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GENETIC DIVERSITY AMONG UPLAND COTTON GENOTYPES FOR DIFFERENT ECONOMIC TRAITS AND RESPONSE TO COTTON LEAF CURL VIRUS (CLCV) DISEASE

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Abstract

Genetic diversity was studied among 13 locally developed elite cotton genotypes and two exotic lines using metroglyph analysis. Different morphological, yield and yield contributing traits and intensity of cotton leaf curl virus disease were recorded. Index scores were allotted to each character of the fifteen cotton genotypes, which indicated the worth of the genotype regarding the character. The performance of genotypes was indicated by total index scores of genotype, which was the sum of the index values with regards to all the characters. Metroglyph scatter diagram indicated the possible occurrence of 6 groups of cotton genotypes. On the basis of this grouping it was concluded that hybridization between genotypes of different groups instead of between genotypes belonging to the same group may be expected to give better cotton recombinants for different economic traits and resistance/tolerance to cotton leaf curl virus disease. The genotypes FH-1000, CIM-443, NIBGE-3, NIBGE-115, NIBGE-160 and NIBGE-253 formed distinct groups and had better tolerance to CLCV. The information generated hence may be utilized for hybridization between distinct genotypes for the creation of genetic variability in cotton.

Introduction

Cotton is the most widely cultivated crop in the world and has attained the main focus of research because cultivars from upland cotton (*Gossypium hirsutum* L.) species meet 90% of the bulk world's cotton demand (Wendel *et al*., 1992). It is also the most significant agricultural commodity in Pakistan that sustains the economy through foreign exchange and employment. Cotton producers in Pakistan are currently faced with rising production costs and static return because of epidemic spread of diseases and heavy losses from cotton pests (Haidar *et al*., 2007). Cotton leaf curl virus (CLCV) disease has emerged as a major disease of cotton in the country. At present genetic diversity for CLCV is very little, creating a continuous threat to cotton productivity in the country. Along with the diversity for CLCV, different morphological traits and yield components also affect the incidence of disease and pests are also very important (Iftikhar *et al.*, 2010).

Maintaining genetic diversity offers a measure of protection against widespread losses from diseases and pests and facilitates the creation of segregating populations (Van Esbroeck *et al*., 1999). Since independence of Pakistan genetic improvement of cotton has led to the evolution of large number of cotton varieties with improved productivity by using both indigenous and exotic germplasm. At present all the breeding material and released varieties are susceptible to CLCV-Burewala strain and scientists are in search of resistant sources to develop the resistant or highly tolerant germplasm. Extensive use of closely related cultivars/genotypes in cotton breeding has resulted in narrowing the genetic base. Therefore, the choice of parents is the most important decision in future cotton breeding programs (Van Esbroeck & Bowman, 1998) and interest in genetic heterogeneity is helpful to limit pests or disease vulnerability. It also provides an ample supply of allelic variation that can be used to create new favorable gene combinations (Rana1 *et al*., 2005).

Punitha & Raveendran (2000) estimated the variability in colored linted cotton (*Gossypium hirsutum* L.) genotypes through metroglyph technique and identified four district groups which showed wide variability for different characters. Likewise, Singh *et al*., (1990) studied the variability and genetic diversity in genetic resources of *Gossypium arboreum* using metroglyph technique. Out of 150 accessions they identified 15 distinct groups for economic and morphological characters. Classificatory techniques were also used to quantify the genetic divergence in a given population of different crops like mungbean (Abbas *et al*., 2010, Sharma *et al*., 1996; Bish *et al*., 1998), rice (Ibrahim *et al*., 1990; Sinha *et al*., 1991; Kharbuli *et al*., 1992; Mahapatra *et al*., 1995; Bharadwaj *et al*., 2001; Cheema *et al*., 2004, Rashid *et al*., 2007), lentil (Asghar *et al*., 2010) and in pigeon pea (Roy & Sharma, 1994). The present study was planned to analyze cotton genotypes by classificatory analysis using Metroglyph technique. The objective of the present investigation was to study the genetic diversity for different economic traits along with CLCV in the available elite cotton genotypes/varieties to develop better recombinants. This would be helpful in choosing suitable genotypes for cotton breeding programs.

Materials and Methods

Thirteen local genotypes *viz*., FH-1000, H-15, CIM-443, CIM-240, MNH-609, MNH-149, MNH-93, NIAB-824, NIAB-884, NIBGE-3, NIBGE-115, NIBGE-160, NIBGE-253, and two exotic lines *i.e.*, Cedix and CP-15/2 (Table 3) were grown at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad during 2007 and 2008. The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each plot consisted of 2 rows of 16m length with plant x row distance of 30 x 75 cm. Standard agronomic practices and plant protection measures were followed. The data were recorded on morphological, yield and yield contributing characters *viz*., cotton leaf curl virus (CLCV) disease score on September 15, CLCV score on 1st week of December, plant height (cm), hairiness (grade), nectries/leaf, monpodial branches/plant, sympodial branches/plant, bolls/plant, boll weight(g) and seed cotton yield/plant. Five plants in each replication were used for recording all the morphological and yield traits.

Plants were classified as resistant and susceptible according to the virus symptoms following the disease rating scale of Akhtar *et al*., (2004). Plant height (cm) was recorded by taking the length of main stem from surface of soil of the plant of the five randomly selected plants in each replication and mean was calculated.

Hairiness was recorded according to the ratting system as described by Bourland *et al*., (2003). Primary grades of this rating system are as follows: 1 (glabrous), 3 (lightly hairy), 5 (moderately hairy), 7 (very hairy), and 9 (pilose). Intermediate grades i.e., 2, 4, 6, and 8, may be assigned if a plant does not appear to fit one of the primary grades. Nectries were noted according to the procedure developed in the form of scale by Stanton *et al*., (1994, Jiang *et al*., (2000), Bourland *et al*., (2003) and Rayburn (1986).

Bolls/plant was counted and cumulative data was maintained for each plant separately and average of plants was recorded in each replication and for each genotype. Average weight per boll (g) was obtained by dividing total weight of yield of seed cotton per plant by number of bolls picked from the same plant. Seed cotton from all the matured bolls was also picked separately from all the plants. The seed cotton was then weighed and the average of seed cotton yield per plant was recorded.

Means for all the characters were used for the analysis of variance following the procedure described by Steel *et al*., (1997). Clustering was done according to Metroglyph analysis proposed by Anderson (1957) and Singh & Chaudhary (1985). The means over replications of the characters were used for this purpose. Two most variable characters which exhibited highest variance (highly significant values of F-calculated) were selected and plotted on X-axis and Y-axis using the values of each genotype. The grouping of the genotypes was carried out on the basis of sum of index scores of all the genotypes in a particular group.

Results and Discussion

All the genotypes showed significant differences for all the characters under study (Table 2). Minimum CLCV score at early stage (September 15) was recorded for NIBGE-253(0.53), NIBGE-3 (0.63) and NIBGE-115 (0.90) and the highest disease score was recorded for Cedix (4.67). Minimum CLCV score at late stage (1st week of December) was recorded for MNH-149 (0.67) and NIBGE-3 (0.78) and the highest disease score was recorded for MNH-93 (3.60). The intensity of CLCV decreased at late stage as compared to early stage in case of FH-1000, H-15, MNH-609, MNH-149, Cedix and CP-15/2**,** whereas intensity of CLCV was increased at later stage as compared to early stage in case of CIM-443, CIM-240, MNH-93, NIAB-824, NIAB-884, NIBGE-3, NIBGE-115, NIBGE-160 and NIBGE-253 (Table 3).

Maximum height was attained by the varieties MNH-149 (154 cm) followed by H-15 (151 cm). Maximum hairiness grade of 5 was scored by NIBGE-3 and NIBGE-115. Highest number of active nectaries/leaf was recorded for Cedix (3) and FH-1000 (2.8). Highest number of monpodial branches per plant was recorded for NIBGE-253 (7.1) and NIBGE-160 (5.1) and sympodial branches per plant was recorded for NIAB-884 (23.7) followed by FH-1000 (21.2) and MNH-149 (21.2). Maximum number of bolls/plant was recorded for MNH-149 (66) followed by FH-1000 (60), whereas maximum boll weight (gm) was produced by NIBGE-160 (4.40) and NIBGE-253 (4.20), respectively.

Maximum seed cotton yield was produced by genotypes FH-1000 (226 g/plant) and MNH-609 (215 g/plant) but these genotypes showed decrease in CLCV intensity at later stage followed by NIBGE-3 (190 g/plant) and NIBGE-253 (189g/plant) which showed lowest CLCV intensity at early stage (Table 2).

According to Anderson' s Metroglyph technique, the index score was allotted to each character of the 15 cotton genotype, which indicated the worth of the genotype regarding the character (Table 1 & Table 5). Two most variable characters i.e., seed cotton yield and plant height were selected and plotted on x-axis and y-axis using the values of each genotype (Fig. 1). Besides the two characters, which were taken on X-axis and Y-axis, all the other characters were represented by rays/arrows on the glyph. Each ray/arrow represents a particular character and it has categorized each character into three classes as low, medium or high. The genotypes that fall in various classes have been shown in Table 4. The length of ray assigned to the characters depends upon the index scores of genotypes for that character (1 for low value, 2 for medium and 3 for highest value). The performance of a genotype was indicated by its total index scores, which was the sum of index values with regards to all the characters.

Table 1. Group number, index scores and cotton genotypes included in each group following Metroglyph technique.

Group number	Genotypes numbers	Genotypes	Group index scores
I	4, 6, 10, 13	CIM-240, MNH-149, NIBGE-3, NIBGE-253	83
II	3, 7, 8, 12	CIM-443, MNH-93, NIAB-824, NIBGE-160	80
III	2,11, 15	H-15, NIBGE-115, CP-15/2	54
IV	1, 5	FH-1000, MNH-609	45
V	9	NIAB-884	18
VI	14	Cedix	17

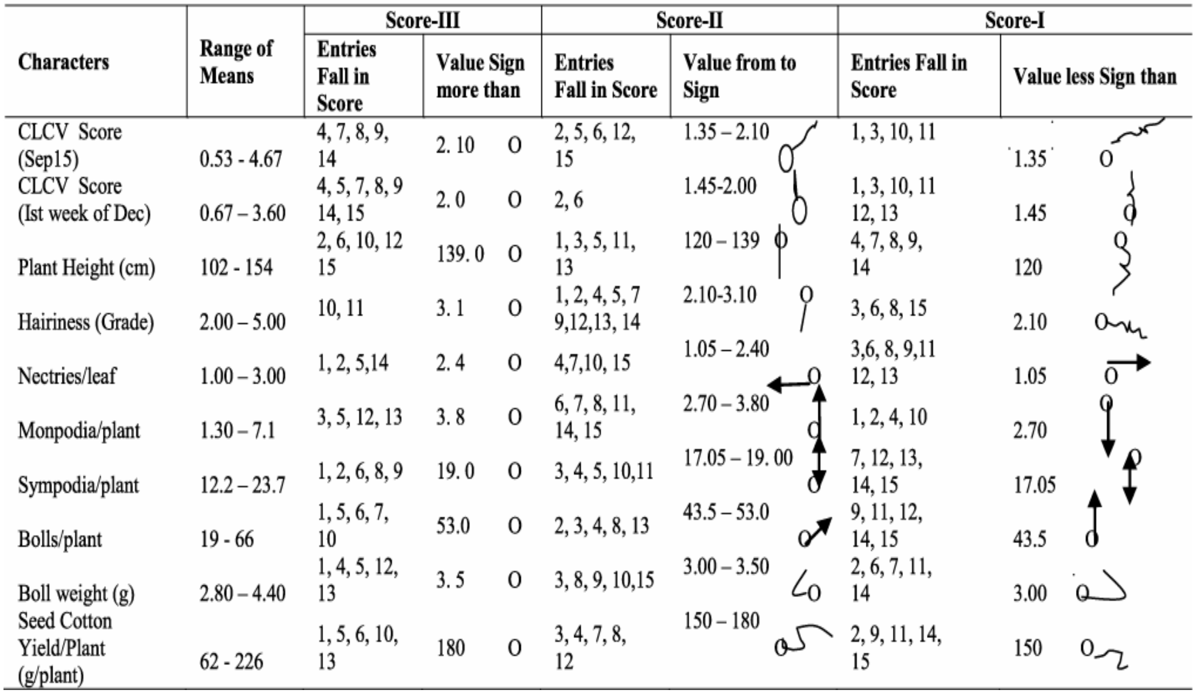
Table 2. Mean squares for different traits among fifteen cotton genotypes.

SOV	df	CLCV (Sep15)	CLCV (Dec 1^{st}week)	Height (cm)	Hairiness (Grade)	Nectries/ Leaf	Monopod /Plant	Sympod. /plant	Bolls/ plant	Boll weight (g)	Yield/plant (g/plant)
Replication	2	0.15	0.22	193.22	0.07	2.24	0.54	3.97	154.36	3.35	2519.56
Genotypes	14	3.15^{**}	2.03^{**}	814.35^{**}	2.61^{**}	1.91^{**}	6.34^{**}	24.56^{**}	399.96^{**}	0.79^{**}	5991.84^{**}
Error	28	0.35	0.60	101.29	0.08	0.10	0.60	5.18	86.03	0.07	1982.58

Table 3. Mean phenotypic values of characters contributing to genetic divergence in fifteen indigenous and exotic genotypes of cotton (*G. hirsutum* L.)

S. No.	Variety/ Line	Institute/ Origin	CLCV (Sep15)	CLCV(Dec 1^{st}week)	Height (cm)	Hairiness (Grade)	Nectries/ Leaf	Monopod /Plant	Sympod. /plant	Bolls/ plant	Boll weight (g)	Yield/ Plant (g/pl)
1.	FH-1000	AARI, Fsd.	1.33	1.22	129	3	2.8	1.9	21.2	60	3.64	226
2.	H-15	UAF, Fsd	1.53	1.50	151	3	2.6	2.4	20.8	52	2.80	149
3.	CIM-443	CCRI, Mul.	1.23	1.44	133	2	1.0	3.9	18.3	47	3.44	165
4.	CIM-240	//	2.20	2.47	109	3	2.3	1.3	18.6	44	3.98	180
5.	MNH-609	CRS, Mul.	2.00	1.89	134	3	2.5	4.2	18.4	59	3.60	215
6.	MNH-149	//	1.60	0.67	154	2	1.0	3.4	21.2	66	2.80	185
7.	MNH-93	//	2.73	3.60	118	3	1.7	3.7	16.9	54	2.89	156
8.	NIAB-824	NIAB, Fsd	2.17	2.67	108	2	1.0	3.5	20.3	47	3.11	163
9.	NIAB-884	//	2.60	3.00	107	3	1.0	1.6	23.7	39	3.23	143
10.	NIBGE-3	NIBGE, Fsd	0.63	0.78	140	5	2.3	2.6	18.4	55	3.37	190
11.	NIBGE-115	//	0.90	1.83	136	5	1.0	3.1	17.1	43	2.92	130
12.	NIBGE-160	//	1.40	1.63	140	3	1.0	5.1	17.0	36	4.40	160
13.	NIBGE-253	//	0.53	1.25	126	3	1.0	7.1	14.4	44	4.20	189
14.	Cedix	Exotic	4.67	2.50	102	3	3.0	3.7	12.2	19	2.92	062
15.	CP-15/2	//	2.03	1.92	143	2	2.3	3.6	17.0	40	3.14	138

Table 4. Range of means and index scores for different quantitative traits of fifteen cotton genotypes.



Characters	Range of Means	Score-III		Score-II		Score-I	
		Entries Fall in Score	Value Sign more than	Entries Fall in Score	Value from to Sign	Entries Fall in Score	Value less Sign than
CLCV Score (Sep15)	0.53 - 4.67	4, 7, 8, 9, 14	2. 10 O	2, 5, 6, 12, 15	1.35 – 2.10 O	1, 3, 10, 11	1.35 O
CLCV Score (Ist week of Dec)	0.67 – 3.60	4, 5, 7, 8, 9 14, 15	2. 0 O	2, 6	1.45-2.00 O	1, 3, 10, 11 12, 13	1.45 O
Plant Height (cm)	102 - 154	2, 6, 10, 12 15	139. 0 O	1, 3, 5, 11, 13	120 – 139 O	4, 7, 8, 9, 14	120 O
Hairiness (Grade)	2.00 – 5.00	10, 11	3. 1 O	1, 2, 4, 5, 7 9,12,13, 14	2.10-3.10 O	3, 6, 8, 15	2.10 O
Nectries/leaf	1.00 – 3.00	1, 2, 5,14	2. 4 O	4,7,10, 15	1.05 – 2.40 ←O	3,6, 8, 9,11 12, 13	1.05 O→
Monpodia/plant	1.30 – 7.1	3, 5, 12, 13	3. 8 O	6, 7, 8, 11, 14, 15	2.70 – 3.80 O↑	1, 2, 4, 10	2.70 O↓
Sympodia/plant	12.2 – 23.7	1, 2, 6, 8, 9	19. 0 O	3, 4, 5, 10,11	17.05 – 19. 00 ↕O	7, 12, 13, 14, 15	17.05 ↕O
Bolls/plant	19 - 66	1, 5, 6, 7, 10	53.0 O	2, 3, 4, 8, 13	43.5 – 53.0 O↗	9, 11, 12, 14, 15	43.5 ↑O
Boll weight (g)	2.80 – 4.40	1, 4, 5, 12, 13	3. 5 O	3, 8, 9, 10,15	3.00 – 3.50 O	2, 6, 7, 11, 14	3.00 O
Seed Cotton Yield/Plant (g/plant)	62 - 226	1, 5, 6, 10, 13	180 O	3, 4, 7, 8, 12	150 – 180 O	2, 9, 11, 14, 15	150 O

Table 5. Score of the ten quantitative traits of fifteen cotton genotypes.

Variety/Line	CLCV (Sep15)	CLCV (Dec 1st week)	Height (cm)	Hairiness (Grade)	Nectries/ Leaf	Monopodia /Plant	Sympodia /plant	Bolls/ plant	Boll weight (g)	Yield/Plant (g/pl)	Total
FH-1000	1	1	2	2	2	1	3	3	3	3	21
H-15	2	2	3	2	2	1	3	3	1	1	20
CIM-443	1	1	2	1	1	3	2	2	2	2	17
CIM-240	3	3	1	2	2	1	2	2	3	2	21
MNH-609	2	2	2	2	2	3	2	3	3	3	24
MNH-149	2	1	3	1	2	2	3	3	1	3	21
MNH-93	3	3	1	2	2	2	1	3	1	2	20
NIAB-824	3	3	1	1	1	2	3	2	2	2	20
NIAB-884	3	3	1	2	1	1	3	1	2	1	18
NIBGE-3	1	1	3	3	2	1	2	3	2	3	21
NIBGE-115	1	2	2	3	1	2	2	1	1	1	16
NIBGE-160	2	2	3	2	1	3	1	1	3	2	20
NIBGE-253	1	1	2	2	1	3	1	2	3	3	19
Cedix	3	3	1	2	2	2	1	1	1	1	17
CP-15/2	2	2	3	2	2	2	1	1	2	1	18

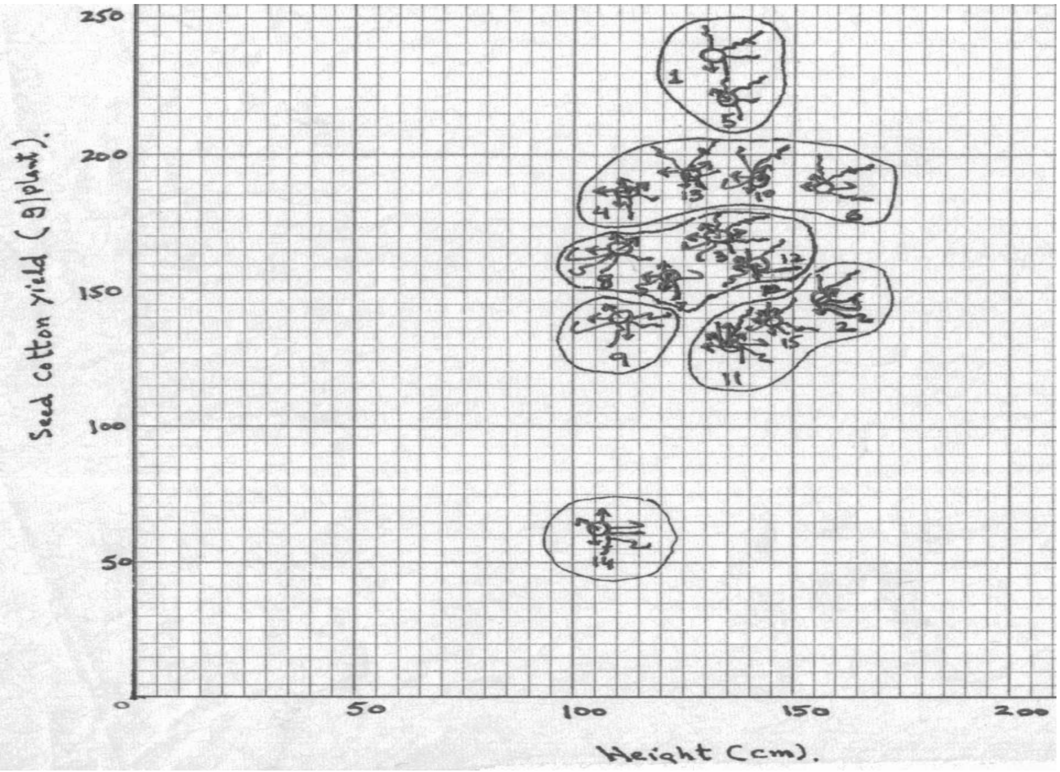


Fig. 1. Metroglyph scatter diagram showing six groups of cotton genotypes.

Cotton genotypes used in this study formed 6 groups (Fig. 1) on the basis of relative dispositioning of genotypes on the graph. These groups were numbered on the basis of net index scores of the group in ascending order. Among genotypes (Table 1) number 4, 6, 10 and 13 (CIM-240 MNH-149, NIBGE-3, NIBGE-253) had the highest index score of 83 as total and formed the Group-I. Similarly, genotype number 3, 7, 8 and 12 (CIM-443, MNH-93, NIAB-824 and NIBGE-160) with total score index of 80 were designated as Group-II. Genotypes number 2, 11 and 15 formed Group- III (H-15, NIBGE-115, CP-15/2) and genotypes 1 and 5 formed the Group-IV (FH-1000, MNH-609), respectively. Genotype number 9 (NIAN-884) and 14 (Cedix) formed the Group- V, and VI, respectively. Group-I and Group-II included 4 genotypes each, likewise Group-III and IV included 3 and 2 genotypes, respectively. Group-V and Group-VI included one genotype each. The results suggested that the metroglyph analysis would be suitable for grouping the genotypes as reported by Chandra (1977). This information can be used in the future hybrid-breeding programme for the improvement of cotton. Hybridization between Group-I and Group-II is expected to give better types. The group with lowest index score (17) was Group-6 which included a single genotype (Cedix) which indicates the presence of genetic diversity in cotton genotypes. The genotypes of the same group had little divergence from each other as compared to the genotypes among different groups. Hybridization between the genotypes of the same group may not provide good segregants. Crosses may be attempted between the genotypes of different groups with high index scores which can give desirable segregants. Similarly, if one is interested in improving a character, which is undesirable or otherwise weak in a genotype, this information might be helpful in identifying the cross/crosses that could be used to obtain the desired results. Singh *et al*., (1990**)** also found the suitability of the technique for preliminary classification of a large number of germplasm and classifying them into distinct groups. Bish *et al*., (1998) demonstrated the patterns of variation at the population level in mungbean and elaborated that this type of analysis was useful in identifying a group of accessions with yield enhancing traits within a highly diverse group of accessions and suggested their potential value in mungbean improvement. Similar findings were given by Ibrahim *et al*., (1990) and Bharadwaj *et al*., 2001in rice.

Conclusion

The suitability of the technique for preliminary classification into distinct groups for qualitative and quantitative characters in cotton was found effective. The genotypes FH-1000, CIM-443, NIBGE-3, NIBGE-115, NIBGE-160 and NIBGE-253 fall in the distinct groups and have shown better tolerance to CLCV. NIBGE-3 and NIBGE-115 also have better hairiness grade. NIAB-884 has very desirable combination of number of monopodial/sympodial branches and also falls in the distinct group. FH-1000 and MNH-609 has shown maximum seed cotton yield per plant and also falls in one distinct group. The information obtained will be utilized for hybridization between the distinct/elite genotypes in diallel fashion followed by induced mutations for creation of genetic variability in cotton.

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