

Project Number: S-009

Project Title: Plant Genetic Resources Conservation and Utilization

Period Covered: 01/2000 through 12/2000

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Participants: <http://www.ars-grin.gov/ars/SoAtlantic/Griffin/pgrcu/s9report.html>

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Accomplishments and Impacts: Conservation of plant germplasm collected throughout the world represents a gene bank for the improvement of agricultural and horticultural crops grown in the U.S. This germplasm contains the genetic diversity necessary to develop needed traits such as resistance to diseases or insects, improved crop quality, greater yields, alternate uses, and new chemical traits to improve crop cultivars. The germplasm collection at the Plant Genetic Resources Conservation Unit contains more than 81,000 accessions representing more than 1480 species and 265 genera. This collection is one of the largest working collections of both seed and clonal accessions in the entire U.S. National Plant Germplasm System. A total of 586 new accessions were added to the genetic resources collection in 2000.

Distributions of 49,257 samples (corms, in-vitro samples, plants, rhizomes, and seeds) were made to users. Of these samples, 43,927 samples were distributed to users in the U.S. and 5,330 samples were distributed to foreign users. A total of 40,327 U.S. distributions were sent to users in states within the S-9 region. Distributions were much greater than in past years due especially to large requests for sorghum accessions (almost 25,000 accessions in one request) and peanut accessions (almost 8,000 in one request). Regenerations were initiated for 3,058 accessions that had low availability, poor germination, or high user interest.

More than 7,261 accessions were backed up for long term storage at the National Seed Storage Laboratory at Ft. Collins, CO, to prevent loss of valuable genetic resources by a disaster at any one germplasm conservation location. Accessions backed up this year included warm season grasses, peppers, peanuts, Vigna, and clover.

Core collections, which are a sample of accessions that are representative of the entire collection, have been created in a number of collections. In 2000, core collections were created for watermelon (251 accessions) and peppers (404) bringing the total number of crops with core collections to nine at the S-9 collection.

Characterization data recorded on accessions during regeneration or obtained from

cooperators is entered into the Germplasm Resource Information Network (GRIN) database to provide researchers with information to help them best select accessions to utilize in their research program. In 2000, more than 361,500 records were created and 130,600 records were modified in the GRIN database. Passport data was updated for more than 11,400 records of warm season grasses, watermelon, and okra from archived written information. Counts and weights were completed on 4,000 inventory samples, over 10,300 inventory samples were transferred to -18 C storage, and more than 17,500 samples were bar coded for rapid identification. Passport data for 6,800 warm season grass accessions was completed and verified. A detailed manual inventory of the warm season grass collection of over 11,200 inventory samples was completed. This process included cleaning, weighing, counting, rebagging, and bar coding each inventory sample.

Sweetpotato and other vegetatively propagated germplasm are often subject to genetic instability. In order to determine the underlying mechanism affecting genetic instability, the sweetpotato genome was probed for the presence of transposable elements in collaboration with scientists at Louisiana State University. Data revealed the presence of retrotransposons in the sweetpotato genome. Knowledge of factors that activate or stabilize these transposable elements could lead to the development of improved germplasm maintenance protocols.

Regeneration and characterization of *Citrullus* germplasm was increased by 50% to 150 accessions per year. Increased regeneration and characterization will increase the availability of seed and useful information to users.

Molecular research was conducted on peanuts and subterranean clover accessions to determine the genetic diversity and redundancy in these germplasm collections. Based on the molecular evidence, some accessions of wild peanut appear to be mixed botanical varieties, *Arachis hypogaea hypogaea* var. *peruviana* and var. *aequatoriana*. These results are supported by morphological information collected from the field. AFLP genetic markers were used to identify genetic variation and redundancy in subterranean clover accessions. Morphological markers are being identified to complement AFLP markers in determining genetic variation and redundancy.

Canavalia ensiformis, *Indigofera spicata*, and *I. nummularifolia* added as a soil amendment reduced root-knot nematode galls by 90%. These species could be used as rotation crops for nematode control and could reduce the use of nematicides and soil fumigants. Also, *Leucaena leucocephala* was identified as having useful phytochemical characteristics.

Seed regeneration of velvetbean, a major phytopharmaceutical and nutraceutical species, can be conducted by growing the plants in the greenhouse for the first year and then transplanting them into the field the second year. This procedure enhances seed production by allowing for additional growth so that the plants can reach maturity prior to a killing frost.

A RT-PCR based method was developed to detect the strain of cowpea aphidborne mosaic virus (CABMV) of peanuts from Brazil. Primers were designed based on the 3' sequence data obtained by cooperators in Tifton, GA. The best approach to detect the virus was to test large batch samples from seedlings produced from seed lots in question. Other approaches using the IC-RT-PCR method for CABMV detection in tandem or in a multiplexing approach with the primers of peanut stripe and peanut mottle viruses did not work.

Vigna germplasm has been selected for resistance to blackeye cowpea mosaic virus and

cucumber mosaic virus. These two viruses cause cowpea stunt, which is the most severe viral disease of cowpea in the U.S. This germplasm will be released in the next year.

Future plans for the Unit are available in the minutes of the S-9 Technical Advisory Committee meeting at: <http://www.ars-grin.gov/ars/SoAtlantic/Griffin/pgrcu/s9report.html>

Publications:

Alabama

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Arkansas

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Florida

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Georgia

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Hawaii

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Kentucky

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Louisiana

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Mississippi

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Puerto Rico

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South Carolina

No publications.

Tennessee

No publications.

Texas

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Virginia

No publications.

USDA-Plant Genetic Resources Conservation Unit

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