

Project Number: S-009
Title: Plant Genetic Resources Conservation and Utilization
Project Duration: From October 1, 2023 to September 30, 2028

Statement of Issues and Justification

A. Need as indicated by stakeholders

Plant genetic resources acquired throughout the world and conserved at the Griffin, Georgia location are crucial components of agricultural production systems that sustain humanity. This project is part of a comprehensive nationwide program, the National Plant Germplasm System (NPGS), to preserve plant genetic resources for present and future researchers and plant breeders. Plant genetic resources are the raw materials essential for the genetic enhancement of crops and are used extensively in support of basic scientific research in numerous disciplines. The genetic resource collections maintained by the USDA, ARS, Plant Genetic Resources Conservation Unit (PGRCU) are recognized globally as valuable sources of genetic diversity for use by the agricultural and horticultural research communities. The plant materials in these collections serve as the foundation materials required by, and utilized in, crop improvement efforts in the areas of plant breeding, biotechnology, plant genetics, plant pathology, entomology, plant biology, and many others.

B. Importance and extent of problem

Food security in the U.S. is largely based on the cultivation of non-indigenous crops that were imported many decades ago. The genetic resources of these crops and their wild relatives are often no longer available from their original locations where the diversity of the crop is often the greatest. The loss or reduction in the genetic diversity in crop species that contribute to the world's food supplies is a potential threat to U.S. and global food security (Khoury et al., 2014). Best management practices are required to ensure efficient, effective, long-term, and secure preservation of sorghum, millet, peanut, vegetable crops, sweetpotato, warm-season grasses, tropical/subtropical legumes, annual clover, cowpea, industrial crops, other crops, and their crop wild relatives (CWRs).

Viability testing and continuous monitoring are required to ensure the highest quality of stored accessions and to optimize regeneration intervals. Secure storage of plant genetic resources at secondary locations is needed to ensure against the loss of plant genetic resources due to natural or manmade disasters. Users of the plant materials in germplasm collections must be able to identify and obtain the most appropriate genetic resources for their research needs. The genetic resources available to meet those needs must be efficiently and effectively distributed. Phenotypic characterization and digital imaging serve to fully document morphological traits. Abiotic and biotic stress resistance data, including drought tolerance, disease resistance, and root system analyses, are needed to identify accessions potentially useful in adapting crops to climate change. Biochemical evaluation data such as oil content, fatty acid composition, mineral content, flavonoid content, capsiate, galactomannan, and protein content are needed to identify accessions with traits offering improved nutritional value. Evaluation of genome sequences and structures in CWRs can provide insight into the evolution, domestication, and expression of genes contributing to disease and pest resistance and important morphological traits in

the cultivated crop species. All these and other data once incorporated into the Germplasm Resources Information Network (GRIN-Global) and other databases, will be accessible worldwide for users to best select germplasm to meet their research needs.

C. Technical feasibility

Cold storage facilities are available for proper conservation, and experienced personnel are available to conduct the mission of acquiring, characterizing, conserving, evaluating, documenting, and distributing genetic resources of agronomic and horticultural crops.

D. Advantages of multistate effort

Crop germplasm collections important to the Southern Region have been supported since 1949 through a partnership designated as the Multistate Research Project S-009 between the USDA-Agricultural Research Service (USDA-ARS) and the Southern State Agricultural Experiment Stations (SSAES). For decades, S-009 has served as a major germplasm repository within the NPGS. Its activities have markedly improved crop technology in the U.S. and abroad, through the acquisition, conservation, characterization, evaluation, and distribution of plant genetic resources and associated information for use in scientific research and crop improvement programs.

E. Benefits or impact of research

The potential benefits expected from attaining the project's objectives include ensuring that S-009 plant genetic resources are well preserved, secure, and able to serve as critical sources of genes for research and crop improvement for vulnerable or threatened sorghum, peanut, chili pepper, watermelon, okra, sweetpotato, tropical/subtropical legume, warm-season grass, annual clover, *Vigna* spp., industrial crop, and other crops and their CWRs. Genetic characterization and phenotypic evaluation information for priority genetic and agronomic traits will enable users to more efficiently identify accessions for their research and breeding activities. Progress in crop genetic improvement projects in the Southern Region, the U.S., and throughout the world will be accelerated as a result of the information on and availability of the genetic resources furnished by this project. Sources of genes for diversifying the genetic background of the previously mentioned crops and their CWRs will be more readily assured; thereby, contributing to the productivity, genetic base, stability, and sustainability of U.S. agricultural production systems.

F. Stakeholders

The stakeholders, customers, and consumers for this project include researchers and plant breeders worldwide who request and utilize these plant genetic resources and associated information for their programs. Many stakeholders and customers are directly involved with this project through the S-009 technical committee or through ten crop-specific Crop Germplasm Committees (CGC) that meet periodically to discuss plant genetic resource acquisition, conservation, management, evaluation, and distribution of the crops curated within this project. Information is provided for users to select the most appropriate genetic resources for their research needs. The users of S-009 plant genetic resources and associated information range from large multinational companies to local specialty seed

companies; from small organic production systems to large high yield production systems; and from basic and applied genetic research to theoretical genomic research.

Related, Current, and Previous Work

S-009 was established in 1949 to enable federal and state cooperators to participate in coordinated efforts to acquire, regenerate, maintain, characterize, evaluate, document, distribute, and utilize plant genetic resources of value to agriculture. Plant genetic resources are the building blocks of genetic variability upon which scientists conduct research and develop improved cultivars and products. S-009 germplasm has been utilized in research resulting in hundreds of publications and numerous crop cultivars. The collection has grown from 811 accessions of 41 genera in 1949 to one of the largest collections of the four NPGS regional multistate projects with over 104,000 accessions of more than 280 genera and over 1600 species. Over 87% of S-009 accessions are available for distribution and over 95% are safely backed up at Ft. Collins, CO (Appendix 1, Table 1). Intervals between seed regenerations are maximized to reduce loss of valuable genetic variability (genetic drift) by storing accessions at -18°C rather than 4°C. Hundreds of requesters per year use these genetic resources in their plant breeding, plant pathology, entomology, molecular biology, genomics, archaeology, anthropology, crop management, ecology, medical, and alternative use studies. This project has had significant impact on numerous research programs, increased agricultural productivity, and provided other public benefits. The new project will continue to provide current and additional plant genetic resources and information to scientists in the region, the nation, and the world.

The conservation of plant genetic resources is essential to preserve and ensure the availability of the genetic diversity vital for safeguarding global food security. Plant genetic diversity provides plant breeders with the material to develop cultivars with increased yield, improved quality, flavor, nutritional value, and resistance to biotic and abiotic stresses. Global food security depends on the extent to which the genetic improvement of crops can meet the challenges of human population increases, climate change, and reduced environmental resources (Ronald, 2011; Upadhyaya et al., 2011; Pautasso, 2012). The Plant Genetic Resources Conservation Unit (PGRCU)/S-009 Multistate Project at Griffin is one of 19 seed and clonal germplasm repositories in the NPGS. The National Laboratory for Genetic Resources Preservation (NLGRP) in Ft. Collins, CO, stores reserve seed of accessions for these 19 other repositories. The NPGS repositories, as well as germplasm repositories in other countries and international centers, have long preserved plant genetic resources for use by present and future researchers throughout the world (Fowler and Hodgkin, 2004). Presently, the NPGS preserves over 605,000 accessions (USDA, ARS, NGRP, 2023). Plant genetic resource collections worldwide consist of a wide range of material with no selection or different levels of selection or development. These collections may include CWRs, primitive landraces, farmer's selections, breeding lines, heirloom varieties, pure lines, germplasm, genetic stocks, and modern cultivars. The goal of germplasm collections is to preserve the genetic diversity found in all species (Nelson, 2011). The S-009 Multistate project strives to conserve the range of genetic variation and diversity located within each crop group maintained at this location.

This project is one of four regionally based multistate projects cooperating with USDA, ARS Units at other locations. Each location is charged with the acquisition, characterization, maintenance, evaluation, documentation, and distribution of specific agronomic and horticultural

crops. Crops are divided among the four projects to prevent duplication of effort. These projects include NE-009 at Geneva, NY; NC-007 at Ames, IA; and W-006 at Pullman, WA. Techniques and procedures for plant genetic resource conservation and collection backup are coordinated with ARS projects at the National Laboratory for Genetic Resources Preservation, Ft. Collins, CO. Acquisition of new accessions and documentation efforts are coordinated with ARS projects at Beltsville, MD. Regeneration of sorghum and other photoperiod-sensitive crops is coordinated with ARS projects at Mayagüez, PR. Regeneration of crops suited for arid conditions is coordinated with ARS projects in Parlier, CA.

Objectives

1. Conserve and regenerate genetic resources of crops and their crop wild relatives (CWRs) of importance to the Southern Region including sorghum, peanut, watermelon, chili peppers, warm-season grasses, cowpea, clover, tropical/subtropical legumes, industrial crops, and others.
2. Conduct characterizations and evaluations of the conserved crops and their CWRs for commercially and agriculturally important traits.
3. Distribute genetic resources and associated information to researchers and plant breeders in the Southern Region and worldwide.

Methods

Objective 1.

The plant genetic resources collection at the Griffin location consists of over 104,000 accessions with 99% maintained as seeds and 1% maintained as clones. Seed of each accession in the collection will be preserved using appropriate cold storage practices to maximize long-term seed viability and to reduce the frequency of regeneration. Original seed and seed of species rarely requested will be maintained solely at -18°C. All other accessions will be maintained as split samples at 4°C and at -18°C. When the distribution sample at 4°C is depleted, seed will be taken from the -18°C sample to replenish the distribution sample. Currently, 87% of accessions maintained as seed have at least one inventory in -18°C. Samples will continue to be split for newly regenerated and acquired accessions.

The number of regenerations conducted each year is dependent upon available resources. Regeneration numbers are estimated as a minimum based on current funding levels. Seed regenerations for most crops will be conducted with 50 or 100 plants per accession for self-pollinated and cross-pollinated species, respectively. At least 1,670 seed-producing accessions will be regenerated each year locally or in collaboration with cooperators at remote locations. Crops regenerated in the greenhouse or in fields at Griffin or Byron, GA, will include approximately 75 tropical and sub-tropical legumes, 30 industrial crops, 50 warm season grass, 300 peanut accessions including CWRs, 100 *Vigna* accessions, and 100 vegetable crop accessions per year. Additional *Vigna* spp., and vegetable accessions may be grown at other locations with the assistance of cooperators, if necessary. Each year, 50 cowpeas, two *Ipomoea* spp., and 3 *Cucurbita* spp. will be regenerated in St. Croix, U.S. Virgin Islands or Mayaguez,

Puerto Rico. A total of 653 pearl millet, 700 finger millet and 1,680 sorghum accessions will also be regenerated in St. Croix over a five-year period. Regeneration of 10 *Cucurbita* spp. will be conducted each year in Parlier, CA. When necessary, accessions of *Citrullus* will be pre-increased in Griffin for subsequent increase by a cooperator.

Accessions to be regenerated will be selected based on low seed viability, low seed numbers, original seed only, age of seed, and demand by the user community. Self-pollinating species will be either directly seeded in the field or started in the greenhouse and transplanted into the field. Species that are photoperiod and/or frost-sensitive (i.e. they flower in the winter when temperatures are too cold in Georgia for seed production) will be grown in a greenhouse for seed regeneration. Cross-pollinated species will be started in the greenhouse and transplanted in the field. Insect-pollinated species will be regenerated in screened cages with honeybees. If outcrossing is limited or unknown in a primarily self-pollinated species, accessions will be regenerated in the greenhouse, spatially isolated in the field, or separated using buffer crops to minimize outcrossing. Wind pollinated species, such as warm-season grass accessions, will be isolated by a distance of at least 25 meters from neighboring accessions of the same species to minimize outcrossing (Johnson et al., 1996).

Germination testing was initiated in 2002 at the Griffin location. To date, the germination of at least one inventory of over 88% of all accessions has been tested. Standard germination tests will be conducted on the entire range of crop and CWRs in the germplasm collection. Germination testing will follow standard procedures developed by the Association of Official Seed Analysts (AOSA, 2011) for major crop species and/or the Handbook of Seed Technology for Genebanks - Volume II: Compendium of Specific Germination Information and Test Recommendations (Ellis et al., 1985). When standardized germination protocols do not exist for a particular species, the crop curator, cooperators at NLGRP, S-009 scientists, and curators or crop experts for other minor crops and CWRs will be consulted for alternative germination techniques. The germination assays provide seed viability information to curators for establishing regeneration priorities. Germination tests will be conducted using 100 seeds for accessions with adequate seed numbers and will follow a sliding scale decreasing to 10 seeds on accessions with minimal seed numbers. Test results will be entered into GRIN-Global.

Accessions are evaluated for trueness to type at various steps in the genebank conservation process. Prior to incorporation into the collection, seeds from completed regenerations are compared to original samples during seed processing. Seed mixtures, incorrect taxonomic identifications, or other concerns are noted during seed cleaning, germination testing, characterizations, or regenerations. Cooperators or users may report that a particular accession is incorrectly identified during their research. When questions arise regarding the trueness to type of regenerated accessions they are referred to the appropriate curator for grow-outs or other evaluations to determine the correct taxon or identification of the sample.

Sweetpotato, perennial wild peanuts which produce few seeds, bamboo, Chinese water chestnuts, bermudagrass, and other warm-season grass accessions are maintained as clones rather than seeds. The sweetpotato clonal collection consists of over 619 accessions maintained in tissue culture. Sweetpotato accessions will be maintained in vitro in a pathogen-free state on semi-solid Murashige and Skoog (MS) media in test tubes on a 10 hour photoperiod at ~20°C and are

recultured every 4 to 12 months to ensure viability and availability. Clonal accessions of 436 warm-season grass, 126 wild peanut, and 6 water chestnut accessions are currently maintained as live plants in the greenhouse or field in Griffin, GA. Clonal bamboo accessions are maintained in separate 5 x 6 m plots at the USDA, ARS, Byron, GA, location.

More than 95% of crop seed accessions are conserved at a second location (NLGRP, Ft. Collins, CO). Backups will be arranged for accessions not already conserved at another location including newly acquired accessions and other accessions. Over time, accessions in the collection will be sent to a third site at Svalbard, Norway, as an additional backup.

Objective 2.

Genebank curators and research scientists need to recognize the needs of the user communities (Fowler and Hodgkin, 2004) including developing countries. Characterization and evaluation data are key prerequisites for efficient utilization of plant germplasm (Esquinas-Alcázar, 2005; Edagbo et al., 2011; Engels and Ebert, 2021). Preserved germplasm needs to be well characterized by using integrated approaches including phenotypic, biochemical, and genotypic analyses to document unique traits among accessions within a collection. Where available, important traits need to be associated with DNA markers. Currently, the associated information for NPGS plant germplasm is documented and maintained in the Germplasm Resources Information Network (GRIN-Global) database. The information on GRIN-Global is publicly available and has greatly benefited end-users such as plant breeders, curators, and scientists. However, the information available for morphological, genetic, biochemical, horticultural and agronomic descriptors is still limited for many species. To overcome these limitations and fill information gaps on the PGRCU accessions, additional data on plant descriptors, morphological characters, genetic, horticultural and agronomic traits, and biochemical traits needs to be generated and confirmed. Associating genotypic and phenotypic data and making it accessible on GRIN-Global (Volk and Richards, 2008; Volk et al., 2021), will benefit the research community.

Basic Descriptor Data and Imaging. Phenotypic crop descriptors are routinely utilized and are available on GRIN-Global to provide basic information on germplasm accessions. Individual descriptors are documented in numerous international publications (IBPGR, 1982; IBPGR, 1984; IPGRI, 1996). The PGRCU utilizes descriptors developed by specific CGCs, crop curators and modified IBPGR descriptor lists. These descriptors are recorded during annual regeneration of accessions or general grow-outs. Descriptors vary for each crop but often include traits related to plant growth habit and morphology (such as plant height, leaf size, seed size, fruit shape or size, midrib, or seed color), phenology (maturity, dormancy), production (seed/fruit yield, foliage yield), and postharvest description of pod and seed traits. Each year, data on regenerated accessions is acquired using a set of standard descriptors, specific to each crop. These data are recorded and uploaded to GRIN-Global. Digital imaging provides a means to visualize and record multiple plant, fruit, or specific seed characteristics. In vegetable, legume, and industrial crop germplasm, characteristics such as fruit characteristics, seed shape, size, and color are often important in assessing the potential value of the accessions. Currently, 26% of the PGRCU collection have at least one digital image on GRIN-Global, with most of the images being of sorghum, cowpea, watermelon, pepper, other cucurbits, peanut, and warm-season grass

accessions. Descriptors and digital images need to be recorded from more accessions and added to GRIN-Global to fill the data gaps for all crops.

Crop specific agronomic and horticultural morphological traits and tolerances to abiotic and biotic stresses are often sought by stakeholders. Disease resistance in CWRs provides additional genotypes for breeding programs (Bohra et al., 2021) to further the development of resistant varieties. Fifty peanut accessions will be evaluated for leaf spot resistance in replicated field plots. Additionally, accessions of 25 peanut CWRs will be evaluated for leaf spot resistance using a modified *in vitro* detached leaf method (Guimaraes et al., 2017; Leal-Bertioli et al., 2009; Melouk and Banks, 1978). Due to global warming and related climate change issues, the identification of drought tolerance in cowpea is essential for the development of improved varieties for use in dry areas. Drought tolerance evaluations in cowpea accessions will be conducted in a greenhouse using previously described methods (Ravelombola et al., 2018; Singh et al., 1999; Verbree et al., 2015). Since minerals in seeds are important components for their health benefits and quality, seeds of 650 cowpea accessions will be analyzed for phosphorus, zinc, and iron (personal communication, William Payne, Univ. of Nevada-Reno).

Biochemical analyses (including oil content, fatty acid composition, protein content, amino acid composition, mineral element content, flavonoids, and other phytochemical traits including capsiate) of genetic resources can be used to identify and quantify useful phytochemicals that contribute to nutritional quality, human health, and bioenergy. In comparison with data on crop descriptors, information on phytochemical characteristics remains limited in GRIN-Global for many crop species including vegetable, medicinal, and nutraceutical genetic resources. Oil content and fatty acid composition for the entire U.S. castor and okra germplasm collections have been evaluated, and accessions with high oil content have been identified for oil or biodiesel production (Jarret et al., 2010; Wang et al., 2011). Variation for oil content and fatty acid compositions from select peanut subspecies and botanical varieties (Wang et al., 2009) have been evaluated. Oil content and fatty acid composition for the entire sesame and cultivated peanut collections have been determined (Wang et al., 2022) as well as for wild peanut species (Wang et al., 2010). Sesame accessions were grown in the field and evaluated for oil, protein, lignan, tocopherol, and fatty acid concentrations (Morris et al., 2021). Protein content has also been evaluated in cowpea seeds stored at 4°C (Morris et al., 2020). Similar work is needed for the *Solanum* spp., pepper, guar, *Indigofera* spp., jute, *Senna* spp., and *Crotalaria brevidens* germplasm. Significant variability in sennoside A and B variation have been identified in *Senna* spp. (Morris et al., 2019). Pepper germplasm has been evaluated for high concentrations of capsinoids (Jarret et al., 2014; Singh et al., 2009). Capsiate is an analog of capsaicin with potential health benefits (Gupta et al., 2021). Flavonoid concentrations and additional biochemicals have been identified and quantified in seeds, immature pods, calyces from several species including peanut, roselle, hyacinth bean, guar, cowpea, mung bean, and others (Sobolev and Cole, 1999; Kirakosyan et al., 2007; Wang and Pittman, 2008; Morris and Wang, 2011; Morris et al., 2012; Morris and Wang, 2015). Using a similar method, flavonoids, and anthocyanins in select accessions of jute, *Senna* spp., and *Crotalaria brevidens* will be evaluated. Galactomannan content will be evaluated from guar and *Indigofera* accessions using a similar method as Gresta et al. (2017). Twenty-five sesame accessions grown in a RCBD with two replicates will be analyzed for high oil, oleate, sesamin, and sesamol. Field grown jute (7 accessions), *Senna* (7 accessions), and *Crotalaria brevidens* (5 accessions) in a RCBD with two

replicates over two years will be analyzed for flavonoids, anthocyanins, and protein. Ten each of guar and *Indigofera* accessions grown in a RCBD will be analyzed for galactomannan content correlations with seed age in cold storage. The oil and protein content, fatty acid composition, amino acid composition, fiber, mineral element concentration, flavonoid, anthocyanin, galactomannan, resveratrol, and flavor-related compounds will be examined by analysis of variance and mean separations using SAS software (SAS Institute, 2002-2005).

Genotyping-by-sequencing proved to be an effective means for quantifying genetic diversity and establishing genetic relationships among and within cultivated eggplants and their wild relatives as reported by Acquadro et al. (2017) and Salgon, et al. (2018). We propose to genotype approximately 800 accessions of eggplant in the USDA eggplant collection (*S. melogena* and several related species). A low coverage whole-genome sequencing approach, similar to that reported for the analysis of *Capsicum* germplasm as described by (Liu et al., 2023), will be utilized. Sampling of plant materials and selection of a core subset from the original population will be accomplished as described by Liu et al., 2023. Phenotypic data on plant and fruit characteristics and digital images will also be acquired over a two-year period. Collaboration will be ongoing with AgriPlex Genomics in the development and evaluation of a medium-density gene chip for use in characterizing pepper (*Capsicum*) germplasm and populations, with The University of Georgia in an examination of sex determination in *Citrullus naudinianus*, and a closer examination of the genome structure of selected wild *Capsicum* species.

Functional DNA markers are developed from the candidate genes for specific traits of interest. Marker Assisted Selection (MAS) can enhance breeding program efficiency by expediting the process of selecting for traits of interest and eliminating undesirable genotypes and phenotypes. New functional DNA markers will be developed from candidate genes by taking advantage of our morphological observation, mutant screening, biochemical analysis, and genetic characterization data. In peanut, various functional DNA markers for high oleate (an important seed oil quality trait leading to longer shelf life and beneficial effects for human health) have been developed (Chu et al., 2007; Barkley et al., 2010; Wang et al., 2015). A high oleate mutant with high resistance to tomato spotted wilt virus (TSWV) was identified by screening the entire U.S. cultivated peanut germplasm collection. The sequenced *FAD2* gene for fatty acid desaturase was useful for identifying polymorphisms which led to amino acid changes and might contribute to changes in fatty acid compositions in sesame (Chen et al., 2014). For integrating both high oleate and leaf spot resistance to breeding lines, new functional *FAD2* markers are required and will be developed from these multi-parents advanced generation inter-cross (MAGIC) lines. Recombinant peanut MAGIC lines (Arrones et al., 2020) with high oleate and leaf spot resistance will be screened for oil content, fatty acid composition, and protein content.

A sorghum panel that consisted of 256 EMS-induced mutant lines has been sequenced. These mutant lines will be deposited into the sorghum collection at Griffin and will be valuable sorghum genetic resources for sorghum association studies. Several useful traits have been identified in this panel and associated with candidate genes (Wang et al., 2021). However, not many useful root traits were identified because root traits are difficult to observe and study. We explored different (hydroponic, sand, and paper pouch) methods for observation of root morphological changes from this sorghum panel. Preliminary data have been collected and some mutant lines with significant root morphology variation were identified, but the root mutant traits

have not been associated with SNP markers (Tishchenko et al., 2020). These mutants will be backcrossed with the wild type (BTx 623) and then F₂ populations will be generated by selfing. Some selected F₂ mutants with clear root morphological changes (traits) will be bulk segregant analysis sequenced (BSAseq). Through sequence analysis, SNP markers associated with the trait or the candidate gene will be identified for the trait (see details in Xin et al., 2021).

Objective 3.

Plant genetic resources (seeds, in-vitro cultures, plants, cuttings, corms, and rhizomes) and associated information will be provided to users worldwide in response to requests received by email, internet, phone, and U.S. Mail. The number of requests varies from year to year with distributions ranging from 28,000 to 51,000 during the last 10 years (Appendix 1, Table 2). All seed orders are processed by the seed storage staff. The time required for filling domestic seed orders averages 2 to 4 weeks from the order receipt to shipment, while foreign seed orders average 8 to 12 weeks from receipt of order to shipment. Order-to-shipment time varies greatly from season to season and year to year depending on the number and size of seed requests. The average time to process clonal requests is species dependent varying greatly between sweetpotato (in tissue culture), warm-season grasses and wild peanuts in the greenhouse, Chinese water chestnuts in hydroponics, and field-grown bamboo. Requests are forwarded by the seed storage staff to crop curators for approval. Plant genetic resources are currently distributed only to bona fide researchers. Additional correspondence with the user will be conducted and utilized as needed to clarify the stated basis for the request. When the request is approved by the curator, seed storage staff prints envelopes and packages seed for shipment. Standard seed quantities are shipped. These quantities are based on the crop, seed availability, difficulty in regeneration, and research need. Prior to shipment of foreign requests, the Office of Foreign Assets Control, U.S. Treasury Department is consulted to ensure that shipments are not restricted to the destination country. Foreign requests are evaluated by the Plant Exchange Office (PEO) and Animal and Plant Health Inspection Service (APHIS) for phytosanitary certificate or import permit requirements to ensure proper procedures are followed. Every effort is made to expedite shipments, however, screening and correspondence often require additional time. Curators routinely respond to information requests by email or telephone on a wide variety of topics including pest and pathogen resistance, cultural requirements, specific horticultural or agronomic traits, quality or yield characteristics, or plant quarantine issues.

Sweetpotato clonal materials will be shipped to the user as small plantlets or *in vitro* cultures. One to three *in vitro* cultures of sweetpotato are typically provided per request depending on the needs of the user. *In vitro* cultures (semi-solid media) are packaged in boxed cardboard sleeves (25 x 150 mm culture tubes) or styrofoam packing material (liquid media). Vegetative material of other *Ipomoea* spp., perennial wild peanuts, Chinese water chestnuts, and warm-season grass accessions which do not produce seed will be shipped bare-root; wrapped in moist paper towels, foam root cubes, or moss; placed in plastic bags; and shipped in packing material within a cardboard box. Constant communication is maintained with the user so that if damage occurs in transit, arrangements for the replacement of damaged materials can be arranged quickly. Nursery certificates issued by the Georgia Department of Agriculture will be kept current to allow for legal domestic distribution of live plant material. Routine inspections of greenhouse facilities and bamboo field plots will be conducted twice a year by the Georgia Department of Agriculture to ensure compliance with the Imported Fire Ant Quarantine, Nematode Quarantine, Federal

Japanese Beetle Quarantine, and North Carolina Tropical Spiderwort Quarantine. In addition, seed storage personnel will query Department of Agriculture websites for the destination state prior to shipment of material to determine if specific state import requirements limit the shipment of live plant material. When it is determined that live plant material cannot be distributed due to state-imposed import restrictions, the requestor will be contacted by the curator. Bamboo rhizomes will be distributed once a year in February to all requesters from the bamboo plots at the USDA, ARS, Byron, GA, location. Proper documentation (e.g. official fire ant stamp) showing legal compliance will be sent with each live plant shipment.

Measurement of Progress and Results

- A. **Outputs.** Regenerations will provide high quality genetic resources for use in research programs. Characterization and evaluation data will be added to GRIN-Global to provide users with more complete information to better select the appropriate accessions for their research uses. Requests for genetic resources will be promptly handled as resources permit, and accessions will be distributed to users worldwide.
- B. **Outcomes or Projected Impacts.** The plant genetic resources conserved and distributed by this project will provide plant breeders and researchers with the necessary materials to develop new and improved crop varieties. The rich genetic diversity conserved in the S-009 collection can provide traits for adaptation to harsh climates, improved nutritional value, and increased yields with fewer inputs. Many of the traits conserved in the PGRCU collection are not available in the current commercial varieties used in crop production and are a source of new traits needed to meet the demands of producing crops in a world with a changing environment and an increasing population. The result is a more secure and sustainable food supply that is highly nutritious and diverse.
- C. **Milestones.** This project is an on-going effort and, in the future, will continue to acquire, characterize, maintain, evaluate, document, and distribute plant genetic resources as it has for the last 74 years. Specific milestones are difficult to establish as all aspects of the project are continuous and fluctuate with changes in resources and research priorities. Viable germplasm, associated information, characterization, and evaluation data will continue to add value to this collection.

Projected Participation

See Appendix 3.

Outreach Plan

Plant genetic resources and associated information will continue to be readily available worldwide on the GRIN-Global website. Information on genetic resources, management procedures, characterizations, evaluations, and distributions will be published by PGRCU scientists and S-009 participants. Information on the S-009 project, including membership, annual reports, and meeting minutes, will be maintained on the S-009 website (www.ars-grin.gov/ars/SoAtlantic/Griffin/pgrcu/s9.html). Newly developed NPGS infographics and an NPGS video are available on the PGRCU homepage that educates the public on the mission of the unit and importance of plant germplasm conservation and utilization

(<https://www.ars.usda.gov/southeast-area/griffin-ga/pgrcu/>). The S-009 Regional Technical Advisory Committee and CGC members publicize crop specific germplasm at their specific institutions or companies. In person tours are given throughout the year to commodity groups, high school students, undergraduate and graduate students, visiting scientists, congressional staffers, and others. Curators will attend national and regional meetings to present information about the germplasm collection and provide updates on current research through formal talks and poster presentations. PGRCU will explore ways to further communicate and promote the importance of the germplasm collection through field days, publications in trade journals, and other media in order to reach a broader audience.

Organization and Governance

S-009 has officers consisting of a Chair, Secretary, and Past Chair. The Secretary is elected to a two-year term and becomes Chair after their term ends. Each year the project reports results, assesses progress, and receives guidance during the annual S-009 committee meeting held at Griffin or at other locations throughout the Southern Region.

Authorization

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Appendix 1.

Table 1. Total number of accessions, number of available accessions, and number of accessions backed up at Ft. Collins, CO for the Griffin germplasm collection, 2013-2022.

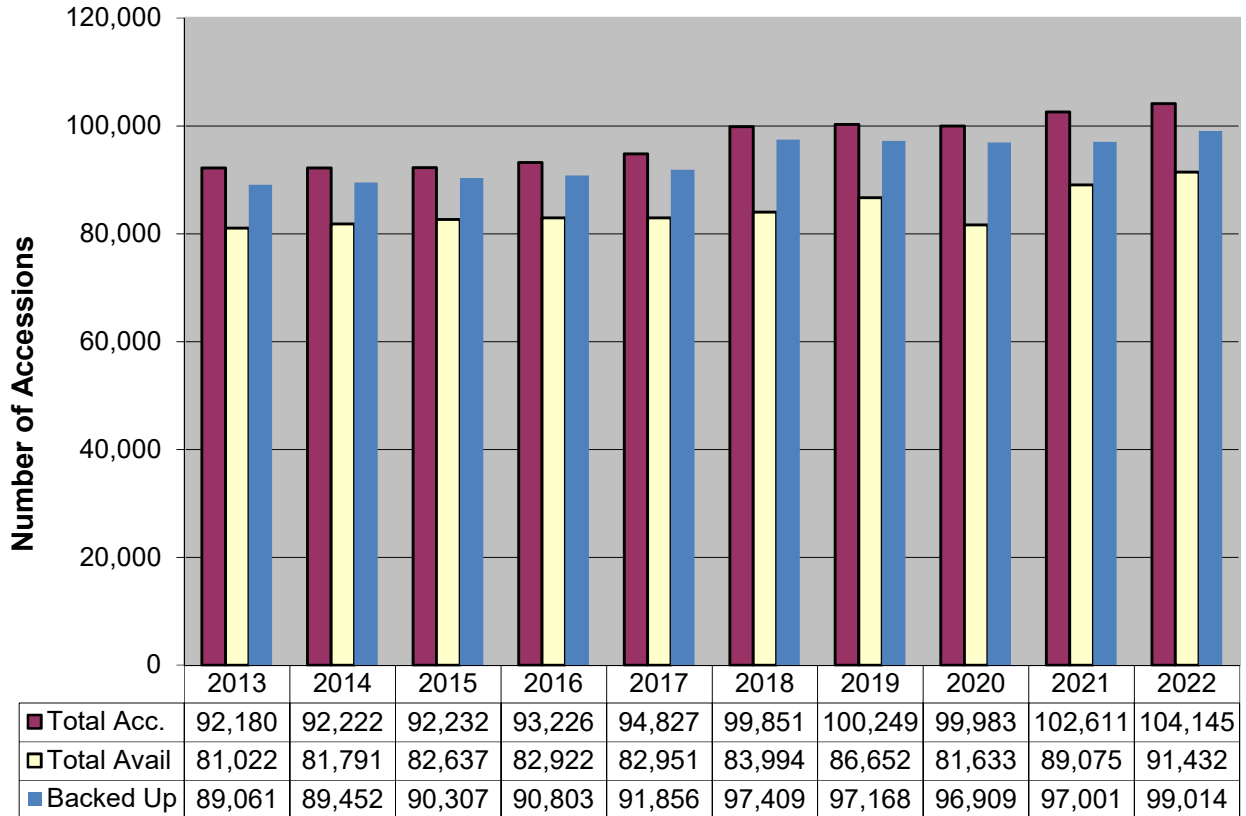
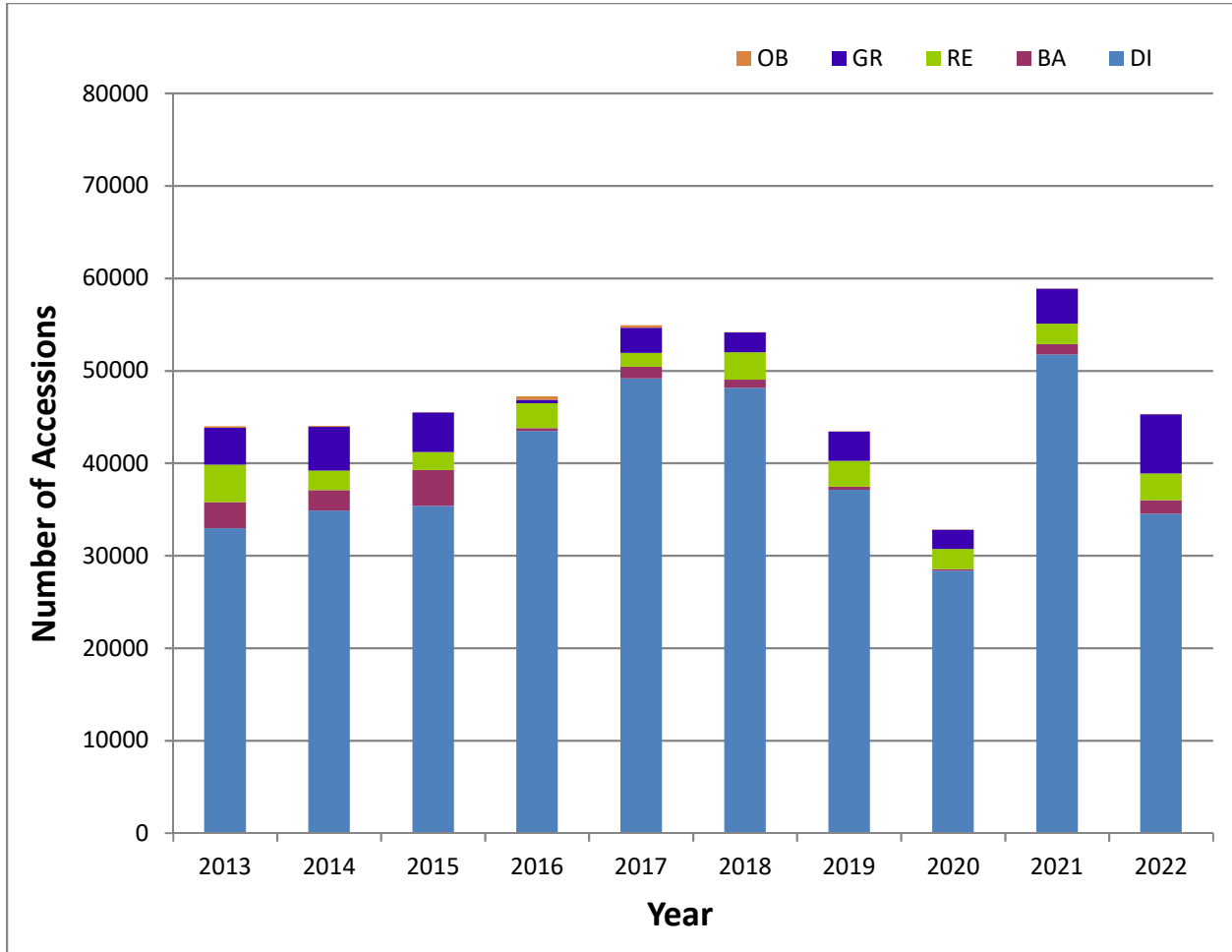


Table 2. Total number of accessions distributed (DI) to researchers in the U.S. and foreign countries and total number of accessions distributed for observations (OB), germination testing (GR), regeneration (RE), and back-up (BA) by the Plant Genetic Resources Conservation Unit, Griffin, GA (2013-2022).



Appendix 2. Response to reviewers' comments

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