

## BREEDING AND GENETICS

### Comparison of Bulk F<sub>2</sub> Performance Testing and Pedigree Selection in Thirty Pima Cotton Populations

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#### ABSTRACT

The objective of early generation testing is to increase breeding efficiency through early identification of superior heterogeneous populations. Bulk F<sub>2</sub> testing has gained adherents among the cotton breeding community with little data to support its efficacy. The goal of this study was to compare bulk F<sub>2</sub> performance with historical pedigree selection records to determine the degree of correspondence between the two methods in identifying superior hybrid pima cotton (*Gossypium barbadense* L.) populations. Thirty hybrid populations, originally created in the USDA-ARS Pima breeding project in 1983 and 1984, were recreated. The F<sub>2</sub> populations of 1983 and 1984 crosses were tested for yield and fiber performance in randomized complete block tests at Maricopa and Safford, AZ in 2000 and 2002, respectively. Pedigree selection records of the 30 populations were summed across F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations, and correlations were run between the summed selection records and F<sub>2</sub> population performance data. Comparisons also were made between F<sub>2</sub> performance of populations and the number of lines each contributed to advanced, replicated testing. Significant correlations were almost entirely lacking between selection records of 1983 crosses and the yield and fiber data of their F<sub>2</sub> populations. A greater number of correlations were observed between field and fiber lab selection numbers of 1984 crosses and the yield and fiber performance of the F<sub>2</sub> populations. These correlations were not consistent between the Maricopa and Safford locations. Weak correspondences were observed between F<sub>2</sub> generation performance of the 30 populations and the number of progeny each contributed to advanced, replicated testing.

The goal of early generation testing is to increase breeding efficiency through the early identification of superior heterogeneous populations. The early elimination of inferior populations and subsequent concentration of selection efforts within superior populations is assumed to result in increased efficiency. The success of the method depends upon accurate evaluation of heterogeneous populations, and assumes that transgressive segregants from inferior populations will not exceed selections from superior populations in performance. The concept of early generation testing in self-pollinating species as a means to identify superior bulk hybrid populations was first described by Immer (1941) and has been used in various crops with varying success.

Numerous variants of early generation testing have been developed and employed. Harlan et al. (1940) used F<sub>2</sub> bulks to identify superior barley (*Hordeum vulgare* L.) populations. Weiss et al. (1947) used F<sub>2,3</sub> families of soybean [*Glycine max* (L.) Merr.] to identify superior families. In a comparison of F<sub>1</sub>-, F<sub>2</sub>-, and F<sub>3</sub>-derived families of soybeans, St. Martin and Gernaldi (2002) concluded that evaluation in all generations gave similar yield gains and therefore the F<sub>2</sub> families selected from the F<sub>1</sub> generation would be the most advantageous for testing. Results from early generation testing, while generally favorable (Cregan and Busch, 1977; Singh et al., 1990, and Singh et al., 1998), have been mixed. Bulk F<sub>2</sub> through F<sub>5</sub> populations of soybean failed to adequately identify crosses possessing superior yield and maturity (Weiss, 1947). Fowler and Heyne (1955) reported poor predictive results from bulk hybrid tests of hard red winter wheat (*Triticum aestivum* L.).

In recent years, early generation F<sub>2</sub> testing has gained adherents among the cotton breeding community (Bowman, 2000), but relatively little information is available concerning the efficacy or efficiency of the method in cotton (Green and Culp, 1989). The one study that found moderate positive correlation between the performance of early generation populations and their descendant pure lines

needs corroboration (Barut, 1998). The goal of the present investigation was to compare F<sub>2</sub> population performance with historical pedigree selection records to determine the degree of correspondence between early generation testing and pedigree selection in identifying superior hybrid populations.

### MATERIALS AND METHODS

The F<sub>2</sub> generation of thirty hybrid populations, originally created in the USDA-ARS Pima cotton breeding program in 1983 and 1984, were re-created for the purpose of comparing F<sub>2</sub> bulk testing with pedigree selection. The Pima breeding program had as its goal the creation of broadly adapted, high yielding commercial cultivars possessing extra-long staple fiber. Parental lines used in creating hybrid populations were selected on the basis of their fiber yield and quality, as determined by previous testing. Parental lines were crossed in a diallel fashion for the sake of efficiency and to create the maximum amount of variability for selection from the chosen parental lines. Field selections within the populations were made on the basis of visual evaluation for fruiting height, plant height, plant productivity, and earliness of maturity. Reselection for fiber quality among the field-selected individuals con-

centrated upon lint percentage, fiber length, fiber strength, and micronaire. The initial F<sub>2</sub> generation selection was performed on populations consisting of plants spaced at 0.3 m intervals on approximately 300 m of row. The size of the F<sub>3</sub> and F<sub>4</sub> generation populations receiving selection varied according to the number of plants selected and progeny advanced from the previous generation. Records of field and fiber quality selections within the F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations of 30 hybrid populations have been compiled (Tables 1 and 2.)

Plant selection numbers within populations of the 1983 and 1984 crosses have been summed across their F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations. Summed selection records were thought more likely to reflect the identification of superior populations within the pedigree breeding program, since it was observed that selection proceeded in a non-linear, somewhat saltatory manner between generations (see populations 8309 and 8313, Table 2.). Further, it was recognized that fiber quality selection numbers within a particular cross population could be dependent upon the number of field selections previously made within that population, leading to a situation where correlation between F<sub>2</sub> performance traits and field selection numbers could contribute to a spurious

Table 1. Parentage and cross numbers of F<sub>2</sub> populations recreated from 1983 and 1984 crossing plans of the USDA-ARS pima cotton breeding program

1983 cross populations			1984 cross populations		
1983 Cross no.	Pedigree	1999 Cross no.	1984 Cross no.	Pedigree	1999 Cross no.
8301	P51x82-201	99527	8401	P62xP59	99201
8302	P51x81-244	99528	8402	P62x82-203	99202
8303	P51x81-272	99529	8403	P62xP64	99203
8304	P51x82-210	99530	8404	P62xP67	99204
8305	P51x82-216	99531	8405	P62xP66	99205
8306	82-201x81-244	99532	8406	P59x82-203	99206
8307	82-201x81-272	99533	8407	P59xP64	99207
8308	82-201x82-210	99534	8408	P59xP67	99208
8309	82-201x82-216	99535	8409	P59xP66	99209
8310	81-244x81-272	99536	8410	82-203xP64	99210
8311	81-244x82-210	99537	8411	82-203xP67	99211
8312	81-244x82-216	99538	8412	82-203xP66	99212
8313	81-272x82-210	99539	8413	P64xP67	99213
8314	81-272x82-216	99540	8414	P64xP66	99214
8315	82-210x82-216	99541	8415	P67xP66	99215

Table 2. Selection records within the 1983 crosses of the USDA-ARS pima breeding program

Cross no.	No. field selected plants				No. plants advanced after fiber Analyses				Ratio of plants advanced
	F <sub>2</sub>	F <sub>3</sub>	F <sub>4</sub>	Total	F <sub>2</sub>	F <sub>3</sub>	F <sub>4</sub>	Total	
8301	131	20	60	211	64	14	21	99	0.47
8302	131	46	39	216	48	9	11	68	0.31
8303	122	38	8	168	47	10	0	57	0.34
8304	63	30	22	115	23	7	0	30	0.26
8305	115	110	115	340	74	42	43	159	0.47
8306	159	277	404	840	93	97	125	315	0.38
8307	150	127	46	323	71	41	11	123	0.38
8308	134	89	22	245	61	24	5	90	0.37
8309	42	31	130	203	27	18	54	99	0.49
8310	80	21	0	101	19	1	0	20	0.20
8311	96	25	17	138	32	5	5	42	0.30
8312	97	51	51	199	52	15	14	81	0.41
8313	155	11	0	166	39	5	0	44	0.27
8314	57	19	9	85	31	5	4	40	0.47
8315	41	5	0	46	24	0	0	24	0.52

correlation between F<sub>2</sub> field performance and fiber selection numbers. To remove this possible bias, fiber selection numbers have been expressed as a ratio of field selection numbers within each population.

The 30 hybrid populations, originally created in 1983 and 1984, were re-created in the field and greenhouse at Maricopa, AZ in 1999. Performance tests of the F<sub>2</sub> populations from 1983 and 1984 crosses, and their parents, were conducted at Maricopa and Safford, AZ in 2000 and 2002, respectively. Tests at both locations in both years were randomized, complete block designs with four replications. Plots at Maricopa and Safford in 2000 were four rows, 12.8 m x 1 m and 14 m x 0.9 m, respectively. Plots at Maricopa and Safford in 2002 were four rows, 12.8 m x 1 m and 10.7 m x 0.9 m, respectively. Fifty normal, full-sized bolls were hand-harvested from the center two rows of each plot for fiber analysis and determination of lint percentage at the end of the season. The center two rows of each plot were then machine-harvested for lint yield determination. A single-row height measurement was made in each plot of the replicated tests at the time of harvest, and is referred to hereafter as plant height. Fiber samples obtained from the hand-har-

vested boll samples were analyzed using individual instrumentation by Star Lab (Knoxville, TN).

Analyses of variance were performed on all F<sub>2</sub> population data (parents excluded) using the general linear model procedure of the Statistical Analysis System (SAS Institute Inc., Cary, NC). Parental data were used to calculate midparent values for all traits measured. Correlations were determined between F<sub>2</sub> performance data and summed field selection numbers, fiber selection numbers, and their ratios. Only traits that received emphasis in the selective process of the pima pedigree breeding program were used in correlation analyses. Comparisons were made between population rankings for F<sub>2</sub> yield, plant height, and fiber traits and the number of progeny individual populations contributed to advanced, replicated testing.

## RESULTS AND DISCUSSION

**Analyses of variance.** Of the 1983 crosses, the F<sub>2</sub> populations differed in yield, plant height, and micronaire at both Maricopa and Safford, AZ in 2000 (Table 3). Lint percentage and fiber length among F<sub>2</sub> populations were different only at the Maricopa site. Fiber strength among F<sub>2</sub> populations was not different at either location. Across locations, the F<sub>2</sub> popu-

Table 3. Mean squares<sup>y</sup> for fiber yield, plant height, lint percentage, fiber length, fiber strength, and fiber micronaire from comparisons of F<sub>2</sub> populations of 1983 and 1984 crosses grown in 2000 and 2002, respectively, at Maricopa and Safford, Arizona

Crosses	Locations	Source of variation	Df <sup>z</sup>	Fiber yield	Plant height	Lint percentage	Fiber property		
							Length	Strength	Micronaire
1983	Maricopa	Replication (R)	3	18520	0.050**	0.0001*	0.0001	7.59**	0.044**
		Population (P)	14	42261**	0.046**	0.0003**	0.0010**	2.07	0.094**
		error	42	8554	0.011	0.00002	0.0004	1.49	0.009
		CV		6.4	8.9	1.3	1.4	4.0	2.4
	Safford	Replication (R)	3	208094**	0.058**	0.0001	0.0030**	2.68*	0.035
		Population (P)	14	20470*	0.022**	0.0003	0.0020	0.80	0.065**
		error	42	8329	0.003	0.00002	0.0006	0.76	0.013
		CV		12.9	6.7	1.3	1.8	2.9	2.6
	Across	Location (L)	1	15981894**	5.129**	0.0014**	0.0074**	0.37	3.072**
		R(L)	6	113306**	0.054**	0.0001**	0.0016**	5.13**	0.039**
		Population (P)	14	40959**	0.056**	0.0006**	0.0025**	1.86	0.143**
		L x P	14	22108**	0.012	0.00002	0.0005	1.01	0.016
error		84	8440	0.007	0.00002	0.0005	1.13	0.011	
CV		8.6	8.4	1.3	1.6	3.5	2.5		
1984	Maricopa	Replication (R)	3	4941	0.014	0.0001	0.0008	1.79	0.001
		Population (P)	14	28467**	0.031**	0.0008**	0.0001	2.87	0.036**
		error	42	10428	0.006	0.0001	0.0003	1.89	0.009
		CV		9.1	6.3	1.7	1.2	4.5	2.3
	Safford	Replication (R)	3	88450*	0.001	0.0001	0.0007*	0.85	0.046*
		Population (P)	14	44556	0.007	0.0009**	0.0006**	3.24*	0.020
		error	42	23231	0.005	0.0001	0.0002	1.47	0.016
		CV		12.1	8.4	2.4	1.1	4.0	2.8
	Across	Location (L)	1	528631**	3.366**	0.0131**	0.0036**	0.99	2.324**
		R(L)	6	46696*	0.007	0.0001	0.0008*	1.32	0.023
		Population (P)	14	37728*	0.028**	0.0017**	0.0004	4.87**	0.040**
		L x P	14	35291*	0.009	0.0001	0.0003	1.24	0.016
error		84	16662	0.005	0.0001	0.0003	1.68	0.013	
CV		10.8	7.2	2.1	1.1	4.3	2.6		

<sup>y</sup> \*, \*\* indicates means are significant at the  $P \leq 0.05$ , and  $P \leq 0.01$ , respectively.

<sup>z</sup> Due to missing plot values, degrees of freedom for the error term were reduced for the yield variable at Maricopa in 2000 and 2002, and at Safford in 2002.

lations of 1983 crosses displayed significant differences for all traits, except for fiber strength. Lint yield was the only trait for which a significant location by population interaction occurred. Among the 1984 crosses, F<sub>2</sub> populations were different for yield, plant height, and micronaire at the Maricopa location, and for fiber length and strength at the Safford location. Lint percentage was the only trait in which

significant population differences were noted at both locations. Across locations, F<sub>2</sub> populations of 1984 crosses were different for all traits, except for fiber length. Lint yield was the only trait for which a significant location by population interaction occurred in the 2002 evaluation of 1984 F<sub>2</sub> populations.

**Correlation of F<sub>2</sub> performance with pedigree selection records.** There was no correlation between

F<sub>2</sub> population performance at Maricopa in 2000 and pedigree selection numbers (summed across F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations) within 1983 crosses (Table 4.). Likewise, no correlations were observed between F<sub>2</sub> performance across the Maricopa and Safford locations and pedigree selection numbers. At the Safford location, the correlation between F<sub>2</sub> plant heights and the number of selections made among F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> populations of the 1983 crosses was negative. The correlation between the fiber strengths of F<sub>2</sub> populations and the pedigree fiber selection ratio was also negative. The significance of this latter correlation is questionable, since the F<sub>2</sub> populations of 1983 crosses were not different in fiber strength at Safford in 2000.

A larger number of significant correlations between F<sub>2</sub> trait performance and pedigree selection records occurred within the 1984 cross populations tested in 2002 (Table 5), but these correlations were

not consistent across the two locations. At Maricopa, F<sub>2</sub> population plant heights and micronaire values were negatively associated with pedigree field selection numbers. Midparent yield and lint percentage of F<sub>2</sub> populations were positively correlated with pedigree fiber selection ratios. The fiber strengths of F<sub>2</sub> populations were negatively correlated with fiber lab selection numbers. Since F<sub>2</sub> populations of 1984 crosses did not differ for fiber strength at Maricopa, the above correlation with fiber lab selection records is questionable. At Safford, F<sub>2</sub> population midparent yields and lint percentages were positively correlated with pedigree fiber selection ratios. The fiber lengths of 1984 F<sub>2</sub> populations were positively correlated with the number of selections made in the field and the number of fiber lab selections. Across the Maricopa and Safford locations, F<sub>2</sub> fiber strength was positively related to the number of field selections, and F<sub>2</sub> micronaire was negatively correlated to field selec-

**Table 4. Correlation coefficients<sup>z</sup> for yield, plant height, and fiber traits of F<sub>2</sub> populations grown at Maricopa and Safford, AZ in 2000 with individual plant selection numbers of 1983 crosses summed across the F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations**

Location	F <sub>2</sub> trait	No. plant selections		Fiber lab/field
		Field	Fiber lab	
Maricopa	Yield	-0.05	0.00	0.28
	Midparent yield	0.04	0.08	0.18
	Height	-0.24	-0.27	-0.24
	Lint percentage	0.02	0.01	0.26
	Length (2.5SL)	-0.01	0.02	0.30
	Strength (T1)	0.00	-0.02	-0.22
	Micronaire	-0.14	-0.13	0.12
Safford	Yield	-0.17	-0.21	-0.13
	Midparent yield	-0.04	0.00	0.25
	Height	-0.53*	-0.58*	-0.39
	Lint percentage	0.31	0.31	0.21
	Length (2.5SL)	-0.39	-0.39	0.07
	Strength (T1)	0.41	0.26	-0.52*
	Micronaire	-0.30	-0.31	-0.09
Across locations	Yield	-0.09	-0.07	0.18
	Midparent yield	0.01	0.05	0.21
	Height	-0.38	-0.42	-0.34
	Lint percentage	0.16	0.15	0.23
	Length (2.5SL)	-0.26	-0.25	0.18
	Strength (T1)	0.19	0.11	-0.41
	Micronaire	-0.22	-0.22	0.03

<sup>z</sup> \* indicates that the correlation coefficient is significant at  $P \leq 0.05$ .

**Table 5. Correlation coefficients<sup>z</sup> for yield, plant height, and fiber traits of F<sub>2</sub> populations grown at Maricopa and Safford, AZ in 2002 with individual plant selection numbers of 1984 crosses summed across the F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations**

Location	F <sub>2</sub> trait	No. plant selections		Fiber lab/field
		Field	Fiber lab	
Maricopa	Yield	0.15	0.43	0.39
	Midparent yield	-0.31	0.13	0.66**
	Height	-0.57*	-0.47	-0.10
	Lint percentage	-0.35	0.11	0.70**
	Length (2.5SL)	0.20	0.42	0.30
	Strength (T1)	0.31	0.66*	0.50
	Micronaire	-0.56*	-0.46	-0.06
Safford	Yield	-0.28	0.09	0.39
	Midparent yield	-0.49	-0.07	0.52*
	Height	-0.23	-0.26	-0.42
	Lint percentage	-0.45	-0.03	0.68**
	Length (2.5SL)	0.59*	0.66**	0.09
	Strength (T1)	0.45	0.38	-0.29
	Micronaire	-0.26	-0.18	0.22
Across locations	Yield	-0.12	0.35	0.53*
	Midparent yield	-0.44	0.01	0.61*
	Height	-0.51	-0.44	-0.22
	Lint percentage	-0.41	0.03	0.70**
	Length (2.5SL)	0.47	0.69**	0.25
	Strength (T1)	0.53*	0.50	-0.18
	Micronaire	-0.57*	-0.47	0.13

<sup>z</sup> \* and \*\* indicate the correlation coefficient is significant at  $P \leq 0.01$  and  $P \leq 0.05$ , respectively.

tions. The F<sub>2</sub> yield and lint percentage, and the midparent yield were positively correlated with fiber selection ratios. Although F<sub>2</sub> fiber length was positively related to fiber lab selection numbers, the meaningfulness of this latter correlation is questionable, because of the lack of fiber length differences among F<sub>2</sub> populations across locations.

In summary, there was poor association of the various traits measured in the F<sub>2</sub> populations and pedigree selection records. Observed correlations were not consistent across the 1983 and 1984 F<sub>2</sub> population sets, or across locations. Lint yield, a trait of great interest to breeders, produced significant location by F<sub>2</sub> population interactions in both the 1983 and 1984 sets of crosses. The early identification of populations exhibiting strong genotype X environment interactions may be one of the advantages of early genera-

tion testing. The only correlation obtained between yield and pedigree selection records occurred between yields of 1984 F<sub>2</sub> populations, across locations, and fiber selection ratios. It is unclear why F<sub>2</sub> yield should correlate positively with a selection ratio that was based upon fiber quality traits.

**Correspondence between F<sub>2</sub> performance and pedigree lines advanced to replicated testing.** In correlating F<sub>2</sub> performance with pedigree selection records, an assumption has been made that populations receiving the highest levels of selection within a pedigree selection program correspond to the “best” populations. This may not be the case, and cumulative plant selection numbers might not even correspond to the identification of superior lines within the pedigree program. Early identification of superior lines within a population actually may lead

to lower numbers of field selections being made within that population in subsequent generations. Conversely, identification of a superior yielding line within a population that possesses poor fiber quality might lead to high numbers of field selections being made in subsequent generations in an attempt to identify better fiber quality, or it may lead to early abandonment and a low number of total selections.

Therefore, it may be informative to compare the performance of F<sub>2</sub> populations to the number of lines these populations ultimately contributed to advanced, replicated testing in the pima pedigree breeding program. Table 6 shows the F<sub>2</sub> yield rankings of 1983 crosses at Maricopa, Safford, and across locations in 2000, and the number of lines from each population that were advanced through pedigree breeding to replicated testing. Population 8312 produced the highest F<sub>2</sub> yields at Maricopa, Safford, and across locations in 2000, and its progeny were identified by pedigree breeding for replicated testing in preliminary, advanced, and regional tests. Population 8305, another population whose progeny were selected for replicated testing by pedigree breeding, exhibited a large F<sub>2</sub> genotype by location interaction for yield. Population 8305 had the second high-

est lint yield at Maricopa, but ranked 14<sup>th</sup> at Safford. Eight lines of population 8309 were selected for preliminary tests through pedigree breeding, two of its lines were advanced to advanced tests, and one line of 8309 was advanced to regional tests, despite its F<sub>2</sub> population being ranked 10<sup>th</sup>, 13<sup>th</sup>, and 12<sup>th</sup> for yield at Maricopa, Safford, and across locations, respectively. Applying a selection intensity of 50% to F<sub>2</sub> yields at Maricopa, populations 8312, 8305, 8311, 8302, 8314, 8303, and 8304 (ranked first through seventh) would be candidates for individual plant selection and further development. Of the above populations, 8311, 8302, 8314, 8303, and 8304 contributed no lines to replicated testing in the pima pedigree breeding program. Applying the same 50% selection intensity to across location F<sub>2</sub> yields, 66% of the lines that were advanced to preliminary tests by pedigree breeding would have been captured, 85% of the lines that were advanced to advanced tests would be captured, and 50% of the lines that were advanced to regional tests would be captured. The correspondence between F<sub>2</sub> yield performance and populations that contributed lines to replicated testing in the pima pedigree breeding program are no better than the correlations between F<sub>2</sub> yield perfor-

**Table 6. Yield rankings of F<sub>2</sub> populations from 1983 crosses at Maricopa, Safford, and across locations in 2000, and the number of lines advanced from each to replicated testing through pedigree breeding**

Cross no.	Yield rank			No. entries advanced to replicated tests		
	Maricopa	Safford	Across Locations	Preliminary	Advanced	Regional
8312	1	1	1	3	3	1
8314	5	2	2	0	0	0
8303	6	4	3	0	0	0
8304	7	5	4	0	0	0
8302	4	12	5	0	0	0
8305	2	14	6	5	3	0
8306	9	6	7	12	5	0
8315	8	8	8	0	0	0
8313	12	7	9	0	0	0
8311	3	9	10	0	0	0
8301	11	11	11	1	0	0
8309	10	13	12	8	2	1
8310	14	3	13	0	0	0
8308	13	15	14	1	0	0
8307	15	10	15	0	0	0

mance and the cumulative pedigree selection numbers of F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> generations.

Somewhat better results were obtained in comparisons between the F<sub>2</sub> population performance of 1984 crosses and the number of lines these populations ultimately contributed to replicated testing in the pima pedigree breeding program. Table 7 shows the correspondence between F<sub>2</sub> performance (considering only F<sub>2</sub> traits that were correlated with cumulative F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> pedigree selection records) and the number of lines advanced to replicated testing from each population. Of the seven 1984 populations that contributed lines to replicated testing in the pedigree breeding program, only three were captured by applying a selection intensity of 50% to F<sub>2</sub> yield, and only two were captured at the 50% level using lint percentage as a criterion. Selecting the upper 50% of F<sub>2</sub> populations for either high fiber strength or low micronaire captured five of the seven 1984 populations that contributed lines to replicated testing in the pedigree breeding program. A selection index that was based upon fiber strength and micronaire produced F<sub>2</sub> rankings similar to fiber strength. One population, 8408, produced F<sub>2</sub> yield,

lint percentage, fiber strength, micronaire, and selection index rankings that indicated it was a good candidate for individual plant selection and development, but it contributed no lines to replicated tests in the pima pedigree-breeding program.

In correlating F<sub>2</sub> performance with pedigree selection records, a major assumption has been made that superior populations receive higher levels of selection. Accepting this assumption, a very poor correspondence was obtained between early generation F<sub>2</sub> performance and cumulative F<sub>2</sub>, F<sub>3</sub>, and F<sub>4</sub> selection records. One also could assume that the net cumulative effect of pedigree selection would be to advance lines from superior populations, but in the present investigation, the correspondence between populations contributing lines to advanced, replicated testing and the F<sub>2</sub> performance of those populations was weak. The poor correspondence between F<sub>2</sub> performance of hybrid populations and the amount of selection practiced within these populations, or the number of lines advanced from these populations contradicts results reported by Barut (1998). Barut reported moderate positive correlations between the performance of early generation

Table 7. Across location rankings of F<sub>2</sub> populations from 1984 crosses for yield, lint percentage, fiber length, fiber strength, and micronaire (mic), and the number of lines advanced from each to replicated testing through pedigree breeding.

Cross no.	Mean ranks				Selection index <sup>z</sup>	No. entries advanced to replicated tests		
	Yield	Lint percentage	Strength (T1)	Mic		Preliminary	Advanced	Regional
8404	10	10	1	14	1	7	6	2
8405	6	8	4	15	2	2	2	1
8415	1	2	3	12	3	2	2	1
8408	4	4	2	7	4	0	0	0
8403	11	11	6	13	5	3	0	0
8402	15	15	5	6	6	1	0	0
8401	7	14	7	11	7	0	0	0
8409	8	6	10	8	8	0	0	0
8414	2	3	11	9	9	9	6	1
8410	14	9	9	3	10	0	0	0
8412	12	7	8	1	11	0	0	0
8411	9	12	15	10	12	1	0	0
8413	5	1	13	5	13	0	0	0
8406	13	13	12	4	14	0	0	0
8407	3	5	14	2	15	0	0	0

<sup>z</sup> The formula for the selection index: strength - (6.84 × micronaire).

cotton populations and their descendant pure lines. Results of the present investigation are similar to those reported in investigations of soybean (Weiss, 1947) and red winter wheat (Fowler and Heyne, 1955), in which early generation bulk tests failed to adequately identify superior crosses. Despite the poor correspondence between early generation F<sub>2</sub> performance and pedigree selection records in the present investigation, no conclusions can be drawn regarding which method has greater efficacy in identifying superior genotypes.

### DISCLAIMER

Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

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