Genetic Improvement of the Pee Dee Cotton Germplasm Collection following Seventy Years of Plant Breeding

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ABSTRACT

One of the most significant, long-term public U.S. Upland cotton (*Gossypium hirsutum* L.) germplasm enhancement programs is known as the Pee Dee germplasm program. The unique, genetic foundation of the Pee Dee germplasm was created using germplasm from Upland, Sea Island (*Gossypium barbadense* L.), and primitive diploid cottons. Since the program's inception in 1935, the Pee Dee germplasm program has released >80 improved germplasm lines and cultivars. In this study, the agronomic and fiber quality performance of Pee Dee germplasm was evaluated across southeastern U.S. environments to estimate genetic improvement within the Pee Dee germplasm program. Results suggest that the Pee Dee germplasm enhancement program has (i) maintained usable genetic variation and (ii) maintained high fiber quality potential while concomitantly improving agronomic performance. Although the results highlight the need to continue improving lint percent, lint yield, and bolls m^{-2}, there is also evidence to suggest that Pee Dee germplasm can continue being utilized to develop the next generation of high-fiber-quality and high-yielding cotton cultivars.

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Abbreviations: G × E, genotype × environment; HVI, high-volume instrument; SSR, simple sequence repeat.

Plant breeding programs develop genetic resources that form the baseline potential of crop production systems. Like many globally important agricultural commodities, continued genetic improvement of cotton (*Gossypium* spp.) is essential to increase both the quantity and quality of cotton production systems. Today, the globalization of cotton textile manufacturing and the adoption of high-speed fiber spinning machinery have increased the global demand for high-quality fiber. Hence, increasing pressure is being placed on cotton breeding programs to increase yields while simultaneously increasing fiber quality.

Genetic improvement of cotton dates to early farmer–seedsmen and scientific strategies date to the rediscovery of Mendel's principles at the turn of the 20th century. Since 1900, many studies have been conducted to quantify levels of genetic gain. Several of these studies, which have been summarized by Calhoun and Bowman (1999), estimate average lint yield genetic gains of approximately 9 kg ha^{-1} yr^{-1}. However, Paterson et al. (2004) reported, from 1985 to 1998, absolute cotton yields began declining at a

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3.3% annual rate (16.8 kg ha^{-1} yr^{-1}). Moreover, the year-to-year variability in absolute yield from 1980 to 1998 was four times greater than in 1960 to 1979. Paterson et al. (2004) suggested that breeders' overexploitation of a few genetic backgrounds, along with the widespread adoption and planting of backcross-derived transgenic cultivars, has created a cotton yield plateau. Subsequent studies attempting to quantify genetic diversity suggested a narrowing of genetic diversity within the primary gene pool of cotton (Abdalla et al., 2001; Lu and Myers, 2002; Rahman et al., 2002; Van Becelaere et al., 2005). Narrow genetic diversity is cause for alarm because genetic diversity must exist for effective plant breeding and genetic improvement efforts.

Bowman et al. (2006) traced the history of 13 different U.S. public cotton breeding and germplasm development programs. Two public germplasm programs highlighted in that report (New Mexico Acala and Pee Dee) were also found to account for >50% of fiber strength improvements present in commercial cultivars (Bowman and Gutierrez, 2003). Interestingly, both germplasm programs have similar complex and unique breeding histories that involve genetic exchange between two tetraploid species (*G. hirsutum* L. and *G. barbadense* L.) and two diploid wild species (*G. arboreum* L. and *G. thurberi* Todaro). Although the amount of gene introgression from wild species in each germplasm program has not been quantified, the moderate genetic similarities reported by Zhang et al. (2005) and Campbell et al. (2009) provide evidence that genetic diversity has been maintained in each program over time. Genetic diversity maintenance within each germplasm program is probably due to each program's unique germplasm foundation and the combination of alternative breeding methods deployed, such as random intermating, modified backcrossing, and composite crossing (Campbell et al., 2009).

The Pee Dee germplasm program was initiated in 1935 to improve the yield and boll weevil (*Anthonomus grandis* Boheman) tolerance of Sea Island cotton (*G. barbadense* L.) and to develop early-maturing Upland cottons (*G. hirsutum* L.) with Sea Island fiber properties (Culp and Harrell, 1973). By the mid-1940s, developing improved Sea Island cottons with adequate yield proved difficult; however, two Upland cotton cultivars (Sealand and Earlistaple) with superior fiber properties were developed and grown commercially. Due to further reduction in Sea Island cotton production during this period, primarily as a result of devastation caused by the boll weevil, the program's objectives shifted from breeding Sea Island cotton to focusing on developing Upland cultivars with improved fiber strength and yield. About this time, unique triple-hybrid strains (*G. arboreum* L. × *G. thurberi* Todaro × *G. hirsutum* L.) with improved fiber strength were developed and distributed to cotton breeding programs (Beasley, 1940; Kerr, 1960). Culp and Harrell (1973) described a complex intercrossing program (e.g., recurrent selection) involving two triple-hybrid strains (TH 108 and TH 171) and several Upland parents (Sealand, Earlistaple, and 'Hopi Acala') that gave rise to the F, J, A, and N Upland progenitor lines that form the basis of the current Pee Dee germplasm program.

In an effort to determine the rate of genetic gain in the Pee Dee germplasm program, Culp and Green (1992) compared the field performance of 20 obsolete and modern Pee Dee germplasm lines developed through the 1970s. They estimated a 14 kg ha^{-1} yr^{-1} increase in lint yield. Using molecular markers, Campbell et al. (2009) characterized the genetic relationships within the Pee Dee germplasm collection and found useful genetic diversity exists. In this report, we examine genetic trends associated with germplasm developed within eight primary breeding cycles of the Pee Dee germplasm program since the development of the F, J, A, and N progenitor lines. The objectives of this research were (i) to evaluate the agronomic and fiber quality performance of Pee Dee germplasm across southeastern U.S. environments, and (ii) to estimate levels of genetic improvement within the Pee Dee germplasm program over time.

MATERIALS AND METHODS

Germplasm Selection

Eighty-two officially released cotton germplasm lines and/or cultivars were selected from the Pee Dee cotton germplasm collection to represent the history of the Pee Dee cotton breeding program. Care was taken to select a range of lines representative of different pedigrees and points in time over the life of the breeding program. The list of germplasm lines and cultivars is provided in Table 1. Based on both breeding cycle and pedigree, the germplasm lines and cultivars were separated into eight different groups. Group 1 represented initial germplasm and cultivar releases that formed the breeding program's foundation. The germplasm lines in this group were derived from complicated intercrosses involving several Upland cotton parents, Sea Island cotton parents, and unique high-fiber-strength triple-hybrid strains. The second, third, and fourth groups were derived primarily from intercrosses involving the germplasm developed in the previous breeding cycle (group). Groups 5 and 6 represented a change in breeding focus; these groups consist of germplasm developed for host plant resistance to boll weevil and other insect pests. Group 7 represented a renewed focus on improving yield and fiber quality. The base germplasm used in the development of Group 7 was derived from crosses involving a line developed in a previous breeding cycle and several lines from the Mississippi Delta gene pool, including 'Delcot 311' (PVP 8100029; Sappenfield, 1980), 'DES 422' (PVP 8100170; Bridge and Chism, 1982), and 'DP 41' (PVP 7900102). Group 8 represented repeated intercrosses primarily involving germplasm developed in Breeding Cycle 7.

For each field trial, a total of two to six check cultivars were selected for comparison purposes. These check cultivars allowed for the Pee Dee germplasm to be compared with commercial cultivars widely grown in the United States. The six checks included the two conventional cultivars Deltapine 491 (DP491, PVP 200100159) and FiberMax 958 (FM958, PVP 200100208). In addition, to adequately compare Pee Dee germplasm with

Table 1. A description of Pee Dee lines evaluated in this study.

Genotype	Pedigree	Group	Registration article
AC 235(9)	Hybrid 313/C6-5	1	Culp and Harrell, 1980b
AC 241	Hybrid 313/C6-5	1	Culp and Harrell, 1980b
Earlistaple 7	Reselection (Tidewater Acala/Coker Wilds)	1	Culp and Harrell, 1980a
Hybrid 330-278	Sealand-542//TH 108/AHA6-1-4/Earlistaple	1	Culp and Harrell, 1980a
FJA 347	F/J//A (Sealand 542, TH 108, AHA 6-1-4, TH 171, Sealand 7, Earlistaple)	1	Culp and Harrell, 1980a
FTA 266	F/T//A (Sealand 542, TH 108, AHA 6-1-4, TH 171, Sealand 7, Earlistaple)	1	Culp and Harrell, 1980a
Sealand 542	Bleak Hall/5 × Coker Wilds	1	Culp and Harrell, 1980a
PD 0259	TH 108, 171, AHA 6-1-4, Earlistaple, Sealand 542, C6-5	2	Harrell and Culp, 1979a
PD 2165	TH 108, 171, AHA 6-1-4, Earlistaple, Sealand 542, C6-5	2	Harrell and Culp, 1979a
PD 4381	Auburn 56/AC 239	2	Harrell and Culp, 1979b
PD 4461	*G. barbadense* "V," Auburn 56, Coker 100 Wilt, Earlistaple	2	Culp and Harrell, 1979b
PD 2164	AC 239/FJA 348	2	Culp and Harrell, 1980b
PD 3246	AC 239/FTA 266	2	Culp and Harrell, 1980b
PD 3249	AC 239/FTA 266	2	Culp and Harrell, 1980b
PD 9223	Coker 421/PD 2164	3	Culp and Harrell, 1979a
PD 9232	Coker 421/PD 2164	3	Culp and Harrell, 1979a
PD 9363	Carolina Queen/PD 9249//PD-2	3	Culp and Harrell, 1979a
PD 9364	Carolina Queen/PD 9249//PD-2	3	Culp and Harrell, 1979a
PD 0109	PD 4381/PD 2165	3	Culp and Harrell, 1980c
PD 0111	PD 4381/PD 2165	3	Culp and Harrell, 1980c
PD 0113	PD 4381/PD 2165	3	Culp and Harrell, 1980c
SC-1	Coker 421/PD 4398	3	Culp and Harrell, 1979d
PD 8619	PD 4461/MO-DEL	3	Culp and Harrell, 1979c
PD 875	DSR-1 × 6-56/PD 8619//PD 8619	4	Harrell and Culp, 1979b
PD-1	PD 4381/PD 8623	4	Culp et al., 1985a
PD-2	FTA 266/ATLAS//AC 239/DIXIE KING	4	Culp et al., 1985b
PD 6044	Delcott 277/PD 9223	4	Culp et al., 1985c
PD 6132	SC-1/PD 9232	4	Culp et al., 1985c
PD 6142	SC-1/PD 9232	4	Culp et al., 1985c
PD 6179	SC-1/PD 8619	4	Culp et al., 1985c
PD 6186	SC-1/PD 8619	4	Culp et al., 1985c
PD 6992	SC-1/PD 8619//Coker 310/PD 7396	4	Culp et al., 1985c
PD-3	PD 9363/PD 9240	4	Culp et al., 1988
PD 695	LA Frego 2/2 × PD 8562	5	Harrell and Culp, 1979b
PD 7388	PD 8619//PD 8619/LA Frego 2	5	Culp et al., 1990a
PD 7439	PD 8650//PD 8650/LA Frego 2	5	Culp et al., 1990a
PD 7458	PD 8499/LA Frego 2//2 × Coker 310	5	Culp et al., 1990a
PD 7496	PD 924//PD 8550/LA Frego 2	5	Culp et al., 1990a
PD 7501	PD 924//PD 8550/LA Frego 2	5	Culp et al., 1990a
PD 7586	PD 9257//PD 8562/LA Frego 2	5	Culp et al., 1990a
PD 7723	PD 6520//PD 8562/LA Frego 2	5	Culp et al., 1990a
PD 0648	PD 695/Deltapine 7146N	6	Culp et al., 1990a
PD 0683	PD 695/PD 869	6	Culp et al., 1990a
PD 0723	PD 695/5-718	6	Culp et al., 1990a
PD 0878	TX-ORS-75C/Deltapine 7146N	6	Culp et al., 1990a
PD 0948	TX-ORS-75C/PD 875	6	Culp et al., 1990a
PD 0738	PD 695/PD 875	6	Culp et al., 1990b
PD 0741	PD 695/PD 875	6	Culp et al., 1990b
PD 0747	PD 695/PD 875	6	Culp et al., 1990b
PD 0753	PD 695/PD 875	6	Culp et al., 1990b
PD 0756	PD 695/PD 875	6	Culp et al., 1990b
PD 0761	PD 695/PD 875	6	Culp et al., 1990b
PD 0762	PD 695/PD 875	6	Culp et al., 1990b
PD 0771	PD 695/PD 875	6	Culp et al., 1990b
PD 0778	PD 695/PD 875	6	Culp et al., 1990b

(cont'd)

Table 1. Continued.

Genotype	Pedigree	Group	Registration article
PD 0781	PD 695/PD 875	6	Culp et al., 1990b
PD 0785	PD 695/PD 875	6	Culp et al., 1990b
PD 0804	PD 695/PD 875	6	Culp et al., 1990b
PD 5363	Delcot 311/PD 6131	7	Green et al., 1991c
PD 5472	McNair 235/PD 6184	7	Green et al., 1991c
PD 5286	DES 422/PD 6044	7	Green et al., 1991b
PD 5529	Deltapine 41/PD 6133	7	Green et al., 1991b
PD 5576	Deltapine 41/PD 3246	7	Green et al., 1991b
PD 5582	Deltapine 41/PD 4461	7	Green et al., 1991b
PD 5246	McNair 220/PD 6171	7	Green et al., 1991a
PD 5256	McNair 220/AC 241	7	Green et al., 1991a
PD 5358	Delcot 311/PD 5657	7	Green et al., 1991a
PD 5377	Delcot 311/PD 6171	7	Green et al., 1991a
PD 5380	Delcot 311/PD 6171	7	Green et al., 1991a
PD-3-14	Sel. PD-3	8	May et al., 1996
PD 93001†	PD-3/Brown lint accession	8	May et al., 1994
PD 93030	PD 5358/PD 5485	8	May and Howle, 1997a
PD 93034	PD 5285/PD 5485	8	May and Howle, 1997a
PD 93057	PD 5265/PD 5485	8	May and Howle, 1997a
PD 93007	PD 5285/PD 5485	8	May and Howle, 1997b
PD 93043	PD 5265/PD 5576	8	May and Howle, 1997b
PD 93046	PD 5358/PD 5485	8	May and Howle, 1997b
PD 93009	PD 5286/PD 5485	8	May and Howle, 1997a
PD 93019	PD 5285/PD 5377	8	May and Howle, 1997a
PD 93021	PD 5286/PD 5377	8	May and Howle, 1997a
PD 94042	JIMIAN 8/PD-3	8	May, 1999
PD 94045	COKER 315/JIMIAN 8	8	May, 2001

† PD 93001 was excluded from all analyses because of highly variable performance related to poor seed germination.

current genetic technology, we included four transgenic, commercial cultivars widely grown in the southeastern United States. These cultivars included Deltapine 444BR (DP444BR, PVP 200300134), Deltapine 555BR (DP555BR, PVP 200200047), FiberMax 960BR (FM960BR, PVP 200400224), and Stoneville 5599BR (ST5599BR, PVP 200300279).

Field Trials

During 2004 to 2006, a total of 14 replicated field trials were conducted across North Carolina, South Carolina, Georgia, and Mississippi. Each trial included the 82 Pee Dee germplasm lines and two to six of the check cultivars. The experimental design for each trial consisted of two to four replicates arranged in an α-lattice incomplete block design. In 2004, trials were conducted at three locations in South Carolina; these locations included the Clemson University Edisto Research and Education Center in Blackville, the Clemson University Pee Dee Research and Education Center in Florence, and the Monsanto Company research station in Hartsville. These trials included the check cultivars DP491 and FM958. Florence and Blackville trials contained four replicates and 14 incomplete blocks of size six. The Hartsville trial contained two replicates and 21 incomplete blocks of size four.

In 2005 and 2006, trials were conducted across North Carolina, South Carolina, Georgia, and Mississippi. Each trial included all six check cultivars. For North Carolina, three replicate trials in each year were conducted at the North Carolina State Upper Coastal Plains Research Station in Rocky Mount, NC. In both years, three replicate trials were conducted at the University of Georgia research station in Tifton, GA. Two replicate trials were conducted at the USDA-ARS Jamie Whitten Research Center in Stoneville, MS. Trials in South Carolina were conducted in Florence (four replicates), Blackville (three replicates), and Hartsville (two replicates), with the exception that 2006 included Florence and Blackville only. In 2005 and 2006, with the exception of Blackville 2006, each replicate of the α-lattice designs contained 22 incomplete blocks of size four. Blackville 2006 contained eight incomplete blocks of size 11.

With the exception of the Stoneville location, plots were two rows 10.6 m to 15.0 m by 76 cm to 100 cm. At the Stoneville location, plots were single rows 10.6 m by 96.5 cm. Trial management followed the established local practices for dryland cotton production at each location. Each plot was harvested with a spindle-type mechanical cotton picker, and total seed cotton weight was recorded. A 25-boll sample was hand-harvested from each plot before harvest to determine boll weight, bolls m^{-2}, seed index, lint percent, and fiber quality properties. Boll weight was determined by dividing the weight of the 25-boll sample by 25. Bolls m^{-2} was determined by dividing the seed cotton yield by the boll weight. All samples from each location were ginned on a common 10-saw laboratory gin and lint percent was determined by dividing the weight of the lint sample after ginning by the weight of the seed cotton sample before ginning. Lint yield was calculated by multiplying the lint percent by the seed cotton yield. In addition, a portion of the lint sample was sent to the Cotton Incorporated Fiber Testing Laboratory (Cary, NC) for determination of high-volume instrument (HVI) and Advanced Fiber Information System (AFIS)

fiber properties. The fiber properties measured include HVI fiber length, HVI fiber strength, HVI elongation, HVI uniformity, HVI micronaire, and AFIS fineness.

Field Data Analysis

All agronomic and fiber quality data were analyzed using a mixed model and the PROC GLM module of SAS version 9.2 (SAS Institute, 2008). The RANDOM statement was included to identify random effects and make *F* tests using the appropriate error term. Initially, individual year–location data were analyzed and homogeneity of variance tests were conducted to determine if a combined analysis of variance could be conducted for each trait. After confirming homogenous error variance for each trait, the data were analyzed using two analysis of variance procedures. For ease of analysis, the replicate and incomplete block terms were combined to form a single "block" term; the block term was considered a random effect. Each year–location trial was considered a single environment; environment was considered a random effect. Genotypes were considered fixed effects.

The first analysis of variance was conducted to test the effects of genotype and the genotype × environment (G × E) interaction. Genotype was further partitioned to test for differences among Pee Dee lines (L), among checks (C), and between the Pee Dee lines and checks (L vs. C). The G × E interactions were then tested for each of the partitioned main effects. The second analysis of variance was conducted to test the effects among the eight Pee Dee germplasm groups and among the lines within each group. The G × E interactions were subsequently tested for each of the partitioned main effects. The least squares means of each genotype (adjusted for experimental design) were calculated for each of the traits measured. To observe the genetic change achieved over time for each trait, the trait mean for each group was plotted as a function of group number. For each trait, a linear regression line was fitted across groups to provide a regression equation describing the genetic change over time.

Molecular Marker Analysis

Simple sequence repeat (SSR) marker data, previously collected on each Pee Dee germplasm line according to the procedure described by Campbell et al. (2009), were used in the following analyses. Briefly, efforts were made to genotype each Pee Dee germplasm line with two SSR markers per chromosome arm (104 total) using polymerase chain reaction, polyacrylamide gel electrophoresis, and ethidium bromide staining. Amplified fragments of each SSR marker–germplasm line combination were scored as 1 or 0, where 1 and 0 indicated the presence or absence of a specific allele (band), respectively. Previously, Campbell et al. (2009) calculated all possible pairwise genetic similarities considering all 82 Pee Dee germplasm lines. However, in this report, mean genetic similarities were estimated within each of the eight Pee Dee germplasm breeding cycles or groups using NTSYSpc version 2.2 (Rohlf, 2005). Genetic similarities between pairs of germplasm lines within each group were measured using the SIMQUAL module by the DICE similarity coefficient based on the proportion of shared alleles (Dice, 1945; Nei and Li, 1979).

RESULTS AND DISCUSSION

Combined Analysis of Variance

Agronomic and fiber quality data were collected on Pee Dee lines and commercial checks across 14 location–year environments. Data on PD 93001 were excluded from all analyses because of highly variable performance related to poor seed germination. Because of mechanical harvesting problems, lint yield and bolls m^{-2} data collected at Hartsville in 2005 and Florence in 2006 were not included in our analysis. Tables 2 and 3 show significant variation among genotypes for all measured agronomic and fiber quality traits. The G × E interactions were significant for all traits except fiber uniformity. Partitioning the genotype variation further showed significant variation among the Pee Dee lines for each agronomic and fiber quality trait. Likewise, partitioning the G × E interactions further showed that Pee Dee lines × E interactions were significant for all traits. Pee Dee lines and checks were significantly different from one another for all traits except boll weight.

Pee Dee Germplasm Groups

In addition to estimating and comparing overall Pee Dee line performance with commercial checks, analysis of variance was conducted to compare the performance of eight cycles or groups of Pee Dee germplasm. Comparing the "among" and "within" group agronomic and fiber quality performance data allows for comparisons across breeding cycles. For each of the agronomic and fiber quality traits measured, significant differences were detected among groups (Tables 4 and 5). Among-groups × E interactions were significant for lint yield, bolls m^{-2}, lint percent, boll weight, fiber strength, fiber length, elongation, micronaire, and fineness.

Group 1

Group 1 consisted of seven germplasm lines representing the first cycle of intercrossing and recurrent selection among the founders of the Pee Dee germplasm program. This group had a mean molecular marker genetic similarity of 0.79 and ranged from 0.61 to 0.88. Significant differences among Group 1 lines were detected for all traits except boll weight (Tables 4 and 5). Analysis of the Group 1 G × E interaction indicated significant differences for fiber length only. Compared with the mean of commercial checks, on average, Group 1 lines produced lower lint percent, lower lint yield, higher seed index, stronger fibers, longer fibers, greater fiber length uniformity, lower micronaire, and finer fibers. Compared with other Pee Dee germplasm groups, Group 1 produced the best fiber quality values for fiber strength, fiber length, micronaire (lower value is better), and fineness (lower value is better). Group 1 produced the lowest mean lint percent and fiber elongation. Compared with other Group 1 genotypes, Sealand 542 (318 kN m kg^{-1}) and

Table 2. Combined analysis of variance of five agronomic traits for Pee Dee germplasm lines and checks evaluated in replicated trials in 14 location–year environments in North Carolina, South Carolina, Georgia, and Mississippi from 2004 to 2006.

		Mean squares			Mean squares		
Source	df	Lint yield	Bolls m^{-2}	df	Lint percent	Boll weight	Seed index
Environment (E)	11	15,548,935**	20,531**	13	1037.8**	31.8**	63.5**
Block (E)	672	96,990**	258**	824	2.8**	0.6**	0.7**
Genotype (G)	86	240,208**	398**	86	49.4**	1.1**	6.5**
Pee Dee line (L)	80	125,435**	277**	80	28.1**	0.9**	4.3**
Check (C)	5	146,752*	669**	5	39.0**	4.2**	25.1**
L vs. C	1	6,904,283**	5,299**	1	1242.0**	0.3	65.8**
G × E	930	49,247**	130**	1102	2.3**	0.4**	0.5*
L × E	876	44,505**	126**	1036	2.1**	0.4**	0.5*
C × E	43	55,916**	134**	53	3.8**	0.3	0.4
L vs. C × E	11	346,628**	397**	13	4.0**	0.4	0.6
Pooled error	1376	27,416	79	1662	1.5	0.3	0.4
CV		14	16		3.2	9.6	6.1

* Significant at the 0.05 level of probability.

** Significant at the 0.01 level of probability.

Table 3. Combined analysis of variance of six fiber quality traits for Pee Dee germplasm lines and checks evaluated in replicated trials in 14 location–year environments in North Carolina, South Carolina, Georgia, and Mississippi from 2004 to 2006.

		Mean squares					
Source	df	Fiber strength	Fiber length	Elongation	Uniformity	Micronaire	Fineness
Environment (E)	13	42,300**	54.4**	92.80**	104.4**	45.75**	24,861**
Block (E)	824	230**	0.9**	0.25**	1.9**	0.11**	76**
Genotype (G)	86	2,372**	8.5**	2.36**	4.9**	0.59**	269**
Pee Dee line (L)	80	2,219**	8.3**	2.13**	4.8**	0.38**	202**
Check (C)	5	4,771**	9.5**	6.44**	3.0	1.20**	593**
L vs. C	1	2,612**	16.8**	2.73**	12.6**	8.02**	2,315**
G × E	1102	169**	0.7**	0.24**	1.1	0.07**	53**
L × E	1036	165**	0.7**	0.24**	1.1	0.07**	50**
C × E	53	168	0.8**	0.18	1.4	0.06	55
L vs. C × E	13	349**	1.4**	0.31*	1.7	0.34**	274**
Pooled error	1662	129	0.5	0.17	1.1	0.05	43
CV		4	2.4	7.72	1.3	5.16	4

* Significant at the 0.05 level of probability.

** Significant at the 0.01 level of probability.

Hybrid 330-278 (322 kN m kg^{-1}) both produced the highest fiber strength. In addition, Sealand 542 produced the highest fiber length (31.4 mm) and lowest fineness (166.0 mg km^{-1}). Each of these genotypes expressed low lint yield potential (889 kg ha^{-1} and 974 kg ha^{-1}, respectively). Overall, these data suggest that the first products of the Pee Dee germplasm program, since the development of the founder germplasm lines, represent excellent sources of fiber quality. However, the data also highlight the poor agronomic performance of Group 1 lines compared with current commercial cultivars.

Group 2

Group 2 consisted of seven germplasm lines representing the second cycle of intercrossing and recurrent selection among the first cycle of Pee Dee germplasm program releases. The group had a mean molecular marker genetic similarity of 0.75 and ranged from 0.60 to 0.86. Significant differences among Group 2 lines were detected for all traits except lint yield and fiber uniformity (Tables 4 and 5). Analysis of the Group 2 G × E interaction indicated significant differences for bolls m^{-2}, lint percent, seed index, fiber strength, fiber length, fiber uniformity, and micronaire. When compared with the mean of commercial checks, on average, Group 2 produced lower lint percent, lower lint yield, fewer bolls m^{-2}, higher seed index, stronger fibers, longer fibers, greater elongation, lower micronaire, and finer fibers (Tables 6 and 7). Compared with Pee Dee germplasm Group 1, Group 2 lines produced higher lint percent, fiber elongation, micronaire, and fineness, accompanied by decreases in fiber strength and fiber length. Of particular note within this group, PD 2164 combined excellent fiber strength (316 kN m kg^{-1}) and lint yield (1030 kg ha^{-1}) performance.

Group 3

Group 3 consisted of nine germplasm lines representing the third cycle of intercrossing and recurrent selection among the first and second cycles of Pee Dee germplasm program. The group had a mean molecular marker genetic similarity

Table 4. Combined analysis of variance of five agronomic traits for eight groups of Pee Dee germplasm lines and checks evaluated in replicated trials in 14 location–year environments in North Carolina, South Carolina, Georgia, and Mississippi from 2004 to 2006.

		Mean squares			Mean squares		
Source	df	Lint yield	Bolls m^{-2}	df	Lint percent	Boll weight	Seed index
Environment (E)	11	15,548,935**	20,531**	13	1037.8**	31.8**	63.5**
Block (E)	672	96,990**	258**	824	2.8**	0.6**	0.7**
Genotype (G)	86	240,208**	398**	86	49.4**	1.1**	6.5**
Among groups (AG)	8	1,469,355**	1,311**	8	352.2**	1.0*	36.2**
Checks	5	154,613*	665**	5	38.7**	4.2**	25.8**
Group 1	6	52,649*	190*	6	25.5**	0.4	2.9**
Group 2	6	31,499	275*	6	11.5**	1.1**	4.9**
Group 3	8	60,056*	223*	8	7.8**	0.3	1.8**
Group 4	9	95,540*	353**	9	13.3**	1.3**	1.6**
Group 5	7	125,012	238	7	22.6**	0.6	2.2**
Group 6	16	62,808*	190*	16	8.9**	1.2**	1.7**
Group 7	10	96,484*	295*	10	4.9**	0.8**	2.0**
Group 8	11	38,225	174*	11	13.3**	0.8*	0.7
G × E	930	49,247**	130**	1102	2.3**	0.4**	0.5*
AG × E	88	115,841**	221**	104	3.4**	0.4**	0.5
Checks × E	43	54,677**	132**	53	3.8**	0.3	0.4
Group 1 × E	66	21,343	88	78	1.6	0.3	0.5
Group 2 × E	63	28,341	108*	75	2.8**	0.3	0.6*
Group 3 × E	88	26,811	107*	104	1.5	0.4**	0.4
Group 4 × E	99	48,477**	130**	117	2.8**	0.3	0.5
Group 5 × E	77	76,454**	203**	91	1.8	0.3	0.5
Group 6 × E	176	32,239	112**	208	1.7	0.4**	0.4
Group 7 × E	109	52,724**	158**	129	1.8*	0.3	0.5
Group 8 × E	121	35,707*	99*	143	2.2**	0.4**	0.4
Pooled error	1376	27,416	79	1662	1.5	0.3	0.4
CV		14	16		3.2	9.6	6.1

* Significant at the 0.05 level of probability.

** Significant at the 0.01 level of probability.

of 0.78 and ranged from 0.64 to 0.90. Group 3 lines differed for all traits except boll weight (Tables 4 and 5). Analysis of the Group 3 G × E interaction indicated significant differences for bolls m^{-2}, boll weight, and micronaire. Similar to Groups 1 and 2, Group 3 lines averaged lower lint percent, lower lint yield, higher boll weight, higher seed index, stronger fibers, longer fibers, greater elongation, greater fiber length uniformity, lower micronaire, and finer fibers than the mean of the commercial checks. Compared with Pee Dee germplasm Group 2, Group 3 produced higher lint percent and lower seed index. Four Group 3 genotypes produced excellent fiber strength and length that included PD 9232 (307 kN m kg^{-1}, 29.2 mm), PD 0109 (304 kN m kg^{-1}, 29.4 mm), PD 0113 (304 kN m kg^{-1}, 29.5 mm), and PD 8619 (305 kN m kg^{-1}, 29.1 mm). Out of these four genotypes, PD 9232 (1137 kg ha^{-1}) and PD 8619 (1095 kg ha^{-1}) produced the highest lint yield potential.

Group 4

Group 4 consisted of 10 germplasm lines representing the fourth cycle of intercrossing and recurrent selection among the releases from the second and third cycles of the Pee Dee germplasm program. The group had a mean molecular marker genetic similarity of 0.74 and ranged from 0.57 to 0.89. Significant differences among Group 4 lines were detected for all traits except fineness (Tables 4 and 5). Analysis of the Group 4 G × E interaction indicated significant differences for lint yield, bolls m^{-2}, lint percent, fiber length, micronaire, and fineness. Continuing the same trend as Groups 1 to 3, compared with the mean of the commercial checks, on average, Group 4 lines produced lower lint percent, lower lint yield, higher boll weight, higher seed index, stronger fibers, longer fibers, greater elongation, greater fiber length uniformity, lower micronaire, and finer fibers (Tables 6 and 7). With the exception of boll weight and fiber elongation, Pee Dee germplasm Group 4 produced similar mean values to Group 3 for each trait measured. Compared with the Group 3 mean, on average, Group 4 produced lower boll weight and higher fiber elongation. Within Group 4, PD 6132 and PD 6186 produced the highest fiber strength, 306 kN m kg^{-1} and 310 kN m kg^{-1}, respectively.

Group 5

Group 5 consisted of eight germplasm lines representing the fifth cycle of Pee Dee germplasm program releases. The group had a mean molecular marker genetic similarity of

Table 5. Combined analysis of variance of six fiber quality traits for eight groups of Pee Dee germplasm lines and checks evaluated in replicated trials in 14 location–year environments in North Carolina, South Carolina, Georgia, and Mississippi from 2004 to 2006.

Source	df	Mean squares					
		Fiber strength	Fiber length	Elongation	Uniformity	Micronaire	Fineness
Environment (E)	13	42,300**	54.4**	92.80**	104.4**	45.75**	24,861**
Block (E)	824	230**	0.9**	0.25**	1.9**	0.11**	76**
Genotype (G)	86	2,372**	8.5**	2.36**	4.9**	0.59**	269**
Among groups (AG)	8	12,254**	34.6**	9.92**	24.3**	1.99**	794**
Checks	5	4,390**	10.0**	6.41**	2.9	0.99**	523**
Group 1	6	1,232**	15.8**	0.77**	2.8*	0.57**	247**
Group 2	6	13,373**	5.2**	1.60**	1.3	0.18*	120**
Group 3	8	1,286**	3.2**	1.05**	4.5**	0.52**	182**
Group 4	9	1,503**	4.8**	1.06**	3.6**	0.42**	98
Group 5	7	958**	2.6**	1.01**	1.9	0.26**	263**
Group 6	16	654**	4.1**	1.46**	1.5	0.20**	103**
Group 7	10	559**	2.2**	0.39*	1.6	0.04	37
Group 8	11	396**	2.6**	0.99**	3.4**	0.29**	152**
G × E	1102	169**	0.7**	0.24**	1.1	0.07**	53**
AG × E	104	268**	1.1**	0.69**	1.2	0.11**	79**
Checks × E	53	195**	0.9**	0.18	1.4	0.08**	63*
Group 1 × E	78	154	0.7**	0.21	1.1	0.05	53
Group 2 × E	75	183**	0.7**	0.14	1.5*	0.08**	40
Group 3 × E	104	146	0.6	0.19	0.9	0.07**	43
Group 4 × E	117	154	0.7**	0.18	1.0	0.08**	56*
Group 5 × E	91	169*	0.5	0.19	1.0	0.05	43
Group 6 × E	208	143	0.7**	0.20	1.1	0.06	46
Group 7 × E	129	148	0.6**	0.18	1.0	0.07*	73**
Group 8 × E	143	136	0.5	0.17	1.1	0.05	46
Pooled error	1662	129	0.5	0.17	1.1	0.05	43
CV		4	2.4	7.72	1.3	5.16	3.7

* Significant at the 0.05 level of probability.

** Significant at the 0.01 level of probability.

0.76 and ranged from 0.64 to 0.90. Based on pedigree information and supporting data presented in germplasm release documents, Group 5 represented a change in breeding focus, shifting from fiber quality to developing germplasm resistant to the boll weevil and other insect pests. Attempts were made to transfer putative host plant insect resistance traits from an experimental line (La. Frego 2) developed by the Louisiana Agricultural Experiment Station. Significant differences among Group 5 lines were detected for lint percent, seed index, fiber strength, fiber length, fiber elongation, micronaire, and fineness (Tables 4 and 5). Analysis of the Group 5 G × E interaction indicated significant differences for lint yield, bolls m^{-2}, and fiber strength. Compared with the mean of commercial checks, on average, Group 5 lines produced lower lint percent, lower lint yield, higher boll weight, higher seed index, lower fiber strength, longer fibers, greater elongation, lower micronaire, and finer fibers (Tables 6 and 7). On average, compared with Pee Dee germplasm Group 4, Group 5 produced lower lint percent, fiber strength, fiber length, micronaire, and fineness. These data suggest that efforts to introduce host plant insect resistance negatively impacted the fiber quality performance of Group 5 germplasm. Within Group 5 genotypes, PD 7439 produced the highest fiber strength and fiber length (299 kN m kg^{-1} and 29.8 mm, respectively).

Group 6

Group 6 consisted of 17 germplasm lines representing the sixth cycle of Pee Dee germplasm program releases. The group had a mean molecular marker genetic similarity of 0.77 and ranged from 0.58 to 0.96. Based on pedigree information and supporting data presented in germplasm release documents, Group 6 followed the Group 5 shift in breeding focus from fiber quality to insect resistance. Group 6 germplasm resulted from intercrosses and selection among fourth and fifth cycle Pee Dee germplasm releases. Significant differences among Group 6 lines were detected for all traits except fiber uniformity (Tables 4 and 5). Analysis of the Group 6 G × E interaction indicated significant differences for bolls m^{-2}, boll weight, and fiber length. Compared with the mean of the commercial checks, on average, Group 6 lines produced lower lint percent, lower lint yield, higher seed index, lower fiber strength, greater elongation, lower micronaire, and finer fibers (Tables 6 and 7). On average, compared with Pee Dee germplasm Group 5, Group 6 produced similar values for each trait measured

Table 6. Comparison of the mean performance of Pee Dee germplasm lines, eight groups of Pee Dee germplasm lines, and checks for five agronomic traits.

Source†	Mean (range)				
	Lint percent	Lint yield	Bolls m^{-2}	Boll weight	Seed index
	%	kg ha^{-1}	no.	g	
Pee Dee lines	37.3	1112	53.2	5.56	11.0
Group 1	35.1 (33.9–36.3)	983 (889–1039)	51.0 (47.1–54.2)	5.50 (5.35–5.66)	11.6 (11.1–12.0)
Group 2	36.3 (35.2–37.2)	1029 (974–1083)	49.7 (45.5–55.6)	5.68 (5.36–6.05)	11.6 (11.1–12.4)
Group 3	37.1 (36.1–38.1)	1083 (1008–1141)	51.5 (44.4–55.8)	5.64 (5.45–5.78)	11.1 (10.8–11.6)
Group 4	37.5 (36.5–38.8)	1090 (968–1213)	52.4 (46.1–59.9)	5.44 (5.08–5.80)	10.9 (10.7–11.5)
Group 5	37.0 (36.2–39.2)	1120 (1033–1247)	53.9 (50.0–59.7)	5.65 (5.46–5.85)	11.0 (10.6–11.4)
Group 6	37.6 (36.5–38.6)	1125 (1011–1225)	53.1 (47.4–60.3)	5.55 (5.02–5.94)	10.6 (10.1–11.1)
Group 7	38.0 (37.4–38.8)	1179 (1132–1257)	55.7 (52.7–60.2)	5.56 (5.27–5.94)	10.9 (10.6–11.3)
Group 8	38.3 (37.4–40.0)	1188 (1144–1287)	56.0 (51.6–61.9)	5.52 (5.15–5.83)	10.8 (10.5–11.0)
Checks	41.0	1386	54.8	5.54	10.0
DP444BR	40.8	1232	49.5	5.13	9.8
DP491	42.3	1410	57.8	5.74	9.6
DP555BR	42.6	1519	60.2	4.92	8.2
FM958	41.2	1404	61.8	5.59	10.8
FM960BR	39.0	1375	50.2	5.87	10.8
ST5599BR	40.2	1377	48.3	5.96	10.8
$LSD_{0.05}$	0.4	64	3.5	0.19	0.2

† DP, Deltapine; FM, FiberMax; ST, Stoneville.

Table 7. Comparison of the mean performance of Pee Dee germplasm lines, eight groups of Pee Dee germplasm lines, and checks for six fiber quality traits.

Source†	Mean (range)					
	Fiber strength	Fiber length	Elongation	Uniformity	Micronaire	Fineness
	kN m kg^{-1}	mm	%		units	mg km^{-1}
Pee Dee lines	296	29.0	5.32	83.2	4.40	174.9
Group 1	311 (304–322)	30.0 (29.1–31.4)	4.74 (4.52–4.98)	83.3 (82.9–83.9)	4.24 (3.95–4.40)	171.1 (166.0–175.0)
Group 2	303 (292–316)	29.2 (28.8–30.1)	5.03 (4.64–5.41)	83.1 (82.9–83.3)	4.39 (4.21–4.59)	174.0 (171.6–181.2)
Group 3	300 (286–307)	29.1 (28.3–29.5)	5.19 (4.91–5.46)	83.3 (82.7–83.7)	4.41 (4.20–4.65)	175.4 (170.8–178.1)
Group 4	300 (284–310)	29.0 (28.4–29.8)	5.35 (5.01–5.64)	83.5 (82.8–84.1)	4.39 (4.17–4.60)	174.1 (172.0–177.6)
Group 5	288 (280–299)	28.7 (28.2–28.7)	5.41 (5.06–5.64)	82.6 (82.9–83.3)	4.52 (4.31–4.65)	178.0 (172.0–182.3)
Group 6	284 (277–296)	28.4 (27.7–29.3)	5.45 (4.83–5.76)	82.6 (82.1–83.1)	4.40 (4.25–4.56)	174.8 (171.7–178.0)
Group 7	300 (294–308)	29.1 (28.6–29.6)	5.52 (5.24–5.74)	83.2 (83.2–84.1)	4.38 (4.30–4.47)	175.0 (173.0–176.9)
Group 8	297 (289–303)	28.9 (28.3–29.3)	5.51 (5.14–5.83)	83.5 (82.5–83.9)	4.42 (4.29–4.72)	175.7 (171.9–182.2)
Checks	294	28.4	4.86	82.7	4.87	183.4
DP444BR	272	27.7	5.84	83.1	4.48	178.2
DP491	300	29.8	5.27	82.9	4.67	177.9
DP555BR	276	27.9	4.90	82.2	4.95	184.1
FM958	303	28.7	4.68	83.3	4.98	183.7
FM960BR	307	27.7	4.39	82.4	4.73	180.3
ST5599BR	284	28.0	5.07	82.5	5.00	191.0
$LSD_{0.05}$	4	0.2	0.15	0.4	0.08	2.3

† DP, Deltapine; FM, FiberMax; ST, Stoneville.

except lint percent, seed index, fiber length, micronaire, and fineness. Group 6 lint percent, micronaire, and fineness represented improvements over Group 5 means. However, the mean fiber strength and fiber length of Group 6 represented the lowest of any Pee Dee germplasm group. Within Group 6, PD 0738 produced the highest fiber strength and fiber length (296 kN m kg^{-1} and 29.3 mm, respectively). These fiber quality data provide additional evidence suggesting that efforts to introduce host plant insect resistance negatively impacted the fiber quality performance of Group 5 and 6 germplasm.

Group 7

Group 7 represented a renewed focus on improving yield and fiber quality; the 11 germplasm lines developed in this group were derived from crosses involving a line developed in breeding cycles before Group 5 and several elite lines from the Mississippi Delta gene pool (Delcot 311,

DES 422, and DP 41). This group had the highest mean molecular marker genetic similarity of any of the Pee Dee groups, averaging 0.82 and ranging from 0.68 to 0.94. Group 7 lines differed for all traits except uniformity, micronaire, and fineness (Tables 4 and 5). Analysis of the Group 7 G × E interaction indicated significant differences for lint yield, bolls m^{-2}, lint percent, fiber length, micronaire, and fineness across the environments tested. Compared with the mean of the commercial checks, on average, Group 7 lines produced lower lint percent, lower lint yield, higher seed index, higher fiber strength, longer fibers, greater elongation, greater fiber length uniformity, lower micronaire, and finer fibers (Tables 6 and 7). Compared with Pee Dee germplasm Group 6, Group 7 produced higher seed index, fiber strength, fiber length, and fiber uniformity. Within Group 7, there were four genotypes that combined good lint yield potential with excellent fiber strength and length. These included PD 5363 (1141 kg ha^{-1}, 307 kN m kg^{-1}, 29.4 mm), PD 5529 (1209 kg ha^{-1}, 304 kN m kg^{-1}, 29.3 mm), PD 5358 (1153 kg ha^{-1}, 308 kN m kg^{-1}, 29.6 mm), and PD 5377 (1132 kg ha^{-1}, 304 kN m kg^{-1}, 29.2 mm). These fiber quality data suggest that following two cycles of breeding removed from focusing on insect resistance, renewed efforts to improve fiber quality recaptured the fiber quality performance of Pee Dee germplasm groups before the Group 7 breeding cycle.

Group 8

Group 8 represented a renewed focus to create a germplasm pool with new combinations of desirable alleles. The group had a mean molecular marker genetic similarity of 0.76 and ranged from 0.63 to 0.94. The 12 germplasm lines developed in this group were primarily derived from intercrosses and selection involving Group 7 Pee Dee germplasm line releases. Hence, excluding Groups 5 and 6 breeding cycles, Group 8 germplasm lines represented the products of at least six cycles of intercrossing and recurrent selection originating with the founders of the Pee Dee germplasm program. Significant differences among Group 8 lines were detected for lint percent, bolls m^{-2}, boll weight, and all fiber quality traits (Tables 4 and 5). Analysis of the Group 8 G × E interaction indicated significant differences for lint percent, lint yield, bolls m^{-2}, and boll weight. These lines performed similarly across environments for seed index and all fiber properties (Tables 4 and 5). Compared with the mean of the commercial checks, on average, Group 8 lines produced lower lint percent, lower lint yield, higher seed index, longer fibers, greater elongation, greater fiber length uniformity, lower micronaire, and finer fibers (Tables 6 and 7). Compared with Pee Dee germplasm Group 7, Group 8 produced similar values for all agronomic and fiber quality traits. Several Group 8 genotypes combined excellent fiber strength and length with good lint yield potential. These genotypes include PD-3-14 (303 kN m kg^{-1}, 29.2 mm, 1174 kg ha^{-1}), PD 93043 (302 kN m kg^{-1}, 29.2 mm, 1176 kg ha^{-1}), and PD 94042 (300 kN m kg^{-1}, 29.1 mm, 1232 kg ha^{-1}).

Genetic Improvement over Time

From the mean values presented in Tables 6 and 7, clearly the Pee Dee germplasm program began its first cycle of breeding with germplasm releases of low yield potential and excellent fiber quality. These releases were a result of the primary breeding focus to improve fiber quality during that time. In subsequent breeding cycles, except for Groups 5 and 6, the program shifted focus to maintaining fiber quality while improving agronomic performance. Overall, the percentage change observed in Group 8 relative to Group 1 for agronomic and fiber quality traits was (i) +9% lint percent, (ii) +21% lint yield, (iii) +10% bolls m^{-2}, (iv) −7% seed index, (v) −4% fiber strength, (vi) −4% fiber length, (vii) +16% fiber elongation, (viii) +4% micronaire, and (ix) +3% fiber fineness. Considering yield component traits, agronomic performance advantages in lint yield were due to increases in lint percent and bolls m^{-2}. This conclusion is consistent with the findings of Bridge et al. (1971) and Culp and Green (1992) that attributed yield increases to selection for high lint percent and a greater number of bolls per unit area. The accompanying 7% decrease in seed index over time likely was due to increased metabolite and nutrient partitioning to developing fibers rather than developing seeds. Although the mean of Group 8 lines produced fiber quality values deficient to Group 1, the fiber quality performance of Group 8 lines still maintained a competitive advantage compared with the selected commercial cultivars. In comparison with commercial cultivars, Group 8 produced superior values for five fiber quality traits, including (i) fiber strength equal to or higher than four cultivars, (ii) fiber length equal to or higher than five cultivars, (iii) higher uniformity than all cultivars, (iv) lower micronaire than all cultivars, and (v) finer fibers than all cultivars.

To evaluate the genetic change over time of the five agronomic and six fiber quality traits measured in this study, Pee Dee germplasm group trait means were regressed on group number. This regression allowed for a measurement of genetic change accounting for each of the eight breeding cycles represented in this study. Figure 1 shows the regressions for each of the five agronomic traits. The Pee Dee germplasm program changed agronomic traits as follows per breeding cycle: (i) lint percent increased 0.4%, (ii) lint yield increased by 28 kg ha^{-1}, (iii) bolls m^{-2} increased by 0.8 bolls, and (iv) seed index decreased 0.1 g. Similarly, Fig. 2 shows the regressions for each of the six fiber quality traits. For these regressions, Groups 5 and 6 were excluded from the analysis because both groups represented outlier data and did not represent

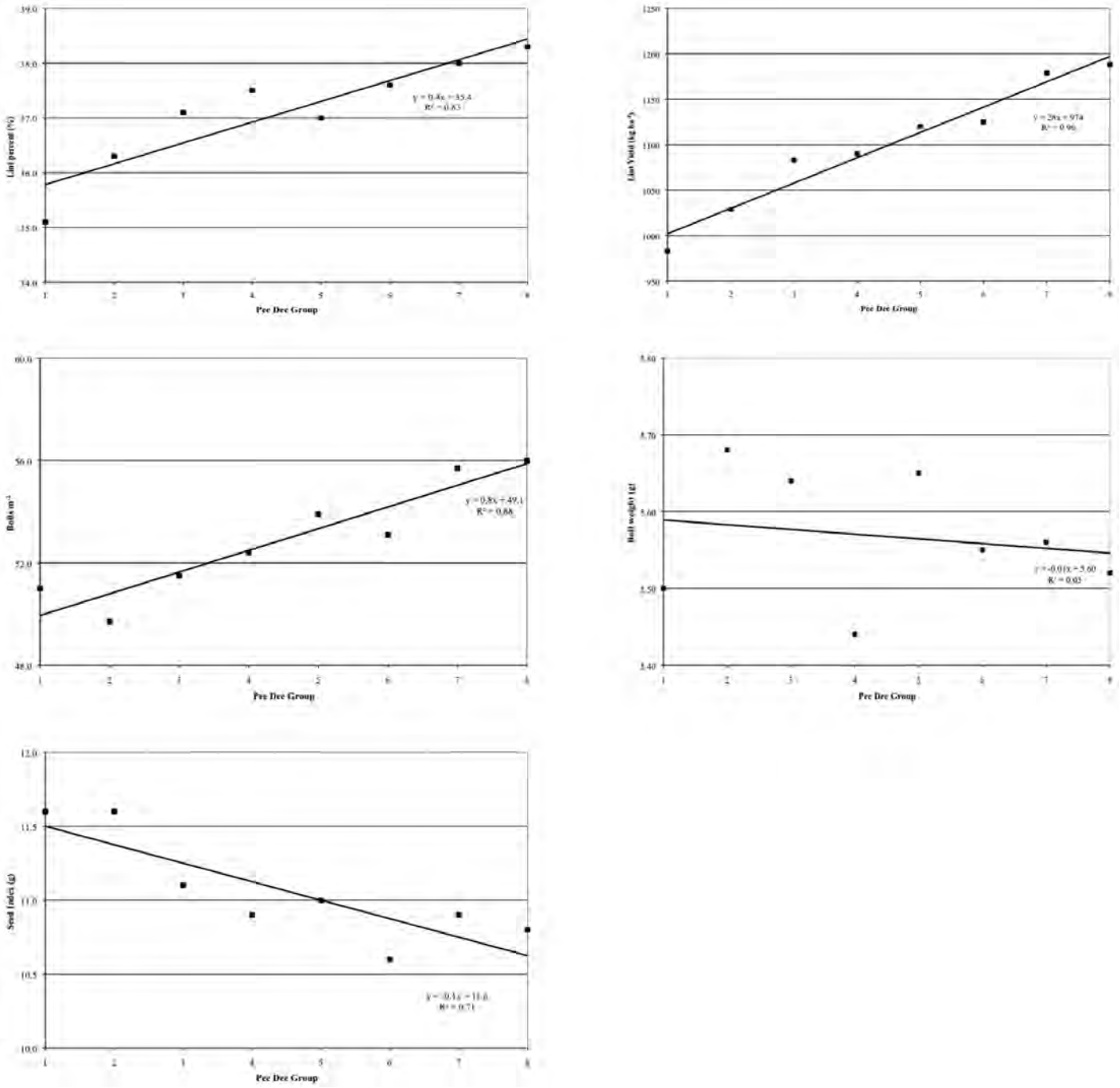

Figure 1. Regressions of cotton lint percent, lint yield, bolls m^{-2}, boll weight, and seed index means on Pee Dee group.

the historical philosophy and objective of the 70-yr-old Pee Dee germplasm program to increase fiber quality. For each breeding cycle, the Pee Dee germplasm program changed fiber quality traits as follows per cycle: (i) fiber strength decreased 2 kN m kg^{-1}, (ii) fiber length decreased by 0.2 mm, (iii) fiber elongation increased by 0.16 mm, and (iv) fineness increased 0.7 mg km^{-1}.

CONCLUSIONS

In this study, genetic improvement of agronomic traits, particularly lint percent and lint yield, has steadily increased approximately 3% per breeding cycle. Most importantly, these genetic gains for agronomic traits occurred while decreasing fiber quality properties <1% per cycle. This is a significant finding, as it provides evidence that the negative relationship between lint yield and fiber quality properties (Culp et al., 1979; Meredith 2005) has been minimized to a great extent through the various breeding methods employed. This would suggest that linkage rather than pleiotropy has been responsible for the negative lint yield and fiber quality relationship, although further research should address this question. As noted by Campbell et al. (2009), the origin of the Pee Dee germplasm program consisted of diverse accessions

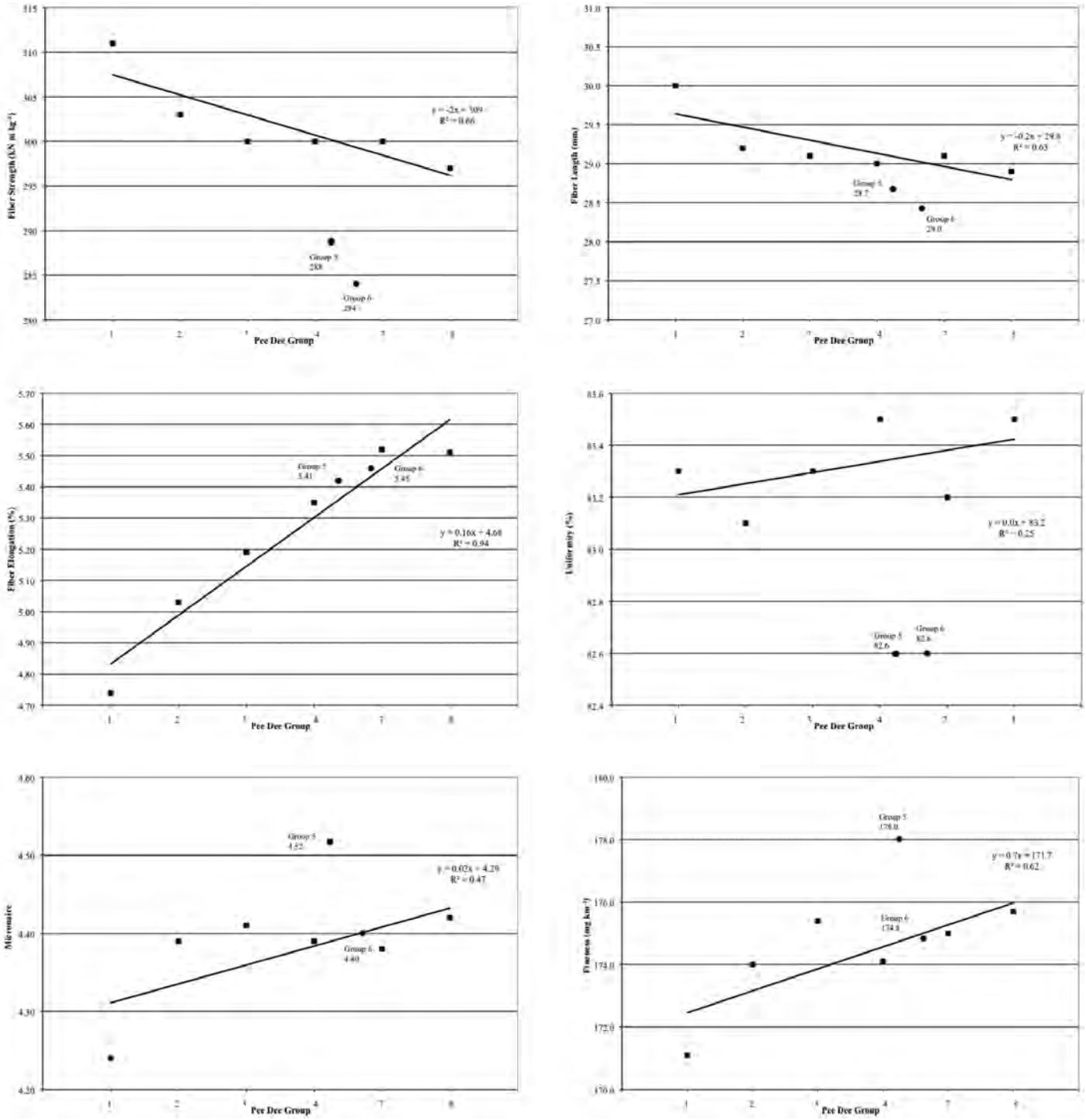

Figure 2. Regressions of cotton fiber strength, fiber length, fiber elongation, uniformity, micronaire, and fineness means on Pee Dee group.

of four cotton species which provided the opportunity for novel combinations of *G. hirsutum*, *G. barbadense*, *G. thurberi*, and *G. arboreum* alleles present within the Pee Dee germplasm program.

Over the course of its 70-yr history, the Pee Dee cotton germplasm enhancement program has made significant genetic gains in efforts to combine improved fiber quality and yield potential. In their analysis of breeding sources of fiber quality, Bowman et al. (2006) documented that Pee Dee germplasm has been extensively used as parents in breeding programs to develop commercial cultivars. Culp and Green (1992) noted that PD 2164 was crossed to 'Stoneville 213' to produce 'DES 56' (PVP 7800041; Bridge and Chism, 1978). Bridge and Meredith (1983) noted that DES 56 represented a significant advance responsible for early maturity and increased yield in the Mississippi Delta. Campbell and Bauer (2007) identified within a subset of Pee Dee germplasm significant genetic variation for agronomic and fiber quality response to supplemental irrigation. Due to increased private sector

investment in cultivar development and the proprietary nature of traits and pedigrees, it is difficult to quantify the extent that Pee Dee germplasm can be traced in the lineages of current commercial cultivars.

This study identified several genotypes from each Pee Dee germplasm group that provide a combination of high fiber quality and lint yield potential and can be immediately utilized in cotton breeding programs. These genotypes include PD 2164 (Group 2), PD 9232 (Group 3), PD 8619 (Group 3), PD 6132 (Group 4), PD 6186 (Group 4), PD 5363 (Group 7), PD 5529 (Group 7), PD 5358 (Group 7), PD 5377 (Group 7), PD-3-14 (Group 8), PD 93043 (Group 8), and PD 94042 (Group 8).

Several final conclusions can be gleaned from the data presented in this study. First, the maintained level of genetic variation over the life of the Pee Dee germplasm program suggests that adequate variation still exists within the germplasm collection that can be exploited to continue genetic improvement. Second, the genetic improvement data for Pee Dee germplasm agronomic and fiber quality performance over the history of the program suggests that breeding methods employed over the last 70 yr have continued improving agronomic performance while maintaining superior fiber quality properties. Third, comparing the agronomic performance of Pee Dee germplasm lines with that of current commercial cultivars identifies a need to continue focusing on improving lint percent, bolls m^{-2}, and lint yield in future breeding efforts involving the Pee Dee germplasm. Although this study provides evidence that continuing the breeding methods used over the course of the Pee Dee germplasm program's history should be effective to continue genetic improvement, it will also be important to introduce new genetic variability into the breeding program from sources present in global cotton germplasm collections that might include wild *G. hirsutum* landraces and other *Gossypium* species (Campbell et al., 2010). Considering the diverse foundation of the Pee Dee germplasm program, future research should also determine the *Gossypium* species origin of the beneficial fiber quality alleles present in the Pee Dee germplasm collection. Such research would aid breeding efforts to select future germplasm lines with the optimum combination of superior fiber quality alleles.

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