

USDA
AGRICULTURAL RESEARCH SERVICE

**NATIONAL PROGRAM 301 –
PLANT GENETIC RESOURCES, GENOMICS, AND GENETIC
IMPROVEMENT**

ACTION PLAN 2008-2013

[REVISED APRIL 2010]



AGRICULTURAL RESEARCH SERVICE
National Program 301
PLANT GENETIC RESOURCES, GENOMICS, AND GENETIC IMPROVEMENT
Action Plan

[REVISED APRIL 2010 TO FACILITATE MERGER WITH NATIONAL PROGRAM 302,
PLANT BIOLOGICAL AND MOLECULAR PROCESSES]

Goal: National Program (NP) 301, *Plant Genetic Resources, Genomics, and Genetic Improvement*, supports research that expands, maintains, and protects our genetic resource base, and increases our knowledge of plant genes, genomes, and biological and molecular processes. Through novel tools and approaches, it manages and delivers vast amounts of genetic, molecular, biological, and phenotypic information. The ultimate goals for the preceding efforts are to improve the production efficiency, sustainability, 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 genes 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 of plant biological and molecular processes; 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 genes 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 gene pools. New breeding theories and strategies will be developed to effectively capture the intrinsic genetic potential in germplasm, especially for key agronomic traits.

Plant breeding has a long history of improving crops through phenotypic or marker-assisted selection, usually without fundamental knowledge of the underlying genes that are involved. However, recent advances in plant molecular biology, genetic engineering, and physiology will enable crops to be improved either by manipulating the existing variability in plant properties, or alternatively by creating new variability when warranted. Knowledge of how to precisely modify biological mechanisms and how to associate molecular and genetic variability with specific phenotypes will potentially enhance the effectiveness of genetic selection, and thereby accelerate and strengthen crop breeding programs.

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 Genetic Improvement National Program (NP 301) is comprised of four components:

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

Relationship of This National Program to the ARS Strategic Plan: Outputs of NP 301 research support the actionable strategies associated with the performance measure shown below from the *ARS Strategic Plan for 2006- 2011*, Strategic Goal 2, Enhance the Competitiveness and Sustainability of Rural and Farm Economies; Objective 2.2: *Increase The Efficiency Of Domestic Agricultural Production And Marketing Systems*.

Performance Measure 2.2.3: Expand, maintain, and protect our genetic resource base, increase our knowledge of genes, genomes, and biological processes, and provide economically and environmentally sound technologies that will improve the production efficiency, health, and value of the Nation's crops. **Target:** New technologies developed and used by ARS customers to increase production efficiency and enhance the economic value and quality of U.S. crop production while decreasing the environmental footprint of production systems.

Component 1: Plant and Microbial Genetic Resource Management

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:

Washington, D.C.
Beltsville, Maryland

Geneva, New York
Urbana, Illinois
Peoria, Illinois
Ames, Iowa
Madison, Wisconsin
Davis, California
Riverside, California
Hilo, Hawaii
Palmer, Alaska
Pullman, Washington

Scientists:

Whittemore, Alan T.; Aker, Scott M.; Luria, Nancy S.
Garvey, Edward J.; Williams, Karen A.; Meinhardt,
Lyndel; Van Berkum, Peter B.; Farr, David F.; Kinard,
Gary R.
Zhong, Gan-Yuan; Robertson, Larry D.
Sachs, Martin. M.; Clough, Steven
Labeda, David P.
Gardner, Candice A.
Spooner, David M.; Bamberg, John B.
Preece, John; Kluepfel, Daniel
Lee, Richard F.
Zee, Francis T.
Hummer, Kim E.
Greene, Stephanie L.; Hu, Jinguo

Corvallis, Oregon
Aberdeen, Idaho
Fort Collins, Colorado
College Station, Texas
Griffin, Georgia
Miami, Florida
Mayaguez, Puerto Rico

Hummer, Kim E.
Bockelman, Harold E.
Ellis, David D.; Walters, Christina T.
Grauke, Larry J.; Percy, Richard
Pederson, Gary A.
Meerow, Alan W.; Schnell, Raymond J.
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:

Beltsville, Maryland
Ithaca, New York
Geneva, New York
Urbana, Illinois
Peoria, Illinois
Ames, Iowa
St. Paul, Minnesota
Albany, California
Aberdeen, Idaho
Fargo, North Dakota
College Station, Texas

Scientists:

Cregan, Perry B.
Buckler, Edward S.; Jannink, Jean-Luc; Ware, Doreen H.
Cousins, Peter S.; Owens, Christopher
Clough, Steven J.
Dowd, Patrick
Shoemaker, Randy C.; Lawrence, Carolyn J.
Samac, Deborah
Anderson, Olin D.; Belknap, William R.; Harmon, Frank G.
Raboy, Victor
Vick, Brady A.; Jauhar, Prem P.; Faris, Justin D.
Klein, Robert R.; Percy, Richard

Beaumont, Texas
Lubbock, Texas
Stillwater, Oklahoma
Stuttgart, Arkansas
Stoneville, Mississippi
Tifton, Georgia

McClung, Anna M.
Xin, Zhanquo
Haung, Yinghua
McClung, Anna M.
Ray, Jeffery D.; Scheffler, Brian E.
Guo, Baozhu

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 gene pools 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:

Washington, D.C.

Beltsville, Maryland

Geneva, New York

Kearneysville, West Virginia

West Lafayette, Indiana

Wooster, Ohio

Columbia, Missouri

Ames, Iowa

East Lansing, Michigan

St. Paul, Minnesota

Madison, Wisconsin

Parlier, California

Salinas, California

Davis, California

Maricopa, Arizona

Pullman, Washington

Scientists:

Pooler, Margaret R.; Reed, Sandra M.;

Olsen, Richard

Stommel, John R.; Haynes, Kathleen G.;

Ehlenfeldt, Mark K.; Pastor Corrales, Marcial A.;

Fazio, Gennaro

Scorza, Ralph

Shukle, Richard H.

Mian, Rouf M.

Gustafson, J. Perry; Oliver, Melvin J.

Palmer, Reid D.; Pollak, Linda M.; Blanco, Michael H.;

Scott, Marvin P.

Cichy, Karen; McGrath, J. Mitchell

Garvin, David F.

Jansky, Shelley H.; Simon, Philipp W.

Ledbetter, Craig A.

McCreight, James D.; Richardson, Kelley

Tai, Thomas

Coffelt, Terry A.

Vandemark, George J.; Steber, Camille M.;

Skinner, Daniel Z.

Prosser, Washington	Brown, Charles R.; Miklas, Phillip N.; Navarre, Duroy
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	Gulya, Thomas
College Station, Texas	Thompson, Tommy E.
Stillwater, Oklahoma	Melouk, Hassan A.
Stuttgart, Arkansas	Gealy, David
Stoneville, Mississippi	Mengistu, Alemu; Meredith, William R.; Scheffler, Jodi A.; Young, Lawrence
Poplarville, Mississippi	Rinehart, Timothy
Mississippi State, Mississippi	Williams, William P.; Jenkins, Johnie N.
Houma, Louisiana	Tew, Thomas L.
Tifton, Georgia	Holbrook, C. Corley; Wilson, Jeffrey
Byron, Georgia	Okie, William R.
Fort Pierce, Florida	Bowman, Kim D.
Canal Point, Florida	Glaz, Barry
Miami, Florida	Schnell, Raymond J.
Mayaguez, Puerto Rico	Porch, Timothy G.
Raleigh, North Carolina	Carter, Thomas E.; Holland, James B.; Krakowsky, Matthew; Marshall, David S.
Charleston, South Carolina	Farnham, Mark W.; Fery, Richard L.

Component 4: Plant Biological and Molecular Processes

Problem Statement 4A: Functional Utilization of Plant Genomes – Translating Plant Genomics into Crop Improvement

In the past 5 years, DNA sequencing of model plant genomes such as Arabidopsis (dicot) and rice (monocot) has contributed to an exponential gain in information about plant genes and gene expression. These efforts have produced vast EST resources and extensive amounts of microarray-based transcript expression data. It is now possible not only to observe whole-genome patterns of gene expression in response to treatment variables, but also to differentiate genetic variation in those responses. New technologies for quantifying gene function through changes in mRNA, protein, and metabolites (transcriptomics, proteomics, metabolomics) create additional opportunities to understand how plants convert their genetic potential into form. Confirming the function of specific gene sequences enables advanced strategies for crop improvement that involve the modification of specific gene targets. However, to support useful applications, the information garnered through plant genomics must be reduced to practice in a timely manner.

- *Advancing From Model Plants to Crop Plants*

Most genomic information is derived from model plants, such as Arabidopsis. However, the extent to which knowledge of model systems can be generalized to the complex genomes of crop plants depends on the degree of synteny or how closely plant species are related on an evolutionary scale. Thus, regulation of many important processes in crop plants often differs from those in model systems. This inadequacy limits the utility of model systems to resolve complex problems in agricultural crops. To remedy this dilemma, ARS research will explore gene-rich regions in important agricultural crops to advance genomics and alleviate the inherent limitations of model plant genomes.

- *Applying Genomics to Crop Improvement*

Gene families or gene networks in crop plants often control complex traits, such as seed quality and vigor, flower color and scent, mineral nutrient use efficiency, and forage digestibility. Knowledge of how these genes interact to influence gene expression in crops is essential to understand inheritance and regulation of traits. Without this knowledge, inheritance of such traits is hard to predict, and assembling the required genes in an improved genotype is difficult. ARS research will analyze, interpret, and use the voluminous increase in crop genomic resources to characterize gene networks governing fundamental processes in crops and identify opportunities for crop improvement.

Research Needs:

Knowledge of how important genes function in model plants will be extended to crop plants. Methods useful in model species, such as gene disruption to identify function, will be modified or extended to systematically define the biological function of crop plant genes. Transcript and protein expression profiles associated with genetic variation in complex traits will be determined to identify genes that control phenotypic expression. DNA sequence differences (polymorphisms) associated with variants of complex traits will be identified to enable mapping, inheritance studies, and eventual manipulation of valuable traits. Multiple sets of information within and across species and environments will be “mined” to relate gene action to plant phenotype and productivity. Quantifying gene action and crop biological processes that contribute to productivity will require application of new algorithms and computational tools for data analysis and integration.

Anticipated Products:

- Description of the function of agriculturally important genes in model plants and agronomic crops.
- Verified knowledge of gene families or genetic networks that mediate or are associated with important traits in agronomic crops.
- Identification of specific genes that mediate end-product traits desired by consumers – such as nutritional content, oil, and grain quality – disease resistance, and abiotic stress tolerance in agricultural crops.
- Voluminous expansion of genomic information on the function and regulation of gene systems that govern the expression of important traits in agricultural crops.
- Expanded macro-array and micro-array capabilities to visualize functional changes in gene expression during the development of agronomic crops species.
- Proteomic technologies to extend genomic understanding to the level of gene products.

Potential Benefits:

Innovative research strategies will yield more comprehensive information about gene action in crops, enabling researchers to directly modify genetic processes governing or influencing crop productivity and quality. Gene discovery will provide new sources of enhanced crop traits for incorporation into breeding programs. New genetic strategies resulting from expanded genomic knowledge will accelerate the enhancement of crop productivity and the exploitation of nutritional and healthful properties of foods.

Problem Statement 4B: Biological Processes that Improve Crop Productivity and Quality

Crop productivity is determined by a plant's capacity to convert energy, nutrients, and water into harvestable yield of high quality and high value. Thus, ample supply of harvestable products is a function of a plant's genetic potential to capture energy, and use available water and nutrients. The molecular and biochemical factors that actuate regulatory mechanisms are poorly understood for fundamental biological processes that underpin crop plant productivity and the production of high-value end products. A highly coordinated integration of research is needed to develop knowledge of how biological processes may be regulated to overcome factors that limit crop yield and quality in a manner that reduces costly inputs, expands area suitable for production, and protects the environment.

- *Understanding Growth and Development*

Biological processes that regulate crop plant growth and development include photosynthesis (conversion of sunlight energy to chemical energy); initiation and growth of reproductive tissues; root and shoot growth; transport of metabolic assimilates from leaves to and among plant organs; and seed development and maturation need to be better understood. These processes often are inefficient or poorly adapted to agricultural growing conditions that may seriously restrict productivity and crop quality. ARS research will develop a better understanding of the fundamental principles governing these processes and findings will be applied to improve crop quality, increase product value, and achieve more sustainable production systems.

- *Understanding Plant Interactions with Their Environment*

Abiotic and biotic stresses during a growing season can significantly limit agronomic crop yield and alter the population dynamics of plant species. Natural plant defense mechanisms often provide only limited protection, and the process of how crops adapt to unfavorable growth environments is poorly understood. ARS research will establish knowledge of how gene networks for fundamental biological processes perceive and translate 'signals' in response to environmental stimuli. Innovations governing fundamental processes that influence crop performance will be incorporated into useful crop protection strategies.

- *Developing High-Value Products*

Plants are increasingly being recognized as sources of compounds that have important roles in nutrition, medicine, or industrial products. Frequently, new phytochemicals are produced as organisms interact with each other, but many materials of interest are produced without external stimulus. ARS research on natural products will help develop new high-value feedstocks for biobased products and pharmaceuticals.

Research Needs:

Knowledge of the processes that regulate growth and development is necessary to develop effective strategies for enhanced crop productivity under variable growing conditions. Hormonal signals that trigger important developmental changes and the genes that control the signaling pathways will be identified. The potential of gene modification to beneficially influence the performance of biological processes will be assessed for ability to enhance crop quality and production efficiency.

Genes important to crop adaptation, tolerance and defense will be identified. The capacity these genes confer on crops to withstand stress or attack will be determined. How crop plants and the organisms that affect them “recognize” and respond to each other will be assessed. Critical sites for intervention will be distinguished by disrupting interactions between organisms.

New sources of novel phytochemicals will be identified. Constituent compounds will be isolated and characterized for appropriate chemical and biological activities. This information will be related to the biosynthetic pathways, genes that control those pathways, and the development of probes to enable rapid screening of plants for new sources of high-value compounds.

Anticipated Products:

- Improved knowledge of how genes and gene networks that mediate crop development and productivity are regulated.
- Improved knowledge of how metabolic processes that mediate crop quality and productivity of agricultural commodities are regulated.
- Technology to enhance flavor, nutritional value, or other quality traits of plant products.
- DNA markers for genes that confer resistance or tolerance to abiotic and biotic stresses. Discovery of genes that govern processes involved in plant adaptation and response to environmental stimuli.
- Knowledge of biological mechanisms and regulatory processes that condition crop response to abiotic and biotic stresses.
- Discovery of genes that condition biological processes associated with crop plant interactions with weeds, fungi, and bacteria.
- Tools and methods to identify specific genes that mediate secondary end-product traits desired by consumers, such as nutritional and pharmaceutical compounds.
- Identification and characterization of functional compounds and components in agricultural commodities and their byproducts that provide the basis for enhanced crop value. New sources of valuable bioactive compounds and potential sources for commercialization identified.

Potential Benefits:

Ability to regulate fundamental biological mechanisms will enable technologies that beneficially alter processes such as photosynthesis, cellulose and lignin accumulation, carbohydrate partitioning to harvested organs, and fruit ripening. Improved efficiency of nutrient assimilation and metabolism will support higher crop productivity and nutritional

value. Knowledge of the basis for crop-environment interaction will lead to enhanced stress tolerance and enhanced ability to maintain productivity in unfavorable growth environments. Breeding for pest and pathogen resistance will be more effective as a result of identifying and characterizing new sources of resistance. Natural products will embody valuable biological, nutritional, pharmacological, or other beneficial materials including domestic source of feedstocks for biobased products.

Problem Statement 4C: Plant Biotechnology Risk Assessment

Genetic engineering offers tremendous promise for improving crop production and protection, making production systems more efficient and sustainable, and providing high-value and high-quality products needed by the world's burgeoning population of consumers. These products can range from foods with enhanced nutrients to biomedical reagents. However, the science of recombinant DNA, both creating the genetically engineered plants and evaluating their impact is in an early stage. Methods used for genetic engineering need to be improved, and the principles that determine the risks of transgenic plants in the environment need to be better elucidated. Research that integrates product development with risk assessment is needed to develop data that will help guide regulatory decisions on management of transgenic crops in a manner that builds public confidence in the safety of products derived from biotechnology.

- *Improving and Assessing Genetic Engineering Technology*

The utility of plant transformation protocols often is limited by low recovery of transformed cells, unpredictable expression of transgenes, inability to control transgene expression, residues of unneeded selectable marker-genes, and limited ability to introduce multiple genes. ARS research will characterize the genetic changes that accompany transformation, determine the mechanisms that alter gene expression and metabolic processes, and elucidate the biological consequences of those alterations.

- *Interaction of Transgenic Plants with Their Environment*

Unbiased and rigorous information is needed to guide regulatory agencies that oversee the deployment of transgenic crops. The possibility of unintended ecological effects of transgenes needs to be maintained as low as possible, using the likelihood of effects from non-transgenic crops as a benchmark for comparison. These include such concerns as deleterious effects from the introgression of transgenes, effects of plant-incorporated protectants, or induced weediness or invasiveness. ARS research will focus on ways to accomplish appropriate recommendations of the National Research Council for biological confinement of transgenic material.

Research Needs:

Methods will be developed that reliably and reproducibly insert single copy genes into a host genome, that limit gene expression, and that remove transgenes from harvested materials once their usefulness is over. Methods will be developed for “pyramiding” multiple genes so that multigenic traits can become feasible targets for transfer. Baseline data will be collected on the changes in global gene expression patterns when plants undergo through a vegetative or sexual reproductive process, for comparison to changes that accompany recombinant DNA manipulation. The deviation of global gene expression patterns from normal will be correlated with plant performance, so that unacceptable levels of variability can be defined.

The evaluation of gene flow from transgenic crops needs to be accompanied by analysis of the ecological effects and the persistence of those genes. Methods will be developed to eliminate transgenes from pollen or, like male sterility, otherwise prevent transgenes from being transmitted during reproduction. The molecular basis of pollen-stigma compatibility will be characterized, so that pollen from transgenic plants can be made incompatible with potential female receptors.

Anticipated Products:

- Improved gene constructs and plant genetic transformation systems that efficiently incorporate genes and enable their stable expression, and that allow expression of multiple genes and limit expression to specified tissues.
- New processes placed in the public domain to the extent possible, promoting public access to them.
- Data that define genetic and epigenetic effects of transformation and comparison of those effects to similar effects of natural reproductive processes, so that thresholds of acceptability can be identified.
- Greater knowledge and technology to remove transgenic DNA from pollen, or other approaches likely to help contain transgene flow in the field and control gene spread. Ability to characterize the nature and likelihood of persistent changes in ecosystems as a result of introducing new transgenic plants, in support of science-based regulation of transgenic crops.

Potential Benefits:

Accomplishments will establish a basis for interpreting variability in global gene and protein expression, as well as shifts in metabolism associated with biotechnologically derived traits. New procedures will expand the scope and reduce the cost of genetic engineering, potentially making it more useful for a wider array of crops. New technology will be advanced that will reduce or eliminate the movement of transgenes from transgenic crops to areas where they are unwanted. Data will help determine whether transgenic crops pose environmental risks. These data will provide a scientific basis for regulatory consideration of transgenics.

Component 4 Resources:

Forty one (41) ARS projects are coded to NP 301 address the research needs identified under Component 4. ARS scientists who are assigned to these projects include:

Albany, CA	Fletcher, Jennifer C.; Hake, Sarah C.; McCormick, Sheila M.; Altenbach, Susan; Blechl, Ann E.; Hurkman, William J.; Vensel, William; Thilmony, Roger; Thomson, James
Ames, IA	Wise, Roger P.
Beltsville, MD	Cooper, Bret; Ehlenfeldt, Mark; Rowland, Lisa; Kuykendall, Larry; Matthews, Benjamin F.; Mattoo, Autar K.; Slovin, Janet P.; Smigocki, Anna C.; Tucker, Mark L.; Lewers, Kim; Natarajan, Savithiry; Polashock, James
Columbia, MO	Flint-Garcia, S; Herman, E.; McMullen, Michael D.; Oliver, Mel; Shaefer, M.; Beuselinck, Paul R.; Bilyeu, Kristen; Krishnan, Hari B.;

	Miernyk, Jan A.
Dawson, GA	Rowland, Diane; Sobolev, Victor, Lamb, Marshall C.; Dang, Phat
Fargo, ND	Dahleen, Lynn S.; Fugate, Karen;
Gainesville, FL	Chourey, Prem S.; Teal, Peter
Hilo, HI	Gonsalves, Dennis; Albert, Henrik
Ithaca, NY	Giovannoni, James J.; Kochian, Leon; Li, Li, Thannhauser, Theo; Yang, Yong; Hokenga, O.
Kearneysville, WV	Artlip, Tim; Bassett, Carole L.; Norelli, John; Wisniewski, Michael
Lubbock, TX	Burke, John J.; Chen, Junping; Mahan, James; McMichael, Bobbie; Payton, Paxton; Velten, Jeffrey; Xin, Zhanguo
Madison, WI	Henson, Cynthia A.; Skadsen, Ronald W.; Wise, Mitchell; Brunet, Johanne; Simon, Philipp W.
New Orleans, LA	Lingle, Sarah E.
Oxford, MS	Baerson, Scott; Dayan, Franck E.; Duke, Stephen O.; Pan, Zhioang
Phoenix, AR	Salvucci, Michael
Raleigh, NC	Burton, Joseph W.; Carter, Tommy; Israel, Daniel W.; Kwanyuen, Prachuab; Taliercio, Earl; Upchurch, Robert
St. Paul, MN	Vance, Carroll
Urbana, IL	Huber, Steven; Ort, Donald R.; Ainsworth, Elizabeth
Washington, DC	Kamo, Kathy; Hammond, John
West Lafayette, IN	Hudson, Karen; Dunkle, Larry