance of reliable genetic, genomic, and phenotypic description data sets achieved via active data curation.
- Easy-to-use public interfaces to data repositories.
- Facile private interfaces to data repositories to aid curators in their work.
- Software and data analysis tools that enable the analysis of genetic and genomic data sets.

Potential Benefits:
The availability of integrated data sets that can be navigated and analyzed with ease will allow researchers and curators to generate and associate new knowledge about the structure and function of plant genomes, thereby enabling the development of improved crop plants. Such improvements should include efficiencies in both time and cost for future genome study and application.

Problem Statement 2B: Structural Comparison and Analysis of Crop Genomes
Genomics has facilitated the identification and mapping of individual candidate genes within segments of genomics, but has yet to show interrelations of these genes and alleles to agronomic traits. Most important agronomic traits are complex and quantitatively inherited. A thorough understanding of genome structure is required before large gains in crop improvement can be realized. Existing tools for genetic and genomic analysis will be improved, including the integration of genetic, physical, and cytogenetic maps for plants. In polyploid crops, the accurate assembly of physical maps from genome sequence information will be facilitated by comparative analyses of syntenic genomes.

Research Needs:
Knowledge of genomic structure is needed to accelerate progress toward improving crop quality, productivity, and resistance to diseases and pests. Genomes within phylogenetically related groups will be mapped, generating data that can be applied to related species. Improvements in genomic technology will be made, including the development of efficient, high-throughput germplasm characterization protocols. Genomic sequences will be aligned and assembled accurately. Genomic technologies will enable accurate positioning of gene isoforms in polyploid species.

Anticipated Products:
- Detailed genetic maps and markers for important agronomic genomes.
- Integrated genetic, physical, and cytogenetic maps.
- Improved tools for genetic and genomic analysis of complex genomes, including polyploid species.
- BAC libraries with extensive ordered and oriented contig assemblies.
- Annotated gene sequences for candidate gene location.
- Custom designed oligonucleotide microarrays for alignment of genomic structure.

Potential Benefits:
Improved knowledge of crop genome architecture that facilitates the identification of a wide range of markers, genes, and genotypes influencing important traits such as disease and pest resistance, environmental stresses, and functional and nutritional quality will accelerate crop improvement.

Problem Statement 2C: Genetic Analyses and Mapping of Important Traits.
Technological advances, as well as innovative analytical approaches, have recently made it possible to associate genomic regions with phenotypic variation for important crop traits. Improved genetic map development is needed to expedite breeding techniques and selection of superior crops. After advantageous alleles for specific traits are identified, dense marker placement on genetic maps will facilitate marker-assisted selection for important agronomic traits.

Research Needs:
Theory for mapping in complex (e.g., polyploid) species, methods to identify the effects of sets of interacting genes, and efficient strategies for dissecting the genetic control of traits in crop species will be developed. Mapping populations and genetic stocks designed for high-resolution mapping will be created, maintained, genotyped, and distributed for multiple crops. High-throughput phenotypic analysis will be applied to discover genes for product quality, resistance to diseases and pests, and tolerance to stressful growing conditions. Mapping and comparative genetic analyses will identify genes and superior alleles controlling these traits.

Anticipated Products:
- New theory and strategies for mapping traits.
- Trait mapping populations and genetic stocks for gene and allele identification, such as near-isogenic lines, recombinant inbred lines, transposon knockouts, and targeting induced local lesions in genomes (TILLING) resources.
- Genes controlling key traits and associated markers will be identified.

Potential Benefits:
Improved theory and the development of publicly available mapping populations will accelerate research by the entire plant research community in multiple species. Newly identified genes and alleles controlling key traits will enable marker-assisted breeding and transgenic strategies for crop improvement.

Component 2 Resources:
Thirty (30) ARS projects that are coded to NP 301 address the research needs identified under Component 2. ARS scientists who are assigned to these projects include:

Location:	Scientists:
Beltsville, Maryland	Cregan, Perry B.
Ithaca, New York	Bradbury, Peter; Buckler, Edward S.; Ware, Doreen H.
Geneva, New York	Cousins, Peter S.; Garris, Amanda J.;
Urbana, Illinois	Clough, Steven J.
Columbia, Missouri	Schaeffer, Mary L.
Ames, Iowa	Shoemaker, Randy C.; Lawrence, Carolyn J.
St. Paul, Minnesota	Rines, Howard W.; Vance, Carroll F.
Albany, California	Anderson, Olin D.; Belknap, William R.; Harmon,Frank G.
Aberdeen, Idaho	Raboy, Victor
Fargo, North Dakota	Vick, Brady A.; Jauhar, Prem P.; Faris, Justin D.

College Station, Texas	Klein, Robert R.; Kohel, Russell J.
Beaumont, Texas	McClung, Anna M.
Lubbock, Texas	Xin, Zhanguo
Stillwater, Oklahoma	Haung, Yinghua
Stuttgart, Arkansas	Eizenga, Georgia C.
Stoneville, Mississippi	Ray, Jeffery D.; Scheffler, Brian E.
Tifton, Georgia	Guo, Baozhu
Raleigh, North Carolina	Vacant

Component 3. Genetic Improvement of Crops

Methods, techniques, and knowledge gained through genomic advances have accelerated the pace of plant improvement and increased the specificity with which plants can be genetically characterized. Time-tested plant breeding approaches that integrate the most effective new technologies will be the cornerstone for genetic improvement of major, specialty, industrial, and other new crops. Strategically coordinated breeding programs are needed to expand the science of plant breeding, and to develop the improved germplasm needed to meet production constraints, consumer needs, sustainable energy demands, and processing challenges, and to address nutritional and toxicological problems in the U.S. food and feed supply.

Problem Statement 3A: Genetic Theory and Methods of Crop Improvement

Efficient and effective genetic improvement of crop plants requires a solid theoretical foundation of principles and methodologies. Suboptimal statistical genetic and breeding theory for handling complications such as genetic associations, differential heritabilities, and genetic drift can impede breeding progress. Inadequate knowledge of quantitative genetic variation, genotype-environment interaction, epigenetic regulation, mutation, and stochastic effects can result in failure or severe restriction in genetic gain and improved plant material. In addition, genetic improvement can be limited in the absence of state-of-the-art methodologies that integrate genomic with genetic knowledge. ARS will develop a better understanding of fundamental plant genetic mechanisms, and apply the findings to improve breeding techniques and methods.

Research Needs:

Methods that integrate genomic with genetic knowledge, such as molecular marker-assisted selection, will be developed for major and specialty crops. The manner in which genetic mechanisms influence selection and genetic improvement will be assessed. Quantitative traits loci (QTLs) will be discovered, validated, and applied in breeding programs.

Anticipated Products:

- Greater knowledge of fundamental plant genetic mechanisms and how they can be applied effectively to crop genetic analyses and crop improvement.
- Improved experimental design and enhanced ability to identify, validate, and utilize QTLs in a broad range of crop species.
- Reliable molecular marker-assisted methods and procedures.

Potential Benefits:
A better understanding of the fundamental plant genetic mechanisms governing quantitative variation will advance breeding theory and lead to the development of novel crop genetic improvement methods, enabling researchers to more accurately and efficiently develop improved crops.

Problem Statement 3B: Capitalizing on Untapped Genetic Diversity
Crops with narrow genetic diversity are vulnerable to changes in pathogen and pest populations, changing agricultural practices, and a changing global environment. ARS will develop and implement procedures to identify and evaluate genetic variability for key traits in crop plants, and incorporate them into crop improvement programs.

Research Needs:
More efficient and effective strategies and methods are needed for identifying, evaluating, and incorporating genetic diversity into adapted breeding pools. Genetic diversity for resistance to biotic and abiotic stress tolerance will be sought. Knowledge and resources will be leveraged to develop cooperative programs between public and private entities to better estimate levels of variability in crops. Genes and gene pools from diverse crop wild relatives will be evaluated, characterized, and introgressed into adapted germplasm. Germplasm with genes for resistance to pests and weather stress will be identified. Breeding lines and germplasm populations will be evaluated. Genotyping and phenotyping of adapted germplasm will be conducted as a basis for deploying genes for improved pest resistance, tolerance to weather stress, crop productivity, and new uses.

Anticipated Products:
- Development of genetic stocks that serve as research tools and potential sources of genes for crop improvement.
- Level of diversity determined for key traits in crops.
- Germplasm with identified resistance (tolerance) to biotic and abiotic stresses
- Identification of germplasm with novel traits and properties that will enable development of new varieties for new uses and agricultural products.
- Evaluation information that contributes to developing crops containing new sources of diverse traits derived from ancestral and wild relatives.

Potential Benefits:
Intrinsic diversity of crops will facilitate the maintenance and development of crops that are durable over time and space. Valuable evaluation data, in concert with genomic characterization, will be readily accessible for accelerating genetic selection and enhancement. Rapid deployment of genes conferring resistance to new and emerging pests and diseases will protect crops from catastrophic losses. The quality, protection, and productivity of new varieties will be maintained and improved to insure that U.S. crops remain competitive.

Problem Statement 3C: Germplasm Enhancement/Release of Improved Genetic Resources and Varieties.

U. S. agriculture requires enhanced germplasm and improved crops that possess high-yield capability, resistance to biotic and abiotic stresses, improved agronomic characteristics, and specific processing and product quality properties. Enhancement of germplasm and the improvement of cultivated varieties through breeding require the accumulation of numerous favorable alleles. Superior crop germplasm and varieties will be developed for diverse, multiple cropping systems (conventional, low and high input, and organic) and competitive global market needs. Crop varieties will be developed to overcome production constraints (biotic and abiotic stresses); have improved processing characteristics; and contain specific end-use qualities (nutritional, food safety, energy, and value-added traits).

Research Needs:

Crop genepools with intrinsic characteristics for increased productivity in diverse cropping systems will be developed. New germplasm and cultivars will be developed that are resistant to diseases and pests; tolerant to abiotic stresses; responsive to variability in climate; and attentive to consumer needs.

Anticipated Products:

- Genomics-integrated, marker-assisted selection breeding programs.
- New and improved germplasm and crop varieties containing desired traits.
- New alternative crops for diverse management and market systems for crop producers.
- Flexible, crop-specific procedures for releasing and protecting plant material.

Potential Benefits:

The varieties and germplasm developed will result in improved crops of all types to serve immediate, as well as future, needs of U.S. agriculture.

Component 3 Resources:

Seventy one (71) ARS projects that are coded to NP 301 address the research needs identified under Component 3. ARS scientists who are assigned to these projects include:

Location:	Scientists:
Washington, D.C.	Griesbach, Robert J.; Pooler, Margaret R.; Reed, Sandra M.; Olsen, Richard
Beltsville, Maryland	Stommel, John R.; Haynes, Kathleen G.; Ehlenfeldt, Mark K.; Pastor Corrales, Marcial A.;
Geneva, New York	Fazio, Gennaro
Kearneysville, West Virginia	Scorza, Ralph
West Lafayette, Indiana	Shukle, Richard H.
Wooster, Ohio	Mian, Rouf M.
Columbia, Missouri	Gustafson, J. Perry; Oliver, Melvin J.
Ames, Iowa	Palmer, Reid D.; Pollak, Linda M.; Blanco, Michael H.; Scott, Marvin P.
East Lansing, Michigan	McGrath, J. Mitchell; Vacant
St. Paul, Minnesota	Garvin, David F.; Vance, Carroll F.
Madison, Wisconsin	Jansky, Shelley H.; Simon, Philipp W.

Parlier, California	Ledbetter, Craig A.
Salinas, California	McCreight, James D.; Lewellen, Robert T.
Davis, California	Tai, Thomas
Maricopa, Arizona	Coffelt, Terry A.
Pullman, Washington	Muehlbauer, Frederick J.; Steber, Camille M.; Skinner, Daniel Z.
Prosser, Washington	Brown, Charles R.; Miklas, Phillip N.
Corvallis, Oregon	Henning, John A.; Bryla, David R.
Aberdeen, Idaho	Novy, Richard G.; Bonman, J. Michael
Kimberly, Idaho	Strausbaugh, Carl A.
Fort Collins, Colorado	Panella, Leonard W.
Manhattan, Kansas	Bowden, Robert L.
Lincoln, Nebraska	Graybosch, Robert A.; Pedersen, Jeffery F.
Fargo, North Dakota	Campbell, Larry G.; Miller, Jerry F.
College Station, Texas	Thompson, Tommy E.
Stillwater, Oklahoma	Melouk, Hassan A.
Stuttgart, Arkansas	Rutger, J. Neil
Stoneville, Mississippi	Mengistu, Alemu; Koger, Clifford; Meredith, William R.; Scheffler, Jodi A.
Poplarville, Mississippi	Spiers, James M.
Mississippi State, Mississippi	Williams, William P.; Jenkins, Johnie N.
New Orleans, Louisiana	Tew, Thomas L.
Tifton, Georgia	Holbrook, C. Corley; Krakowsky, Matthew D.
Byron, Georgia	Okie, William R.
Fort Pierce, Florida	Bowman, Kim D.
Canal Point, Florida	Vacant
Miami, Florida	Schnell, Raymond J.
Mayaguez, Puerto Rico	Porch, Timothy G.
Raleigh, North Carolina	Carter, Thomas E.; Holland, James B.; Marshall, David S.
Charleston, South Carolina	Farnham, Mark W.; Fery, Richard L.; Bohac, Janice R.