

NATURE OF GENETIC DIVERGENCE AMONG SOME COTTON GENOTYPES

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Genetic divergence is the basis for any crop improvement programme. The knowledge of genetic variation existing in the germplasm is an important and essential aspect for initiating any crop breeding programme because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related parents.

Classificatory techniques are being used to quantify the genetic divergence in a given population of cotton using cluster analysis to select some promising plants (Abd El-Baky 2006; Abd El-Sayyed *et al.*, 2006). As such a quantification of the degree of divergence would be of help in choosing suitable genotypes for on-going cotton breeding programme.

Metroglyph analysis is a simple technique used for preliminary grouping of accessions. With the help of this technique, breeders can easily predict genotypes which have high index scores and can fall into different clusters to be crossed giving maximum variability of good combinations of characters. Khan *et al.* (2007) found that metroglyph analysis and index score were a useful tool to assess genetic variability among cotton population. Likewise, Haidar *et al.* (2012) used metroglyph analysis to classify thirteen locally developed elite cotton geno-

types and two exotic lines (*Gossypium hirsutum* L.) into six clusters for some qualitative and quantitative characters.

Mahalanobis's D^2 statistic provides a quantitative method to determine the divergence among the biological populations and has been applied successfully in plant species. Parresuman and Patil (2014) grouped 86 intra-*hirsutum* lines for 15 yield attributes and quality characters into nine clusters, using Mahalanobis D^2 statistic to measure the genetic divergence. The inter cluster distances were found to be greater than intra cluster distances, revealing considerable amount of genetic diversity among the studied genotypes.

The present study was planned to analyze twenty cotton genotypes using Mahalanobis D^2 technique to estimate the dissimilarity coefficients and metroglyph analysis to classify cotton genotypes into different clusters, to develop better recombinants between groups and helping in choosing suitable genotypes for cotton breeding programs.

MATERIALS AND METHODS

The present investigation consisted of the selfed seeds of twenty cotton genotypes belonging to *Gossypium barbadense* L. Origin and pedigree of these genotypes

are shown in Table (1). These genotypes were raised in a completely randomized block design with three replications during the growing seasons 2012 and 2013 at Sakha Experimental Station, Kafr El-Sheikh, Agricultural Research Center, Egypt. Each genotype was sown in two rows of 7 m length spaced at 70 cm between rows and plants. All other normal agronomic practices were followed for growing the cotton crop.

At maturity, ten randomly cotton plants were selected for studying four yield parameters, boll weight (BW) in grams, seed cotton yield per plant (SCY) in grams lint yield per plant (LY) in grams and lint percentage (L%). Also, three fiber quality characters were tested at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt; fiber length (FL) as span length at 2.5% by the digital fibrograph, fiber fineness (FF) as a micronaire value and fiber strength (FS) as pressley index.

Data were subjected to the analysis of variance (Steel *et al.*, 1997), followed by genetic divergence was estimated by Mahalanobis D^2 statistic as described by Rao (1952). While, the D^2 distance for inter and intra cluster between different groups using Toucher's method as outlined by Rao (1952). The contribution of each character to total genetic divergence for the number of times that appeared first in ranking was calculated according to Singh and Chaudhary (1979).

Metroglyph analysis using the index score method was also applied (Anderson, 1957). A scatter diagram was plotted taking the most two variable characters, viz., seed cotton yield as ordinate (X axis) and lint percentage as abscissa (Y axis). All the other characters were represented as rays at different positions on the glyph. Each ray was represented for a particular character obtained by dividing the range of variation into three equal classes giving the grades low, medium and high for each character. The length of ray assigned to the characters was depended upon the index scores of genotype for that character (1 for low value, 2 for medium and 3 for the highest value). The glyph positions and rays were used to assess the variability pattern and correlated traits for assessment of their divergent groups. Each genotype had a special number and is represented as a glyph which is the intersection point of mean values of X and Y coordinates as described by Chandra (1977). The index values and the position of rays and arrows for the different characters are given in Table (2). The number to each cluster was allotted on the basis of net index score of the cluster in ascending order.

RESULTS AND DISCUSSION

Mean values of the studied quantitative characters among twenty cotton genotypes are shown in Table (3). The analysis of variance using quantitative characters revealed that mean squares due to genotypes were highly significant for all the studied characters indicating exist-

ence of considerable genetic divergence among these genotypes, which reflecting the genetic diverse back ground, and exhibiting their different geographical origin and pedigree (Table 4).

Among the genotypes, genotype Giza 86 x 10229 (G5) had the highest index score for all individual characters except fiber length and fiber strength which scored (2) for these characters (Table 3). These results appear that the genotypes having high index scores may be crossed with those having minimum index scores to give maximum variability for good combinations of characters. These informations seemed to be useful for the breeders interested in creating desired level of variability for a specific engineering the crosses.

The genetic divergence was estimated by Mahalanobis D^2 statistic to calculate the genetic dissimilarity coefficients among these cotton genotypes. D^2 values ranged from 3.263 to 190.89, corresponding to all possible combinations among twenty cotton genotypes taking two genotypes at a time. These estimates were treated as Chi-square values, which showed that most of the all dissimilarity coefficients were significant or highly significant as described by Singh and Chaudhary (1979). The genetic dissimilarity coefficient, the highest between Giza 90 (G6) and Pima high yield (G17) while, the lowest among Giza 70 (G10) and Giza 88 (G12) (Table 5). These results reflect that high D^2 value was due to genetic dis-

similarity, while low D^2 values reflect genetic similarity among genotypes.

The contribution degree of each character towards total genetic divergence among all combinations between the twenty cotton genotypes was counted for the number of times it appeared first in ranking (Fig. 1 and Table 6). This was used as a criterion for the contribution of each character to the total genetic divergence. The major contribution to the total genetic divergence showed that seed cotton yield had the highest contribution 64.211% followed by fiber strength (19.474%), accounting for about 83% of total genetic divergence. It was due to genetic dissimilarity among the genotypes for these characters.

Lint percentage and fiber length were very negligible (0.526%) to the total genetic divergence; this might be due to genetic similarity among the genotypes for these characters. These results showed that to select genetically diverse genotypes for hybridization, the material should be screened for important traits, while, the rest traits based upon the breeding programme targets (Parresuman and Patil, 2014).

According to metroglyph analysis, the twenty cotton genotypes formed eight distinct clusters. Cluster I had the maximum number of genotypes with four, followed by clusters II, III and IV with three genotypes while clusters V, VI and VII had two genotypes, while cluster VIII has a unique genotype (Table 7). Cluster I consisted of four genotypes; G6, G7, G8

and G18; had the highest index score of 47 as a total. While, cluster VIII had a unique genotype, G13, with the minimum index score of 13 as a total.

The scatter diagram used seed cotton yield as x-axis and lint percentage as y-axis using the values of each genotype as shown in Fig. (2). Each axis was divided into three categories based on range of variation, low for seed cotton yield (105.5-145.904 g/plant), medium (145.904-191.133 g/plant) and high (191.133-283.6 g/plant). Also, lint percentage divided to low (32.389-36.621 %), medium (36.621-38.802%) and high (38.802-41.871%). These characters were selected based upon the objective of Egyptian cotton breeding programme. Parresuman and Patil (2014) noticed that in order to select genetically diverse genotypes the material should be screened for important traits, while the other traits can then be considered based upon the breeding objective. The scatter diagram grouped all the genotypes into eight clusters. The other studied characters were plotted on the scatter diagram. Each character was represented by a glyph or rayed glyph. The length of the rays indicated the mean value of the studied character. A long ray indicates a high mean value and a short ray indicates the medium mean value. A glyph having no rays represents a low mean value.

Mahalanobis D^2 measure the genetic distance between two clusters (inter-cluster) and within a cluster (intra-cluster) as presented in Table (8). The inter-cluster

distance values ranged from 11.381 between clusters III and VI and 178.902 between clusters I and V. The inter-cluster D^2 values were highly significant between all clusters except, between clusters III and VI and clusters VII and VIII were not significant, which was exhibiting less genetic divergence. These divergent clusters, which are closer to each other, would not be expected to yield transgressive segregants or display heterosis. Crossing between these distinct clusters may increase variability and expected transgressive segregants in hybridization. While, the intra-cluster D^2 values ranged from 3.263 for cluster VII to 47.806 for cluster II. The average intra-cluster distance between the members of cluster II followed by clusters IV, V and I, suggesting that genotypes in cluster III was more diverse than genotypes in other clusters.

D^2 values proved to be effective procedure in genetic divergence for cotton breeding programme because hybridization followed by selection depending primarily on the selection of parents which having high genetic variability for different characters, will lead to accumulation of favorable genes in a selected variety (Thiyagu *et al.*, 2011; Parresuman and Patil, 2014).

Hybridization between clusters I or II which having the maximum index score with clusters VII or VIII possessing minimum index score is expected to maximize population variance. This information could be useful for breeders interested in creating desirable level of variability for a

specific character and thus would be helpful in identifying and engineering the crosses. The metroglyph analysis would be a suitable technique for grouping genotypes into different clusters based on their genetic dissimilarity back ground. The information furnished would be helpful to the breeder in the selection of superior genotypes which may be directly improved or utilized as parents in hybridization program for the development of future varieties. Khan *et al.* (2007), Shakeel *et al.* (2011) and Haidar *et al.* (2012) found the suitability of this technique for preliminary classification a large number of germplasm into distinct clusters depending on dissimilarity back ground.

SUMMARY

Inherent divergence and parenthood of germplasm could play an important role in genetic improvement of cotton. The present investigation was conducted to assess the genetic divergence among fourteen locally cotton genotypes and six exotic genotypes using multivariate Mahalanobis D^2 statistics and metroglyph analysis. The results showed highly significant differences among these genotypes for all the studied quantitative characters. The Mahalanobis D^2 statistics showed that the dissimilarity coefficients were significant and highly significant, which ranged from 3.263 to 190.89, indicating highly genetic divergence for these cotton genotypes. Seed cotton yield and fiber strength were account about 83% of total genetic divergence. The metroglyph analysis grouped these genotypes into

eight different clusters based on seven quantitative cotton characters. The inter-cluster D^2 values ranged from 11.381 to 178.902 between these groups, while, the intra-cluster D^2 values ranged from 3.263 to 47.806 within each group. On the basis of this grouping, it was concluded that hybridization between genotypes of different clusters might be expected to give new genetic recombinants for different economic characters. These informations could be utilized for hybridization between distinct genotypes to increase genetic cotton variability.

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Table (1): Origin and pedigree of the studied cotton genotypes.

No.	Genotypes	Origin	Pedigree
1	Giza 75	Egypt	Giza 67 / Giza 69
2	Giza 85	Egypt	Giza 67 / C.B 58
3	Giza 86	Egypt	Giza 75 / Giza 81
4	Giza 89	Egypt	Giza 75 / Russian 6022
5	10229 / Giza 86	Egypt	10299 // Giza 75 / Giza 81
6	Giza 90	Egypt	Giza 83 / Dandara
7	Giza 90 / Australly	Egypt	Giza 83 / Dandara // Australly
8	Giza 83 // Giza 75 / 5844 /// Giza 80	Egypt	Giza 83 // Giza 75 / 5844 /// Giza 80
9	Giza 45	Egypt	Giza 28 / Giza 7
10	Giza 70	Egypt	Giza 59a / Giza 51b
11	Giza 87	Egypt	(Giza 77 / Giza 45) a
12	Giza 88	Egypt	(Giza 77 / Giza 45) b
13	Giza 92	Egypt	Giza 84 //Giza 74/Giza 68
14	Giza 93	Egypt	Giza 77 / Pima S7
15	Suvin	Indian	Sujata x Vincent
16	Early Pima	America	Unknown
17	Pima high yield	America	Unknown
18	Pima high percentage	America	Unknown
19	Pima S6	America	5934-23-2-6 / 5903-98-4-4
20	Pima S7	America	6614-91-93 / 6907-513-509-501

Table (2): Class intervals for the studied seven quantitative characters.

Characters	Range of means	Score I		Score II			Score III	
		Less than	Sign than	From	To	Sign than	Greater than	Sign than
Boll weight	2.486-3.557	2.874	○	2.874	3.090	○	3.090	○
Seed cotton yield	105.5-283.6	145.904	○	145.90	191.133	○	191.133	○
Lint yield	42.21-110.87	53.920		53.920	71.700		71.700	
Lint percentage	32.389-41.871	36.621		36.621	38.802		38.802	
Fiber length	30.793-37.473	33.397	○	33.397	35.264	○	35.264	○
Fiber fineness	3.060-4.889	3.663	○	3.663	4.120	○	4.120	○
Fiber strength	9.173-11.773	10.215	○	10.215	10.847	○	10.847	○

Table (3): Phenotypic mean performance and index score for the studied quantitative characters among twenty cotton genotypes.

Genotypes	Boll weight	Seed cotton yield	Lint yield	Lint percentage	Fiber length	Fiber fineness	Fiber strength	Index score
Giza 75	2.944 2	217.489 3	77.500 3	35.830 1	33.489 2	4.033 2	10.189 1	14
Giza 85	2.918 2	197.983 3	72.067 3	36.279 1	33.694 2	3.756 2	10.017 1	14
Giza 86	3.089 2	178.842 2	68.194 2	38.222 2	34.144 2	4.533 3	10.033 1	14
Giza 89	3.369 3	265.933 3	94.856 3	35.799 1	32.844 1	4.889 3	9.700 1	15
10229 / Giza 86	3.557 3	260.080 3	105.787 3	40.616 3	34.333 2	4.507 3	10.247 2	19
Giza 90	2.487 1	105.507 1	42.207 1	40.127 3	31.833 1	3.927 2	9.173 1	10
Giza 90 / Australly	3.000 2	114.087 1	46.660 1	40.827 3	30.960 1	4.620 3	9.800 1	12
Giza 83 // Giza 75 / 5844 /// Giza 80	3.047 2	140.487 1	57.193 2	40.677 3	30.793 1	4.067 3	10.067 1	13
Giza 45	2.727 1	165.987 2	53.640 1	32.389 1	37.353 3	3.140 1	11.007 3	12
Giza 70	2.847 1	132.053 1	46.607 1	35.361 1	35.993 3	3.833 2	11.187 3	12
Giza 87	3.124 3	155.860 2	54.467 2	34.979 1	37.198 3	3.367 1	11.233 3	15
Giza 88	2.813 1	129.220 1	46.420 1	35.814 1	37.473 3	3.420 1	11.320 3	11
Giza 92	3.247 3	118.993 1	43.800 1	36.828 2	34.893 2	3.527 1	11.400 3	13
Giza 93	2.787 1	169.820 2	63.347 2	37.438 2	36.820 3	3.060 1	11.773 3	14
Suvin	2.972 2	148.713 2	44.047 1	37.286 2	32.067 1	3.767 2	10.420 2	12
Early Pima	2.983 2	156.789 2	61.700 2	39.243 3	32.950 1	4.128 3	10.200 2	15
Pima high yield	3.060 2	283.611 3	110.867 3	38.981 3	33.044 1	4.456 3	10.111 1	16
Pima high per- centage	2.833 1	125.417 1	52.550 1	41.871 3	36.133 3	3.200 1	11.550 3	13
Pima S6	3.176 3	151.900 2	59.933 2	39.839 3	34.189 2	3.733 2	10.111 1	15
Pima S7	2.667 1	151.600 2	54.333 2	35.825 1	36.400 3	3.873 2	11.073 3	14
Mean	2.982	168.519	62.809	37.711	34.330	3.892	10.531	
LSD at 0.05	0.653	105.686	37.628	3.544	2.114	0.709	1.043	
LSD at 0.01	0.895	139.118	49.531	4.666	2.783	0.933	1.373	

Table (4): Combined analysis of variance for the studied quantitative characters among twenty cotton genotypes.

Mean Squares								
S.O.V	df	Boll weight	Seed cotton yield	Lint yield	Lint percentage	Fiber length	Fiber fineness	Fiber strength
Replications	2	0.409	2956.122	500.322	4.398	2.057	0.677	1.171
Genotypes	19	0.364**	15996.815**	2468.190**	37.131**	27.227**	1.633**	3.117**
Years	1	3.333**	3000.000**	3000.000**	14.700**	14.700**	2.700**	13.333**
Error	97	0.025	655.210	83.054	0.737	0.262	0.029	0.064

* and ** Significant at 0.05 and 0.01, respectively.

Table (5): Genetic divergence estimated by Mahalanobis D^2 among the studied twenty cotton genotypes.

Genotypes	Giza 75	Giza 85	Giza 86	Giza 89	10229/Giza 86	Giza 90	Giza90/Australly	Giza 83//Giza 75/5844/// Giza 80	Giza 45	Giza 70	Giza 87	Giza 88	Giza 92	Giza 93	Suvin	Early Pima	Pima high yield	Pima high per-centage	Pima S6
Giza 85	20.25																		
Giza 86	39.83**	19.64																	
Giza 89	51.47**	71.68**	91.1**																
10229/Giza 86	51.36**	70.80**	89.5**	13.40															
Giza 90	117.5**	97.27**	77.8**	168.9**	167**														
Giza90/Australly	108.1**	87.82**	68.3**	159.4**	157**	9.789													
Giza 83//Giza 75/5844/// Giza 80	79.82**	59.62**	40.1**	131.0**	129**	38.08**	28.43												
Giza 45	57.00**	37.32**	20.60	108.2**	107**	62.31**	53.46**	27.86											
Giza 70	90.89**	70.72**	51.6**	142.3**	141**	27.71	19.50	15.48	34.81*										
Giza 87	65.91**	45.82**	27.18	117.3**	116**	52.40**	43.39**	17.86	10.49	25.11									
Giza 88	93.67**	73.50**	54.3**	145.1**	143**	25.20	17.33	17.70	37.62**	3.26	27.84								
Giza 92	104.1**	83.91**	64.6**	155.5**	154**	14.50	8.217	25.98	48.28**	13.49	38.49**	10.92							
Giza 93	49.89**	29.73*	10.86	101.2**	99.8**	67.99**	58.62**	30.80*	11.63	41.38**	16.74	44.02**	54.49**						
Suvin	76.50**	56.71**	38.6**	127.7**	127**	43.36**	34.93**	15.93	21.05	17.43	13.86	20.44	29.87*	29.03					
Early Pima	62.81**	42.59**	23.04	114.1**	112**	54.89**	45.34**	17.11	14.75	29.41*	9.543	32.05*	41.95**	13.94	19.53				
Pima high yield	74.13**	94.05**	113**	24.07	24.16	190.89**	181**	152.8**	131.0**	164.6**	139.7**	167.3**	177.7**	123.4**	150.5**	136.2**			
Pima high per-centage	95.63**	75.41**	55.8**	146.9**	144**	23.04	14.00	16.78	41.69**	11.05	31.29*	9.520	12.04	45.91**	25.57	32.98*	168.6**		
Pima S6	68.02**	47.79**	28.23	119.3**	117**	49.73**	40.22**	12.25	17.46	24.41	8.923	26.93	36.80**	18.67	16.54	5.39	141.2**	27.68	
Pima S7	69.91**	49.74**	30.77*	121.3**	120**	48.11**	39.02**	13.70	14.85	21.02	4.473	23.76	34.32*	20.42	11.64	10.28	143.6**	26.94	7.32

* and ** Significant at 0.05 and 0.01 (X^2 at 0.05 and 0.01 for 18 degrees of freedom = 28.87 and 34.81, respectively).

Table (6): Contribution Degree of each character towards total genetic divergence among studied cotton genotypes.

Characters	Boll weight	Seed cotton yield	Lint yield	Lint percentage	Fiber length	Fiber fineness	Fiber strength	Total
First ranking	7	122	12	1	1	10	37	190
Contribution %	3.684	64.211	6.316	0.526	0.526	5.263	19.474	100

Table (7): Cluster number, cluster index scores and cotton genotypes included in each group following Metroglyph technique.

Cluster No.	Genotypes No.	Cluster index scores
I	6, 7, 8, 18	47
II	1, 2, 4	43
III	9, 11, 20	41
IV	3, 14, 15	40
V	5, 17	35
VI	16, 19	30
VII	10, 12	23
VIII	13	13

Table (8): Average intra (Diagonal values) and inter (Above diagonal values) cluster divergence D^2 and D (square roots of D^2 values in the parenthesis) values of eight groups for twenty cotton genotypes for seven quantitative characters.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	21.686** (4.657)	110.624** (10.518)	45.363** (6.735)	47.114** (6.864)	178.902** (13.375)	35.029** (5.919)	17.941** (4.236)	15.187* (3.897)
II		47.806** (6.914)	74.748** (8.646)	65.834** (8.114)	42.991** (6.557)	75.781** (8.705)	123.634** (11.119)	114.543** (10.703)
III			9.938 (3.152)	19.644** (4.432)	175.435** (13.245)	11.381 (3.374)	43.503** (6.596)	40.366** (6.354)
IV				26.194** (5.118)	117.314** (10.831)	19.997** (4.472)	38.219** (6.182)	49.682** (7.049)
V					24.169** (4.916)	161.084** (12.692)	154.266** (12.420)	165.971** (12.883)
VI						5.396 (2.323)	161.084** (12.692)	39.379** (6.275)
VII							3.263* (1.806)	12.209 (3.494)

* and ** Significant at 0.05 and 0.01 (X^2 at 0.05 and 0.01 for 6 degrees of freedom = 12.59 and 16.81, respectively).

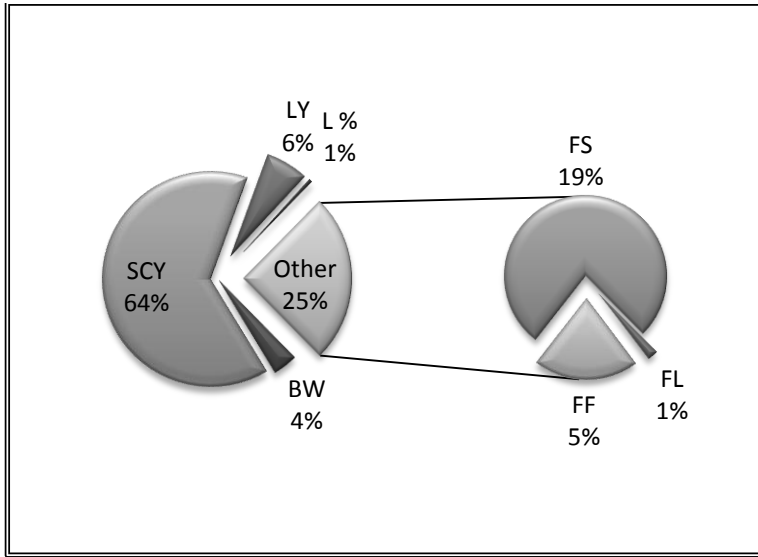


Fig. (1): Contribution degree of each character towards total genetic divergence among studied cotton genotypes.

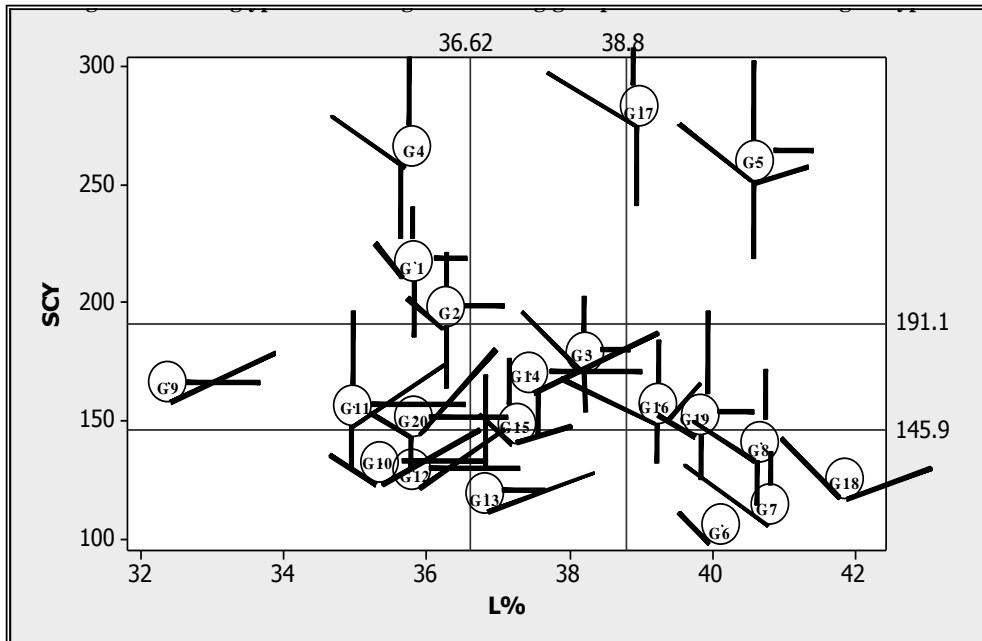


Fig. (2): Metroglyph scatter diagram showing groups formed from cotton genotypes.