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(Multistate Research Project)

Duration: October 2003 to September 30, 2013

Administrative Advisor(s): [\[Gerald Arkin \]](#)NIFA Reps: [\[AnnMarie Thro\]](#) [\[Michael Fitzner\]](#)**Statement of Issues and Justification**

Project's Primary Website is at <http://www.ars-grin.gov/ars/SoAtlantic/Griffin/pgrcu/s9.html> (direct link can be found under LINKS)

Plant genetic resources, along with water, air, soil, minerals, and crop management practices, are crucial parts of the agricultural production system that sustains humanity. The stability of the agricultural system of the United States and of the Southern Region is based primarily on non-indigenous crops such as peanuts, sorghum, bermudagrass, and many other crops that were imported years ago. Relatively few crops (sunflower, artichokes, nuts, and berries) of commercial importance are indigenous to the United States. These facts establish that for proper homeland security of American food and fiber, plant genetic resources must be preserved for both current and future research use. For years, there was no effective system in the U.S. for long-term conservation and utilization of indigenous and introduced plant genetic resources. The 80th U.S. Congress enacted the Research and Marketing Act of 1946 (Public Law 733), which established Regional Research Funds, some of which were allocated to support a system of four regional projects devoted to conserving and distributing plant germplasm. This system has evolved into the U.S. National Plant Germplasm System (NPGS), a cooperative effort of public (federal and state) and private organizations which seek to conserve plant genetic diversity by acquiring, preserving, evaluating, documenting, and distributing plant germplasm. Four Regional Plant Introduction Stations (RPIS) that have been supported by the Regional Research Funds serve as major management sites for germplasm in the NPGS, and each is responsible for a particular group of crops. Crop collections of importance to the Southern Region have been supported since 1949 through a joint partnership, designated as Multi-state Research Project S-009, between the U.S. Department of Agriculture-Agricultural Research Service's (USDA-ARS) Plant Genetic Resources Conservation Unit (PGRCU) and the Southern State Agricultural Experiment Stations (SSAES). For over 50 years, the S-009 Project has served as a major component of the NPGS, and its activities have markedly improved crop technology in the U.S. and abroad, by providing plant genetic resources and associated information.

Plant genetic resources collected from throughout the world are a valuable source of genetic diversity for the improvement of agricultural and horticultural crops grown in the Southern Region and the U.S. These resources impact current research programs by providing accessible, viable, well-characterized and documented plant genetic resources for the scientific research community in the southern region, the U.S., and the world. Plant breeders, geneticists, plant pathologists, entomologists, archaeologists, anthropologists, ecologists, and other scientists benefit from access to a wide range of genetic variation that they may subsequently utilize in crop-specific

selection, characterization, and evaluation studies (Appendices 1 and 2). Genetic resources will impact future research and generations by ensuring that crop genetic diversity, including wild relatives of crops, are available for utilization in research whose specific objectives are not yet known.

Genetic uniformity in American crop systems increases crop vulnerability to pests, diseases, and stresses. Gene banks ensure conservation of the genetic diversity necessary to quickly respond to problems arising as a result of crop vulnerability. Proper classification of accessions and evaluation of genetic diversity in collections will facilitate the identification of duplicate accessions and gaps within individual collections and help ensure that genetic diversity is conserved in an effective and efficient manner. These activities will also result in the development and adoption of improved management practices that will increase germplasm utility and availability.

Selection of the most appropriate germplasm for the desired objectives of users' research programs will be facilitated by providing well-documented passport, characterization, and evaluation data. Users will be assisted in attaining current and future research goals including the development of new alternative or value-added crops, pest and disease resistant crops, and crops with greater yield potential. Users will be provided with associated information on accessions to most efficiently utilize plant genetic resources in their research program. Researchers will be provided with access to the maximum genetic diversity possible in support of their research goals by minimizing the occurrence of duplicate accessions and acquiring unique materials to fill diversity gaps in the collections. Customers will be provided with molecular markers, breeding lines, and new knowledge about species and accessions in the collection. The greatest benefits to the general public come indirectly via seed and clonal genetic resources distributed through this project which result in new cultivars or value-added crops for use by farmers as well as various companies interested in plants with nutraceutical, pharmaceutical, pesticidal, or industrial uses. These genetic resources and associated information will aid in the discovery of new knowledge by scientists throughout the world.

Research scientists and support staff in public universities, private companies, foundations, government agencies, international research centers, foreign universities, and foreign companies utilize the information and germplasm provided by this project. The general public is the ultimate customer reaping the benefits of a more abundant and stable food supply with improved nutritional characteristics, nutraceutical qualities, and/or environmental sustainability.

### **Related, Current and Previous Work**

The Southern Multi-state Research Project S-009 was established in 1949 to enable the USDA-ARS, other federal agencies, SSAES (Alabama, Arkansas, Florida, Georgia, Kentucky, Louisiana, Mississippi, North Carolina, Oklahoma, Puerto Rico, South Carolina, Tennessee, Texas, Virginia, and the U.S. Virgin Islands), and other cooperators to participate in coordinated efforts to acquire, regenerate, maintain, characterize, evaluate, document, enhance, distribute, and utilize plant germplasm of potential value to agriculture. Similar Multi-state research projects, Western (W-6), Northeastern (NE-9), and North Central (NC-7), have a corresponding mission for their respective regions. Despite similarities among the activities at these locations, unique regional interests and responsibilities direct the specific efforts of each site and crops are divided among the sites to prevent duplication of effort.

The various sites of the NPGS, such as the PGRCU/S-009 Project at Griffin, are interdependent. The PGRCU works with other NPGS sites to facilitate the easy movement of germplasm and associated information. Staff from all NPGS sites meet as the Plant Germplasm Operations Committee (PGOC) to discuss common problems and share solutions. The Germplasm Resources Information Network (GRIN) database

([www.ars-grin.gov/npgs/](http://www.ars-grin.gov/npgs/)) facilitates communication between the sites. The S-009 Regional Technical Advisory Committee (RTAC) meets every third or fourth year jointly with the RTACs of the other three Multi-state projects to facilitate coordination of plant germplasm management nationwide. The PGRCU staff also works closely with the following Crop Germplasm Committees (CGC): Capsicum, Clover and Special Purpose Forage Legumes, Cucurbit, Forage and Turf Grass, New Crops, Peanut, Sorghum, Sweetpotato, and Vigna. The CGCs have significant representation of interested scientists from the Southern Region. Staff at the PGRCU, in cooperation with the Animal and Plant Health Inspection Service (APHIS), the Georgia State Department of Agriculture, and other state and federal agencies, collaborate to minimize the introduction and dissemination of new pathogens and pests through quarantine and inspection of germplasm.

The total germplasm collection maintained at Griffin has increased to 82,566 accessions (Appendix 3) consisting of 1,433 species and 246 genera of crops including vegetable crops (okra, pepper, watermelon, squash, eggplant, gourds), cowpea, mung bean, legumes (clover, guar, winged bean), peanuts, warm season grasses, bamboo, castor bean, sesame, pearl millet, sorghum, and others. These genetic resources are impacting current research programs by providing access to a wide range of genetic variation that researchers utilize in crop-specific selection, characterization, and evaluation studies. In the last 5 years, more than 2,800 orders containing almost 120,000 accessions have been processed and distributed to users in all 50 states and at least 35 foreign countries (Appendix 4). Over 79,000 accessions were sent to users throughout the Southern Region (Appendix 5). Associated information for accessions was updated in the GRIN database with over 1.2 million records created and 0.7 million records modified in the last 5 years. Backing up germplasm by maintaining accessions at two sites reduces the risk of losing valuable germplasm. Since 1996, the percentage of germplasm from Griffin backed up at the National Center for Genetic Resources Preservation (NCGRP) in Ft. Collins, CO, has increased from approximately 36% to 87% (Appendix 3). This year sweetpotato tissue cultures are being shipped to NCGRP to backup this clonal collection. The number of accessions in the germplasm collection at Griffin has increased by 7,729 accessions since 1996 (Appendix 3). Currently, 84% of the accessions in the collection are available for distribution (Appendix 3).

## Objectives

1. Conserve genetic resources and associated information for a broad spectrum of crops and related species.
2. Develop and apply new or improved evaluation procedures and marker-based approaches to assess diversity of genetic resources in the collections and evaluate materials for useful traits.
3. Transfer technology to researchers and plant breeders in the Southern Region and worldwide in the form of plant genetic resources and associated information.
- 4.

## Methods

Methods: The Multi-state Research Projects (S-9, W-6, NC-7, and NE-9) that support the four Regional Plant Introduction Stations are major components of the national effort to provide genetic resources and associated information for research by public and private-sector cooperators throughout the U.S. and worldwide. Because of the continual need for new and improved crops and for plant genetic resources for research, the S-009 Project is, by nature, a long-term effort. Consequently, its organization, and its technical aspects in general, change relatively little from year-to-year.

The S-009 Multi-state Project is effective because of close cooperation between federal, state, and private sectors. The USDA-ARS currently provides 84% of the PGRCU's annual budget (Appendix 6), including funds for 29 federal employees (Appendix 7), general operations, and equipment. Federal facilities include buildings for seed storage, processing and distribution, headhouse offices and laboratories, screenhouse, field maintenance shop, and storage building. Over 12,500 sq. ft. of federal greenhouse space is available for clonal germplasm maintenance, quarantine control, and seed regeneration. Two refrigerated cold rooms (1,600 sq. ft. total) at 4 C and two freezer cold rooms (1,050 sq. ft. total) at -18 C are utilized to store the entire seed collection. Seed regenerations are conducted on 19 acres of federal land located at the ARS Fruit and Nut Research Unit, Byron, GA.. The USDA-ARS also provides funds for plant exploration and for specialized technical assistance at the USDA-ARS Area and National levels. The Directors of the SSAESs provide 16% of the current federal-state partnership's annual budget (Appendix 6) in the form of S-009 funding taken "off-the-top" of the Regional Research Funds (RRF) received from the USDA Cooperative State Research, Education, and Extension Service (CSREES). Funds are utilized for 10 state employees (Appendix 7) and general operations. The faculty of each land-grant university of the Southern Region provides representatives to the S-009 Regional Technical Advisory Committee (RTAC) which provides technical advice to the project. The State of Georgia, through the University of Georgia, College of Agriculture and Environmental Sciences, Georgia Experiment Station in Griffin, Georgia, provides facilities and significant other local assistance to the S-009 Project. Administrative operations, offices, and molecular laboratory facilities are located in a University of Georgia building. Other state facilities utilized by the S-009 Multi-state Project include buildings for seed storage, germination laboratory, tissue culture clonal preservation, other laboratories, offices, and over 3,600 sq. ft. of state greenhouse space. Seed regenerations and field research are conducted on 15 acres of state land located near the Griffin campus.

Many other researchers and institutions in the U.S. actively manage germplasm within their specialties, but none has the total "system" approach of the NPGS. Individual states and the private sector lack the coordinated structure and critical mass of trained curatorial staff, assembled during the last 50 years, necessary to duplicate the germplasm management capabilities represented by our site and others in the U.S. National Plant Germplasm System. Some of the NPGS's major components include:

A. The National Genetic Resources Advisory Committee (NGRAC) advises the Secretary of Agriculture and NPGS personnel on plant, animal, and microbial germplasm and plant genome matters.

B. The Plant Germplasm Operations Committee (PGOC) evaluates, ranks, and recommends funding for plant exploration proposals and advises the NGRAC, USDA-ARS National Program Staff, and USDA-ARS line managers regarding the NPGS.

C. About 40 Crop Germplasm Committees (CGC) have been established to help advise the NPGS and its curators regarding genetic vulnerability of particular crops, descriptor lists, germplasm characterization, evaluation and enhancement programs, and needs for additional germplasm acquisitions including preservation of germplasm collections in danger of being lost. Many of the CGCs are chaired by or include faculty members of the land-grant universities in the Southern Region who provide invaluable technical assistance to the NPGS for conserving and managing plant germplasm.

D. The S-009 Regional Technical Advisory Committee (S-009 RTAC) provides technical guidance to the S-009 Multi-state Research Project and to the PGRCU. It is composed of an administrative advisor, a regional coordinator, representatives of each SSAES plus Puerto Rico and the U.S. Virgin Islands, and a number of ex officio members (Appendix 8).

E. The National Center for Genetic Resources Preservation (NCGRP), formerly the National Seed Storage Laboratory, preserves the base collection, which is the security backup for the entire NPGS. NCGRP utilizes long-term storage conditions and conducts research regarding optimal germplasm maintenance practices.

F. The National Germplasm Resources Laboratory (NGRL) directs international activities of germplasm exchange and acquisition, quarantine matters, ecogeographic studies, GRIN database management, CGC coordination, and related activities.

G. The Plant Genetic Resources Conservation Unit (PGRCU) at Griffin, Georgia is staffed by research scientists, curators, and technical support. The Unit manages the facilities, equipment, and land necessary to acquire, maintain, regenerate, characterize, evaluate, enhance, and distribute more than 82,000 accessions (representing 246 genera and 1,433 species) in its collection, and the associated passport and descriptive data.

Objective 1: Customers and users of the germplasm collection are continually in need of new sources of genetic variation to evaluate in their research program. Additional plant genetic resources for the germplasm collection may be acquired from several sources including collecting trips, germplasm exchanges, donations from University or industry breeding programs, and private donations. Opportunities for acquisition change from year to year and are often difficult to anticipate in a 10-year planning process. Curators as well as CGC and S-009 RTAC members remain current on the status of local, state, regional, national, and worldwide crop-specific collections that may be in danger of being lost and act quickly to prevent loss of valuable genetic resources if at all possible. All acquisitions are carefully evaluated for duplication, redundancy, and usefulness in improving the genetic diversity of the present U.S. collection, often in consultation with CGC and S-009 RTAC scientists. As possible acquisitions can not be clearly defined in advance, only known plant exploration trips that have already been proposed or will be proposed by project scientists in the next few years will be noted. Plant exploration trip proposals have been and will be submitted to the U.S. Plant Exchange Office (PEO) for competitive funding.

Wild perennial *Arachis* spp. are utilized for forage production in the southeastern U.S., but few accessions are currently available for evaluation. A collection trip, funded by the U.S. Plant Exchange Office, is planned for May 26 through June 10, 2003 to collect wild *Arachis* germplasm in Paraguay. Germplasm of wild *Arachis* will be collected from areas in Departments of Concepcion and Amambay not visited in a collection effort conducted in 2002. Germplasm will be collected as seeds or as vegetative material with at least 50 accessions planned to be collected. Collected material will be shared with and evaluated by S-009 RTAC and other scientists working on *Arachis* spp.

Many native *Ipomoea* spp., that may have commercial potential or potential uses in sweetpotato improvement or other research activities, are not represented in the U.S. germplasm collection. Sixteen different *Ipomoea* spp. are targeted for collection in the southwestern U.S. and possibly northern Mexico beginning in September through December 2003 and in subsequent years through at least 2006. Collected material will be evaluated by S-009 RTAC and other southeastern U.S. scientists working on *Ipomoea* spp.

Viability testing is an essential component of any genebank. Users need viable seed to utilize in their research and curators need to know accession viability to prioritize regenerations. Standard germination tests will be conducted on the entire range of crop and wild relative accessions in the collection with at least 6,000 - 8,000 accessions/yr tested. Germination testing will follow standard procedures developed by the Association of Official Seed Analysts (AOSA, 2000) for major crop species and/or by cooperators at the National Center for Genetic Resources Preservation (NCGRP) for minor crops and wild relatives. Germination tests will be conducted with no replication

using 100 seeds for accessions with adequate seed numbers and follow a sliding scale decreasing to 10 seeds on accessions with only 200 seeds. Germination test results will be documented on GRIN.

Seed of each accession maintained in the collection will be preserved in appropriate cold storage to maximize long-term seed viability. Two refrigerated cold rooms at 4 C and two freezer cold rooms at -18 C store all accessions. Species with seed that can not tolerate -18 C storage will be maintained in coffee bags at 4 C. All other species will be maintained as split samples in 4 and -18 C. The bulk of the seed of each accession will be maintained in heat-sealed aluminum foil bags at -18 C, while a small distribution sample to handle expected requests for at least the next 5 years will be maintained in glycine-lined coffee bags at 4 C. Back up samples will be sent to NCGRP for the remaining 13% of collection not already backed up.

Through the advice provided by S-009 RTAC and other scientists, regeneration protocols for increasing seed and clonal plant material will be determined and improved regeneration techniques will be developed to increase seed and clones from species requiring seasonal extension and photoperiodism. Standard crop-specific protocols have been developed in the past and are already in use for most crops (Operations handbook for germplasm maintenance, 1994, PGRCU, Griffin). Crops that will be regenerated include peanuts, cowpeas, special-purpose legumes, annual clovers, warm-season grasses, watermelon, peppers, sweetpotato, okra, *Curcubita moschata*, *Ipomoea* spp., miscellaneous cucurbits, *Solanum* spp., castorbean, *Hibiscus* spp., guar, winged bean, sesame, and *Leucaena* spp. Sorghum, cowpea, misc. cucurbits, and other legumes with photoperiod concerns will be regenerated in St. Croix, Puerto Rico, and other sites in collaboration with local scientists. Additional regenerations will be conducted with S-009 RTAC scientists or other collaborators where possible. Curators will conduct at least 2,000 seed and clonal regenerations per year at both Byron and Griffin, GA. Selection of accessions will be based on importance, seed viability, age (> 10 year old seed), original seed only, and low seed numbers. Self pollinated species will be planted in the field or greenhouse. Cross pollinated species pollinated by insects will be grown in the field in screen cages with honey bees utilized for pollination. Species requiring wind pollination, such as grass species and *Hibiscus* spp., will be planted in isolation or within tall plant buffers. Sweetpotato clones will be maintained and regenerated using tissue culture methods or converted to botanical seed, as appropriate. Continuous monitoring for pests will be accomplished by collaboration with a Plant Pathologist and/or Entomologist.

Correct taxonomic identification of plant genetic resources facilitates efforts to conserve biodiversity. The grass, sweetpotato, Capsicum, and other CGCs and S-009 RTAC scientists have expressed concerns over apparent mis-identification of crop-related species. Representative examples of taxa to be examined will be grown to flowering in the field or greenhouse and keyed to species by the curator, or identified in collaboration with a cooperating botanical authority. Herbarium specimens will be prepared for unknown species, and submitted to a botanical authority for identification. Once taxonomic questions are resolved, the herbarium specimens will be stored on site for future reference. Accessions will be further characterized via sequencing of a chloroplast gene (Prather et al., 2000), a nuclear gene (Mathews et al., 2000; Small et al., 1998) and the internal transcribed spacer (ITS) regions of the nuclear ribosomal DNA (Miller and Mann, 1999). Sequence comparisons will be conducted to establish, support, or question species classification. Relationships among species will be determined by sequence analysis comparisons using currently available software programs such as MEGA (Kumar et al., 1993), PAUP (Swofford, 1991), CLUSTAL, and others.

Objective 2: Careful characterization of accessions within the germplasm collection is necessary to ensure accession homogeneity. Curators will observe and collect

characterization or evaluation descriptors for each accession of their crops. Curators will work cooperatively with S-009 RTAC scientists and other collaborators to evaluate accessions within the germplasm collection for economically important traits. Crop descriptors to be utilized are listed on the GRIN website for each crop and will be modified by curators and collaborators as required. Digital images of crop species and characterization data on accessions regenerated throughout the season will be incorporated into GRIN. As procedures for regeneration for various crops are crop specific, the procedures for regeneration will be determined by the curator of the crop; while evaluation procedures will be determined in cooperation with S-009 RTAC scientists and other collaborators. Evaluations and other research projects will be conducted on species, other than those noted in the following sections, in response to needs identified by users, S-009 RTAC scientists, or curators during the term of this project.

New uses for plant genetic resources have been identified as a need through consultation with customers on the new crops, clover/special-purpose legumes, and other CGCs. Value-added traits within plant genetic resources will be identified and evaluated for their usefulness in providing valuable health promoting and protecting phytochemicals. Velvetbean accessions will be evaluated for their nematode (*Meloidogyne incognita* or *M. arenaria*) and fungus gnat reduction capacity. Velvetbean leaf, stem, and flower tissues harvested from field plots will be dried, ground, mixed with soil, and inoculated with eggs of *M. incognita* or *M. arenaria*. Tomato seedlings will be planted into the soil and roots examined for galls after 6-8 weeks. Tissues from velvetbean accessions which inhibit egg hatching will be used for chemical analysis to identify the active component(s). Tissues will also be added to fungus gnat (*Bradysia coprophila*) cultures to observe whether there is any effect on larval development or mortality. Plant and seed production studies will be conducted at Griffin, Ashburn, and Americus, GA for determination of best genotypes from guar, hyacinth bean, subterranean clover, and velvetbean for use as new alternative crops in the southeastern U.S.

Pungency is a primary quality determining factor in chili peppers (*Capsicum* spp.). The presence or absence of pungency is a characteristic that is frequently utilized as the basis of selection of specific genotypes from the genebank. However, there are limited data on this characteristic. In order to remedy this situation, fruit of at least 400 accessions in the *Capsicum* core collection will be analyzed for total capsaicinoids. Capsaicinoids will be quantified using an enzyme immunoassay as described by Perkins et al. (2002).

Approaches for pathogen research are dictated by priorities established by crop-specific CGCs for diseases of importance for control. Newly acquired germplasm will be tested by enzyme-linked immunosorbent assay (ELISA) for possible contaminating viruses (Gillaspie et al., 1995). Plants showing symptoms of disease in regeneration plots are tested serologically. If there are symptoms on plants that cannot be explained by the viruses detected, a search for a new virus will be done. These possible new pathogens will be tested biologically in a host range test, checked via transmission electron microscopy, and then obtain pertinent antisera and/or primers for RT-PCR identification.

The identification of pathogen-resistant germplasm will involve two approaches. First, plants of cowpea and peanut in regeneration plots will be observed for pathogen symptoms and lines showing no symptoms of cucumber mosaic virus in cowpeas or tomato spotted wilt and/or peanut stunt virus in peanut will be tested serologically. The second approach will be to actively screen members of the cowpea core collection and wild peanut collection for virus resistance. If DNA markers associated with resistance are found, they will be tested in greenhouse and field tests and then utilized in screening tests. Plant lines with known resistance to important pathogens will be

tested against SSR markers such as those published by Li et al. (2001) for cowpea and others published for peanut by Hopkins et al. (1999). SNP markers (Kaderali et al., 2003) will also be tested to determine whether any of the markers are associated with resistance. Markers showing possible association with resistance will be tested further with resistant and susceptible lines under field conditions. Marker-based approaches will be utilized in cooperation with S-009 RTAC scientists or other collaborators to clearly identify diverse accessions that may contain useful traits. To develop novel SSR markers in peanut, an SSR enriched genomic library generated from DNA isolated from *Arachis hypogaea* will be probed, hybridizing colonies will be sequenced via the Beckman DNA sequencer CEQ 8000 and sequences edited. Sequence data generated will be screened against GenBank to identify homologies and candidate primers will be screened using a set of 24 genetically divergent *A. hypogaea* accessions to determine if the SSR locus is polymorphic. Primers amplifying polymorphic loci will be dye-labeled and tested with a larger number of plant genotypes in order to determine their usefulness.

To maximize efficiency in the maintenance and utilization of germplasm collections and validate the core collections, AFLPs and SSRs will be employed in cooperation with S-009 RTAC scientists or other collaborators to examine germplasm genetic diversity. First, to address the amount of introduced genetic diversity arising from the acquisition of wild *Arachis* species, new accessions will be fingerprinted using the Beckman AFLP primer set. Also, 600 *Arachis hypogaea* accessions comprising the core collection will also be fingerprinted using SSR markers. Secondly, the *Vigna* collection will be sampled to determine the amount and partitioning of genetic diversity within the collection. Thirdly, the entire sweetpotato collection will be analyzed using AFLPs via a collaborative effort between Southern Regional scientists. A core collection for sweetpotato will be selected based on these and other data.

Objective 3: Plant genetic resources in the form of seeds, in-vitro cultures, plants, and rhizomes will be sent to S-009 RTAC scientists and other researchers in the U.S. and worldwide in response to their requests. Once received, all requests are given to the curator for that crop who determines the availability of the material, evaluates the research use of the material, and approves or disapproves the request. A standard seed quantity (often 100 seeds), dependent upon the crop, seed availability, and difficulty in regeneration, is shipped. Clonal materials are shipped to the user as small plantlets or rarely in-vitro cultures.

The Germplasm Resources Information Network (GRIN) manages all the passport, characterization, and evaluation data for the collection maintained in this project. Accessions are characterized and evaluated for crop-specific descriptors developed in consultation with the appropriate CGC. Data from these descriptors is then entered into the GRIN system for access by all public users of genetic resources. Germplasm users will be encouraged through contacts with CGC members and S-009 RTAC members to submit their evaluation data on accessions to this project for entry into GRIN. A complete record is maintained in GRIN of every distribution of an accession to users. Curators and staff routinely respond to requests for information on various topics relative to specific genetic resources issues or for information on the NPGS. Requests for information are received by phone, FAX, e-mail, and U.S. Mail.

## Measurement of Progress and Results

### Outputs:

- Plant explorations and other acquisitions will fill taxonomic gaps in collections of crop-related species and newly introduced materials will represent a source of genes and gene complexes for crop improvement, the development of alternative crops, and other research activities.



- Germination tests will be completed on seed samples of all newly-regenerated accessions. Germination tests will also be conducted on the backlog of accessions maintained in the collection with the goal of testing at least one inventory sample of each accession maintained in the germplasm collection. Regeneration priorities will be established based on seed viability as measured in germination tests rather than by seed age as germination data becomes available. Seed samples of all new regenerations and all accessions of species commonly distributed will be split into distribution and bulk storage samples.
- Seed regenerations from thousands of regenerated accessions from the germplasm collection will provide users with high quality plant genetic resources available for use in their research programs.
- Studies will assist in the taxonomic identification of plant materials that have not been previously classified and for the re-identification of plant materials whose identification is suspect. When determined, proper taxonomic identification will be documented in GRIN. Unique DNA sequence data will be produced from a wide array of plant species. Placement of these data into a publicly available database (e.g. GenBank) will facilitate their use in systematic studies with these, and other crop-related species. DNA sequence data acquired from individual species will serve as a reference against which additional existing and new introductions may be compared.
- Phenotypic characterization and descriptor data will provide all users with the data and information needed to conduct their research program. Use of portable data logging devices and barcodes will improve speed and accuracy of data handling and reduce identification errors. Novel and valuable traits for use such as nutraceuticals, phytopharmaceuticals, industrial, and pesticidal products will be identified, analyzed, and utilized by scientists, industries, and producers.
- Output 6: Identification of pathogen resistance in the germplasm will be a big step toward the control of pathogens through breeding as well as through elimination of spread. A variety of molecular markers will be isolated, characterized, and evaluated and may be used to estimate genetic diversity among accessions of crop species within the germplasm collection. The genetic analyses performed will differentiate between accessions and partition the genetic variance for the collections which will enable more efficient curation and acquisition priorities. All requests for genetic resources will be handled promptly with most requests approved by the curators within the first week and shipped to users within the second week. Requests for large numbers of accessions will take longer depending on the number of accessions requested. An average of at least 20,000 accessions/year will be shipped to requesters from the collections. All passport, characterization, and evaluation data available for each accession will be documented in the GRIN database for use by curators internally and users in the Southern Region, U.S., and worldwide. A total of 120,000 to 150,000 data records/year will be entered into GRIN. All requests for information on genetic resources will be handled promptly, completely and professionally.

### **Outcomes or projected Impacts:**

- Demand for genetic resources maintained at Griffin has greatly increased in the last few years. In 1992-1999, an average of 13,500 accessions of all crops maintained at Griffin were sent each year to customers worldwide upon request. In the last three years, demand has increased to an average of 31,800 accessions requested each year. Demand for sorghum, the largest of the national seed collections maintained at Griffin, has increased from 3,400 seed samples each year in 1992-1999 to 17,300 seed samples each year in 2000-2002. Already in 2003, over 35,000 accessions have either been distributed to customers or requested by customers. This increase in demand indicates that more users are recognizing the vital role that genetic resources play in their

research program. Accessions distributed from the collections have been and will continue to be utilized in a vast array of research studies throughout the Southern Region and the world. Each year it is noted that more and more accessions are used by people in research outside of traditional plant breeding. Requests come from scientists in agronomy, genetics, molecular biology, plant pathology, entomology, botany, anthropology, archeology, medical fields, pharmaceutical, nutritional, ecology, homeland security, energy, animal science, artistic, and aquatic areas. For example, germplasm requests include new uses such as public demonstrations at Epcot Center, Department of Defense uses, classroom plant and seed identification, church demo project (Heifer Project Int.), switchgrass biofuel use, archaeobotany and anthropology use (India, Africa, and Asia agricultural origins), sorghum use for paper pulp, peanut protein profile to identify allergy reaction differences, velvetbean for wildlife management, gourmet chile for Pacific Rim cuisine, botanical artist painting Solanaceae, develop plant cell cultures for drug discovery, identification of archaeological specimens, bermudagrass adaptability on fields fertilized with animal waste, vegetable juice to help nutrients get into blood stream of cancer patients, kenaf for biofiltration research, sorghum syrup making, seed for baking and candy industry, exhibit of plants used for paper making, green manure crop in California deserts, fish control research, fiber and dye plants used by fiber artist, and phytopharmaceutical and energetic uses. Impact of the genetic resources distributed from these collections affect many scientific fields.

### **Milestones:**

( ): This project continues to acquire, characterize, maintain, evaluate, document, and distribute genetic resources as it has for the past 54 years. Much of the process of genetic resource preservation changes little from year to year. There are some much-needed milestones that will be achieved during the 10-year duration of this project. This includes obtaining germination data on all accessions to determine viability for users and for regeneration priorities, making corrections in taxonomic identification of accessions, having better long-term preservation of the collection by maintaining the bulk of the accessions in -18 C storage, and, in particular, using molecular methodology to better characterize the genetic variability located within the collections.

### **Projected Participation**

Include a completed [Appendix E](#)

### **Outreach Plan**

The availability of and associated information on the genetic resources maintained at Griffin will continue to be readily available worldwide on the GRIN website on the Internet. Users can search for accessions and request genetic resources directly from this web site. Information on genetic resources, management procedures, characterizations, evaluations, and distributions will be published by PGRCU scientists and S-009 research participants in refereed and non-refereed publications, proceedings articles, abstracts, informational bulletins, and publications for the general public. Information on the S-009 project, including members, annual reports, and minutes, will be maintained on the S-009 website ([www.ars-grin.gov/ars/SoAtlantic/Griffin/pgrcu/s9.html](http://www.ars-grin.gov/ars/SoAtlantic/Griffin/pgrcu/s9.html)).

### **Organization/Governance**

The technical committee uses a standard form of governance with officers consisting

of a chair, secretary, and past-chair. A secretary is elected to a one-year term and becomes chair the following year. Each year the project reports results, assesses progress, and receives guidance in the following manner: - annual meetings with the S-009 Regional Technical Advisory committee. - annual meetings with each of the nine CGCs (Capsicum, Clover and Special Purpose Forage Legumes, Cucurbit, Forage and Turf Grass, New Crops, Peanut, Sorghum, Sweetpotato, and Vigna) that deal with crops maintained at Griffin.

### Literature Cited

Association of Official Seed Analysts. 2000. Rules for testing seeds. AOSA. Gillaspie, A. G., Jr., M. S. Hopkins, D. L. Pinnow, and R. O. Hampton. 1995.

Seedborne viruses in preintroduction cowpea seed lots and establishment of virus-free accessions. *Plant Dis.* 79:388-391.

Hopkins, M.S., A.M. Casa, T. Wang, S.E. Mitchell, R.E. Dean, G.D. Kochert, and S. Kresovich. 1999. Discovery and characterization of polymorphic simple sequence repeats (SSRs) in peanut. *Crop Sci.* 39:1243-1247.

Kaderali, L., A. Deshpande, J.P. Nolan, and P.S. White. 2003. Primer-design for multiplexing genotyping. *Nucleic Acid Res.* 31:1796-1802.

Kumar, S., K. Tamura and M. Nei. 1993. MEGA, Molecular Evolutionary Genetics Analysis version 1.0. Institute of Molecular Evolutionary Genetics. The Pennsylvania State University, University Park, PA.

Li, C.D., P.E. Eckstein, M.Y. Lu, B.G. Rossnagel, and G.J. Scoles. 2001. Targeted development of a microsatellite marker associated with a true loose smut resistance gene in barley (*Hordeum vulgare* L.). *Molecular Breeding* 8 (3): 235-242.

Mathews, S., R.C. Tsai and E.A. Kellogg. 2000. Phylogenetic structure in the grass family (Poaceae); Evidence from the nuclear gene phytochrome B. *Amer. J. Bot.* 87:96-107.

Miller, R.E. and M.D. Mann. 1999. Phylogenetic systematics of *Ipomoea* spp. (Convolvulaceae) based on ITS and waxy sequences. *Systematic Botany* 24:209-227.

Perkins, B, R. Bushway, K. Guthrie, T. Fan, B. Stewart, A. Prince and M. Williams. 2002. Determination of capsaicinoids in salsa by liquid chromatography and enzyme immunoassay. *J. AOAC International* 85:82-85.

Prather, L.A., C.J. Ferguson, and R.K. Jansen. 2000. Polemoniaceae phylogeny and classification: implications of sequence data from the chloroplast gene *ndhF*. *Amer. J. Bot.* 87:1300-1308.

Small, R.L., J.A. Ryburn, R.C. Cronn, T. Seelanan, and J.F. Wendel. 1998. The tortoise and the hare: Choosing between noncoding plastome and nuclear *adh* sequences for phylogeny reconstruction in a recently diverged plant group. *Amer. J. Bot.* 85:1301-1315.

Swofford, D.L. 1991. PAUP: Phylogenetic analysis using parsimony, version 3.0. - Computer software. U.S. Natural History Survey, Champaign, IL.

### Attachments

[[Appendix1-publications.doc](#)] [[Appendix\\_8.htm](#)] [[appendix2-publications.doc](#)] [[appendix3-7.doc](#)]

### Land Grant Participating States/Institutions

AL, AR, FL, GA, GU, HI, KY, LA, MS, NC, OK, PR, SC, TN, TX, VI, VA

**Non Land Grant Participating States/Institutions**

USDA/ARS

**Signatures:**

s:/Gerald Arkin

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