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GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF COTTON YIELD AND ITS COMPONENTS OF GMS BASED HYBRIDS IN UPLAND COTTON (*Gossypium hirsutum* L.)

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ABSTRACT

The present investigation was undertaken to study phenotypic stability of parents and hybrids. The experimental material consisted of nine parents (seven females and two males) and their fourteen resultant crosses that were made in GMS system grown in kharif 2002 at three locations viz., Surat, Hansot and Bharuch. The Eberhart and Russell model (1966) of stability analysis was carried out to study the genotype x environment interaction for seed cotton yield and its component traits. The analysis revealed that environment component was considerably higher than genotypes and genotypes x environment component for all the characters. Looking to the overall performance the parental lines LH-900, LRK-516and G(B) 20 were the most stable parent in seed cotton yield and the cross PH 93 x G.Cot.10, LRK 516 x G.Cot.10 and G(B) 20 x G.Cot.10 with desirable stability.

Key words : *gossypium hirsutum, genotype x environments, stability analysis*

The genotype and environment plays important effect on the crop variety performance in which it grows. It is observed that genotype x environment interaction varies with different genotypes in different environments. This interaction is a result of changes in cultivar's relative performance across environments, due to differential responses of the genotypes to various soil, climate and biotic factor. Therefore, the analysis of genotype x environment interaction becomes an important tool employed by breeders for evaluating varietal adaptation. Hence stability analysis was carried out to identify stable accessions so as to develop high yielding hybrids and superior crosses.

MATERIALS AND METHODS

The study includes 24 entries comprising of 14 F_1s, (GMS based hybrids),7 females and 2 males and 1 check were evaluated during *kharif* 2002 at three locations *viz*., Surat, Bharuch and Hansot. The trials were conducted in a Randomised Block design (RBD), replicated thrice in the three different locations. The parents and F_1s with standard checks were represented by a single row plot of 14 plants, placed at 120 cm x 45 cm. All the agronomical practices and plant protection measures were followed as and when required to raise a good crop of cotton. Five random competitive plants excluding border ones were selected from each row in each replication to record observations on seed cotton yield per plant, number of bolls per plant, boll weight, number of seeds per boll, ginning per centage, 2.5 per cent span length and fibre strength. The characters were recorded in the field and laboratory and the mean values were subjected for statistical analysis.

RESULTS AND DISCUSSON

According to the model of (1), a variety may said to be stable over different environments, if it shows unit regression co-efficient (bi=1) with lowest deviation (non significant) from the regression (S^2di = 0). With these conditions, high and desirable *per se* performance of variety over environments is also a positive point to rate the variety/hybrid as a better and stable genotype.

The magnitude of G x E interactions and stability parameters for various traits were estimated as per the procedure outlined by (1). The mean squares for phenotypic stability for different traits are presented in Table-1.

The mean squares for phenotypic stability for different traits are presented in Table-1. The mean squares due to genotypes were found to be significant for all the characters when tested against pooled error except the mean squares of fibre length. However, these were significant when tested against pooled deviation. The mean SS due to environments were significant for all the characters except number of seeds per boll, ginning percentage and fibre strength when tested against pooled error. However, fibre strength was significant when tested against pooled deviation. Similarly genotype x environment interactions were significant for all the characters except fibre length and fibre strength. The mean squares due to environments (linear) were significant for all the characters except fibre strength in GMS based hybrids .Whereas, GMS methods of fibre strength were significant against pooled deviation. On the other hand, the mean squares due to genotype x

Table-1 : Analysis of variance (mean squares) for phenotypic stability for Seed cotton yield per plant (g), number of bolls per plant, boll weight, Ginning percentage (%), 2.5 per cent span length (mm) and Fibre strength (g/tex)

Source of variation	DF	Seed cotton yield per plant (g)	Number of bolls per plant	Boll weight (g)	Ginning percentage (%)	2.5 per cent span length (mm)	Fibre strength (g/tex)
Genotypes (G)	22	1377.34**	172.61**	0.47**	19.27**	3.73*	2.64
Environment (E)	2	11514.66**	86.43**	4.86**	3.10	32.44**	3.45
G × E	44	271.65**	34.80**	0.22**	6.58**	1.54	0.93
Environments (linear)	1	23029.61**	172.89**	9.72**	6.22	64.86**	6.92
G ×E (linear)	22	267.58**	42.75**	0.32**	3.96	1.13	1.03
Pooled deviation	23	263.72**	25.68**	0.11**	8.81*	1.86	0.79
Pooled error	132	64.74	9.40	0.04	5.45	2.51	4.37

*,** Significant at 5 and 1 per cent probability levels against pooled error.

Table-2 : Stability parameters of different genotypes for seed cotton yield per plant (g), number of seeds per boll and boll weight (g)

Genotypes	Seed cotton yield per plant (g)			Number of bolls per plant			Boll weight (g)		
	Mean	b_i	S^2d^i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
76 IH 20	93.49	0.44	405.75**	30.00	1.69	12.95*	3.58	0.38	0.35**
LH 900	86.50	1.47	-21.57	27.90	1.82	15.62**	3.10	1.54	-0.02
PH 93	75.89	0.43	14.64	29.76	-0.99	-2.55	3.07	1.72	0.01
LRA 5166	81.27	0.42	487.07**	31.67	-0.07	54.97**	2.86	1.15	0.04
LRK 516	96.40	0.92	-1.63	26.33	1.54	-1.87	4.00	0.90	-0.01
G(B) 20	104.78	1.09	84.59*	31.38	3.90	24.56**	3.78	0.18	0.02
G.Cot. 100	84.03	1.07	20.15	28.36	3.35	11.10	3.32	0.43	-0.02
G.Cot. 10	104.15	0.91	-20.08	33.40	2.30	-2.18	3.30	0.24	-0.01
DHY 286-1	90.93	1.13	-7.90	26.09	2.12	2.89	3.60	0.31	0.27**
76 IH 20 x G.Cot.10	106.35	1.55	863.45**	44.44	0.55	60.91**	3.31	1.70	-0.01
76 IH 20 x DHY 286-1	128.08	2.27	2282.77**	45.16	3.32	182.62**	3.76	2.29	0.01
LH 900 x G.Cot.10	83.92	0.69	-20.80	28.71	2.42	-3.08	3.83	-0.17	-0.02
LH 900 x DHY 286-1	125.18	1.54	3.22	42.38	2.50	0.68	4.16	1.21	-0.02
PH 93 x G.Cot.10	105.03	0.82	48.37	42.51	0.54	23.12**	3.52	0.45	0.00
PH 93 x DHY 286-1	104.51	0.26	236.69	41.64	-5.09	-3.11	3.37	2.08	0.00
LRA 5166 x G.Cot.10	127.10	1.96	-10.58	44.42	3.97	-2.02	3.87	1.25	0.09**
LRA 5166 x DHY 286-1	107.10	0.78	212.26**	42.76	0.00	15.93**	3.44	1.79	0.41**
LRK 516 x G.Cot.10	117.86	1.02	371.31**	38.80	-2.25	45.48**	3.97	-0.63	0.15**
LRK 516 x DHY 286-1	146.70	0.44	317.58**	44.62	-0.70	-0.20	4.26	1.19	0.12**
G(B) 20 x G.Cot.10	154.05	1.03	267.92**	48.58	0.67	63.62**	4.04	0.31	0.12**
G(B) 20 x DHY 286-1	168.42	0.98	-18.53	45.29	-4.41	5.77	4.00	2.88	0.09**
G.Cot.100 x G.Cot.10	126.46	0.85	53.11	40.29	2.94	1.84	4.31	0.05	0.07
G.Cot.100 x DHY 286-1	112.33	0.95	1.53	45.38	-1.67	11.46*	3.41	1.75	0.64
Mean	108.72	-	-	37.38	-	-	3.64	-	-
S.E.+	11.48	0.51	-	3.58	1.84	-	0.24	0.52	-

environments (linear) were significant for all the characters. Pooled deviation were significant for the characters of ginning percentage and seed cotton yield per plant (2, 3).

The estimates of stability parameters computed to evaluate relative stability of different genotypes over a range of environments are presented in Table 2 and 3. The results are described below :

Seed cotton yield per plant : Among the parents LH 900, LRK 516, G(B) 20, G.Cot.100, G.Cot.10 and DHY 286-1 recorded high mean values with nearer to one regression coefficient and low and non significant

Table-3 : Stability parameters of different genotypes for ginning percentage (%), 2.5 per cent span length (mm) and fibre strength (g/tex)

Genotypes	Ginning percentage %			2.5 per cent span length (mm)			Fibre strength (g/tex)		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
76 IH 20	31.59	-0.64	-1.76	23.15	1.88	-0.47	17.57	2.29	-0.61
LH 900	34.77	-0.64	-1.53	23.46	1.17	-0.74	16.48	3.08	-0.16
PH 93	41.26	-4.25	-1.67	22.28	1.51	-0.04	17.89	2.64	-0.76
LRA 5166	35.38	1.04	1.30	24.56	1.58	4.71**	18.18	1.65	0.51
LRK 516	37.03	1.49	-1.74	25.62	-0.35	2.21	19.08	0.87	-0.73
G(B) 20	34.90	3.02	13.19**	25.14	0.70	-0.08	18.91	-0.68	-1.03
G.Cot. 100	33.67	-2.91	2.97	27.30	1.90	0.18	19.59	-0.23	-1.45
G.Cot. 10	36.08	-1.70	-1.80	23.23	0.77	1.97	18.36	-1.18	-1.14
DHY 286-1	36.33	4.93	-1.70	24.91	0.63	-0.63	20.17	-3.02	-0.93
76 IH 20 x G.Cot.10	38.62	0.96	-1.82	23.66	0.78	0.79	18.30	4.21	-1.46
76 IH 20 x DHY 286-1	35.91	-4.61	12.75**	24.56	1.03	-0.66	19.36	3.66	-0.54
LH 900 x G.Cot.10	32.79	-4.64	21.42**	23.55	0.64	1.22	18.04	1.54	1.49
LH 900 x DHY 286-1	35.78	2.75	0.46	26.15	1.83	-0.71	19.17	1.68	-0.62
PH 93 x G.Cot.10	41.43	1.16	23.14**	24.40	1.39	0.05	17.56	-0.82	-0.68
PH 93 x DHY 286-1	39.19	1.86	19.55**	23.32	1.38	2.13	18.14	1.01	-0.92
LRA 5166 x G.Cot.10	36.82	2.82	13.97**	24.28	0.83	0.11	19.74	-0.11	-1.26
LRA 5166 x DHY 286-1	34.98	8.58	10.28**	23.96	1.80	-0.82	17.68	2.83	-1.37
LRK 516 x G.Cot.10	34.30	0.14	-0.49	25.06	1.35	-0.56	19.44	2.83	1.88
LRK 516 x DHY 286-1	33.55	1.29	13.93**	23.88	0.58	-0.76	20.17	0.50	-1.44
G(B) 20 x G.Cot.10	37.03	7.19	14.09**	24.42	-0.23	4.80**	19.09	-1.70	-1.46
G(B) 20 x DHY 286-1	33.61	1.18	16.25**	24.47	0.98	4.53**	19.46	0.77	-1.18
G.Cot.100 x G.Cot.10	34.26	8.50	11.83**	23.50	0.08	5.83**	19.46	2.06	-0.13
G.Cot.100 x DHY 286-1	28.67	-4.04	-1.82	23.17	0.78	0.56	18.52	2.06	-1.35
Mean	35.99	-	-	24.26	-	-	18.71	-	-
S.E.+	2.09	5.70	-	0.96	0.81	-	0.62	1.62	-

deviation from regression except G(B) 20 which showed significant deviation from regression. In GMS based crosses, six viz., PH 93 x G.Cot.10, LRK 516 x G.Cot.10, G(B) 20 x G.Cot.10, G(B) 20 x DHY 286-1, G.Cot.100 x G.Cot.10 and G.Cot.100 x DHY 286-1 recorded high mean values with regression coefficient approximately equal to one and low S^2di values.

Number of bolls per plant : In GMS method, the parents viz., LH 900, LRK 516, G.Cot.10 and DHY 286-1 recorded high mean greater than one regression coefficient and lower S^2di values. The crosses 76 IH 20 x G.Cot.10, PH 93 x G.Cot.10, G(B) 20 x G.Cot.10, G(B) 20 x DHY 286-1 and G.Cot.100 x DHY 286-1 showed high mean values with bi values less than unity and significant values of deviation from regression.

Boll weight : The parents viz., LRK 516 and LRA 5166 registered high mean values, regression coefficient equal to approximately unity and low deviation from regression.In GMS based crosses, LH 900 x DHY 286-1, LRA 516 x G.Cot.10 and LRK 516 x DHY 286-1 showed high mean values, nearer to one regression coefficient and significant deviation from regression except LH 900 x DHY 286-1.

Ginning percentage (%) : In GMS method, the parents LRA 5166 and LRK 516 registered high mean values with regression coefficient nearer to one and low and non significant deviation from regression. The crosses viz., 76 IH 20 x G.Cot.10, PH 93 x G.Cot.10 and G(B) 20 x DHY 286-1 recorded high mean with approximately equal to one regression coefficient and significant deviation from regression, whereas 76 IH 20 x G.Cot.10 showed low S^2di value.

Taken into account while selecting/evaluating genotypes for stability performance across the environments. To measure stability of genotypes across the environments, deviations from 2.5 per cent span length (mm).

The parent LH 900 showed high mean value with approximately equal to one regression coefficient and low deviation from regression. The parents G.Cot.100 and LRA 5166 recorded highest mean values with bi greater than one and low S^2di value. In GMS based crosses, 76

IH 20 x DHY 286-1, LRA 5166 x G.Cot.10 and G(B) 20 x DHY 286-1 exhibited high mean values, approximately equal to one regression coefficient and low S^2di.

Fibre strength (g/tex) : The parent LRK 516 recorded high mean value with nearer to one regression coefficient and low deviation from regression, whereas the parents G.Cot.100, G.Cot.10 and DHY 286-1 registered highest mean with less than one bi and low deviation from regression. In GMS based crosses, PH 93 x DHY 286-1 and G(B) 20 x DHY 286-1 recorded high mean values with nearer to one regression coefficient and low deviation from regression.

It was concluded that seed cotton yield and its related traits may be regression (S^2di) appeared to be more important criteria than regression coefficient (bi). (4) have also emphasized that the linear regression (bi) may simply be regarded as a measure of response of particular genotype and deviations from regression (S^2di) should be given more weightage as a measure of stability. The result also indicated that, in some environments, distribution of rainfall during the growing period is the determining factor for the performance of cotton genotypes. Accordingly, the mean and deviation from regression of each genotype were considered for stability and linear regression was used for testing the varietal response. Genotypes with high mean, bi = 1 with non significant S^2 di are suitable for general adaptation, *i.e.,* suitable over all environmental conditions and they are considered as stable genotypes and genotypes with high mean, bi > 1 with non significant s^2di are considered as below average in stability. Such genotypes tend to respond favorably to better environments but gives poor yield in unfavorable environments. Hence they are suitable for favorable environments. Whereas genotypes with high mean, bi < 1 with non significant s^2di do not respond favourably to improved environmental conditions and hence, it could be regarded as specifically adapted to poor environments.

Taking into account of all the parameters of stability it can be inferred that among the parents LH-900, LRK-516, G(B) 20, G.Cot.100, G.Cot.10 and DHY 286-1 recorded high mean values with nearer to one regression coefficient and low deviation from regression except G(B) 20 which showed significant deviation from regression and PH 93 x G.Cot.10, LRK 516 x G.Cot.10, G(B) 20 x G.Cot.10, G(B) 20 x DHY 286-1, G.Cot.100 x G.Cot.10 and G.Cot.100 x DHY 286-1 recorded high mean values with regression coefficient approximately equal to one and low S^2di values. These genotypes can be considered as most stable and can be recommended for wider adaptability.

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