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Genetic Diversity of U.S. Upland Cotton Cultivars Released between 1980 and 1990

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ABSTRACT

Sustained genetic advance requires that genetically diverse parents be mated to form segregating populations for selection. Genetic diversity of U.S. cotton (*Gossypium hirsutum* L.) cultivars has not been extensively quantified. We assessed diversity among 126 Upland cotton cultivars released between 1980 and 1990 by use of coefficient of parentage (CP). In computing CP, we utilized assumptions appropriate for self-pollinated crops. Mean CP among the 126 cultivars was 0.07, implying a genetically diverse group. However, cluster analysis revealed 12 distinct gene pools, with mean within-cluster CP = 0.25 and between-cluster CP = 0.04. Overall, clusters corresponded to area of cultivar origin. The CP analysis indicates that Acala-type cultivars are more diverse than those bred in the Mississippi Delta or southeastern USA. A trend in germplasm usage in the late 1980s was the repeated mating of genetically related material, or reselection within germplasm, to develop proprietary cultivars. To ensure continued progress in cotton improvement, we suggest that cotton breeders consider the pedigree of parents prior to population synthesis.

GENETIC DIVERSITY among cultivars reduces vulnerability of the crop to a disease or insect pathogen. In cotton, diversity is important also for long-term improvement in lint yield and fiber quality. Recently, the pedigrees of all cotton cultivars released in the U.S. between 1970 and 1990 were enumerated (Calhoun et al., 1994), which allowed CP (Malécot, 1948) to be calculated. Subsequently, CP among 260 cotton cultivars released between 1970 and 1990 were tabulated (Bowman et al., 1995). Using CP as a measure of genetic relationship, diversity can be estimated among cotton cultivars.

Pedigree analysis was used to assess genetic diversity in several crops including peanut (*Arachis hypogaea* L.; Knauft and Gorbet, 1989), soybean [*Glycine max* (L). Merr.]; Carter et al., 1993) and wheat (*Triticum aestivum* L.; Cox et al., 1985b). Pedigree analysis has not been applied extensively to Upland cotton cultivars. Duvick (1984) used the number of released cultivars and the number in development to assess diversity in the major row crops. For all of the crops, including cotton, he reasoned that with a large number of released cultivars and those in development, genetic diversity was adequate. More recently, Brown (1991) used various multivariate analytic approaches with lint yield, fiber, and seed properties to estimate diversity among entries in the 1987 National Cotton Variety Test. He concluded that Mississippi Delta, Central, and Texas Plains cultivars were more genetically diverse than eastern USA and Acala types. Finally, Wendel and Brubaker (1993) found little variation for allozyme and restriction fragment length polymorphism in a survey of Upland cottons.

Cotton has a long history of cultivation in North America, and many pedigrees trace back to a few introductions in the 1600s (Calhoun et al., 1994; Bowman et al., 1995). Selection within local varieties and occasional outcrosses directed the first 200 yr of cotton cultivar development. Many of the pedigrees of modern cultivars are characterized also by the common presence of a few lines, e.g., 'Empire' and 'Stoneville 2'. Consequently, the genetic base of modern cultivars might be narrow. The objective of this study was to use cluster analysis of CP, and thus assess diversity among cotton cultivars released between 1980 and 1990.

MATERIALS AND METHODS

The year of release or, if not available, the first two digits of the plant variety protection number listed in Calhoun et al. (1994), was used to determine that about 126 cotton cultivars were released between 1980 and 1990. The CP values among the 126 cultivars were extracted from tables in Bowman et al. (1995). Genetic assumptions necessary to calculate CP in our study conform to those for a self-pollinated crop (Murphy et al., 1986; Knauft and Gorbett, 1989).

Groups of related cultivars were found through cluster analysis of the CP values. Prior to cluster analysis, the CPs were converted to a measure of distance by subtracting one from each CP. Subsequently, the average linkage algorithm (Anderberg, 1973, p. 131–155) of SAS (SAS Inst., 1990) was applied to 1-CP. A dendrogram was drawn from the cluster analysis with PROC TREE. The dendrogram was partitioned at the 13-cluster level, resulting in a minimum cluster content of three cultivars for all but one cluster. Average CP within and between clusters was calculated after deleting the cluster containing a single cultivar.

To gain insight on germplasm utilization in cotton breeding, pedigrees of cultivars in each cluster were searched to determine parents shared by all the cultivars. For each common parent, the average number of generations removed from the cultivars in a cluster was calculated. We used generation in this context to reflect man-made crosses, natural outcrosses, or re-selections from germplasm lines-cultivars and not the number of generations of selfing during cultivar development.

RESULTS AND DISCUSSION

The 126 cotton cultivars in this study represent a diverse array of agronomic traits including maturity, disease resistance, plant type, boll type (e.g., picker vs. stripper), yield, and fiber properties (e.g., strong-fibered Acala vs. lower fiber strength Texas Plains). This level of phenotypic variability suggests that genetic variability would not be limited. Considering that the mean CP was only 0.07, genetic diversity is high among this set of 126 cultivars. On a scale of 0 to 1.0, a CP of 0.07 suggests a low degree of relationship. The cluster analysis

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Abbreviations: CP, coefficient of parentage.

Table 1. List of cotton cultivars released in the U.S. between 1980 and 1990, cluster designation, common parent within cluster, and average no. generations common parent is removed.

No. cultivar	Common parent	Generations removed
Cluster 1		
1. Arkot 518	Stoneville 2	8
2. BR-636		
3. Coker 130		
4. Coker 139		
5. Coker 208		
6. Coker 315		
7. Coker 320		
8. Coker 500		
9. Coker 3131		
10. Coker 4360		
11. Delcott 344		
12. Deltapine 20		
13. Deltapine 30		
14. Deltapine 50		
15. Deltapine 51		
16. Deltapine 69		
17. Deltapine 77		
18. Deltapine 90		
19. Deltapine 120		
20. Deltapine 5415		
21. Deltapine 5690		
22. Deltapine DNSL		
23. Deltapine SR-980		
24. DES 422		
25. Dunn 325		
26. Georgia King		
27. Tifcot 56		
28. Hyperformer HS 23		
29. Hyperformer HS 46		
30. Kings Acala MS		
31. PD-1		
32. PD-2		
33. PD-3		
34. Stoneville BR-110		
35. Stoneville BR-115		
36. Stoneville KC 311		
37. Stoneville KC 380		
38. Salcot 10		
39. SureGrow 1001		
40. S-35		
41. SV 13		
42. SV 93		
43. Terra C-30		
44. Terra C-40		
Cluster 2		
45. Bronco 360	Lankart	4
46. Bronco 625		
47. DC 886		
48. Lankart 175		
49. Lankart 311		
Cluster 3		
50. Cascot BR-1	Empire	6
51. Cascot C-13		
52. Earlycot 48		
53. G & P 74+		
54. G & P 1005		
55. G & P 5479		
56. Pioneer PR 80		
57. Tamcot CAB-CS		
58. Tamcot CD3H		
59. Tamcot GCNH		
60. Tamcot HQ 95		
61. DC 827		
62. Delcot 311		
63. Delcot 390		
64. Deltapine SR-482		
65. Dunn 219		
66. Dunn 224		
67. Dunn 1002		
68. Dunn 1047		
69. Dunn HS 120		
Cluster 4		
70. DES 119	Stoneville 7	3
71. LA 887		
72. Seed Source S-55		
73. Stoneville 112		
74. Stoneville 302		
75. Stoneville 453		
76. Stoneville 506		
77. Stoneville 825		
78. Stoneville 907		
79. Terra 207		
Cluster 5		
80. Dunn 400	Paymaster 18	2
81. GSC 1093	Paymaster 111	2
82. Paymaster 147		
83. Paymaster 404		
84. Paymaster 505		
Cluster 6		
85. GSC 20	CA 398	2
86. GSC 25		
87. Simwalt 82		
Cluster 7		
88. Acala 1517-91	#1 Acala	8
89. Acala Maxxa	#3 Acala	9
90. Acala Prema	Hopi Moencopi	6
91. Acala Royale		
92. Acala SJC-1		
93. Germains 352		
94. Germains 356		
95. Germains 362		
96. Germains 363		
97. Germains 410		
98. Germains 445		
99. Germains 510		
100. Germains 555		
101. Paymaster HS 200		
Cluster 8		
102. 7563	DeltaPine 15	4
103. Deltapine SR-383	Acala 49	6
104. Deltapine SR-5	Hartsville	6
105. Paymaster HS 26	Stoneville 20	7
106. Southland 400		
107. Southland M1		
108. Terra SR 10		
Cluster 9		
109. Acala 1517-77BR	AHA 6	7
110. Acala 1517-88	9136	4
111. Acala 1517-SR1	Acala 49W	4
112. Acala 1517-SR2		
Cluster 10		
113. Rogers 7590	Rogers LG 10	2
114. Rogers LG 86		
115. Rogers LG 102		
Cluster 11		
116. Cencot	92k	6
117. Lankart 142	61k	6
118. Lankart 511		
119. Lankart PR 75		
120. Paymaster 892		
Cluster 12		
121. Earlycot 32A	Line D	3
122. GSC 27		
123. GSC 30		
124. GSC 71+		
125. QuapawD		
Cluster 13		
126. SI Samrong 60		

Table 2. Average coefficient of parentage (CP) within-cluster (underlined on diagonal) and between-cluster (below the diagonal) for clusters 1-12 in Table 1.

Cluster no.	1	2	3	4	5	6	7	8	9	10	11	12
1	0.20											
2	0.03	0.34										
3	0.05	0.03	0.19									
4	0.09	0.02	0.06	0.27								
5	0.04	0.09	0.06	0.04	0.34							
6	0.02	0.01	0.04	0.01	0.03	0.25						
7	0.04	0.01	0.03	0.02	0.02	0.04	0.18					
8	0.07	0.04	0.06	0.06	0.05	0.07	0.06	0.23				
9	0.05	0.01	0.01	0.04	0.02	0.02	0.07	0.04	0.28			
10	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	0.31		
11	0.07	0.04	0.08	0.05	0.07	0.04	0.03	0.07	0.02	<0.01	0.17	
12	0.05	0.04	0.05	0.06	0.07	0.02	0.03	0.04	0.02	0.02	0.05	0.19

revealed cultivar groups with mean CP greater than 0.07, however.

Cluster 1 was composed primarily of 44 southeastern U.S. and Mississippi Delta bred cultivars (Table 1). The mean CP was 0.20, indicating a degree of relationship near that of cultivars derived from crosses with a common parent. All of these cultivars share genes through the obsolete cultivar Stoneville 2 (Calhoun et al., 1994). On average, Stoneville 2 occurs 13 times in the pedigree of each cultivar, but is about eight generations removed (Table 1). Among the 17 cultivars in this cluster released between 1987 and 1990, we observed an alarming trend toward erosion of the genetic base, resulting from the extensive use of the same cultivars as parents. Eight of the 17 cultivars have 'Deltapine 90' as a parent, and seven have highly related lines from the McNair breeding program as parents. Even though these 44 cultivars are moderately related, they possess a range in maturity, lint yield, and fiber properties (USDA, 1990). For example, among cultivars still widely grown (USDA, 1993), Deltapine 90 is considered late-maturing but has fiber properties considered desirable by textile mills. In contrast, 'Deltapine 50' is early-maturing and has fiber properties that meet the minimum standards for use by textile mills.

Breeding programs in Texas are responsible for cultivars forming eight of the 12 clusters (Table 1). Cotton hectareage in Texas has been sufficiently large to support numerous cotton breeding programs for the stripper and picker production areas. The terms stripper and picker denote different harvest methods. With stripper-type cottons, intact bolls are stripped from the plant and the seedcotton is separated from the remaining boll components. The term picker-type denotes cottons where the seedcotton is separated from the boll while the boll is attached to the plant. Clusters 2, 5, and 10 contain the most highly related cultivars, while Clusters 3, 7, 11, and 12 contain the least related cultivars (Table 2). In general, these clusters are also genetically distinct from each other, reflecting the lack of recent germplasm exchange among breeding programs.

Cluster 2 was composed of five Texas-Plains-type cultivars from the Lankart, Bronco, and Dawson Seed Companies (Table 1). Mean CP was 0.34, reflecting the extensive use of Lankart derived lines in the pedigrees. Released in 1915, the cultivar Lankart occurs about two times in the pedigree of each cultivar and is about four generations removed.

Cluster 3 had 20 cultivars from the Tamcot, G & P, Custom Ag. Services, Dunn, and Deltapine breeding programs. Mean CP was 0.19, making this a more divergent group than Cluster 2. The cultivar Empire appears extensively in these pedigrees, about eight times per cultivar, but is about six generations removed. Surprisingly, two Mississippi Delta-type cultivars, Delcot 311 and Delcot 390, appear in the same cluster as the stripper-type cottons, 'Cascot BR-1' and 'Cascot C-13'. Fiber properties of Mississippi Delta cottons are phenotypically diverse from the stripper cottons (USDA, 1990), and one would not predict that they would cluster together.

Cluster 5, composed of three Paymaster, one Gro-Agri Seed Co., and one Dunn Seed Farms cultivar, illustrates the influence of Paymaster-derived germplasm on Texas cotton cultivars. All five cultivars share 'Paymaster 18' and 'Paymaster 111' in their pedigree and are an average of only two generations removed. Besides Cluster 2, Cluster 5 had the highest mean CP (0.34) of the 12 clusters (Table 2).

Cluster 6, containing three cultivars, had a mean CP of 0.25, similar to that for half-sibs derived from crossing inbred parents (Tables 1, 2). These cultivars share the obsolete germplasm line CA 398 as a grandparent.

Texas-Plains cultivars comprise Cluster 8, with mean CP of 0.23. These cultivars share four obsolete cultivars in common, Deltapine 15, Acala 49, Hartsville, and Stoneville 20 (Table 1); but, they are four to seven generations removed. Although these cultivars share germplasm such as Deltapine 15 and Hartsville with Mississippi Delta and southeastern USA cultivars (Calhoun et al., 1994), these lines are far removed in the pedigrees. Their genetic contribution, and thus CP between the three groups of cultivars, is low.

Three cultivars from the Rogers breeding program make up Cluster 10. These cultivars are the most genetically isolated of the 126 cultivars in this study (Table 2) with common parent 'Rogers LG-10'. However, to an unknown extent, the apparent genetic isolation may reflect poor pedigree information since the pedigree of Rogers LG-10 is not well described (Calhoun et al., 1994).

Clusters 11 and 12, composed of Texas-bred cultivars, are primarily stripper-type cottons (Table 1). Cluster 11, with three Lankart cultivars, a Cencot, and a Paymaster cultivar share the Tamcot breeding lines 92K and 61K, although on average they are some six generations removed. Cultivars in Cluster 12 are descendants of a complex crossing program involving the combination of seven or more parents. A common parent only three generations removed from these stripper cultivars is line D, composed of 'Roldo Rowden', 'Empire WR', and 'BBR'. Although cultivars in Clusters 11 and 12 share many of the same parents relatively recently in their pedigree, the mean CP among them is not higher due to the number of parents combined together.

The influence of germplasm from the Stoneville Pedigreed Seed Co. is evident from the cultivar composition of Cluster 4. Six of the 10 cultivars are products of the Stoneville breeding program, while the remaining four cultivars descend from obsolete Stoneville cultivars. Released in 1956, 'Stoneville 7' occurs, on average, twice in the pedigree of these 10 cultivars and is three generations removed. Despite some degree of genetic uniformity, with a mean CP of 0.27, these cultivars possess a range of adaptation, lint yield, and fiber properties. The cultivars DES 119 and LA 887 have unusually broad adaptation from the Mississippi Delta to North Carolina. Cultivars such as Stoneville 453, 506, and 907 are among the earliest maturing in the cluster, and perform best in the Mississippi Delta where early maturity aids in pest management and harvest prior to deterioration of climatic conditions (Jenkins et al., 1990).

Acala-type cotton cultivars are produced from Texas to California and are noted for excellent fiber properties, particularly fiber strength (USDA, 1990). For cultivars to be marketed in the Central Valley of California, they must pass rigorous standards for fiber quality and must be equal or greater in lint yield to a standard cultivar. This restriction on performance might suggest a narrow genetic base resulting from the intermating of phenotypically similar germplasm with respect to fiber properties. However, Cluster 7, primarily composed of California Acala types, only has a mean CP of 0.18. This indicates a relatively divergent set of cultivars given the constraints on the acceptance of California Acalas as cultivars. The remaining cluster of Acalas (Cluster 9) was derived entirely from the public breeding program at New Mexico State University. Composed of only four cultivars, two of which are full-sibs (Acala 1517-SR1 and Acala 1517-SR2), the mean CP was 0.28. The most recent cultivar developed in the New Mexico Acala program, Acala 1517-91, does not cluster with its predecessor 'Acala 1517-88'. Their CP is only 0.08 and indicates that despite a mean CP of 0.28 for the four New Mexico Acalas in Cluster 9, genetic diversity remains in this program. These data support the findings of Brown (1991) in that a cluster analysis of New Mexico Acalas based on seed and fiber properties implied a relatively broad genetic base.

The free exchange and utilization of genetically diverse germplasm is essential to prevent genetic uniformity. The cluster analysis and pedigrees of cultivars developed between 1980 and 1990 indicate that certain germplasm lines (e.g., Empire) have been freely exchanged and have contributed to the breeding of such phenotypically diverse cottons as the Acala, Stripper, and Southeastern types. Much of this exchange and utilization of germplasm occurred early in the development of the 126 cultivars. A trend of germplasm use in the late 1980s was toward re-selection within and repeated crossing of genetically related material (e.g., Deltapine 90 and 'McNair 235') for the development of proprietary cultivars. Should this pattern of germplasm usage and selection for similar performance continue, genetic uniformity will increase.

We recognize that CP has limitations as a measure of genetic distance. In computing CP, we assumed that all parents were homozygous and homogeneous (Bowman et al., 1995), and thus, our estimates of CP may overestimate genetic relationships since they do not reflect outcrossing or residual segregation after early generation plant selections are made. Cotton can experience outcrossing, almost exclusively by entomophilous vectors as the pollen does not move well by wind (Niles and Feaster, 1984). Outcrossing rates are influenced by frequency of insecticide use and local level of pollinating insects and, consequently, have varied to an unquantified extent since the beginning of cotton culture in the early 1600s (Calhoun et al., 1994; Bowman et al., 1995). Additionally, 'PD-3' and presumably other cultivars are derived from the bulk seed increase of early generation plant selections (Culp et al., 1988) and violate the assumption of a single genotype when used in a cross. As such, we chose to be consistent in our assumptions necessary to calculate CP and have invoked those for self-pollinated crops (Bowman et al., 1995). Alternatively, we could have used assumptions appropriate to open-pollinated genotypes in the calculation of CP (Gerdes and Tracy, 1994).

The potential bias introduced by selection on whether CP represents a realistic measure of genetic distance has been highlighted in similar studies using CP to estimate diversity (Cox et al., 1985a; Knauft and Gorbet, 1989). Our CPs may overestimate diversity for certain cultivar types. Examples are Acala cultivars selected to meet rigid standards for fiber quality in the one-quality-by-law district of California and those developed for the Mississippi Delta. Cotton is a genetically indeterminate plant that has been modified to act similar to an annual outside the tropics (Lee, 1984). Additional changes of the cotton plant towards early maturity have been emphasized in the breeding of cotton cultivars for certain geographical areas, such as the Mississippi Delta, as a means to avoid insect pests and reduce production costs (Niles and Feaster, 1984). Although crop maturity is considered a quantitatively inherited trait, generations of selection for early maturity would tend to fix some portion of even a large number of genes governing maturity. We can then speculate that the mean CP of 0.27 for the 10 Delta bred cultivars in Cluster 4 may imply more genetic diversity than actually exists. For the California Acala cultivars, despite narrow standards for fiber quality,

improved cultivars continue to be developed (Cooper, 1992), implying that genetic diversity remains.

Cultivars from the same cross derived from the same F_2 plant would have higher CP than that reported in Bowman et al. (1995) and could influence cluster composition in this study (Falconer, 1989). The pedigrees of cotton cultivars do not contain this level of detail (Calhoun et al., 1994) and for this instance, CP would underestimate genetic distance. These considerations make it difficult to assess whether CP over or underestimates genetic diversity.

Despite some limitations as a measure of genetic distance, pedigree analysis can indicate which cultivars are less likely to possess similar genes. When crossed to produce segregating populations, they may offer an opportunity to generate more genetic variation than from mating cultivars with high CP. Our data suggest that the genetic base of cotton may be on a downward trend due to the increasingly proprietary nature of germplasm and the tendency to repeatedly use the same parents in matings. Mating cultivars from different clusters would be a step toward broadening the genetic base of current cultivar development efforts. It is imperative then that public breeding programs continue efforts at enhancement of diverse germplasm with subsequent free exchange. If private breeding firms with the goal of producing and marketing cultivars and generally not germplasm enhancement and free-exchange are the only breeding efforts allowed to survive, long-term gain in lint yield and fiber quality might not be sustained.

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