Comparative Efficiency of Three Selection Methods for Yield and Quality of Cotton (Gossypium hirsutum L.)

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ABSTRACT

The comparative efficiency of three selection methods, honeycomb pedigree selection (HC), pedigree selection (PS) and single-seed descent (SSD), was assessed in an F_2 cotton population in two locations. The best five lines derived by each method in each location after five cycles of selection, along with check varieties were tested in comparative experiments in the F_6 generation at both locations. The analysis of variance revealed significant differences for yield and quality within lines and locations but the genotype x location interaction was not significant for any of the traits studied except the mean boll weight. On the basis of the mean yield and the number of superior lines derived by each method as compared to the check varieties, HC lines were superior to PS and SSD lines in seed cotton yield, fiber length and mean boll weight. HC lines, however were not better than the best check cultivar Eva. No significant differences were identified between the material of the three methods in plant height, lint percentage and fiber strength. The lines that originated from the PS method were not significantly different in seed cotton yield from those originating from the SSD method. Finally, the material derived by PS was earlier in maturity than the material derived by HC and SSD.

Introduction

The traditional pedigree selection is widely applied in cotton. Thus, Feaster and Turcotte (1970) suggested that crossing among varieties and strains followed by selection will probably be the most satisfactory breeding method for varietal improvement in cotton. In addition, Culp and Harrell (1973) stated that any breeding method that increases hybridization and recombination is desirable. The same authors concluded that removal of undesirable plants or selections of the most desirable ones in early generations may be equally important in the varietal process. Fasoulas (1988) attributed the low efficiency of the conventional selection procedures for yield to our inability to control soil heterogeneity and plant competition. Thus, he developed the honeycomb method (Fasoulas and Fasoula 1995). Roupakias *et al.* (1997) reported that honeycomb selection was effective in early generation selection of faba beans. Similarly, Gill *et al.* (1995) reported that honeycomb method exhibited superiority over pedigree selection, single seed descent and bulk methods for yield in mungbean. The present study was undertaken to evaluate the comparative effectiveness of honeycomb pedigree selection (HC), the conventional pedigree selection (PS) and single seed descent (SSD) in cotton.

Materials and Methods

The material used was an F_2 which originated from the *G. hirsutum* cross: Pee Dee (an early accession) x

[71414 (PU1) x 71467 (E-AC)]. This cross was the most promising out of eight crosses evaluated by Galanopoulou-Sendouka and Roupakias (1998). Four cycles of selection were applied (1990, 1992, 1993 and 1994) in two locations (A=Sindos and B=Veria) without artificial selfing the selected plants. Individual plants were selected during the first three cycles, while family selection was applied in the fourth cycle.

Honeycomb method (HC). During the spring of 1990, 1160 F_2 seeds were grown in honeycomb arrangement (NR-1) in each of the two locations. The plant-to-plant spacing was 116 cm. Seedcotton was collected and weighed individually for each plant. The selection pressure applied was 5.3% and a plant was selected when it outyielded all the surrounding plants in the moving grid. Selected plants were evaluated for lint quality. The best 10 plants from each location, based on yield and quality, together with the control (Sindos 80), progressed to the next generation in both locations. They were planted in an R-21 honeycomb design. The same procedure was applied for two more cycles.

In the F_5, progeny of the 21 plants (21 families) selected in the F_4 were evaluated at both locations on the basis of the mean yield per plant, the value of combined criterion ($CC = \overline{X}^2 (\overline{X} - S) / S$) (Fasoulas and Fasoula 1995) and the lint quality measured on a sample (mixture of one boll per plant) from each family. Subsequently, the best five families (lines)

were selected from each location. These lines were further evaluated in the F_6 together with the lines selected from the other methods.

The HONEY microcomputer program (Batzios and Roupakias, 1997) was used to select individual plants in each cycle and family evaluation in the F_5.

Conventional Pedigree Selection (PS). During 1990, 1025 F_2 plants were grown in each location in one plots (41 rows), 10m in length, with row-to-row and plant-to-plant spacing of 100 cm and 40 cm respectively. In each location, 3-5 plants per row were visually selected, based on their phenotype during the flowering period. A second phenotypic selection was applied before harvesting. The best 36 plants were selected (18 from each location) based on the yielding ability and the lint quality of the visually selected plants. These were made the progeny rows, at both locations, in the following generation. The same procedure was repeated for two more cycles.

In the F_5 generation at both locations, the lines were evaluated on the basis of their seedcotton yield and the quality traits. Quality was measured in a sample of 30 random bolls collected from each row. Finally, the best 10 rows (5 from each location) having both good yielding ability and good lint quality were selected. These lines were further evaluated in the comparison experiments at both locations.

Single Seed Descent (SSD). Two seeds were collected from each F_2 plant grown in the honeycomb design at each location. The F_3 seeds collected from each location were grown in rows the following year in the same location. The same procedure was applied till the F_5 generation, when one boll was collected from each plant in each of the two locations. Thus, two mixtures of seeds (one per location) were obtained and used in the comparison experiments. These seed mixtures represent the unselected F_6 generation.

Comparison of HC lines (HCL), PS lines (PSL) and SSD lines (SSDL). In 1995 one experiment was conducted in each location to compare the selected HCL, PSL and SSDL with three Greek cultivars (Sindos 80, Eva and Korina). A balanced lattice experimental design was used, each plot consisting of one row, 10m long. Row spacing was 1m and plant distance on the row about 0.07 m. From the 25 lines compared, 10 lines (5 from each location) were derived by the HC method, 10 lines (5 from each location) by the PS, 2 lines were mixtures (one from each location) that originated from the SSD procedure and 3 were the controls.

A randomized blocks design analysis of variance was used since the relative effectiveness of the balanced lattice design was very small (101%). The criteria for comparing the evaluated lines were seedcotton yield, mean maturity date index (MMD) (Christidis and Harrison, 1955), plant height, boll weight and lint quality characters.

Results and Discussion

In the F_6 the mean yield of HC lines was significantly higher than that of PS lines, the unselected SSD populations and the average of the three check cultivars (Table 1). Although none of the 22 lines derived from the three selection methods was superior to the best check cultivar (Eva), nine out of the ten HC lines were not significantly different from this cultivar (Table 2). In contrast, only one out of the ten PS lines was not significantly different from the best check. In addition, six out of the ten HC lines as compared to only one out of the ten PS lines, yielded significantly higher than the unselected SSD population. Similar results have been reported by Gill *et al.* (1995) in mungbean (Vigna radiata L.).

The HC lines also had higher mean boll weight and longer fibers than PS lines, the SSD population or the controls (Tables 1, 2). No differences were identified in plant height, fiber strength (pressley index) and lint percentage among the lines resulting from the three methods and the controls. The PS lines, however, were earlier than the HC lines and the unselected SSD population. No interaction was observed between location and genotype for any character studied, except the mean boll weight. This is probably due to the across site selection applied. If this is the case, then across site selection applied in properly selected sites could produce more stable lines. It is worth mentioning that the ten F_6 HC lines originated from three F_2 plants, while the ten PS lines originated from eight F_2 plants. This, together with the better performance of the HC lines, suggests that HC selection for yield was more effective in the early generations than PS. If this has a wider application, then HC selection is a unique method for early generation selection. Indeed, effective HC early generation has been reported by other workers (Lungu *et al.*, 1987; Roupakias *et al.*, 1997).

In conclusion, in this study, HC pedigree selection was found to be more effective than the conventional PS for deriving superior lines with high seedcotton yield and good lint quality characters.

References

Batzios, D., and D. Roupakias. (1997): HONEY: A microcomputer program for honeycomb designs analysis. Crop Sci. 37:744-747.

Christidis, B.G. and G.J. Harrison. (1955): Cotton Growing Problems. McGraw-Hill Book Co., New York. 633 pp.

Culp, T.W., and D.C. Harrell. (1973): Breeding methods for improving yield and fiber quality of upland cotton. Crop Sci. 13:686-689.

Fasoulas, A. (1988): The honeycomb methodology of plant breeding. Dept. of Genetics and Plant Breeding, Arist. Univ. of Thessaloniki, Greece. Pp.42-49.

Fasoulas, A., and V. Fasoula. (1995): Honeycomb Selection Designs. Plant Breeding Rev. 13:87-139.

Feaster, C.V., and E.L. Turcotte. (1970): Breeding methods for improving Pima cotton and their implications on variety maintenance. Crop Sci. 10:707-709.

Galanopoulou-Sendouca S. and D.G. Roupakias. (1998): Heterosis of cotton F_1 hybrids and its relationship to the mean yield of advanced unselected generations. (Submitted).

Gill, J. S., M.M. Verma, R.K. Gumber, and J.S. Brar. (1995): Comparative efficiency of four selection methods for deriving high-yielding lines in mungbean (*Vigna radiata L.* Wilczek). Theor. Appl. Genet. 90:554-560.

Lungu, D.M., P.J.Kaltsikes and E.N. Larter. (1987): Honeycomb selection for yield in early generations of spring wheat. Euphytica 36:831-839.

Roupakias, D., A. Zesopoulou, S. Kazolea, G. Dalkalitses, A. Mavromatis, and T. Lazaridou. (1997): Effectiveness of early generation selection under two plant densities in faba bean (*Vicia faba L.*). Euphytica 93:63-70.

Table 1. Means of seedcotton yield (Kg/1000 m^2) and qualitative characters of the material derived by three selection methods.

Selection Method	Seedcotton yield	Plant height (cm)	MMD (index)	GOT (%)	Mean Boll wt. (g)	Micro-naire value	Pressley Index	Staple Length (mm)	Unifor-mity
HCL	390 a	99 a	10.3 a	38.2 a	6.5 a	4.11 b	8.08 a	30.3 a	48.8 b
PSL	336 c	96 a	8.0 b	38.5 a	5.7 b	4.31 a	8.01 a	29.7 b	48.8 b
SSDL	331 c	99 a	10.7 a	38.9 a	5.8 b	4.34 a	8.11 a	29.2 c	49.7 a
Checks	360 b	97 a	6.1 c	38.5 a	5.6 b	3.79 c	8.04 a	29.8 b	48.4 b

Means followed by the same letter, do not differ significantly at the 0.05 level (LSD test)

Table 2. Means of agronomic and qualitative characters of the material derived by three selection methods (means of the two locations).

Selected lines	Seedcotton yield kg /1000m²	Plant Height (cm)	MMD Index	GOT (%)	Mean boll wt. (g)	Micro-naire value	Pressley index	Staple length (mm)	Unifor-mity
HCÁ1	411 ab	100 a-c	10.6 a-c	37.6 c-g	6.5 bc	3.99 e-g	8.19 a-d	30.5 a-d	49.1 b-e
HCÁ5	345 c-f	97 a-d	11.3 a	37.5 d-g	6.4 b-d	3.87 f-h	8.20 a-d	30.9 a	48.1 d-g
HCÁ9	360 b-f	97 a-d	9.9 a-e	37.7 c-g	7.1 a	3.98 e-g	8.16 a-e	29.9 a-f	49.7 bc
HCÁ13	396 a-c	103 ab	10.9 ab	38.4 b-g	6.5 bc	4.02 d-g	8.00 a-e	30.6 a-c	48.7 b-g
HCÁ19	367 b-f	101 ab	10.9 ab	38.8 a-g	6.8 ab	4.42 a-c	8.11 a-e	30.3 a-e	48.2 d-g
HCÂ1	413 ab	106 a	11.3 a	37.2 fg	6.2 c-e	4.07 c-g	8.19 a-d	30.9 a	48.7 b-g
HCÂ11	399 a-c	96 a-d	10.3 a-e	39.9 ab	6.4 b-d	4.07 c-g	7.81 de	29.9 a-f	49.3 b-e
HCÂ15	381 a-e	99 a-d	9.5 a-f	38.7 a-g	6.4 b-d	4.37 a-d	8.29 ab	30.1 a-f	48.4 b-g
HCÂ17	434 a	97 a-d	7.8 c-g	37.3 e-g	6.7 ab	3.99 e-g	7.96 b-e	29.8 b-g	49.7 b-d
HCÂ19	396 a-c	99 a-d	10.3 a-e	38.7 a-g	6.5 bc	4.35 a-e	7.91 b-e	30.2 a-f	48.2 d-g
PSÁ2	324 fg	103 ab	10.8 a-c	39.1 a-f	6.1 c-e	4.13 c-g	8.13 a-e	29.9 a-f	48.9 b-f
PSÁ4	410 ab	97 a-d	7.4 e-h	38.7 a-g	5.4 hi	4.55 ab	7.87 b-e	28.4 h	51.2 a
PSÁ23	284 g	87 cd	6.6 f-I	38.4 b-g	5.3 h-j	4.33 a-e	8.28 ab	29.7 c-g	47.6 f-h
PSÁ25	349 c-f	97 a-d	6.9 f-I	39.4 a-e	5.3 h-l	4.34 a-e	7.86 b-e	28.8 gh	49.6 b-d
PSÁ39	323 fg	103 ab	10.5 a-c	37.1 g	6.4 bc	4.68 a	7.72 e	29.6 c-g	49.4 b-e
PSÂ12	328 e-g	86 d	4.8 hi	38.7 a-g	5.0 ij	4.23 b-f	8.12 a-e	29.3 e-h	48.1 e-g
PSÂ13	327 e-g	95 a-d	8.1 b-g	38.7 a-g	5.5 gh	4.20 b-g	8.24 a-c	30.5 a-d	49.0 b-f
PSÂ25	336 d-g	92 b-d	10.6 a-c	37.3 e-g	5.9 e-g	4.38 a-d	7.76 de	29.3 e-h	49.3 b-e
PSÂ27	323 fg	101 ab	6.7 f-I	37.5 d-g	5.9 d-f	4.19 b-g	8.07 a-e	30.8 ab	48.5 b-g
PSÂ28	351 c-f	95 a-d	7.5 d-h	40.1 ab	6.1 c-e	4.09 c-g	8.04 a-e	30.1 a-f	46.5 h
SSDÁ	335 d-g	97 a-d	9.5 a-f	39.1 a-d	5.5 gh	4.24 b-f	7.84 c-e	28.8 gh	49.7 bc
SSDÂ	328 e-g	103 abc	12.0 a	38.4 b-g	6.0 d-f	4.43 a-c	8.38 a	29.5 d-g	48.8 b
Sindos 80	282 g	100 a-c	4.2 I	40.6 a	4.9 j	3.87 f-h	7.93 b-e	29.2 f-h	48.5 b-g
Eva	409 ab	93 a-d	6.4 g-I	35.1 h	6.2 c-e	3.63 h	7.92 b-e	29.9 b-g	47.3 gh
Korina	388 a-d	96 a-d	7.9 b-g	39.7 a-c	5.6 f-h	3.85 gh	8.26 a-c	30.3 a-e	48.3 c-g
CV%	15.8	11.3	35.3	4.4	6.5	7.57	4.40	2.9	2.5

Means followed by the same letter, do not differ significantly at the 0.05 level (Duncan's test)