



# Asian Journal of Plant Sciences

ISSN 1682-3974

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## A Clustering Study on Selection of Parents in Cotton Breeding

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**Abstract:** The genotypes obtained from Gene-Stock Collection of Nazilli Cotton Research Institute were characterized by clustering analysis for fiber properties. Hierarchical clustering was carried out using UPGMA (Unweighted Paired Group Method using Arithmetic Averages) for fiber length, fiber fineness and fiber strength and 10 groups were defined. Cluster B and cluster I contain 5 and 3 genotypes with having considerable values for fiber length and fiber fineness. The cluster B contains Askabat 100, Sealand 542, Giza 45, Delcerro and Ege 69 which had long stable and finest fiber characteristics. Cluster I were Giza 75, Giza 70 and ED 110. Also, it could be defined that Cluster B and I were late maturity and low lint percentage. The choosing of parents from these clusters may be a problem in terms of earliness and lint percentage for long stable cotton breeding.

**Key words:** Long staple cotton breeding, choosing of parent, cluster analysis

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### INTRODUCTION

Genetic variability is required to achieve genetic gains in a breeding program. Estimation of genetic variability among genotypes can be based on qualitative and quantitative traits (Spagnoletti-Zeuli and Qualset, 1987; Souza and Sorrells, 1991; Van Beuningen and Busch, 1997). Also, Esbroeck and Bowman (1998) revealed that breeders rely on genetic variation between parents to create unique gene combinations necessary for new superior cultivars. In cotton breeding, pedigree breeding schemes are followed by most private and public breeders. The number one factor in choosing parents continues to be yield; stability is the number two factor. The majority of parental material for private breeders is from lines developed in-house, while public breeders use a more balanced source of in-house material, commercial cultivars and other public germplasm (Bowman, 2000). The success of the breeding program is largely depended on true selection of parents. Selection of parents for quantitative traits is not as easy as qualitative one and high performing parents may not produce good segregates (Barut *et al.*, 2000).

Extensive use of closely-related cultivars by producers could result in vulnerability is widely recognized, however, there are conflicting views concerning the importance of genetically-distant parents to cultivar improvement. According to quantitative genetic theory, the probability of producing unique genotypes increases in proportion to the number of genes

for which parents differ (genetic distance). However, past success in developing high-yielding cultivars from the mating of closely-related parents has lead some to question the importance of genetically-diverse parents to crop improvement.

Numerous mating schemes are used to develop breeding populations. Line×tester and partial diallele matings can be used to identify parents with high general combining ability for use in future crosses. These parents are obtained from Gene-Stock Collection of Nazilli Cotton Research Institute. A catalogue of material in the collection, including selected seed and fiber properties of many accessions, is available (Cagırgan and Barut, 2000). This material are re-grown during 3-4 growing seasons and sent to Turkey cotton breeders.

The objective of this study was to examined the cotton germplasm for especially long stable cotton breeding in Nazilli Cotton Research Institute.

### MATERIALS AND METHODS

This study was conducted at Nazilli Cotton Research Institute (latitude; 37°44'-37°-49' N and longitude; 27°44'-27°50' E). Eighty-one cotton genotypes of genetic stocks (*Gossypium hirsutum* L. and *Gossypium barbadense* L.) were used as a material (Table 1). The plots were 12 m length and consisted of one each row. The planting norm was 0.7×0.2 m, the density was 71420 plant ha<sup>-1</sup>. Conventional growing practices were applied though growing season for Aegean Region of Turkey.

Table 1: Eighty-one cotton genotypes of genetic stocks (*G. hirsutum* L. and *G. barbadense* L.)

No.	Genotypes	No.	Genotypes	No.	Genotypes	No.	Genotypes
1	153 F	21	DAK 6	41	Mc Namara	61	Siokra 133
2	Acala 151 7/77	22	Delcerro	42	Nazilli 87	62	Siokra 324
3	Acala S.J.1	23	Deltaopal	43	Nazilli 143	63	ST 250/1
4	Acala S.J.2	24	Yellow Fiber	44	Nazilli 84-S	64	Stoneville 453
5	Acala S.J.5	25	DP-388	45	Nazilli 87	65	Stoneville 474
6	Aktas 3	26	DPL 15/21	46	Nazilli M-39	66	Stoneville 506
7	Aleppo-1	27	DPL 50	47	N. M-503 (93-7)	67	Stoneville 69132
8	Askabat 100	28	DPL 5690	48	Nazilli M-503	68	Stoneville 7/A
9	Auburn	29	DPL 90	49	Okra 201	69	Stoneville 731/N
10	Beliizvor 432	30	ED 110	50	Okra 204	70	Stoneville 825
11	Blightmaster	31	Ege 69	51	Paymaster 404	71	Stoneville 907
12	Bulgaria C 3996	32	Ersan 92	52	Sahel 1	72	Tabladilla 16
13	CABU'CS 2-1-83	33	Giza 45	53	Sayar 314	73	Tamcot CABCS
14	Carmen	34	Giza 70	54	Sealand 542	74	Tamcot CD3H
15	Carolina Queen	35	Giza 75	55	SG 125	75	Tamcot HQ95
16	Chirpan 603	36	Glandless 86	56	SG 404	76	Tamcot SP21-E
17	Coker 100 A/2	37	Dark Yellow	57	SG 501	77	Tamcot SP37-H
18	Coker 310	38	Lankart 57	58	Sicala 33	78	Tashkent 1
19	Cukurova 1518	39	Maras 92	59	Siokra 1/4	79	Veret
20	Cun S2	40	Mc Nair 235	60	Siokra 107-B	80	Vulcano
						81	Green fiber

Genotypes in genetic stocks were evaluated from the point of plant height (PH;cm), first picking percentage (FPP; %), Number of Days Boll Opening (NDBO; day), Boll Opening Degree Days (BODD), Boll Weight (BW; g), seed index (SI; g) and lint percentage (LP; %), fiber length (mm), fiber fineness (mic) and fiber strength (g/tex). Hierarchical clustering was carried out using UPGMA (Unweighted Paired Group Method using Arithmetic Averages) for fiber length, fiber fineness and fiber strength which was recommended when the different size of groups and number of characters were used (Rincon *et al.*, 1996).

## RESULTS AND DISCUSSION

The cotton quality parameters, fiber length, fiber fineness and fiber strength concerning genotypes were used to compute a dendrogram showing Euclidian distance in order to define relationships among the genotypes. Ten groups were defined by cluster analysis and distribution of fiber length and fiber fineness of cluster groups were presented in Cluster B and I contain 5 and 3 genotypes with having considerable values for fiber length and fiber fineness, respectively. In the cluster B, 8 (Askabat 100; *G. barbadense* L.), 54 (Sealand 542; *G. hirsutum* L.), 33 (Giza 45; *G. barbadense* L.), 22 (Delcerro; *G. arboreum* × *G. thurberi* × *G. hirsutum* L.), 31 (Ege 69; *G. hirsutum* L.) had long stable and finest fiber characteristics. Cluster I were 35 (Giza 75; *G. barbadense* L.), 34 (Giza 70; *G. barbadense* L.) and 30 (ED 110; *G. hirsutum* L.). The pedigrees of Ege 69 and ED 110 are 2421-A Russian × Sealand 542 and Ege 69 × Delcerro, respectively. Otherwise, when the mean and standard

errors of genotype characteristics were evaluated in Table 2, FPP, NDBO and BODD of Cluster B were 45.48±24.62%, 124.00±7.78 days and 1372.40±67.57 growing degree-days, respectively. These values for Cluster I were 29.17±27.23%, 132.33±12.42 days and 1439.33±106.04 growing degree-days, respectively. It could be defined that Cluster B and I had high plant height and seed index, late maturity and low lint percentage. The choosing of parents from these clusters may be a problem in terms of earliness and lint percentage for long stable cotton breeding.

Cluster J, H, F, G, E and D, total 65 genotypes, were in range of stable length for upland cotton (from 28.0 mm to 32.00 mm). Also, there were three different groups for fiber fineness. Fiber fineness values of first, second and third groups ranged from 3.0 to 3.8 mic, 3.8-4.7 mic and 4.7-5.5 mic., respectively (Fig. 1). H group (Carmen, DPL 5690 and Sicala 33) had the longest fiber length in these groups, while these genotypes considerate with late maturity characteristics. Cluster D include Stoneville's cultivars (Stoneville 453 for South Eastern Anatolia Region's standard cultivar); Nazilli 84-S, Nazilli 87 and Nazilli 143 (cultivars improved by Nazilli Cotton Research Institute and standard cultivars for Aegean Region; Sayar 314 (standard cultivar for Cukurova Region); Dp 388 and DAK 6 with having thicker fiber, higher lint percentage and the highest seed index.

Green fiber (81), 153 F (1) and Okra 201 (49) were in Cluster A and this group had short and finest fiber. Also, this cluster could be defined as late maturity and lower boll weight. Cluster C include Aleppo 1 (Syria origin) and Dark Yellow Fiber and had short and coarse fibers. Also, Mc Namara (41; Red Leaf) and Yellow fiber (24) genotypes showed similar characteristics.

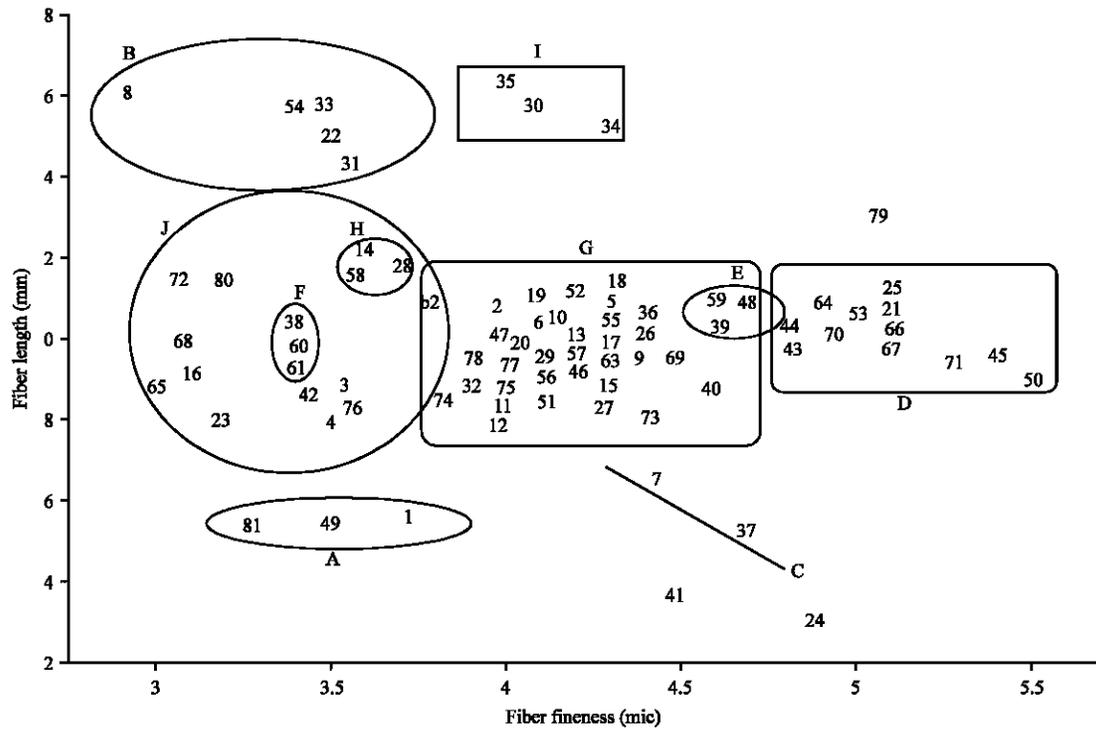


Fig. 1: Clusters include different numbers of genotypes

Table 2: Mean±SE of genotype characters of cluster groups

Cluster	PH (cm)	FPP (%)	NDBO (day)	BODD (°C)	BW (g)	SI (g)	LP (%)
A	118.33±7.64	40.17±11.81	124.33±18.01	1368.33±159.58	4.80±1.08	10.60±0.70	32.17±9.58
B	117.40±19.28	45.48±24.62	124.00±7.78	1372.40±67.57	5.18±1.61	11.64±2.43	33.90±2.07
C	107.50±24.75	61.25±21.00	120.00±7.07	1337.50±67.18	5.80±1.84	11.00±0.99	37.35±0.64
D	103.42±17.59	46.48±14.92	118.33±7.32	1317.92±65.43	5.94±0.96	12.03±1.03	41.18±1.48
E	143.33±23.25	55.60±5.72	122.67±5.69	1360.00±50.76	6.37±0.32	11.30±1.51	40.70±2.26
F	94.00±24.25	46.53±6.39	122.67±2.31	1363.33±21.94	5.60±1.68	10.10±1.65	37.83±3.23
G	101.65±17.35	57.06±18.61	117.65±7.86	1307.97±84.75	6.06±0.66	10.99±1.16	39.71±1.79
H	118.33±10.21	32.87±8.55	122.67±7.02	1360.00±63.55	5.20±0.80	9.00±0.89	41.27±1.75
I	143.00±52.03	29.17±27.23	132.33±12.42	1439.33±106.04	4.57±1.59	11.90±0.66	33.47±1.89
J	105.70±19.94	56.21±23.89	115.40±10.24	1278.00±120.39	5.79±0.71	9.67±1.09	38.83±1.86
Deve Tüyü	90	48.5	117	1307	4.7	8.1	33
Mc Namara	120	9.5	130	1425	3.5	8.5	23.5
Veret	95	32.7	120	1338	6.6	13.9	38.9

PH; Plant Height, FPP; First Picking Percentage, NDBO; Day Number of Days Boll Opening, BODD; Boll Opening Degree Days, BW; Boll Weight, SI; Seed Index, LP; Lint Percentage

The NDBO and BODD values of Carmen (14; Cluster H) and Nazilli 84 S (44; Cluster D), Aegean Region standard cotton cultivars, were 130; 1425 and 119; 1327. The first factor in choosing parents continues to be yield; stability is the second factor (Esbroeck and Bowman, 1998). According to same authors, adapted cultivars have been intercrossed to such extent that a cross involving distantly-related parents requires the use of un-adapted germplasm. Unay *et al.* (2003) and Sezener *et al.* (2006) revealed that Nazilli 84 S was the most stable variety for lint yield, while Carmen was group

of the mid-adaptation to all environments. In the long staple cotton breeding, the genotypes in Cluster B and I should be crossed to Aegean Region standard cotton cultivars, Nazilli 84 S and Carmen. In the cluster B I, Askabat 100, Giza 45, Giza 75 and Giza 70 belong to *Gossypium barbadense* L. The probable *barbadense*×*hirsutum* crosses could contain a large number of undesirable genes or gene combinations especially for maturity or earliness. Therefore, long staple cotton breeding programs should contain upland genotypes such as Sealand 542, Delcerro and Ege 69.

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