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RESEARCH ARTICLE

Status of the USA cotton germplasm collection and crop vulnerability

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Abstract The National Plant Germplasm System (NPGS) is a cooperative effort among State, Federal and Private organizations aimed at preserving one of agriculture's greatest assets: plant genetic diversity. The NPGS serves the scientific community by collecting, storing, and distributing germplasm as well as maintaining a searchable database of trait descriptors. Serving the NPGS, a Crop Germplasm

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Committee (CGC) is elected for each crop and is comprised of a group of scientists concerned with development, maintenance, characterization, and utilization of germplasm collections. Each CGC serves in an advisory role and provides a status report every seven years to determine scientific efforts, adequacy of germplasm base representation, and progress in breeding through utilization of germplasm. In addition, each committee can call attention to areas of concerns regarding facilities and staffing associated with the maintenance, collection, and taxonomic activities for a specific crop within the system. The following report was developed by the CGC for cotton and provides a record of collections, activities, concerns, crop vulnerabilities, and recommendations associated with the cotton collection for the period 1997–2005. Information provided within this document is a much expanded and detailed description of a report provided to the NPGS and includes the most exhaustive citation of germplasm depositions and research activity descriptions available anywhere in the USA for this time period. This documentation will be a valuable resource to breeders, geneticists, and taxonomists with an interest in this important food and fiber crop.

Keywords Cotton · Crop vulnerability · Germplasm collection and evaluation · *Gossypium* · National plant germplasm system · Taxonomy

Introduction

Cotton, *Gossypium* spp., is grown as a source of fiber, food, and feed. Presently, 51 species constitute this genus, with a new species being discovered on an average of once every four years for the past 30 years. In just the last 7 years, 12 new species have been described. Of the 51 species now described, four are cultivated, *G. hirsutum* L. and *G. barbadense* L. which are tetraploid ($2n = 4x = 52$), and *G. arboretum* L. and *G. herbaceum* L. which are diploid ($2n = 2x = 26$). *G. hirsutum* is by far the most widely grown species worldwide.

In the United States cotton is grown coast-to-coast including seventeen states from the Carolinas to California. It is produced on 13–15 million acres with a return of over 5 billion dollars annually for its fiber and seed by-products. Although cotton is grown mostly for fiber, its seeds are an important source of food oil, and the meal is a protein-rich by-product used as feed for ruminant livestock. It is fed as whole cottonseed and there is interest in eliminating seed gossypol to extend the usage of cotton's high protein meal to non-ruminant consumers. Cotton seed meal could become an important source of protein, especially in third world countries, where low protein diets are the rule.

Historically, market prices for cotton fiber have been quite volatile. Cotton, being a global commodity, can have its price affected by international swings between over and under supply. Several years ago, the U.S. cotton industry experienced record high prices for cotton. In more recent times, the price per pound of cotton has dipped below the 50 cent mark. The most obvious contributing factor for lower prices is an ever increasing percentage of retail consumption of imported cotton. Cotton imports at the retail level from China have nearly doubled in the last 7 years. Increased production, reduced domestic consumption, and a drastic increase in foreign imports have taken a toll on the price of cotton. When combined with a reduction in the number of U.S. textile mills, a much greater portion of the U.S. cotton crop competes in a larger world market. Prices for extra-long staple (ELS) cotton, primarily Pima and Egyptian cultivars, have fluctuated during the last seven years from 85 cents to $1.16 per pound for grade number one. The current price of grade one, staple 46 San Joaquin Pima cotton is $1.14 per pound. Exports of ELS cotton currently exceed annual production (reducing year end carry-over). The retail value of the entire U.S. cotton crop for the 1993/1994 season was estimated at more than $120 billion annually (National Cotton Council of America).

Present germplasm activities

Germplasm acquisition

Collection trips

Since the last assessment of the status of cotton germplasm, twelve acquisition trips have been made (Table 1). Seven of these were funded totally or in part by USDA, ARS. Ten of the trips were primarily in situ explorations, while two of the trips were made

Table 1 Foreign cotton germplasm acquisition trips since 1985

Year	Location	Objectives	Principals
1985	Caribbean Islands, S. Florida	Feral and wild *G. hirsutum* and *G. barbadense*	Schwendiman et al. (1986)
1985	Central and NW Australia	Wild diploid species, G and K genomes	Stewart et al. (1987)
1986	Galapagos Islands	Wild and feral *Gossypium*, AD_5 *G. darwinii*, AD_2 *G. barbadense*, $D_{3\text{-}k}$ *G. klotzschianum*	Percival and Wilson
1988	NE Brazil	AD_4 *G. mustelinum*, AD_1 *G. hirsutum* race Marie Galante	Stewart et al. (1989)
1990	SW Mexico	Wild diploid species, D genome	DeJoode
1990	NW Mexico and Baja California	Wild diploid species, D genome	Percival et al. (1992)
1993	N and W Australia	Wild diploid species, G and K genomes	Stewart et al. (1997)
1995	SW Mexico	Wild diploid species, D genomes	Wendel and Cota
2002	Southern Mexico	Dooryard and feral cottons representing designated landraces of cotton, wild diploid *Gossypium* species	Ulloa et al. (2006b) and Stewart et al. (2004)
2003	Nayarit, Mexico	Wild *G. hirsutum* and *G. aridum* species	Ulloa et al. (2006b)

primarily in an effort to obtain germplasm held ex situ by other countries. Collecting trips included two trips to Australia, five trips to Mexico, and one trip each to the Galapagos Islands, the Caribbean Islands, and Northeast Brazil. During this time period twelve new species of *Gossypium* were described and an additional new species description is in manuscript. Seven of the new species were identified as a result of the collections listed in Table 1.

Germplasm exchange

The two germplasm exchange trips included visits to India, China, Russia, and Uzbekistan. Germplasm exchange activities are listed in Table 2.

Germplasm depositions

Plant breeding activities have led to release, registration, and deposition of breeding lines and cultivars with the National Cotton Collection. A list of depositions recorded since the last update of this is presented in Table 3.

Characterization

The systematic collection of trait descriptors is conducted principally but not exclusively by the curator of the working collection of the National Collection of *Gossypium* Germplasm. Descriptor data is sometimes collected by public and private scientists on smaller subsets of the collection to help fill gaps in the GRIN database and perhaps discover useful germplasm for breeding programs or other goal oriented research projects.

Descriptor definitions/updates

Several descriptors are lacking (glandless, nectariless, frego bract, "segregating") in the GRIN database and the need for an improved measure of the descriptor "productiveness" has been suggested. The establishment of a standard "check" would facilitate accessing productivity or yield in different environments. A descriptor committee has been established and is currently working to update and define the current list of descriptors.

Table 2 Germplasm exchange activities reported

Year	Location	Objectives	Principals
1994	India and China	Germplasm exchange, primarily to obtain A-genome species	Percival and Kohel
1995	Russia, Uzbekistan, and India	Germplasm exchange, primarily to obtain materials from the Vavilov Institute and follow up on A-genome acquisitions	Percival and Kohel

Table 3 Germplasm depositions recorded since the 1997 Cotton Germplasm Status Report

Institution	Germplasm[a]	Name	Reference
USDA-ARS, CPSWPRC, Florence, SC	3 Germplasm Lines	PD 93007, PD 93043, and PD 93046	May and Howle (1997a)
USDA-ARS, CPSWPRC, Florence, SC	6 Germplasm Lines	PD 93009, PD 93019, PD 93021, PD 93030, PD 93034, and PD 93057	May and Howle (1997b)
USDA-ARS, USALARC, Maricopa, AZ	2 Elite Breeding Lines (Pima)	89590 and 8810	Percy (1998)
USDA-ARS, CPSWPRC, Florence, SC	1 Germplasm Line	PD 94042	May (1999)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	3 Root-Knot Resistant Germplasm Lines	TAM 2561 RKNR, TAM 2562 RKNR, and TAM 2571 RKNR	Starr and Wayne Smith (1999)
USDA-ARS, CPSWPRC, Florence, SC	58 RILs derived from PD-3-14/Simian-2	PD-3-14 and Simian-2 RILs	May (2000)
North Carolina State Univ., Raleigh, NC	1 Elite Breeding Line	NC 72	Bowman (2001)
Northeast Res. and Ext. Center, Arkansas State Univ., Keiser, AR	2 Germplasm Lines	Arkot A306 and Arkot A314	Bourland and Wayne Smith (2001)
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	1 Elite Cultivar	GA161	May et al. (2001)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Silverleaf Whitefly Resistant Germplasm	TAM 90C-19s and TAM 90 J-57s	Smith (2001a)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Three Morphological Variant Germplasm Lines	TAM 91A-104 fg, TAM 91C-95Ls, and TAM 90O-24L	Smith (2001b)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Fusarium Wilt Resistant Germplasm	TAM 90K-3	Smith (2001c)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	High-Yielding Germplasm	TAM 88G-104	Smith (2001d)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Registration of Nine Germplasm Lines with Improved Fiber Strength	PI 614942–PI 614950	Smith (2001e)
USDA-ARS, CPSWPRC, Florence, SC	1 Germplasm Line	PD 94045	May (2001)
USDA-ARS, USALARC, Maricopa, AZ	6 Germplasm Lines (Pima)	PS-6ne, PS-6Lo, PS-6neLo, P62ne, P62Lo, and P62neLo	Percy (2001)
Miss. Agric. Exp. Stn., Mississippi State Univ., Mississippi State, MS	1 Improved Variety	Miscot 8806	Wallace et al. (2002)
USDA-ARS, CPSWPRC, Florence, SC	1 Germplasm Line	PD 97100	May (2002)
USDA-ARS, CSRL, Mississippi State, MS	16 Day-neutral Primitive Accession Germplasm Lines	PI 628762–PI 628777	McCarty and Jenkins (2002)
USDA-ARS, USALARC, Maricopa, AZ	5 Elite Breeding Lines (Pima)	93252, 93260, 94217, 94218, and 94220	Percy (2002)

Table 3 continued

Institution	Germplasm[a]	Name	Reference
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Registration of Eleven Multi-Adversity Resistant Germplasm Lines	CD3HG2CABS-1-91 CD3HGCBU8S-1-91 LBCBHGDPIS1-91 CUBQHGRPIS-1-92 PD23CD3HGS-1-93 CBD3HGDPIH-1-91 LBCHUD3HGH-1-91 CD3HGCULBH-1-91 CDRCIQCUBH-2-92 CDARCILBCH-1-92 CUBQHGRPIH-1-92	Thaxton and El-Zik (2003a)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Smooth-Leaf Germplasm Line with Improved Fiber Length	TAM 94WE-37s	Smith (2003a)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Germplasm Lines with Improved Fiber Length	TAM 94L-25 and TAM 94 J-3	Smith (2003b)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	1 Improved Variety	Tamcot Luxor	Thaxton and El-Zik (2003b)
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	1 Elite Breeding Line	GA98028	May (2004)
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	1 Elite Breeding Line	GA96-211	May et al. (2004b)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Eleven Multi-adversity Resistant Germplasm Lines	MAR-7B and PI 634320–PI 634327	Thaxton and El-Zik (2004a)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	1 Improved Variety	Tamcot Pyramid	Thaxton and El-Zik (2004b)
Texas Agric. Exp. Station, College Station, TX; USDA-ARS, CSRL, Mississippi State, MS	17 Upland Lines Disomic for *G. barbadense* Chromosome or Arm Substitutions	PI636346 to PI636362	Stelly et al. (2005)
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	1 Elite Breeding Line	GA98033	May et al. (2004a)
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	1 Elite Breeding Line	GA98066	May et al. (2005)
Miss. Agric. Exp. Stn., Mississippi State Univ., Mississippi State, MS	1 Improved Variety	Miscot 8839	Wallace (2005)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Glabrous Germplasm Line	TAM 96WD-69s	Thaxton and Smith (2005a)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Germplasm Line with Improved Fiber Length and Strength	TAM 96WD-18	Thaxton and Smith (2005b)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Germplasm Lines with High Fiber Strength	TAM 98D-102 and TAM 98D-99ne	Thaxton and Smith (2005c)

Table 3 continued

Institution	Germplasm[a]	Name	Reference
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	High Yielding Cotton Cultivar	Tamcot 22	Thaxton and Smith (2005d)
USDA-ARS, CSRL, Mississippi State, MS	21 Day-neutral Primitive Accession Germplasm Lines	PI 636697–PI 636717	McCarty and Jenkins (2005a)
USDA-ARS, CSRL, Mississippi State, MS	14 Primitive Derived Germplasm Lines with Improved Fiber Strength	PI 639148–PI 639161	McCarty and Jenkins (2005b)
USDA-ARS, CPRU, College Station, TX/ Syngenta Inc.	3 Germplasm Lines	RN96425, RN96527, RN96625-1	Cook and Robinson (2005)
USDA-ARS, USALARC, Maricopa, AZ	3 Elite Breeding Lines	AGC85, AGC208, and AGC375	Percy et al. (2006)
USDA-ARS, WICSRU, Shafter, CA	1 Elite Breeding Line	SJ-U86	Ulloa et al. (2006a)

[a] All germplasm depositions are *G. hirsutum* species unless noted otherwise

Collection of descriptor data

Subsets of the national collection are often grown and evaluated as potential sources of genetic variability for use in cotton improvement programs. Collection of GRIN descriptors can contribute to fill gaps in the GRIN database. Every effort should be made to insure that this information finds it way into the GRIN database. The imminent hiring of a new USDA-ARS Cotton Curator will no doubt facilitate coordination of this effort. Activities that encompass more than 1400 accessions resulting in the collection of all or a subset of GRIN related descriptors are listed in Table 4.

Evaluation

Evaluation efforts include studies conducted as research projects or adjuncts to other research by public and private investigators. These latter evaluations usually involve subsets of varying sizes of the germplasm collection and often are not systematic or exhaustive in their approach. The latter type of investigation, being highly goal oriented, often does not report 'negative' results from evaluations. Numerous evaluations are being conducted by university and federal investigators to address needs and issues to further our understanding of cytogenetics, plant biochemistry, regeneration, plant-pest interactions (insects, nematodes, fungal and bacterial pathogens) and physiological stresses. Evaluation efforts that have been undertaken, and/or are currently in progress since the last status report are listed below by broad categories.

Cytogenetic evaluations

A number of chromosomally hemizygous hypoaneuploid interspecific (*G. hirsutum*, *G. barbadense*, *G. tomentosum* Nutt. ex Seem., *G. mustelinum* Miers ex G. Watt) chromosome substitution F_1 hybrids were developed, genomic tools for mapping were developed. The cytogenetic constitution of reniform nematode immune backcrosses (*G. hirsutum*, *G. longicalyx* J. B. Hutch. et B. J. S. Lee, *G. armourianum* Kearney, *G. barbadense*) were characterized during this period (Dighe et al. 2005). Activities related to cytogenetic evaluations reported during this period are presented in Table 5.

Table 4 Germplasm accessions characterized for GRIN descriptors and other traits

Institution	Germplasm[a]	Activity
Miss. Agric. Exp. Stn., Mississippi State Univ., Mississippi State, MS	189 Accessions of the Uzbekistan Collection	Evaluated for GRIN descriptors and lint yield
Miss. Agric. Exp. Stn., Mississippi State Univ., Mississippi State, MS	155 Accessions of the Shafter, CA Collection	Evaluated for GRIN descriptors and lint yield
LSU AgCenter, Louisiana State University, Baton Rouge, LA	200 Accessions of the Uzbekistan Collection	Evaluated for GRIN descriptors and lint yield
LSU AgCenter, Louisiana State University, Baton Rouge, LA	154 Accessions of the Shafter, CA Collection	Evaluated for GRIN descriptors and lint yield
USDA-ARS, USALARC, Maricopa, AZ	69 Accessions of the Russian Collection (*G. barbadense*)	Evaluated for GRIN descriptors and lint yield
USDA-ARS, USALARC, Maricopa, AZ	59 Accessions of the Uzbekistan Collection (*G. barbadense*)	Evaluated for GRIN descriptors and lint yield
USDA-ARS, WICSRU, Shafter, CA	550 Accessions including Landraces of Mexico and recent collections	Evaluated for GRIN descriptors, lint yield and characterization with microsatellites or SSR markers
USDA-ARS, WICSRU, Shafter, CA	75 Accessions including Diploid species of the D genome collected from recent explorations	Evaluated for GRIN descriptors, lint yield and characterization with microsatellites or SSR markers

[a] All germplasm accessions are *G. hirsutum* species unless noted otherwise

Table 5 Cytogenetic and biochemical evaluations of germplasm

Institution	Germplasm	Activity
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	*G. hirsutum*	Development and identification of hypoaneuploids
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX/USDA-ARS, CSRL, Mississippi State, MS	*G. hirsutum*, *G. barbadense*	Developed chromosomally hemizygous hypoaneuploid interspecific chromosome substitution F1 hybrids. Developed and shared DNA panels for molecular marker localization and genome mapping. Used them to develop monosomic and then disomic alien chromosome substitutions, followed by evaluation and release
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX/USDA-ARS, CSRL, Mississippi State, MS	*G. hirsutum*, *G. tomentosum*, *G. mustelinum*	Developed chromosomally hemizygous hypoaneuploid interspecific chromosome substitution F1 hybrids. Developed and shared DNA panels for molecular marker localization and genome mapping. Iteratively backcrossed to develop alien chromosome substitution lines
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	*G. hirsutum*	Developed methods for high quality fluorescence in situ hybridization (FISH) to cotton mitotic and meiotic chromatin, and DNA fibers as a genomics tool (for physical mapping of repetitive sequences and molecular markers, coalescence, identification and orientation of linkage groups, and differentiation of subgenomes)
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX/USDA-ARS, SPARC, College Station, TX	*G. hirsutum*, *G. longicalyx*, *G. armourianum*, *G. herbaceum*	Characterized cytogenetic constitutions of conventional backcrosses immune to the reniform nematode. Recovered euploid resistant types
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Germplasm line GA98033 (*G. hirsutum*)	Found variation in plant tissue culture regeneration then evaluated for plant cell embryogenesis and embryo germination

Biochemical (gossypol, tannins, tissue culture, regeneration, etc.)

Activity reported (Table 5) observation of genetic variation for tissue culture regeneration potential.

Insect resistance

Research activities related to host plant insect resistance evaluations on approximately 300 lines (day-neutral accessions, race stocks, substitution lines) are presented in Table 6.

Table 6 Evaluation of germplasm for insect, pathogen, and nematode host plant resistance

Institution	Germplasm	Activity
USDA-ARS, CSRL, Mississippi State, MS	168 Day-neutral primitive accessions (*G. hirsutum*)	Evaluated accessions for resistance to tobacco budworm in field plots
USDA-ARS, CSRL, Mississippi State, MS	Chromosome substitution lines (CS-B), (*G. hirsutum*)	Evaluated 13 chromosome substitutions lines for resistance to tobacco budworm in field plots
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	Approx. 110 Converted Race Stocks (CRS) and Tam 96WD-69s (*G. hirsutum*)	Evaluated for tolerance/resistance to cotton fleahopper
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	7 Converted Race Stocks (CRS), (*G. hirsutum*)	Evaluated for tolerance/resistance to silverleaf whitefly
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	30 High Tannin Lines, 100 Converted Race Stocks, and multiple obsolete cultivars (*G. hirsutum*)	Screened germplasm for resistance to *Rhizoctonia solani*
Alabama Agric. Exp. Stn., Auburn University, Auburn, AL	Entire TX collection of *G. hirsutum* (approx. 2500 accessions)	Evaluated in greenhouse for resistance to reniform nematode (*Rotylenchulus reniformis*)
LSU AgCenter, Louisiana State University, Batron Rouge, LA	150 Accessions from the Texas Race Stocks (*G. hirsutum*)	Evaluated for field resistance to root-knot nematode (*Meloidogyne incognita*)
USDA-ARS, CSRL, Mississippi State, MS	79 Day-neutral primitive accessions	Evaluated in greenhouse for resistance to root knot nematode (*Meloidogyne incognita*)
USDA-ARS, CSRL, Mississippi State, MS	8 day-neutral race stock accessions (*G. arboreum* and *G. hirsutum*)	Evaluated in greenhouse for resistance to reniform nematode (*Rotylenchus reniformis*)
USDA-ARS, CPRU, College Station, TX	1419 Accessions from the Texas Race Stocks (*G. hirsutum*) and 850 accessions from the GB collection (G. *barbadense*)	Measured reniform nematode resistance in greenhouse/growth chamber
USDA-ARS, CPRU, College Station, TX	Accessions A1-17, A2-87, TX-110, TX-1348, GB-13, GB-49, GB-264, GB-536, GB-713 (*G. hirsutum* and *G. barbadense*)	Measure reniform nematode resistance and root density to 122 cm depth in fields in Texas, Louisiana, Mississippi, and Alabama, also in microplots/growth chamber
USDA-ARS, CPRU, College Station, TX	A2-27, A2-41, A2-83, A2-87, A2-100, A1-17, F1-1, F1-3, TX-893, Auburn 623, Auburn 634, DesAnom277 (SA2457), DesArb16 (SA2458), DesArb277 (SA2459), DesHaf16 (SA2460), DesHerb16 (SA2461), DesTom16 (SA2462), DesBarb16 (SA2508), DesHaf277 (SA2509), DesAnom16 (SA2544), DesLong16 (SA 2546), DesHerb277 (SA2545), (*G. hirsutum*)	Measure reniform nematode resistance in growth chamber assay
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Population developed from the interspecific cross of Pima S6 (*G. barbadense*) with M120 (*G. hirsutum*)	Evaluate breeding population for nematode resistance QTLs

Seed quality

No activity reports related to seed quality submitted for this update.

Disease resistance

Approximately 130 lines/converted race stocks, listed in Table 6, were evaluated for resistance to the cotton seedling disease pathogen, *Rhizoctonia solani* Kühn.

Nematode resistance evaluation

A large number of accessions (>3,500), that included both *G. hirsutum* and *G. arboreum* species were evaluated for resistance to the reniform (*Rotylenchulus reniformis* Linford et Oliveira) and root-knot (*Meloidogyne incognita* Kofoid et White) nematodes. Activities related to evaluation of germplasm for response to nematodes are listed in Table 6.

Stress evaluation

Approximately 1,500 accessions of *G. hirsutum* were evaluated for heat, drought, or salt tolerance and three populations of *G. barbadense* were developed to study the inheritance of Early Foliar Decline (EFD) in Pima. Activities related to evaluation of germplasm for environmental stresses are reported in Table 7.

Agronomic and fiber quality evaluations

Reported activities listed in Table 8 include evaluation of several recombinant inbred line (RIL) populations (*G. hirsutum* and *G. barbadense*), 151 *G. hirsutum* day-neutral primitive accessions, 13 CS-B lines (*G. barbadense* chromosomes/chromosome arms introgressed into *G. hirsutum*), and interspecific crosses of *G. hirsutum* with *G. barbadense* and *G. mustelinum* which were evaluated for yield, fiber quality, fiber quality QTLs and other agronomically important traits.

Taxonomic evaluation

See previous description of "Collection Trips" under heading of "Acquisitions". Twelve new species of *Gossypium* have been described and an additional new species description is underway. More than 300 lines evaluated for gene diversity and taxonomic relationship are reported in Table 9.

Systematic large scale evaluation

Over 150 entries, including breeding lines, race stocks and obsolete cultivars evaluated for a range of agronomic traits are reported in Table 10.

Enhancement

Enhancement, or developmental breeding, in cotton is an on-going pursuit within private, state, and federal agencies. As specially funded public

Table 7 Evaluation of germplasm for response to environmental stresses

Institution	Germplasm	Activity
Alabama Agric. Exp. Stn., Auburn University, Auburn, AL	Approx. 1,380 accessions of the TX collection *(G. hirsutum)*	Evaluated for tolerance to heat stress by determining chlorophyll fluorescence following exposure to high temperature (55°C) for 1 h
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	100 Converted Race Stocks, and multiple obsolete cultivars (*G. hirsutum*)	Greenhouse screen for seedling drought and salt tolerance in containers
USDA-ARS, USALARC, Maricopa, AZ	3 populations (*G. barbadense*)	Created and evaluated populations for inheritance of tolerance to early foliar decline in Pima cotton
USDA-ARS, CPSWPRC, Florence, SC	13 Pee Dee germplasm lines and varieties (*G. hirsutum*)	Evaluated for yield and fiber quality response to supplemental irrigation
Georgia Agric. Exp. Station, Univ. of Georgia, Athens, GA	*G. barbadense/G. hirsutum* interspecific population selected under drought and irrigated conditions	Evaluated populations for markers that are correlated with drought stress

Table 8 Evaluation of *Gossypium* sp. for agronomic and fiber quality traits

Institution	Germplasm	Activity
USDA-ARS, USALARC, Maricopa, AZ	Introgressed RIL population, NM24016/TM-1	Evaluated population for fiber, agronomic, and physiological characteristics related to heat stress
USDA-ARS, USALARC, Maricopa, AZ	RIL population, Pima S-6/89590 (*G. barbadense*)	Created a RIL population for fiber quality investigation and evaluated lines for fiber quality
USDA-ARS, WICSRU, Shafter, CA	RIL population, Pima S-6/89590 (*G. barbadense*)	RIL population for fiber quality investigation and evaluated lines for fiber quality, genetic and QTL mapping
USDA-ARS, CSRL, Mississippi State, MS	16 Day-neutral primitive accessions	Evaluated for yield and fiber traits in replicated field trials (McCarty and Jenkins 2001)
USDA-ARS, CSRL, Mississippi State, MS	21 Day-neutral primitive accessions	Evaluated for yield and fiber traits in replicated field trials (McCarty and Jenkins 2004)
USDA-ARS, CSRL, Mississippi State, MS	114 Day-neutral primitive accessions	Evaluated day-neutral accessions and their F2 bulks crossed with two cultivars for yield and fiber traits in replicated field trials (McCarty et al. 2005)
USDA-ARS, CSRL, Mississippi State, MS	Chromosome substitution lines (CS-B)	Crossed 13 CS-B lines with five elite cultivars and determined GCA and SCA for agronomic and fiber properties
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Interspecific crosses between *G. barbadense* and *G. hirsutum*	Mapping fiber quality trait QTLs genome-wide/Fine mapping of fiber length QTLs on chr. 1/Evaluating this Near Isogenic Introgression Line (NIIL) series particularly for fiber quality QTLs, their individual impact on fiber quality as well as other potential traits, and possible parents with a view to stack the fiber quality QTLs
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Interspecific crosses between *G. mustelinum* and *G. hirsutum*	Evaluating a Near Isogenic Introgression Line (NIIL) series particularly for fiber quality QTLs and their individual impact on fiber quality as well as other potential traits
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Approx. 50 crosses/year among elite Univ. of Georgia breeding lines with promising non-transgenic commercial cultivars and germplasm lines	Yield, fiber quality, and lint percentage evaluated throughout the filial generations as the germplasm approaches heterogeneous homozygosity through selfing
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Population developed from crosses of extra long fiber length material with introgressed markers and material with known QTL for fiber strength	Re-evaluation for length/strength fiber traits and developing stacked lines for an enhanced germplasm resource

[a] All germplasm accessions are *G. hirsutum* species unless noted otherwise

Table 9 Taxonomic evaluation of germplasm

Institution	Germplasm	Activity
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	>300 germplasm lines/cultivars of US Upland cotton (*G. hirsutum*)	Evaluated for gene diversity and taxonomic relationship with in geographic placement of breeding locations

programs, enhancement projects generally have had goals with regional or beltwide impact and broad appeal. Since many enhancement projects out of necessity begin with identification of desirable or suitable genetic materials, the line between evaluation and enhancement becomes blurred. A partial listing of current or recent enhancement programs and projects are listed.

Table 10 Systematic large scale evaluation of germplasm

Institution	Germplasm	Activity
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	80 Converted Race Stock BC3F2 populations (*G. hirsutum*)	Agronomic and fiber property evaluation at two locations in Texas and one in Georgia
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	10 Current and obsolete cultivars (*G. hirsutum*)	Performance of cultivars covering release dates over the past 10 decades in different planting densities
USDA-ARS, CPSWPRC, Florence, SC	82 Released Pee Dee varieties and germplasm (*G. hirsutum*)	Evaluated for yield potential, fiber quality, and adaptation in multi-location trials from 2004 to 2006

Metabolic efficiency studies

No activity reports related to metabolic efficiency submitted for this update.

Photoperiodic flowering response conversion

Much of the *G. hirsutum* and *G. barbadense* collections, being of tropical origin, are photoperiodic in flowering response and require conversion to a day-neutral status before the variability of these collections can be exploited. USDA-ARS, Miss. State, MS (funded) and Phoenix, AZ (unfunded) have ongoing conversion programs. Table 11 lists germplasm enhancement efforts through photoperiodic conversion activities.

Host plant resistance

Activities reported included the development of more than 200 germplasm lines which were evaluated for resistance/tolerance to one or more insect pests (*Lygus* sp., aphids, whiteflies and *Heliothis* sp., bollworms, budworms pests) and 300 germplasm lines (*G. hirsutum* and *G. barbadense*) evaluated for Fusarium wilt [*Fusarium oxysporum* f. sp. *vasinfectum* (FOV) Atk. Sny et Hans]. A number of enhancement activities (Table 12) reported efforts in the development and evaluation root-knot and reniform nematode tolerance via introgression (*G. barbadense*, triple hybrid) and marker assisted selection.

Molecular genetics, mapping, foreign gene identification and cloning

Activity reported in Table 13 included development of mapping population to identify QTLs for within boll yield components and fiber quality.

Fiber trait quality improvement

Activities reported in Table 14 included *G. hirsutum* fiber quality improvement via introgression (*G. barbadense*, *G. mustilineum*), selection of improved fiber quality day-neutral accessions, and re-introduction of genetic variability from various sources (Sea Island, Egyptian, triple hybrid).

Diversification of cytoplasm

No activity reports related to diversification of cytoplasm submitted for this update.

Table 11 Photoperiodic conversion activities

Institution	Germplasm	Activity
USDA-ARS, USALARC, Maricopa, AZ	Approx. 250 lines from National Collection (*G. hirsutum*)	Convert tropical short day flowering accession to day neutrality
USDA-ARS, CSRL, Mississippi State, MS	Primitive race stocks from National Collection (*G. hirsutum*)	Convert tropical short day flowering accession to day-neutrality. Since 2000 selected day-neutral plants in approximately 500 segregating F2 populations of race stocks by day-neutral donor parent

Table 12 Activities related to enhancement of germplasm for host plant resistance

Institution	Germplasm	Activity
North Carolina State Univ., Raleigh, NC	Gene pool resulting from a cross of three upland (*G. hirsutum*) cultivars and a Sea Island (*G. barbadense*) cotton	Screened for tolerance to thrips
Miss. Agric. Exp. Stn., Mississippi State Univ., Mississippi State, MS	Approx. 90 lines (*G. hirsutum*) developed from a wide range of genotypes	Evaluated for tolerance/resistance to Lygus (tarnished plant bug)
LSU AgCenter, Louisiana State University, Batron Rouge, LA	Approx. 30 lines (*G. hirsutum*) developed from high calyx glanding genotypes	Developed via mating advanced breeding lines with high calyx glanding trait for resistance to Heliothis pests
USDA-ARS, WICSRU, Shafter, CA	Approx. 90 lines (*G. hirsutum*) developed from a wide range of genotypes	Evaluated for tolerance/resistance to Lygus, aphids, and white flies
USDA-ARS, WICSRU, Shafter, CA	Approx. 300 accessions, germplasm and developed populations (*G. hirsutum* and *G. barbadense*)	Breeding for resistance to Fusarium wilt (FOV) under greenhouse and field conditions, in addition molecular tagging of resistant gene(s)
Georgia Agric. Exp. Station, Univ. of Georgia, Tifton, GA	Populations developed from PD94042 × M120 and PD94042 × M155 (*G. hirsutum*)	Development of germplasm lines/cultivars resistant to root-knot nematodes using markers linked to nematode resistance QTLs
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	TX110 (*G. barbadense)* reniform resistant crossed with M315	Breeding for resistance to reniform nematode
USDA-ARS, CPRU, College Station, TX, USDA-ARS, CSRL, Mississippi State, MS	GB-713 (*G. barbadense*)	Introgress reniform nematode resistance into *G. hirsutum* through fourth backcross and develop markers
USDA-ARS, CPRU, College Station, TX	*G. longicalyx*	Introgress reniform nematode resistance into *G. hirsutum* via triple species hybrids through eighth backcross and develop markers
USDA-ARS, CPRU, College Station, TX, USDA-ARS, CSRL, Mississippi State, MS	TX-25, TX-748, TX-1586, TX-1828, TX-1860, TX-2469 (*G. hirsutum*)	Identify reniform nematode-resistant F2 from half diallel cross and backcross into *G. hirsutum* to develop resistance via transgressive segregation

Table 13 Enhancement and development of a population for mapping

Institution	Germplasm	Activity
LSU AgCenter, Louisiana State University, Baton Rouge, LA	Intraspecific *G. hirsutum* mapping population (Paymaster 54 × PD2165)	Identified via AFLPs several QTL associated with within boll yield components and fiber quality

Preservation

The National Collection of *Gossypium* Germplasm is housed at the Southern Plains Agricultural Research Center (SPARC), Crop Germplasm Research Unit, College Station, TX. At present the collection contains 9332 accessions representing 49 species from 74 countries and/or political jurisdictions, assigned to three germplasm pools (Tables 15, 16, 17). The various *Gossypium* components of the National Plant Germplasm System (NPGS) are:

Working collection

Responsible for implementing or coordinating of the acquisition, increase, documentation, distribution, characterization, and evaluation.

(a) Upland germplasm—3,132 accessions, primarily of *G. hirsutum.*
(b) Primitive race germplasm—2,120 accessions, primarily of wild or primitive races of *G. hirsutum.*

Table 14 Activities related to enhancement of germplasm for improved fiber quality traits

Institution	Germplasm	Activity
USDA-ARS, USALARC, Maricopa, AZ, USDA-ARS, WICSRU, Shafter, CA, USDA-ARS, CPSWPRC, Florence, SC, LSU AgCenter, Louisiana State University, Batron Rouge, LA, LSU AgCenter, Louisiana State University, Batron Rouge, LA	Introgressed (*G. hirsutum*) germplasm pool	Project to simultaneously improve heat tolerance and fiber quality, create high fiber quality, heat tolerant germplasm pool, and release improved germplasm
USDA-ARS, USALARC, Maricopa, AZ	Elite Pima (*G. barbadense*)	Improve Pima fiber quality; re-introduce variability from Sea Island and Egyptian sources
USDA-ARS, WICSRU, Shafter, CA	Germplasm (approx. 600 accessions) and developed populations (*G. hirsutum* and *G. barbadense*)	Improve Acala, non-Acala Upland, and Pima fiber quality; re-introduce genetic variability from different sources, including Sea Island and Egyptian sources
USDA-ARS, CSRL, Mississippi State, MS	Day-neutral germplasm with improved fiber strength (*G. hirsutum*)	Selected day-neutral lines derived from primitive accessions and crossed them to cultivars and evaluated their breeding merit
Texas Agric. Exp. Stn., Texas A&M Univ., College Station, TX	*G. mustilineum*, *G. barbadense*, and CRS material	Introgression of germplasm to improve fiber properties
USDA-ARS, CPSWPRC, Florence, SC	Elite Pee Dee lines (*G. hirsutum*)	Improve fiber quality; improve yield potential; re-introduce variability from Sea Island and triple hybrid sources

Table 15 Currently recognized *Gossypium* species within the primary (1°) germplasm pool

Species	Genome	Notes
G. hirsutum L.	$(AD)_1$	Current & obsolete cultivars, breeding stocks, primitive and wild accessions
G. barbadense L.	$(AD)_2$	Current & obsolete cultivars, breeding stocks, primitive and wild accessions
G. tomentosum Nutt. ex Seem.	$(AD)_3$	Wild, Hawaiian Islands
G. mustelinum Miers ex G. Watt	$(AD)_4$	Wild, NE Brazil
G. darwinii G. Watt	$(AD)_5$	Wild, Galapagos Islands

(c) *G. barbadense* germplasm—1,585 accessions of primitive germplasm, obsolete cultivars and current cultivars.
(d) Asiatic germplasm—1,924 accessions of the diploid species *G. arboreum* (1,730 accessions) and *G. herbaceum* (194 accessions).
(e) Wild species germplasm—581 accessions representing over 40 species of wild diploid and tetraploid *Gossypium* spp.

Base collection

Responsible for the long-term storage and preservation of the germplasm maintained at National Plant Genetic Resource Center (NPGRC), Colorado State Univ., Fort Collins, CO.

Ad hoc collections

Collections which are not formally included in the NPGS.

(a) Genetic stocks—maintained at USDA, ARS, College Station, TX, and Phoenix, AZ.
(b) Cytogenetic stocks—maintained at TAES, College Station, TX.

The Cotton Winter Nursery in Tecoman, Colima, Mexico is the primary location for increasing accessions, and it is essential for the increase of long

Table 16 Currently recognized *Gossypium* species within the secondary (2°) germplasm pool

Species	Genome[a]	Notes
G. herbaceum L.	A_1	Cultivars and land races of Africa and Asia Minor; one wild from South Africa
G. arboreum L.	A_2	Cultivars, landraces from Asia Minor to SE Asia and China; some African
G. anomalum Wawra	B_1	Wild, two subspecies from Sahel and SW Africa
G. triphyllum (Harv.) Hochr.	B_2	Wild, SW Africa
G. capitis-viridis Mauer	B_3	Wild, Cape Verde Islands
G. trifurcatum Vollesen	(B)	Wild, Somalia
G. longicalyx J. B. Hutch. et B. J. S. Lee	F_1	Wild, trailing shrub, East Central Africa
G. thurberi Tod.	D_1	Wild, Sonora Desert
G. armourianum Kearney	$D_{2\text{-}1}$	Wild, Baja California
G. harknessii Brandegee	$D_{2\text{-}2}$	Wild, Baja California
G. davidsonii Kellogg	$D_{3\text{-}d}$	Wild, Baja California
G. klotschianum Andersson	$D_{3\text{-}k}$	Wild, Galapagos Islands
G. aridum (Rose et Standl.) Skovst.	D_4	Wild, arborescent, Pacific slopes of Mexico
G. raimondii Ulbr.	D_5	Wild, Pacific slopes of Peru
G. gossypioides (Ulbr.) Standl.	D_6	Wild, South central Mexico
G. lobatum Gentry	D_7	Wild, arborescent, SW Mexico
G. trilobum (DC.) Skovst.	D_8	Wild, West central Mexico
G. laxum L. Ll. Phillips	D_9	Wild, arborescent, SW Mexico
G. turneri Fryxell	D_{10}	Wild, NW Mexico
G. schwendimanii Fryxell et S. D. Koch	D_{11}	Wild, arborescent, SW Mexico
sp. *nov.*	(D)	Eastern Guerrero, Mexico

[a] Where used, ( ) indicates provisional genomic placement for the species in question

seasoned or photoperiodic accessions of *G. hirsutum* or *G. barbadense*. In addition, several hundred lines or accessions are grown in the field and greenhouse at College Station, Texas each year as space and funds allow.

Seed renewal of accessions comprising the germplasm collection is currently being performed on a priority basis determined by the curator. Previously, all accessions were renewed on a seven year schedule. Prior to that (1993), seed increases were performed on a five-year schedule, when the newly combined collection was consolidated and increases were required for NPGRC and College Station, TX. Seed renewals are restricted by static funding and increasing costs. Sixty-five thousand dollars of the USDA, ARS, SPARC, CGRU recurring funds for cotton germplasm maintenance are dedicated to seed increase and renewal, and a further 100 thousand dollars of the cotton research budget has been directed recently to maintain the Cotton Winter Nursery operated by the Cotton Winter Nursery Steering Committee. This nursery is a vital component of the germplasm preservation program and its continued existence is crucial.

A list of currently recognized *Gossypium* species in the primary (1°), secondary (2°) and tertiary (3°) germplasm pools are presented in Tables 15, 16, 17.

Germplasm needs

Collection

Seven species of *Gossypium* were collected during a 2002 expedition to Mexico (Ulloa et al. 2003, 2006b). Species collected (and number of accessions)

Table 17 Currently recognized *Gossypium* species within the tertiary (3°) germplasm pool

Species	Genome[a]	Notes
G. sturtianum J.H. Willis	C_1	Wild, ornamental, Central Australia
G. robinsonii F. Muell.	C_2	Wild, West Australia
G. bickii Prokh.	G_1	Wild, Central Australia
G. australe F. Muell.	(G)	Wild, North Transaustralia
G. nelsonii Fryxell	(G)	Wild, Central Australia
G. costulatum Tod.	(K)	Wild, decumbent, North Kimberley of West Australia
G. cunninghamii Tod.	(K)	Wild, ascending, Northern tip of NT, Australia
G. enthyle Fryxell et al.	(K)	Wild, erect, North Kimberley, Australia
G. exgiuum Fryxell et al.	(K)	Wild, prostrate, North Kimberley, Australia
G. londonerriense Fryxell et al.	(K)	Wild, ascending, North Kimberley, Australia
G. marchantii Fryxell et al.	(K)	Wild decumbent, Australia
G. nobile Fryxell et al.	(K)	Wild, erect, North Kimberley, Australia
G. pilosum Fryxell	(K)	Wild, ascending, North Kimberley, Australia
G. populifolium (Benth.) F. Muell. ex Tod	(K)	Wild, ascending, North Kimberley, Australia
G. pulchellum (C. A. Gardner) Fryxell	(K)	Wild, erect, North Kimberley, Australia
G. rotundifolium Fryxell et al.	(K)	Wild, prostrate, North Kimberley, Australia
G. anapoides J. M. Stewart et al., nom. inval.	(K)	Wild, erect, North Kimberley, Australia
G. stocksii Mast.	E_1	Wild, Arabian Peninsula and Horn of Africa
G. somalense (Gürke) J. B. Hutch.	E_2	Horn of Africa and Sudan
G. areysianum Deflers	E_3	Arabian Peninsula
G. Incanum (O. Schwartz) Hillc.	E_4	Arabian Peninsula
G. bricchettii (Ulbr.) Vollesen	(E)	Somalia
G. benadirense Mattei	(E)	Somalia, Ethiopia, Kenya
G. vollensenii Fryxell	(E)	Somalia

[a] Where used, ( ) indicate provisional genomic placement for the species in question

included: *G. aridum* (Rose et Standl.) Skovst. (15), *G. barbadense* (9), *G. gossypioides* (Ulbr.) Standl. (2), *G. hirsutum* (52), *G. laxum* L. Ll. Phillips (5), *G. lobatum* Gentry (1) and *G. schwendimanii* Fryxell et S. D. Koch (2). Fifty-six *Gossypium* seed accessions were collected during a 2003 expedition to Mexico. The five species (and number of accessions) collected during this expedition were: *G. aridum* (9), *G. hirsutum* (33), *G. laxum* (1), *G. lobatum* (10) and *G. schwendimanii* (1). The identification of accessions of the diploid species should be considered tentative until nursery specimens have been grown and compared.

Collection efforts in the last 14 years have improved the diversity available in some germplasm pools. In others, particularly in the dooryard or commensal accessions of the cultivated tetraploid species, modernization and the development of a global economy threaten their continued existence. Small personal plantings and dooryard plants have been abandoned in favor of commercial cultivars—setting up a now-or-never situation for collection. High priority should be placed on obtaining threatened commensal or dooryard accessions of the tetraploid species. In all germplasm pools, unplanned opportunities may arise to obtain germplasm, filling previously identified deficiencies. Such 'targets of opportunity' as exchange projects with countries which maintain collections should receive high priority when they arise, and should be aggressively pursued. Below are listed some of the germplasm collections, categories, or geographical regions identified as germplasm acquisition priorities.

Germplasm exchange

(a) Russian, Uzbekistan, and other cotton growing republics of the former Soviet Union—Recent contacts indicate that it may be possible to develop an exchange agreement with the above countries. A problem will be funding. It is highly likely that we will have to supply all funding for such a project—which may entail such activities as seed renewal at the collections' present location prior to exchange.
(b) Colombia, Greece and Turkey—These countries are known to maintain collections. However at present we are not aware of the numbers or type of materials in these collections or of the possibility of exchange agreements.
(c) Montpellier, France—2,500 accessions from CIRAD acquired by TAES, Lubbock, TX should be added to the collection, possibly as an ad hoc collection until further described.

South America

The greatest deficiency in the primary germplasm pool of the germplasm collection is the under-representation of the diversity of *G. barbadense* and *G. mustelinum* from South America. A wild diploid species related to one of the subgenomes of the cultivated tetraploid cotton species, *G. raimondii* Ulbr. also is native to South America.

(a) *G. barbadense*—Feral and ruderal germplasm is rapidly being lost to development in an area which has been under-collected. This area roughly encompasses northern Argentina, eastern Bolivia, and parts of Paraguay and Brazil. Collection in this area is a high priority and should be pursued as an independent objective.
(b) Peru is the center of origin and diversity of *G. barbadense* and encompasses the total range of *G. raimondii* (the diploid species thought to be a relative of one of the progenitors of tetraploid cotton). Obtaining germplasm from Peru is a priority and a contact has been established which may be highly productive.
(c) *G. mustelinum*, a relic species resembling the original ancestor of tetraploid cottons, appears to be restricted to small and widely spaced locations in NE Brazil, where it may be threatened with extinction. U.S. scientists should cooperate with Brazilian counterparts to determine the true extent of its distribution and vulnerability as well as conserve its genetic diversity ex situ.

Secondary germplasm pool

(a) A-genome species (*G. arboreum* and *G. herbaceum*). Countering the recent acquisition of 1,180 accessions of *G. arboreum* from an Indian collection is an apparent high level of redundancy in this material. Regional diversity known to exist among the A-genome diploid species, but poorly represented in the collection is as follows:
    (1) South Africa—The only known wild representatives of the *G. herbaceum* species, assumed to be the progenitors of the cultigen, occur in South Africa. These populations are very poorly represented in the collection and should be extensively collected.
    (2) Southeast Asia (other than India). *G. arboreum* is known to exist throughout SE Asia (Nepal, Bangladesh, Burma, Thailand, Loas, Vietnam, Cambodia, Malaysia, Indonesia) as dooryard plants or in small family plots. The representation of these genotypes in the U.S. collection is very poor, and the amount of diversity is unknown. Exchanges, regional surveys, and collection of this germplasm are a high priority.
    (3) Other areas—A-genome cottons have spread to other areas of the world by human activities and have been locally adapted in small plot cultivation. Primary areas for additional acquisitions are the African Sahel, and the countries of Asia Minor eastward (Turkey, Iraq, Iran, Pakistan). These should be obtained as opportunity arises.
(b) D-genome wild diploid species—Collecting expeditions in the last 10 years have provided good representation of *G. davidsonii* Kellogg, *G. armourianum*, *G. harknessii* Brandegee, *G. thurberi* Tod., and *G. turneri* Fryxell. Based

on the collecting expedition in Mexico in 2002, *G. turneri* seems to be in good shape for the moment (Ulloa et al. 2003, 2006b). The most widely distributed and most taxonomically diverse species, *G. aridum*, is surprisingly one of the least represented. Special effort should be made to obtain representative seed samples from throughout the range of this species. Ulloa and Stewart made a collection (US-72) in Eastern Guerrero in 2002 that will most likely be a newly described species (Ulloa et al. 2003, 2006b). It was added as sp. nov. under the D group. The species belongs with the *G. aridum* group (subsection *Erioxylum*). In the 2002 trip report it is designated as US-72 *G.* cf. *aridum*. Concurrently, additional populations of *G. lobatum*, *G. laxum*, *G. schwendimanii*, and *G. gossypioides* should be collected in this effort. Special attention should be given to obtaining samples from the range of *G. trilobum* (DC.) Skovst., which has an extensive range but is poorly represented in the U.S. collection. In 2002 and 2003, Ulloa and Stewart searched in Morelos, Mexico, Michoacan, and Jalisco at locations were *G. trilobum* had been collected in the past (Ulloa et al. 2006b). The site where *G. trilobum* was collected in Jalisco is now a part of suburban Guadalajara. They looked around parts of the canyon areas E and NE of Guadalajara, but did not find it. After this trip, Stewart is ready to modify Fryxell's (1979) statement that *G. trilobum* is widespread, to "The habitats of this once wide-spread species have been severely eroded by urbanization and agricultural development, such that now the species is rare, and its existence in the wild appears to be threatened."

(c) B- and F-genome species. These African species (five total) are represented by four or less accessions in the Wild Species Collection, all of unknown provenance. One species (*G. trifurcatum* Vollesen) recently described from herbarium specimens is not represented in the collection. By virtue of their status in the secondary germplasm pool, their proven record of possessing a range of host plant resistances, and sparse representation in the collection, acquisition of documented accessions of these species is important.

Tertiary germplasm pool (species of Australia, and Afro-Arabia)

Collections in Australia, including the addition of seven new *Gossypium* species and extensive representation of the geographic range covered by the genus, have made significant contributions to the available diversity. However, Afro-Arabian species are very poorly represented. No accessions are available for three Afro-Arabian species, and the remaining four are represented by three or fewer accessions, of unknown provenance in most cases. The Horn of Africa, where many of these species occur, appears to be an area of diversity for *Gossypium* and should be explored extensively when the political environment allows this to be done safely. Species on the Arabian Peninsula should be collected as soon as opportunity and inclination of potential collectors coincide.

Characterization

The Germplasm Resource Information Network (GRIN) database for *Gossypium* is sorely deficient in trait descriptor data. Descriptor data from small subsets of germplasm are often collected by various public scientists. This effort, however, lacks a central organized effort. If centrally directed, duplication of work could be avoided, and germplasm subsets could be identified for systematic evaluation. A centrally directed approach is needed to fill the large gaps in the GRIN database. An organized collective effort by public scientists would greatly supplement efforts of the curator.

Descriptor definitions/updates

Several morphological traits which are absent from the current list of trait descriptors need to be added. Descriptors are also needed to indicate segregation. Descriptor data for fiber traits collected prior to HVI testing need to be converted or re-tested.

Collection of descriptor data

Guidelines/procedures for field trials to provide a degree of standardization for collection of descriptor data would be useful. Environment has a significant impact on fiber property values. Designating one or

two cultivars as a common check in field trials would provide a standard for comparison of fiber property values collected in different environments. Passport data to be recorded during collection of descriptor data should be standardized.

Evaluation

Pest tolerance/resistance stress evaluation

A coordinated systematic effort to evaluate the cotton germplasm collection is needed to identify useful sources of biotic and abiotic resistance/tolerance.

Taxonomic evaluation

Countering the considerable taxonomic activity utilizing biochemical and molecular approaches that has occurred in the past 10 years is the retirement and subsequent elimination of a taxonomic specialist position dedicated to the genus at ARS in College Station, TX. The permanent herbarium collection of *Gossypium* was transferred to the New York Botanical Garden (NYBG.org) to provide continued access and preservation of the collection. Recent discoveries of new species, the likelihood that additional taxa will be discovered, and the continued redefinition of species' distribution, all indicate the need of continued support of taxonomic activities focused on the *Gossypium* genus.

Molecular genome characterization and mapping

A high density molecular marker map based on PCR-markers has been produced using an interspecific population of the two tetraploid species. Further, the primer sequences for many of the mapped SSR markers have now been deposited in a public database. Therefore, a project should be implemented to establish a molecular fingerprint of all accessions to minimize duplication and unnecessary evaluations of redundant accessions in the collection. These data could also be utilized in the establishment of a "core collection." The development of a standard set of SSR markers that represents the diversity across the cotton genome is needed.

Fiber quality evaluation

Recent advances in fiber measurement instrumentation promises greater precision in measuring fiber properties contributing to superior end-products. However, fiber properties measured by the new instrumentation do not always correspond to traits previously measured. There is a need for inheritance studies of the fiber properties being measured by new instrumentation and an evaluation of the germplasm for these traits.

Enhancement

Recommendations addressing some of the more immediate needs encompassing enhancement and requiring specific funding are as follows:

Metabolic efficiency

(a) Water use efficiency—Develop germplasm adapted to semiarid regions where water shortage is becoming the limiting factor.
(b) High temperature adaptability—Develop germplasm with ability to withstand stresses related to high temperature in both *G. hirsutum* and *G. barbadense*.

Gene transfer

(a) Introgression of genes from wild races and through interspecific hybridization—The primary and secondary germplasm pools contain extensive genetic diversity that has not been utilized. Desirable heritable traits (insect, pathogen, and environmental stress resistance, unique fiber properties, biochemical properties; etc) from primitive races and the secondary germplasm pool should be identified and transferred into acceptable agronomic genotypes. Transfer of desirable traits between species requires interspecific hybridization, and for the secondary germplasm pool, enhancement of the diploid germplasm is required. With the latter, development of breeding methodology, including development of molecular techniques, is required.
(b) Patterns of genetic and geographical variation in the collections need to be analyzed to better screen for desirable genes. Genes that have a unique function (e.g., abiotic resistance) seem to be grouped in material from specific geographic areas.
(c) A major stumbling block to the efficient utilization of genetic engineering methodologies in

foreign gene transfer to cotton has been the reliance on techniques which require tissue culture regeneration from a very limited "regenerable" germplasm. The use of regenerable germplasm outside of the Coker family has been reported. Identification, acquisition, and utilization of additional regenerable germplasm could increase the diversity of transgenic donor parents. Improvements in genetic engineering methods that do not require plant regeneration or regeneration methodologies, i.e., are genotype independent, are required.

(d) Identification and transfer of useful genetic variation from the primary germplasm pool is impeded for a large portion of the germplasm collection by the photoperiodic nature of tropical accessions. Conversion of photoperiodic *G. hirsutum* race stocks to a day-neutral flowering status is being conducted by a funded USDA, ARS program at Mississippi State, Mississippi. Conversion of *G. barbadense* germplasm is being performed within a USDA, ARS project located in Phoenix, Arizona. The conversion programs should continue; however, the scope and pace of *G. barbadense* conversion has been impeded by the lack of allocated funding for this purpose.

As previously stated, many enhancement projects out of necessity begin with identification of desirable or suitable genetic materials, blurring the line between evaluation and enhancement efforts. Meaningful enhancement efforts for insect, pathogen, or environmental stress resistance, fiber property improvement, performance characteristics, etc., are dependent upon adequate characterization of the germplasm.

Preservation

Working collection

With the accession number in the collection approaching 9,000 entries, there is a need to increase storage space. This would entail expanding vault carrying capacity, increasing drying and refrigeration, and increasing labor to handle the additional volume. Storage space limitations became acute by the summer of 1998 with the increase of 1,183 accessions acquired from India.

Due to static budgets and increasing costs, seed renewal and increase is now performed on an 'as needed basis' at 'the discretion of the curator'. With the new, indefinite criteria for seed renewal, it would be prudent to set up facilities to do periodic germination testing and establish guidelines for the periodicity of testing. Such testing would insure that accessions are increased on a timely basis and might save money by eliminating some unnecessary seed renewals.

Identity preservation

One of the primary functions of descriptor data is to ensure that the integrity of accessions in the collection is being maintained. The use of molecular and biochemical analysis could be a very useful addition—especially in materials that must be grown at remote sites and require trips to collect descriptor data. Molecular fingerprints and biochemical analysis also might save money by allowing the identification and elimination of duplicate accessions in the collection.

Recommendations

Priority of action categories are outlined as follows:

(a) Characterization
(b) Preservation
(c) Collection
(d) Enhancement
(e) Evaluation

Specific priority activities within each category have been outlined in each section of the report above (Germplasm Needs).

Funding needs

It is unlikely that any substantial funding for NPGS, outside of ARS, will be forthcoming in the foreseeable future, from either state or private organizations that have an interest in promotion of cotton. All cotton producing states reported in this document are operating under austere budgets. However, it would be prudent to have a long-range plan for germplasm needs in place, anticipating that the economic woes will change for the better.

Status of crop vulnerability

Genetic diversity is believed to provide a buffer against adverse effects of sudden increases in the virulence of pathogens or pests. An oft-cited example of the danger of genetic uniformity is the Southern corn leaf blight crisis of the 1970s (Ullstrup 1972). The majority of corn hybrids at that time shared a common cytoplasm that was used because it greatly facilitated hybrid seed production. This cytoplasm, and all hybrids using the cytoplasm, proved to be highly susceptible to a race of Southern corn leaf blight. Since that time, greater attention to the preservation and expansion of genetic diversity has been encouraged in all crops, although the encouragement is not always heeded.

Diversity—estimates from pedigrees and molecular markers

Genetic diversity in cotton has been estimated by both pedigree studies and molecular markers. Calhoun et al. (1994, 1997) compiled pedigrees of Upland and Pima cotton cultivars released between 1970 and 1995. Bowman et al. (1996, 1997) estimated an average coefficient of parentage (CP) of 0.07 among 260 cultivars released between 1970 and 1990 and concluded the genetic base was not narrow. May et al. (1995) found a CP of 0.07 among 126 cultivars indicating genetic diversity as a group. However, diversity was much reduced within cultivars of similar origin. These studies suggest that genetic diversity is available but only a few germplasm lines have been used in the development of commercial varieties.

Van Esbroeck et al. (1998) observed the frequent use of relatively few parents in the creation of cultivars while Van Esbroeck and Bowman (1998) stated that only four germplasm lines out of 668 registered in Crop Science can be found in pedigrees of commercially successful cultivars during the period from 1987 to 1996. Finally, Van Esbroeck et al. (1999) suggested pedigree-derived genetic distances have overestimated diversity among cultivars due to relatedness of ancestral lines. Thus, cotton germplasm may not be as diverse as reported CP values indicate (Van Becelaere et al. 2005).

The cultivated Uplands represent an estimated 1% of the potential genetic variability available. Molecular markers (RFLPs, RAPDs, and SSRs) have also been used to characterize the cotton germplasm diversity. Results indicated that there is narrow genetic base among the cultivated cotton germplasm (Ulloa et al. 1999; Gutiérrez et al. 2002). An underlying theme of most formal studies of diversity in cotton crop germplasm is that genetic diversity exists in the primary gene pool, but there is much room for broadening the gene base of the commercial germplasm.

Diversity—as measured by most popular upland cultivars by region

Estimated acreage (USDA/AMS) planted to the most popular Upland cultivars during the 2004 growing season is listed in Table 18. In the Southeast, two cultivars (DP 555 BG/RR and DP 444 BG/RR) accounted for 44.5% of the acreage. Six of the top seven cultivars in this region represent a single seed company. Four out of six of these cultivars have the common parent DP 90 in their background (46.4% of the acreage) and three have DP 50 as a common parent in their background (16% of the acreage). The Southeast region would appear to have less diversity than any other region due to popularity of related cultivars. The same two cultivars (DP 555 BG/RR and DP 444 BG/RR) dominated acreage (36.4%) in the South Central region. In the Southwest, the largest cotton growing region in the U.S., acreage is generally represented by a larger number of cultivars than the remaining growing regions. Although the acreage in this region is represented by a greater number of cultivars, the degree of diversity among these cultivars is not known. The seven most popular cultivars in this region occupied only 39.5% of the acreage. However, five of the most popular cultivars for this region are represented by a single seed company, and are perhaps more likely to be related. In the West, PHY 72 Acala accounted for 23.2% of the acreage. Just four cultivars, all Acala types, occupied more than 62.2% of the acreage in the West. With the exception of the Southwest, one-quarter to one-third of the acreage in each region was planted to a single cultivar (DP 555 BG/RR).

Coefficients of parentage (CP) weighted for acreage provided in the 1997 Cotton Germplasm Status Report indicated that diversity among leading cultivars in 1995 ranged from 0.24 for the Southwest to

Table 18 Estimated percentage of most popular Upland cotton cultivars planted for each growing region in 2004

Southeast	DP 555 BG/RR	DP 444 BG/RR	DP 451 B/RR	ST 5599 BR	DP 449 BG/RR	DP 458 B/RR	DP 5690 RR
	35.01%	9.51%	7.83%	4.89%	4.30%	4.00%	3.07%
South Central	DP 555 BG/RR	DP 444 BG/RR	ST 5599 BR	PM 1218 BG/RR	ST 4892 BR	FM 960 BR	DP 451 B/RR
	22.52%	13.99%	12.89%	12.78%	11.36%	4.35%	4.14%
Southwest	FM 958	FM 989 RR	FM 832	AFD 3511 RR	DP 5690	FM 960 BR	FM 989
	11.23%	6.26%	5.73%	4.85%	3.91%	3.88%	3.66%
West	PHY 72 Acala	Acala RIATA RR	Acala SIERRA RR	DP 449 BG/RR	DP 448 B	PHY 78 Acala	DP 555 BG/RR
	23.20%	13.77%	12.80%	12.46%	4.65%	4.10%	3.64%
USA	DP 555 BG/RR	DP 444 BG/RR	FM 958	ST 5599 BR	ST 4892 BR	PM 1218 BG/RR	FM 960 BR
	14.89%	6.50%	5.27%	5.11%	4.21%	3.72%	3.60%

0.34 for the West. Coefficient of parentage values are not available for 2004 leading cultivars. However, some inference concerning diversity can be suggested based upon acreage occupied by leading cultivars reported in the 1997 Status Report with current leading cultivars. In 1995, 70% of the acreage in the West and 50% of the acreage in the Southwest was occupied by two cultivars. In 2004, the two leading cultivars in the West and Southwest occupied only 37% and 17.5 % of the acreage, respectively.

Diversity—as measured by most popular upland cultivars across regions

The most popular cultivar planted in the U.S.A., DP 555 BG/RR occupied 14.9% of the acreage in 2004 while the remaining top six cultivars occupied 28.4% of the total Upland acreage (Table 18). The genetic diversity among all available cultivars (i.e., available diversity) generally is higher than the diversity that exists among widely grown cultivars (i.e. diversity in current use) because producers within a region tend to plant a few, preferred cultivars. Risk of loss due to genetic vulnerability, therefore, would tend to be greater within a specific growing region compared to the entire Upland acreage.

Diversity—transgenic cultivars

While the diversity represented in commercial cotton production in any year and/or region may be somewhat limited, we do not appear to be in a situation similar to the corn industry of the 1970s when virtually all commercial production shared a common cytoplasm. However, the development of transgenic cotton cultivars may have introduced a linkage group common to transgenic cultivars. With the exception of Texas, New Mexico, Arizona, and California, >90% of the acreage in each cotton growing state was planted to transgenic cultivars in 2003. All currently grown commercial transgenic cultivars were derived through backcross breeding utilizing a common transgene donor parent (Coker 312) due to ease of somatic embryo formation. Even though the recently released Bollgard II™ gene was inserted via particle gun bombardment, the recipient genotype (DP 50B) was developed utilizing a Coker donor (Mahaffey et al. 2000). The recently developed VIP technology which utilizes an exotoxin as opposed to

the more common delta-endotoxin Bt cultivars, was also derived from a Coker donor parent (Mascarenhas et al. 2003). The extent to which the use of a single donor genotype has resulted in a common linkage group among transgenic cotton cultivars is not known. The effect that genetic engineering may have on genetic diversity in the future is unclear. On one hand, these new technologies make it possible to incorporate traits (variability) that are not otherwise available. However, the current trend in applying these technologies may serve to decrease background genetic diversity. The reliance of the present generation of transgenic lines on tissue culture regeneration from a very limited "regenerable" germplasm has restricted genetic variability. Further, most programs utilizing transgenes rely heavily or exclusively on backcrossing to incorporate foreign genes into a desired genotype, a strategy that does nothing to expand genetic diversity (Bowman et al. 2003). Backcrossing programs act as a drag to the replacement of old cultivars with substantially different new cultivars; instead they create cultivars that differ by only a few alleles from their predecessors. By incorporating transgenes into traditional cross-and-select breeding programs, the industry can benefit from novel and valuable traits while maintaining background genetic diversity. The degree of increased risk as a result of the widespread adoption of transgenics which utilize traits derived from a single donor parent should be determined.

Diversity—Pima cotton

The diversity of commercially produced Pima (*G. barbadense* L.) cotton is not known with the same precision as that of *G. hirsutum*. Until the early 1990s, it was the practice of the American Pima cotton industry to grow a single cultivar (sometimes two) at any given time. This circumstance left the commercial Pima industry vulnerable to any "new" disease, insect, or other adversity which might arise. The advent of private Pima breeding programs in the 1990s increased both the number of available cultivars and the apparent diversity of commercial germplasm. Countering this apparent diversity was the fact that all commercial cultivars at that time originated from a single germplasm pool maintained by the USDA-ARS. In recent years the germplasm of commercial companies has matured and diversified. At present, nine commercial cultivars are being grown on a relatively small acreage (Table 19). Again, the apparent diversity of the Pima crop does not hold up when one inspects regional planting patterns. In 2004, over 66% of the Pima acreage in the San Joaquin valley of California was planted to two cultivars. More dramatically, 70% and 92% of the acreage in Texas and New Mexico, respectively, were planted to a single cultivar. The regional adaptation of cultivars and the economics of cultivars competing for a relatively small acreage restrict the ability to diversify—leaving the crop vulnerable to new or introduced threats. This is a situation that is unlikely to change significantly unless increasing Pima acreage improves the economic viability of increased cultivar numbers.

Other species

Little is known about the two commercially produced diploid species, other than germplasm resources and diversity are thought to be large. Research to identify superior agronomic genotypes suitable for production in the U.S. has been initiated recently.

Our greatest opportunity to reduce or minimize genetic vulnerability in cotton lies in greater and more efficient use of our feral and/or exotic germplasm. Public sector programs, both federal and state, must take the lead in developing and enhancing this

Table 19 Estimated percentage of American Pima cotton cultivars planted for each state in 2004

State	BR007 (%)	DP 340 (%)	DP 744 (%)	DP HTO (%)	HA 195 (%)	PHY 76 (%)	PHY 800 (%)	S-6 (%)	S-7 (%)
Arizona	0.00	43.29	5.23	30.66	0.00	0.00	0.00	0.00	20.83
California	0.24	20.01	16.26	0.46	3.73	12.21	46.17	0.00	0.93
New Mexico	0.00	91.71	4.19	0.00	0.00	2.05	2.05	0.00	0.00
Texas	0.00	70.00	5.00	10.00	0.00	0.00	0.00	15.00	0.00
USA	0.21	26.73	14.81	1.60	3.26	10.72	40.37	1.25	1.06

valuable wealth of germplasm. Cooperative research projects and multi-state projects such as Regional Project S-304, are instruments through which federal and state workers maintain and study the *Gossypium* germpool and coordinate research on the genetics, cytogenetics, pathology, taxonomy, and entomology of cotton. Increasing the scope of this work will assist in a better understanding of the diversity existing in *Gossypium*, of the heritable systems of the cotton plant, and of the systematics of the genus. More complete evaluations and enhancements of all the materials in the existing collection, and new materials added to the collection, would generally increase available germplasm for use by cotton plant breeders as needs arise in an ever-changing cotton industry.

Potential threats

Fusarium wilt

Fusarium wilt [*Fusarium oxysporum* f. sp. *vasinfectum* (FOV)] is a foliar disease of cotton common to most cotton regions of the U.S.A. The disease was first described in the U.S.A. in 1892 and continues to result in sporadic losses each year. The Western growing region (Arizona and California) of the U.S.A. has been particularly conducive to this disease. Efforts directed towards the development of wilt-tolerant cultivars at the USDA-ARS Western Integrated Cropping Systems Research, Shafter CA and other programs have prevented this disease from escalating into serious losses. A recent survey of FOV isolates from California identified a new virulent race 4 of the pathogen (Davis et al. 2003). Race 4 was found to be highly virulent on Pima but less virulent on Acala genotypes. More importantly, the survey of California FOV isolates failed to identify the highly virulent Australian fungal genotypes (VCG 01111 & VCG 01112). Since first being recognized in Queensland during the 1992/1993 growing season, the disease (which does not require presence of nematodes) is now widespread in Southern Queensland. Evidence suggests that the pathogen is dispersed via soil, crop residue, and machinery. As a result, Australia has implemented an industry-wide effort to minimize the potential threat to productivity (Allen 2002). Very little resistance has been observed in Australian cultivars, and under severe infestation, plant mortality has exceeded 60%. Cultivars resistant to FOV in the U.S.A. were fully susceptible to the pathogen when grown in Australia. Even though the California Cotton ginners and Growers Association has requested a halt to the importation of cotton seed for feed, imports permits have been allowed to continue. Imported seed is fumigated, however it is most likely not 100% effective against this seed borne pathogen. It has been estimated that 40% of the U.S.A. cotton production would be at risk if the Australian isolates were introduced. Breeders in Australia claim to have found various sources of resistance, including the native Australian diploid species of *Gossypium* and are being utilized. Introduction of this pathogen would in all probability result in significant disruption of US cotton production via reduced yields. If this pathogen was introduced into US soils, the cotton industry would be wise to draw upon the experiences of the Australian cotton industry. An immediate response could be the adoption of a quarantine program similar to the Australian program. Efforts to identify and incorporate resistance to FOV would be facilitated through collaboration with scientists in Australia.

Leaf curl virus

The cotton leaf curl disease (CLCuD), is caused by a whitefly (*Bemisia tabaci*) transmitted begomovirus [Cotton Leaf Curl Virus (CLCuV)] (Jones 2003). Symptoms of this disease include curling of leaf margins, swelling and darkening of veins, and formation of enations on the veins which may develop into cup-like leaf structures (Briddon 2003). Although recognized in Pakistan as a sporadic problem more than 40 years ago, the disease has reached epidemic proportions over the last 15 years and has spread into neighboring India (Briddon and Markham 2000). Recognition that the introduction of a popular new cultivar (S12) coincided with the beginning of this epidemic, tolerant cultivars were developed. Cultivars in Pakistan previously resistant to CLCuV succumbed to the virus during the 2001 growing season suggesting the emergence of a new strain (with DNA ß satellite component) of the virus (Mansoor et al. 2003). Loss to the Pakistan economy was estimated at US$5 billion between 1992 and 1997 due to the CLCuD. While a few tolerant Pakistan cultivars were initially developed in the past, most, if not all cultivars now appear susceptible to this pathogen and most likely would include all US cultivars. The "Desi" cotton

(*Gossypium arboreum*), native to Pakistan, is reportedly immune to the pathogen and may be a potential source of resistance. As this pathogen is entirely vector dependent, any area prone to whitefly infestations would be at risk if the CLCuV were to reach and survive in the USA. This would place a large portion of USA acreage at high risk of significant losses.

Risk of high-consequence plant disease/pests—summary

If the leading cotton cultivar in a region was lost to disease or insect susceptibility, there is certainly the possibility that closely related cultivars (approaching 50% of the acreage in some regions) also would be lost. "Lost", as used here, means that the cultivar(s) would no longer be commercially useful due to disease or pest susceptibility; it is unlikely that such susceptibility would result in the total loss of production of affected cultivars. In the event that a portion of the currently popular cultivars were lost due to an endogenous pest, it appears at the present time that there are adequate genetic resources available to address the situation. The evolution of a new, but endogenous virulent pest strain, would hopefully be identified early enough to provide time for the identification and utilization of resistant germplasm to prevent an epidemic. Replacement cultivars could include cultivars that are grown currently on a minor acreage, cultivars from other regions, or older cultivars that have been recently replaced. Such loss of current popular cultivars would cause a temporary disruption in the industry as necessary adjustments were made.

An introduced pathogen, such as the CLCuV, could potentially result in a greater disruption of the cotton industry. All US cultivars are presumably susceptible to this pathogen. All efforts to identify sources of tolerance/resistance to this pathogen as a preemptive measure to safeguard US cotton should be encouraged. Control of the whitefly vector, in addition to breeding efforts, however, would provide an added response option to this pathogen. The introduction of virulent Australian isolates of FOV appears to be a real possibility and poses a threat to significant acreage in USA. Breeders in Australia are actively searching for sources of resistance to this pathogen. Cooperative efforts in this endeavor should be encouraged. Furthermore, measures to prevent introduction of this pathogen should be pursued. Australia could serve as a model in prevention and containment should this pathogen be introduced.

The view that we presently have adequate genetic resources for our current pest populations does not mean that breeders should relax their vigilance to maintain and expand genetic diversity. Most formal studies of genetic diversity in cotton imply that there is considerable room for improvement. The development and widespread adoption of transgenic cultivars may have inadvertently introduced one or more linkage groups in cultivars occupying a majority of US cotton acreage. The potential risk (genetic vulnerability) as a result of industry wide use of Coker derived transgenics should be determined.

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