

Genetic Base of Upland Cotton Cultivars Released between 1970 and 1990

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ABSTRACT

Most cotton (*Gossypium* spp.) breeders today, without recourse to critical data, assume that the genetic base in modern New World cotton cultivars is narrow. The objectives of this study were to: (i) determine the average coefficient of parentage for 260 upland cotton (*G. hirsutum* L.) cultivars released between 1970 and 1990; and (ii) determine the contributions of a number of public and private breeding programs and of various ancestral lines to the genetic diversity of those cultivars. Coefficients of parentage among 260 cultivars showed an average value of 0.07. This estimate suggests substantial remaining diversity. This conclusion must take into account possible bias from widespread reselection of cotton cultivars and the accompanying assumption of a genetic correlation of 0.75 between generations. The most influential breeding programs, in terms of genetic contributions to cultivar development, were Stoneville Pedigreed Seed Company, Coker's Pedigreed Seed Company, and New Mexico Agricultural Experiment Station. Historically, the most influential cultivar is Stoneville 2. The genetic contribution of 54 ancestral lines, including nine introductions, accounted for less than 25% of the total genetic variation among the 260 cultivars. This low value is thought to result from the loss of genetic information through the process of reselection. The genetic base in modern cotton cultivars is not particularly narrow and continue to offer opportunities for cultivar improvement.

DURING THE 20TH CENTURY, public and private institutions have been deeply involved in cotton (*Gossypium hirsutum* L.) improvement. Private breeding efforts have produced new cultivars. Public breeding efforts, on the other hand, have been involved primarily in the development of improved germplasm. The contribution of these public breeding programs thus indirectly influences cultivar development. Contributions from public and private institutions can be evaluated through pedigree analysis.

With some crops, breeders have relied heavily on the contributions of one, or a few, ancestors. For example, hard red winter wheat (*Triticum aestivum* L.) breeding has centered, until recently, around a single ancestor 'Turkey' (Cox et al., 1986). A major contribution by a single germplasm source may result in genetic uniformity and hence potential vulnerability.

We summarized pedigrees of cotton cultivars released between 1970 and 1990 (Calhoun et al., 1994) and coefficients of parentage among 260 upland cotton cultivars (Bowman et al., 1995). From this information, it is possible to assess the genetic contribution of specific source materials (ancestors, introductions, and other influential parental germplasm) and the genetic contribution of specific breeding programs. Such estimates could be of value for identifying programs having breeding lines with a narrow genetic base.

Before the introduction and wide use of insecticides, cotton was often subject to high rates of natural hybridization, primarily by bumblebees (*Bombus* spp.) (Bowman et al., in press). Introductions and reselections from growers' fields resulted in the development of at least 612 described cotton cultivars by 1907 (Ware, 1950).

Although outcrossing rates are lower today, reselection continues to be an important method for developing new cultivars. The potential of cotton to cross-pollinate has facilitated genetic gain through reselection. Manning (1963) showed a 24 to 32% yield increase in an upland cultivar after 10 generations of reselection. Of the 285 upland cultivars released between 1970 and 1990, 91 were direct selections from other cultivars or from germplasm lines (Calhoun et al., 1994). Examination of the pedigrees from cultivars released between 1970 and 1990 shows 236 cases of reselection in the development of the 260 cultivars described in Bowman et al. (in press).

The large number of reselections in the pedigrees of modern cotton cultivars may suggest a narrow germplasm base and thus the potential for genetic vulnerability. The objectives of this study were to: (i) determine the average coefficient of parentage of the 260 cotton cultivars described in Bowman et al. 1995, (ii) determine the genetic contribution of various public and private breeding programs, and (iii) calculate the genetic contribution of various ancestral lines to the genetic diversity of modern cotton cultivars.

MATERIALS AND METHODS

For this review, we used pedigree information released between 1970 and 1990 (Calhoun et al., 1994), and coefficients of parentage of 260 upland cultivars (Bowman et al., in press). Bowman et al. (in press) outlined the methods for calculating the coefficient of parentage (r), the assumptions made, and the computer program used.

We determined the influence of breeding programs by the number of lines appearing in the pedigrees of the 260 cultivars. We identified the 16 most influential programs and determined the number of cultivars each program released between 1970 and 1990 and the number of cultivars influenced by the program. Any combination resulting in 12 defined an influential program. The number 12 is nearly 5% of the 260 cultivars released and there appeared to be a demarcation between programs with 12 and fewer influential lines.

We estimated the average genetic contribution of each of 49 breeding programs (15 public and 34 private) to the 260 cultivars examined by calculation of r , assuming that all influential lines were unrelated (Gizlice et al., 1994). The most influential line from each program is defined as the one having the highest average genetic contribution to the 260 cultivars. Note that the genetic contribution of an influential line to a cultivar and their r value is the same only when all of the influential lines are not related by pedigree. To estimate the genetic diversity within each program, we calculated the average r value between all influential lines within each program. This computation involved calculation of r from complete pedigrees.

Ancestors generally have been defined as genetic material

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forming the foundation of cultivar development efforts and with no known pedigree (Gizlice et al., 1994). In the pedigrees of the 260 cotton cultivars, 52 parental lines exist with unknown or ambiguous pedigrees, along with eight parental lines that trace back as far as records exist, and 11 other lines introduced at a much later date from foreign countries (Calhoun et al., 1994). Ancestors are herein defined as the set of eight lines that trace back to the beginning of record keeping (early 1600s) through which the pedigrees of all 260 cultivars can be enumerated (Calhoun et al., 1994). Since none of the ancestors were native to the early cotton growing region of the USA (Georgia, North and South Carolina, and Virginia), one could easily consider most as introductions. Genetic contributions from ancestors and introductions were determined by the same procedure used to estimate genetic contribution of breeding programs, i.e., all were assumed to be unrelated. We calculated the number of generations removed in the pedigrees of modern cultivars, and the frequency with which the ancestors and introductions appear in the pedigrees of 260 recent cultivars to provide a perspective on their contribution to modern cultivars.

RESULTS AND DISCUSSION

The average coefficient of parentage for all 260 cotton cultivars described by Bowman et al. (in press) was 0.07, suggesting substantial genetic variation. Coefficients for other representative crops were as follows: 0.13 for 258 public soybean [*Glycine max* L. (Merr.)] cultivars released between 1947 and 1988 (Gizlice et al., 1993), 0.17 for 122 elite soybean lines (Sneller, 1994), 0.15 to 0.42 for oat (*Avena sativa* L.) cultivars (Rodgers et al., 1983), 0.11 and 0.10 for two- and six-rowed barley (*Hordeum vulgare* L.) cultivars, respectively (Martin et al., 1991), 0.21 for Virginia peanut (*Arachis hypogaea* L.) cultivars released since 1969 (Knauff and Gorbet, 1989), 0.19 for soft red winter wheat (*Triticum aestivum* L.), and 0.26 for hard red winter wheat (Murphy et al., 1986). The argument could be made that the large number of cotton parents with unknown pedigrees (71) and the high incidence of reselection, whereby 25% of the genetic material was assumed unaccounted for (original assumption of $r = 0.75$ between a genotype and a reselection from it) contributed to the low r value.

The 16 influential breeding programs included eight public institutions [State Agricultural Experiment Station (AES), and USDA-ARS] and eight private companies. These programs had 7 to 45 lines that were found in the pedigrees of 260 cotton cultivars released between 1970 and 1990 (Table 1). Delta and Pine Land Company and Texas AES College Station had 45 and 40 influential lines, respectively. Delta and Pine Land Company released 28 cultivars in the two decades of this study, which far exceeds the next most productive breeding program, Paymaster/Cargill, with 16 cultivars. The Texas AES-Lubbock program does not release cultivars but, through germplasm releases, furnishes the bulk of the genetic material for stripper-harvested cottons developed for the High Plains area. One program, Dunn, had lines that influenced only their own cultivars which explains why the number of influential lines is the same as the number of cultivars released in Table 1. The public breeding programs USDA-ARS Shafter, CA, Missouri

Table 1. Number of influential lines, cultivars released, frequency in other pedigrees, and number of upland cotton cultivars influenced by 16 cotton breeding programs for the period 1970-1990.

| Breeding program | Influential lines† | Cultivars released‡ | Frequency | Cultivars |
|-------------------------------|--------------------|---------------------|---------------------|------------------------|
| | | | in other pedigrees§ | influenced by program¶ |
| Coker Pedigreed Seed Co. | 26 | 15 | 259 | 102 |
| Delta and Pine Land Co. | 45 | 28 | 63 | 52 |
| Delta Experiment Station, MS | 9 | 5 | 17 | 15 |
| Dunn Seed Farms | 12 | 12 | 0 | 0 |
| GroAgri Seed Co. | 15 | 12 | 5 | 5 |
| Lankart Seed Farms | 14 | 6 | 58 | 48 |
| McNair/Northrup King | 10 | 7 | 6 | 6 |
| Missouri AES | 7 | 5 | 9 | 9 |
| New Mexico AES | 18 | 11 | 150 | 112 |
| Oklahoma AES | 8 | 6 | 12 | 11 |
| Paymaster/Cargill Seeds | 22 | 16 | 56 | 49 |
| Stoneville Pedigreed Seed Co. | 22 | 12 | 383 | 216 |
| Texas AES-College Station | 40 | 11 | 64 | 48 |
| Texas AES-Lubbock | 22 | 0 | 74 | 59 |
| USDA-ARS Shafter, CA | 7 | 5 | 24 | 24 |
| USDA-ARS & South Carolina AES | 19 | 4 | 34 | 33 |

† Number of lines developed in the breeding program indicated that are found in the pedigrees of 260 cotton cultivars released between 1970 and 1990.

‡ Number of cultivars released between 1970 and 1990.

§ Number of times germplasm is found in other cultivars released between 1970 and 1990 not developed by the breeding program indicated.

¶ Number of cultivars released between 1970 and 1990 with germplasm from the breeding program indicated, excluding cultivars developed by the same program.

AES, and Oklahoma AES have been closed, although cotton continues to be a major agronomic crop in those areas.

Stoneville, Coker, and New Mexico AES lines appeared in the pedigrees of other cultivars more often than any other program's lines. Consequently, those programs influenced a larger percentage of cultivars; Stoneville influenced 87% (216) of the 248 other cultivars released; New Mexico AES influenced 45% (112) of the 249 other cultivars; and Coker influenced 42% (102) of the 245 other cultivars.

The mean genetic contribution, as defined by the proportion of genes, to all 260 cultivars for the 16 programs ranged from 0.004 to 0.01 (Table 2). Stoneville was noted above to have influential lines that appeared in the pedigrees of other cultivars 383 times. However, its mean genetic contribution was only 0.01. Although this was the highest average genetic contribution, it is extremely low. It reflects the fact that most of the influential Stoneville lines were not involved in the most recent crosses (Calhoun et al., 1994), as well as the dilution effect of averaging over all 260 cultivars and all influential lines in the program.

Stoneville 2 was the most influential line with an average r value of 0.09 (Table 2). CA614 from the Texas AES-Lubbock program was the second most influential line ($r = 0.03$).

GroAgri Seed Company, which is no longer in existence, had the most closely related lines ($r = 0.26$) while the New Mexico AES program had the most distantly

Table 2. Mean genetic contribution, most influential line, genetic contribution of most influential line, and average r value within 16 major cotton breeding programs for 1970-1990.

| Breeding program | Mean genetic contribution† | Most influential line | Genetic contribution of most influential line | Average r value within program |
|-------------------------------|----------------------------|-----------------------|---|----------------------------------|
| | r | | r | r |
| Coker Pedigreed Seed Co. | 0.006 | Coker 100W | 0.03 | 0.09 |
| Delta and Pine Land Co. | 0.005 | Deltapine 15 | 0.03 | 0.10 |
| Delta Experiment Station, MS | 0.007 | DES 56 | 0.02 | 0.07 |
| Dunn Seed Farms | 0.004 | — | — | 0.08 |
| GroAgri Seed Co. | 0.004 | Stripper 31 | 0.01 | 0.26 |
| Lankart Seed Farms | 0.008 | Lankart 57 | 0.02 | 0.07 |
| McNair/Northrup King | 0.005 | McNair 235 | 0.01 | 0.09 |
| Missouri AES | 0.005 | Delcot 277 | 0.01 | 0.09 |
| New Mexico AES | 0.007 | Acala 1517 | 0.03 | 0.05 |
| Oklahoma AES | 0.009 | Oklahoma 4-1-3-6B2 | 0.01 | 0.05 |
| Paymaster/Cargill Seeds | 0.006 | Paymaster 54 | 0.02 | 0.06 |
| Stoneville Pedigreed Seed Co. | 0.010 | Stoneville 2 | 0.09 | 0.08 |
| Texas AES-College Station | 0.005 | B4LK | 0.02 | 0.08 |
| Texas AES-Lubbock | 0.008 | CA614 | 0.03 | 0.06 |
| USDA-ARS Shafter, CA | 0.005 | AXTE | 0.01 | 0.05 |
| USDA-ARS & South Carolina AES | 0.006 | PD 2165 | 0.02 | 0.09 |

† Average r value of each program with all 260 cotton cultivars released between 1970 and 1990.

related lines ($r = 0.05$) (Table 2). The majority of programs had r values ranging from 0.05 to 0.09. These values suggest that a considerable level of genetic diversity exists in most programs if it is assumed that only the best material becomes an influential line.

Arizona AES and Georgia AES have each provided five influential lines (Table 3). Germain Seeds and Lambright have released eight cultivars while Hurd's, Rilcot, and Rogers each released seven cultivars from 1970 to 1990. The majority of the 33 programs in Table 3 are

Table 3. Number of influential lines and upland cotton cultivars released from 1970 to 1990 in 33 other breeding programs.

| Breeding program | Influential lines | Cultivars released |
|----------------------------|-------------------|--------------------|
| | | no. |
| Agronomics, Inc. | 0 | 4 |
| All-Tex | 0 | 6 |
| Arizona AES | 5 | 1 |
| Arkansas AES | 0 | 2 |
| Auburn (Alabama AES) | 2 | 0 |
| Bronco | 0 | 4 |
| Brownfield Seed | 0 | 2 |
| Custom Ag Services | 0 | 6 |
| Dawson Seed Company | 0 | 3 |
| G & P Seed Company | 0 | 5 |
| Germain Seeds | 0 | 8 |
| Georgia AES | 5 | 3 |
| Growers Seed Association | 0 | 1 |
| Holland Cottonseed Company | 1 | 2 |
| Hurd's | 0 | 7 |
| Hyperformer Seed Company | 0 | 2 |
| J & S Research Company | 0 | 3 |
| Lambright | 0 | 8 |
| Lockett | 2 | 2 |
| Louisiana AES | 1 | 1 |
| Northern Star Seed Farms | 0 | 3 |
| Pioneer | 0 | 2 |
| Ranger Seed Company | 0 | 6 |
| Rilcot Seed Company | 0 | 7 |
| Rogers Cotton Seed Company | 0 | 7 |
| Seed Source, Inc. | 0 | 2 |
| Southland | 0 | 2 |
| Southwest | 1 | 3 |
| Sure-Grow | 1 | 1 |
| Technical Seed Proc. | 0 | 4 |
| Tennessee AES | 2 | 1 |
| Terra International | 0 | 4 |
| USDA-ARS Stoneville | 2 | 0 |

located in the High Plains area where 20% of the U.S. cotton acreage is found. Only seven of the 33 programs are public and only four of these public programs are still in existence (Arkansas AES, Louisiana AES, Georgia AES, and USDA-ARS Stoneville).

The cumulative genetic contribution of all eight ancestors was 0.21 (Table 4). Among the eight ancestors, the upland cultivar Acala with a genetic contribution eight generations removed, had the highest mean genetic contribution (0.063) and appeared in 73% of the pedigrees of the 260 modern upland cultivars. The cultivar Mexican Cotton, seven generations removed, had a genetic contribution almost as high (0.054) and appeared in more than 93% of modern pedigrees. Four other ancestors (three upland—Eastern Green Seed, Siam, and Burling's Mexican, and one extra-long staple cotton—Sea Island, *G. barbadense* L.) had lower genetic contributions and are 14 to 15 generations removed from the modern cultivars. However, they are all parents of Petit Gult and appear in 92 to 95% of modern pedigrees through that cultivar. The other upland cultivar, Kekchi, appears in 26% of the modern pedigrees, and the other extra-long staple cultivar, Pima, appears in less than 1% of modern pedigrees.

Table 4. Genetic contributions, generation remoteness, and frequency in pedigrees for eight cotton ancestors of upland cultivars released between 1970-1990.

| Ancestor | Mean genetic contribution† | Cumulative contribution | Minimum generations removed | Frequency in pedigrees‡ |
|--------------------|----------------------------|-------------------------|-----------------------------|-------------------------|
| | r | r | no. | |
| Acala | 0.063 | 0.063 | 8 | 0.731 |
| Mexican Cotton | 0.054 | 0.117 | 7 | 0.938 |
| Eastern Green Seed | 0.030 | 0.147 | 14 | 0.946 |
| Burling's Mexican | 0.026 | 0.173 | 14 | 0.919 |
| Kekchi | 0.020 | 0.193 | 3 | 0.262 |
| Sea Island | 0.010 | 0.203 | 14 | 0.919 |
| Siam | 0.007 | 0.211 | 15 | 0.919 |
| Pima | 0.001 | 0.211 | 3 | 0.004 |

† Average r value of each ancestor with all 260 cotton cultivars released.

‡ Frequency of ancestor germplasm found in cultivars released between 1970-1990.

Nine of the 11 lines identified as introductions that were analyzed had a cumulative genetic contribution of only 0.03 to the modern cultivars (Table 5). The primitive upland cultivar Hopi Moencopi, originally grown by the Hopi Indians of Arizona, had a mean genetic contribution of <0.01 but appeared in 39% of the pedigrees of the modern cultivars. KP and K3131 are upland cultivars that were introduced into modern U.S. breeding programs from Africa, and CB3051 was introduced from Yugoslavia; all appeared in less than 10% of the modern pedigrees. The line A2D1, which appears in 27% of the modern pedigrees, is not an introduction in the strictest sense but is a hybrid between two diploid species, *G. arboreum* L. and *G. thurberi* Tod. The triple hybrids, through which A2D1 contributed genes, resulted from the cross of A2D1 with *G. hirsutum* L. However, A2D1 is an introduction in the sense that it was the source of useful genes (for high fiber strength) that were transferred into upland cotton, mainly by breeders in the USDA-ARS Pee Dee program at Florence, SC.

The other introductions listed in Table 5 are representatives of *G. barbadense* L. The first three were introduced from Egypt: the Bar 4/16 Sakel and Egyptian cultivars, and Jumel, a tree cotton. The fourth, Tanguis, is a line that was introduced from Peru. None of these introductions appear in more than 17% of the modern pedigrees.

The genetic contribution of ancestors and introductions appears low, similar to results of the barley study by Martin et al. (1991). Their explanation for the low *r* value, the loss of genetic information due to reselection, is consistent with the findings in our study.

The 37 parental lines, other than those defined as ancestors or introductions but with unknown pedigrees, accounted for only 0.53% of the genetic variability even though the lines as a group appeared in nearly 74% of the pedigrees. Less than 25% of the genetic variability in the 260 modern upland cotton cultivars is accounted for by eight ancestors, nine introductions, and 37 other parental lines. Establishing a subset of ancestors which accounts for a large percentage of useful genetic variability does not appear possible for cotton as it was for soybean (Gizlice et al., 1994). In addition, seed is available for very few of the introductions and ancestors for this purpose.

Table 5. Genetic contributions, generation remoteness, and frequency in pedigrees for nine introductions on upland cotton cultivars released between 1970-1990.

| Introduction | Mean genetic contribution† | Cumulative contribution | Minimum generations removed | Frequency in pedigrees‡ |
|----------------|----------------------------|-------------------------|-----------------------------|-------------------------|
| | <i>r</i> | <i>r</i> | no. | |
| Hopi Moencopi | 0.009 | 0.009 | 5 | 0.392 |
| BAR 4/16 SAKEL | 0.006 | 0.015 | 5 | 0.169 |
| CB 3051 | 0.006 | 0.021 | 3 | 0.027 |
| KP | 0.005 | 0.026 | 5 | 0.096 |
| K 3131 | 0.003 | 0.029 | 5 | 0.062 |
| Tanguis | 0.002 | 0.031 | 3 | 0.150 |
| Egyptian | 0.002 | 0.033 | 6 | 0.058 |
| A2D1 | 0.001 | 0.034 | 11 | 0.273 |
| Jumel | 0.001 | 0.034 | 6 | 0.004 |

† Average *r* value of each introduction with all 260 cotton cultivars released.

‡ Frequency of introduction germplasm found in cultivars released between 1970-1990.

Many breeders believe that the germplasm base for upland cotton is narrow. However, the average *r* of 0.07 among the 260 cultivars suggests a wide genetic base. Our analysis of the genetic contribution of ancestors, introductions, parental lines, and breeding programs also suggests a wide germplasm base. Any conclusion from this study must be tempered by the realization that reselection and its accompanying loss of 25% information of the genetic contribution serves to dilute any genetic relationship. Given the nature of pollination in cotton, i.e., a tendency toward outcrossing, an *r* value of 0.75 may not be unrealistic.

These data highlight the contribution of individual breeding programs to genetic diversity of cotton. The private breeding firm Stoneville Pedigreed Seed Company influenced the most cultivars. The New Mexico AES, the Texas AES (College Station and Lubbock), and the USDA-ARS Pee Dee breeding programs also impacted cotton cultivar development significantly between 1970 and 1990. Recent releases from the Louisiana AES, Georgia AES, and Delta Experiment Station MS programs should have a significant impact on future cultivar development. We anticipate that the impact of Delta and Pine Land Company will increase due to almost exclusive use of their material as a source of the smooth leaf trait. Public cotton breeding programs should continue germplasm enhancement and germplasm exchange with private breeding programs. Erosion of genetic diversity in cotton could occur if private breeding programs with generally short-term goals become the dominant vehicle for cotton germplasm improvement.

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Genetic Analysis of Primitive Cotton Germplasm Accessions

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ABSTRACT

The recent conversion of primitive cotton (*Gossypium hirsutum* L.) stocks to the day-neutral flowering habit has effectively made these accessions readily available for direct use in plant breeding programs. Genetic analysis of these accessions would be useful in ascertaining parental material for improvement of specific traits. The objective of this study was to estimate genetic variances for 13 yield, fiber, and other agronomic traits in 79 accessions and 11 cultivars. A minimum norm quadratic unbiased estimation (MINQUE) method was used for estimating genetic variance components and an adjusted unbiased prediction method for predicting genetic effects. Additive \times environment interaction variances were significant for lint yield and node of first fruiting branch. The additive variance components made relatively high contributions to the phenotypic variances for lint percentage and boll size. Additive variances were relatively low for other traits. Narrow-sense heritabilities ranged from 8 to 50% for the traits studied. The proportion of accessions displaying significant, positive effects ranged from 12.7% for 50% span length to 30.4% for lint percentage and 2.5 span length. Positive additive effects for yield, lint percentage, and fiber traits except micronaire and negative effects for N1FB, NOMS, and plant height could be considered favorable effects. Although 16 of the primitive accessions showed significant positive additive effects for lint yield, only MDN-74 and MDN-101 could be predicted to produce stronger fiber, as well as higher lint yield and lint percentage. Results indicate that many primitive accessions may be used in crosses with commercial cultivars without serious loss of agronomic potential in the progeny.

THE USE of tropical cotton accessions in temperate environment breeding programs has been advocated for many years (O'Kelly, 1950), but few introduced accessions have found their way into successful cultivars. Few introductions of such germplasm were made in the USA until the 1940s. On collection trips in 1946, 1947, and 1948 to the presumed center of origin (Mexico and Central America) of upland cotton, more than 600 primitive accessions were collected and brought into the USA (Anonymous, 1974).

Previous research has shown that tropical accessions have useful genetic variability for insect and disease resistance and fiber quality (Percival, 1987; Meredith, 1991; McCarty and Jenkins, 1992; Jenkins and Parrott,

1978; Jenkins et al., 1978; Jenkins et al., 1979 a,b). Despite numerous attempts to use exotic germplasm, only a relatively small number of improved lines such as Acala 4-42 (Hyer and Bassett, 1985), Auburn 623 (Sheperd, 1974), MWR-1 and MWR-2 (McCarty et al., 1986), and MHR-17 and MHR-18 (Jenkins et al., 1988) have any significant amount of tropical or semitropical background. Tropical germplasm accessions have found limited use in temperate areas for several reasons: (i) tropical accessions are poorly adapted to temperate regions, mainly because of photoperiod sensitivity (Fryxell, 1984); (ii) unfavorable linkages in tropical accessions are difficult to overcome (Meredith, 1984; Percival and Kohel, 1990; McCarty and Jenkins, 1992); (iii) few extensive evaluations of tropical accessions have been made with respect to use in temperate climates (McCarty and Jenkins, 1992); and (iv) U.S. Cotton Belt germplasm is relatively good, and still has enough genetic variability to allow breeders to develop new improved releases in a relatively short time. As a result, there is little basis for using introduced tropical accessions in the U.S. Cotton Belt.

A program has been in progress for many years to introduce genes for day-neutrality into tropical germplasm accessions with a backcrossing scheme designed to disturb the genotype as little as possible and thus to have the new germplasm directly available for crossing and incorporation into cotton breeding programs (McCarty et al., 1979). Seventy-nine BC₄F₃ and BC₄F₄ progenies were evaluated for several agronomic and fiber traits and results indicated that there was useful genetic variability in these day-neutral cotton lines (McCarty and Jenkins, 1992). The objective of this experiment was to estimate genetic variances for several agronomic and fiber traits in BC₄F₄ day-neutral versions of 79 primitive accessions to aid cotton breeders in utilizing these accessions in their breeding programs.

MATERIALS AND METHODS

Seventy-nine day-neutral (MDN) accessions were developed by crossing each of the photoperiodic accessions as males to 'Deltapine 16' (DPL-16) in the winter cotton breeding nursery

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Abbreviations: INL, internode length; MIC, micronaire; MINQUE, minimum norm quadratic unbiased estimation; N1FB, node of the first fruiting branch; NOMS, nodes on main stem; σ_p^2 , phenotypic variance; V_n/V_p , narrow-sense heritability; H_b , broad-sense heritability; MDN, day-neutral accession.