

**NC-7 Report
Summary
By
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Peanut Germplasm Report Oct. 5, 2009

During the time-frame 2008-2009 I had requested three items from the NPGS, i.e., 195145 – 18APR08 (2 items) and 198509 – 26AUG08 (1 item).

These materials were requested simply to replace three items which had been lost from our wild peanut germplasm collection. We did not have any specific program working to use these three lines, we simply wanted to make sure they were preserved in our Texas Collection.

Impact of Germplasm

The three lines reported above have had no specific impact on our program, however, numerous other PI materials have had a large effect on our program for oil quality changes in peanut product, disease and nematode resistance, and improved agronomic traits.

In the past the Texas A&M University System and Agencies have released 16 new peanut cultivars and five germplasm lines. All but one of these 21 accessions had their parentage rooted deep into the NPGS. Only the first release, Spantex, could not be associated with a plant introduction. In reality that may not be true, but records do not exist to trace the original source of the “landrace” line that Spantex was selected from in the late 1940’s. All the other 20 lines can be traced directly back to one or more PI’s that came through the NPGS.

The impact of NPGS germplasm on Texas peanut production has been significant. At one point in the late 1960’s the Texas A&M release, ‘Starr’, was grown on ca. 95% of the Texas peanut acreage, and near 75% of the total US peanut acreage. At present (2008 crop) slightly more than 50% of Texas peanuts were planted to TAMU released cultivars. Data are not yet available on the 2009 crop.

The Texas AgriLife Research peanut improvement program continues to utilize and evaluate numerous PI lines of peanut. One area of research is evaluation and breeding for improved oil content in peanut. A new forage peanut release is in progress with selected material derived from PI262819. Peanut minicore accessions were evaluated in the field for tolerance to drought and salt stress in separate experiments. Data are being analyzed for drought stress. Most accessions tested under high salt did not survive to maturity; however, a few did. These experiments will be repeated in 2009.

I will not report of the germplasm releases (distribution) from the TAMU program since 2007 because I was not senior author. I shall leave that reporting to Michael Baring (Tamnut OL06 and Tamrun OL07) and Mark Burow (Germplasm line, TxAG-8). Two MS Thesis’ are here reported that involved NPGS germplasm, although neither deal with the three lines I requested since 2007.

1. Baring, M.R. 2007. Selection of a Multiple Disease Resistant runner-type Peanut. A thesis submitted to the Office of Graduate Studies in partial fulfillment for the degree of Master of Science. Texas A&M University, College Station, TX 77843. 50 pp.
2. Williams, E.J. 2008. Determination of Seed Size in Relationship to the Distance from the Main Axis in *Arachis* L. A thesis submitted to the Graduate College in partial fulfillment for the degree of Master of Science. Tarleton State University, Stephenville, TX 76401. 108 pp.

Grasses Re: NC-7 Report (Dariusz Malinowski)

The germplasm ordered from USDA-GRIN on 6/6/2008 included summer-dormant and summer-active types of *Poa secunda*, *Melica* spp., and *Elymus* spp. The purpose of ordering the germplasm was to increase seed of these grasses for future experiments on mechanisms of summer dormancy in cool-season grasses, in addition to currently evaluated summer-dormant and summer-active grasses of the *Festuca*, *Dactylis*, and *Lolium* genera. The initial goal of increasing seed amount of these grasses was met in 2009. Future experiments including this germplasm are planned for 2010 and beyond.

Impact:

Based in major part on results of research conducted at the Texas AgriLife Research Center at Vernon during 2000-2009, summer-dormant cool-season grasses have been proven more persistent and productive in the Southern Great Plains when compared with traditionally recommended, summer-active types. Repeated severe droughts in this region often result in failure of wheat and other traditional forage crops to support cattle requirements during winter and summer. Exceptional tolerance of summer-dormant cool-season grasses to summer drought and high forage production in early fall to early winter, and again in early spring, makes them the only choice to complement winter wheat pastures. Flecha MaxQ and Prosper summer-dormant tall fescue were included on the list of recommended grasses for Texas in 2009. Future research will determine mechanisms of summer dormancy as a tool to select for this trait in forage grass breeding programs.

No publications have been produced at this time.

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Cotton NC 7 Report (Wayne Smith)

Five upland cotton families were identified in 2002 by the Cotton Improvement Lab, Department of Soil and Crop Sciences at Texas A&M University that exhibited exceptional fiber lengths and fiber bundle strength equal to or better than most non-Acala cultivars available to upland cotton producers in the United States. Thirty strains from these five families had upper half mean length (UHML) exceeding 32 mm and several equaled or exceeded the minimum UHML in the pima or extra long staple (ELS), 34.8

mm, loan schedule when grown in one or more environments. Eight germplasm lines exhibiting the ELS trait were released in 2009 (Smith et al., 2009a). The source of these improved traits appears to be the common parent of the five families, TAM 94L-25 or its sib line 94L-2, which may have a unique combination of alleles for fiber quality derived by decades of breeding and contributions from several breeding programs in the United States. TAM 94 L-25 was released by Texas AgriLife Research in 2003 (Smith, 2003). Additional upland ELS strains are under development and evaluation.

Bechere, E., D. Auld, R. Cantrell, E. Hequet, M. Krifa, S. Misra, and C.W. Smith. 2007. Registration of TTU 0774-3-3 and TTU 0808-1-6-1 upland cotton germplasm lines with improved fiber length and strength. *J. Plt. Reg.* 1:58-59.

Ragsdale, P.I., and C.W. Smith. 2007. Germplasm Potential for Trait Improvement in Upland Cotton Diallel Analysis of Within-Boll Seed Yield Components. *Crop Sci.* 47:1013-1017.

Schwartz, B.M., and C. Wayne Smith. 2008. Genetic gain in yield potential of upland cotton under varying plant densities. *Crop Sci.* 48:601-605.

Schwartz, B.M., and C. Wayne Smith. 2008. Genetic gain in fiber properties of upland cotton under varying plant densities. *Crop Sci.* 48:1321-1327.

Gardunia, B., C. Braden, and W. Smith. 2008. Applying quantile regression to analysis of AFIS cotton fiber distribution. *Crop Sci.* 48:1328-1336.

Smith, C.W., P.S. Thaxton, S. Hague, E. Hequet, and D. Jones. 2008. Registration of TAM 01E-22 upland cotton germplasm line with improved fiber strength and length. *Journal of Plant Registration* 2:129-131.

Smith, C.W., S. Hague, E. Hequet, P.S. Thaxton, and I.N. Brown. 2008. Development of extra long staple upland cotton. *Crop Sci.* 48:1823-1831.

Smith, C.W., S. Hague, P.S. Thaxton, E. Hequet, and D. Jones. 2009a. Registration of eight extra long staple upland cotton germplasm lines. *J. Plant Registration* 3:81-85.

Longenberger, P., C.W. Smith, S.E. Duke, and B.L. McMichael. 2009. Evaluation of chlorophyll fluorescence as a tool for the identification of drought tolerance in cotton. *Euphytica* 166:25-33. (March 09)

Braden, C.A., C.W. Smith, and E.F. Hequet. 2009. Combining ability for fiber length in near-long staple upland cotton. *Crop Sci.* 49:1638-1646.

Smith, C.W., C.A. Braden, and E.F. Hequet. 2009b. Generation mean analysis of near long staple fiber length in TAM 94L-25 upland cotton. *Crop Sci* 49:1638-1646.

Smith, C. W., C.A. Braden, and E.F. Hequet. 2009c. Genetic analysis of fiber length uniformity in upland cotton. *Crop Sci.* (accepted)

Legumes (Ray Smith)

Crimson clover, lablab and cowpea accessions are being evaluated and used as parents in the Texas AgriLife Research (Texas A&M Univ. System) forage legume breeding

program. Plant introduction lines of safflower were evaluated on the Texas High Plains and the results for specific lines were published.

Research was conducted at the USDA-ARS Children's Nutrition Research Center at Houston, TX on PI accessions of *Teramnus labialis* (L.) Spreng. Seeds of this wild relative of soybean are collected and used as a food source by tribal populations in Asia. In order to assess the potential of this legume to provide dietary minerals for humans, fourteen PI accessions were grown under controlled, nutrient-replete conditions and seeds were harvested for mineral analysis. Seed concentrations of phosphorus (P), potassium (K), sodium (Na), iron (Fe), copper (Cu), manganese (Mn), and zinc (Zn) were found to fall within the range of published values for several cultivated grain legumes (including soybean), while calcium (Ca) and magnesium (Mg) were higher in *Teramnus labialis* seeds.

Cucurbits

Cucurbit PI lines were evaluated in the TAMU Vegetable and Fruit Improvement Center. Numerous evaluations and crosses were made to initiate screening for health beneficial phytochemicals in cucurbits.

Publications

Oswalt, J.S., C.C. Lowery, R.C. Johnson, and D.L. Auld. 2008. Development of Safflower as a New Winter Crop for the Texas High Plains. Nakamaya, F.S. and C.A. Gardner, eds. 20th Annual AAIC Meeting – New Crops & Bioproducts Development: Program and Abstracts. College Station, TX. p. 61.

Oswalt, J.S., C.C. Lowery, R.C. Johnson, and D.L. Auld. 2008. Development of Safflower as a New Winter Crop for the Texas High Plains. Safflower: Unexploited Potential and World Adaptability – Abstract Book, 7th International Safflower Conference. Wagga Wagga, Australia, p. 40.

Maize(Seth Murray)

The material requested by the Quantitative Genetics and Maize Breeding program is being used for identifying new alleles conditioning traits such as grain mold resistance (especially *A. flavus*) and increased biomass production (extremely delayed flowering, tillering, perennialism). We would expect to only find these alleles in tropical backgrounds as they have been traditionally selected against in elite Midwestern dent germplasm. By combining these lines with our elite Texas material and elite Midwestern ex-PVP material, also ordered, we hope to increase both yield of grain and biomass and disease resistance. Finally, association mapping is a valuable technique to map genetic loci for traits of interest. In obtaining a set of lines already genotyped by the USDA we plan to collect phenotypic information on aflatoxin resistance to map QTL of interest. Grusak, M.A. 2008. Genetic diversity for seed mineral composition in the wild legume *Teramnus labialis*. *Plant Foods Hum Nutr* 63:105-109