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Stability analysis for seed cotton yield and its components of conventional, GMS and CMS 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 forty two resultant crosses that were made in conventional (14), GMS (14) and CMS (14) system 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 in three methods, the parental line G(B) 20 was the most stable parent in seed cotton yield and the cross G(B) 20 x G.Cot.10 with desirable stability.

Keywords: *Gossypium hirsutum*, genotype x environments, stability analysis

Introduction

A variety having good adaptability is one that consistently gives stable performance over wide range of environments (Frey, 1964)^[4]. Thus stability depends upon the relative sensitivity of a genotype to varied environments. An individual may react to variable environments in such a way that its development is buffered against environmental variation and the same adaptive phenotype being produced in varying environments. 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. In the present investigation when these parameters were studied for each genotype separately, none of the parents/hybrids exhibited average stability for all the characters. Thus any generalization regarding stability of genotype for all the characters is too difficult since the genotype may not simultaneously exhibit uniform responsiveness and stability patterns for these characters (Bhandari 1980; Gill and Singh 1982 and Pvasia and Shukla, 1997)^[1, 5, 9]. It is therefore suggested that in order to produce stable hybrid actual testing of hybrids over a range of environments would be necessary.

Material and methods

The study includes 52 entries comprising of conventional based hybrids (14 F₁s), GMS based hybrids (14 F₁s) and CMS based hybrids (14 F₁s), 7 females and 2 males and 1 check were evaluated 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 environmental conditions encountered during crop period are given in Table. The parents and F₁s 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, 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

Genotype x environment (G x E) interaction measures the differential response of genotypes to changes in the environments. This interaction plays an important role in the efficiency of selection programme.

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The magnitude of G x E interactions and stability parameters for various traits were estimated as per the procedure outlined by Eberhart and Russell (1966)^[3].

Analysis of variance for stability

The mean squares for phenotypic stability for different traits are presented in Table 1 to Table 4. The mean squares due to genotypes were found to be significant for all the characters when tested against pooled error except the mean squares for GMS hybrid of fibre length and for conventional and CMS hybrids of fibre strength. However, these were significant when tested against pooled deviation. The mean SS due to environments were significant for all the characters except number of monopodia per plant, number of seeds per boll, ginning percentage and GMS and CMS based hybrids for 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 days to 50 per

cent flowering, fibre length and fibre strength. The mean squares due to environments (linear) were significant for all the characters except number of monopodia per plant in conventional and CMS based hybrids, seed index and ginning percentage in CMS hybrids, and fibre strength in GMS and CMS based hybrids. Whereas, GMS and CMS methods of fibre strength were significant against pooled deviation. On the other hand, the mean squares due to genotype x environments (linear) were significant for all the characters except days to 50 per cent flowering, number of sympodia per plant in GMS and CMS method, seed index, ginning percentage, fibre length and fibre strength in conventional and CMS method. Pooled deviation were significant for the characters viz., number of monopodia per plant, conventional method of sympodia per plant, number of bolls per plant, boll weight, conventional method of seeds per boll, GMS and CMS method of ginning percentage and seed cotton yield per plant.

Table 1: Analysis of variance (mean squares) for phenotypic stability for days to 50 per cent flowering, plant height (cm) and number of monopodia per plant

Source of variation	DF	Days to 50 per cent flowering			Plant height (cm)			Number of monopodia per plant		
		CON	GMS	CMS	CON	GMS	CMS	CON	GMS	CMS
Genotypes(G)	22	154.81**	128.77**	156.66**	1174.26**	1236.58**	1110.74**	1.38**	0.93**	1.16**
Environments (E)	2	281.97**	174.38**	215.47**	1491.93**	12465.39**	2113.10**	0.18	0.39	0.17
G X E	44	6.16	7.43	7.64	102.28**	80.77	125.54**	0.61**	0.65**	0.42**
Environments (Linear)	1	563.87**	348.79**	430.94**	3184.09**	4930.67**	4226.05**	0.36	0.78*	0.35
G X E (Linear)	22	6.32	8.76	7.43	161.94**	137.13**	167.14**	0.45**	0.67**	0.34**
Pooled deviation	23	5.75	5.84	7.51	40.77	23.36	80.30	0.74**	0.59**	0.48**
Pooled error	132	12.19	11.20	10.42	78.73	69.30	74.20	0.20	0.20	0.19

Table 2: Analysis of variance (mean squares) for phenotypic stability for number of sympodia per plant, number of bolls per plant and boll weight (g)

Source of variation	DF	Number of sympodia per plant			Number of bolls per plant			Boll weight (g)		
		CON	GMS	CMS	CON	GMS	CMS	CON	GMS	CMS
Genotypes(G)	22	42.57**	39.69**	28.34**	210.78**	172.61**	166.02**	0.59**	0.47**	0.42**
Environments (E)	2	98.50**	113.83**	198.62**	340.58**	86.43**	251.20**	5.64**	4.86**	3.69**
G X E	44	13.85**	13.23**	14.84**	338.78**	34.80**	29.51**	0.24**	0.22**	0.16**
Environments (Linear)	1	197.01**	227.66**	397.25**	681.17**	172.89**	502.45**	11.28**	9.72**	7.38**
G X E (Linear)	22	12.34*	12.22	14.61	35.52**	42.75**	34.86**	0.37**	0.32**	0.19**
Pooled deviation	23	14.69**	13.62	14.42	30.64**	25.68**	23.11**	0.11**	0.11**	0.13**
Pooled error	132	7.56	9.21	10.14	7.80	9.40	10.58	0.04	0.04	0.05

*, ** Significant at 5 and 1 per cent probability levels against pooled error 0.02E

Table 3: Analysis of variance (mean squares) for phenotypic stability for number of seeds per boll, seed index (g) and ginning percentage (%)

Source of variation	DF	Number of seeds per boll			Seed index (g)			Ginning percentage (%)		
		CON	GMS	CMS	CON	GMS	CMS	CON	GMS	CMS
Genotypes(G)	22	28.13**	32.22**	28.24**	3.04**	2.42**	2.88**	28.74**	19.27**	19.27**
Environments (E)	2	15.39	15.67	17.96	6.12**	3.75*	0.70	5.65	3.10	8.64
G X E	44	10.01**	13.58**	9.26**	1.50*	1.36**	1.19**	7.49**	6.58**	10.09**
Environments (Linear)	1	30.79*	31.35*	35.94*	12.25**	7.50**	1.40	11.27	6.22	17.29
G X E (Linear)	22	7.11	16.93**	6.07	2.01**	1.77*	1.80**	6.75	3.96	11.72
Pooled deviation	23	12.36**	10.29	11.91	0.95	0.91	0.49	7.88	8.81*	8.09*
Pooled error	132	6.49	6.80	7.95	1.09	1.12	1.02	5.84	5.45	4.74

Table 4: Analysis of variance (mean squares) for phenotypic stability for seed cotton yield per plant (g), 2.5 per cent span length (mm) and fibre strength (g/tex)

Source of variation	DF	Seed cotton yield per plant (g)			2.5 per cent span length (mm)			Fibre strength (g/tex)		
		CON	GMS	CMS	CON	GMS	CMS	CON	GMS	CMS
Genotypes(G)	22	1652.77**	1377.34**	1019.54**	6.44**	3.73	5.54**	2.82	2.64	4.03**
Environments (E)	2	18595.41**	11514.66**	19221.51**	45.00**	32.44**	54.22**	7.46**	3.45	2.58
G X E	44	332.21**	271.65**	303.13**	2.32	1.54	2.37	1.49	0.93	0.57
Environments (Linear)	1	37191.13**	23029.61**	28443.10**	90.02**	64.86**	108.44**	49.91**	6.92	5.17
G X E (Linear)	22	455.52**	267.58**	244.03**	1.66	1.13	1.90	1.64	1.03	0.77
Pooled deviation	23	199.81**	263.72**	348.48**	2.85	1.86	2.72	1.27	0.79	0.36
Pooled error	132	73.66	64.74	62.29	3.05	2.51	2.67	2.02	4.37	2.43

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

Stability parameters

The estimates of stability parameters computed to evaluate relative stability of different genotypes over a range of

environments are presented in Table 5 to Table 16. The results are described below:

Table 5: Stability parameters of different genotypes for days to 50 per cent flowering

Genotypes	CON			GMS			CMS		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
76 IH 20	65.89	1.44	-2.48	65.89	1.83	-1.74	65.89	1.67	-3.31
LH 900	62.67	1.17	8.70	62.67	1.47	9.93	62.62	1.49	1.13
PH 93	54.78	1.69	-3.71	54.78	2.15	-3.55	54.78	1.85	2.81
LRA 5166	60.89	1.27	-4.03	60.89	1.61	-3.73	60.89	1.40	-0.78
LRK 516	51.33	1.65	-3.90	51.33	2.10	-3.68	51.33	1.81	1.71
G(B) 20	59.89	1.08	-4.07	59.89	1.78	-3.71	59.89	1.21	-2.03
G.Cot. 100	71.44	0.73	3.35	71.44	0.91	4.11	71.44	0.96	-0.18
G.Cot. 10	61.44	0.69	-0.35	61.44	0.87	0.29	61.44	0.87	-2.28
DHY 286-1	69.56	1.15	-3.93	69.56	1.46	-3.49	69.56	1.30	-2.52
76 IH 20 x G.Cot.10	58.56	1.30	1.49	55.11	1.70	-0.88	53.11	1.20	7.61
76 IH 20 x DHY 286-1	65.00	1.17	12.04	62.67	1.01	-0.63	58.78	0.14	-1.55
LH 900 x G.Cot.10	61.44	1.53	41.71**	60.67	0.33	27.24**	56.11	1.48	40.44**
LH 900 x DHY 286-1	64.56	0.93	-0.50	60.00	-0.11	-1.90	58.56	0.40	15.15*
PH 93 x G.Cot.10	52.33	1.62	4.34	50.78	0.95	-0.35	47.00	1.33	-2.98
PH 93 x DHY 286-1	62.44	1.05	-1.88	60.00	1.32	-2.02	56.00	1.52	-3.02
LRA 5166 x G.Cot.10	55.56	1.06	-3.83	52.89	1.46	-3.50	50.67	1.28	16.49**
LRA 5166 x DHY 286-1	65.78	0.06	8.81	60.33	-0.32	-3.72	60.78	0.66	8.20
LRK 516 x G.Cot.10	44.67	1.19	-4.04	48.67	-0.12	12.93	44.67	-0.26	3.49
LRK 516 x DHY 286-1	59.22	1.24	-4.01	58.78	0.36	-2.03	53.44	0.78	-3.48
G(B) 20 x G.Cot.10	55.00	0.44	-4.05	53.67	1.12	5.97	50.11	0.52	-1.77
G(B) 20 x DHY 286-1	66.33	0.52	-1.96	64.33	1.60	1.55	62.67	1.18	26.28**
G.Cot.100 x G.Cot.10	69.22	-0.04	3.52	66.67	-0.29	19.02**	63.11	-0.54	-3.46
G.Cot.100 x DHY 286-1	76.22	0.07	-2.33	73.22	0.21	2.34	70.33	0.56	-3.16
Mean	61.48	-	-	60.29	-	-	58.40	-	-
S.E. \pm	1.69	0.08	-	1.70	0.62	-	1.93	0.63	-

Table 6: Stability parameters of different genotypes for plant height (cm)

Genotypes	CON			GMS			CMS		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
76 IH 20	128.57	1.95	-9.47	128.57	1.60	-23.10	128.57	1.72	-24.61
LH 900	99.76	1.79	-18.51	99.76	1.45	-21.99	99.76	1.56	-23.04
PH 93	119.04	2.09	-24.83	119.04	1.67	-12.47	119.04	1.80	-12.15
LRA 5166	93.86	2.16	-25.32	93.86	1.68	-10.74	93.86	1.81	-10.26
LRK 516	85.51	2.15	1.01	85.51	1.77	-22.77	85.51	1.91	-24.67
G(B) 20	97.01	2.53	137.80**	97.01	2.15	29.56	97.01	2.33	22.63
G.Cot. 100	119.99	1.76	4.60	119.95	1.46	-20.10	119.99	1.58	-22.56
G.Cot. 10	107.43	1.76	-16.99	107.43	1.43	-22.58	107.43	1.54	-23.80
DHY 286-1	99.49	1.59	-25.92	99.49	1.26	-15.22	99.49	1.36	-15.59
76 IH 20 x G.Cot.10	139.41	1.37	-26.03	129.02	0.39	25.52	143.53	0.76	142.98**
76 IH 20 x DHY 286-1	135.11	1.60	-26.20	130.95	1.25	21.01	136.37	1.99	-24.75
LH 900 x G.Cot.10	86.83	0.70	-22.06	83.59	0.93	-19.72	91.11	0.10	-23.95
LH 900 x DHY 286-1	86.68	0.99	73.92	91.86	0.89	38.96	97.26	1.15	94.49*
PH 93 x G.Cot.10	126.38	-0.46	2.35	124.06	0.13	-21.76	131.44	0.33	-19.02
PH 93 x DHY 286-1	122.16	1.15	49.05	125.52	1.56	-16.70	136.08	1.28	94.79*
LRA 5166 x G.Cot.10	84.73	0.24	-8.77	82.22	0.03	-6.02	101.51	0.71	21.22
LRA 5166 x DHY 286-1	92.62	-0.91	129.15**	9.26	0.17	4.02	116.59	0.18	278.46**
LRK 516 x G.Cot.10	75.65	1.18	-25.90	73.31	1.19	-13.20	88.05	0.92	-7.53
LRK 516 x DHY 286-1	78.33	-0.43	60.10	65.93	0.89	-17.36	86.48	-1.21	-17.95
G(B) 20 x G.Cot.10	131.18	-0.47	14.51	133.59	0.56	11.77	137.64	-0.42	383.45**
G(B) 20 x DHY 286-1	102.95	-1.31	127.61**	105.52	-1.12	57.41	115.57	-1.08	513.13**
G.Cot.100 x G.Cot.10	129.92	0.89	-26.23	128.09	-0.24	84.51*	134.15	1.21	-5.56
G.Cot.100 x DHY 286-1	116.46	0.73	-5.08	119.91	1.91	-22.91	129.86	1.76	-16.79
Mean	106.91	-	-	105.89	-	-	118.75	-	-
S.E. \pm	4.51	0.54	-	3.41	0.33	-	6.33	0.66	-

Table 7: Stability parameters of different genotypes for number of monopodia per plant

Genotypes	CON			GMS			CMS		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
76 IH 20	2.16	6.23	-0.07	2.16	3.88	0.04	2.16	-2.75	0.44**
LH 900	2.40	9.63	0.05	2.40	6.69	0.02	2.40	-2.47	1.45**
PH 93	2.31	-10.13	-0.02	2.31	-5.48	0.60**	2.31	6.66	0.94**
LRA 5166	2.60	2.59	-0.06	2.60	1.31	-0.01	2.60	-1.94	-0.01
LRK 516	2.24	1.57	0.20	2.24	-0.44	0.23	2.24	-3.95	-0.06
G(B) 20	1.69	-3.44	-0.07	1.69	-2.07	-0.03	1.69	1.70	0.08
G.Cot. 100	2.07	3.17	0.12	2.07	3.04	-0.04	2.07	1.39	0.25*
G.Cot. 10	2.27	-9.03	-0.07	2.27	-5.44	0.23	2.27	6.66	0.94**
DHY 286-1	2.80	1.92	-0.05	2.80	-1.83	-0.07	2.80	0.04	0.02
76 IH 20 x G.Cot.10	3.24	-4.95	0.07	3.47	7.35	0.13	3.53	3.38	0.43**
76 IH 20 x DHY 286-1	2.31	-5.80	2.77**	3.04	0.85	1.51**	2.07	10.46	0.10
LH 900 x G.Cot.10	2.16	0.53	0.50**	2.98	8.93	-0.06	2.80	-6.42	1.25**
LH 900 x DHY 286-1	3.31	-3.79	1.09**	2.29	-1.03	3.65**	2.84	6.13	-0.06
PH 93 x G.Cot.10	3.33	7.62	0.85**	3.53	3.58	0.07	3.07	3.37	0.30**
PH 93 x DHY 286-1	2.04	2.09	0.16	2.53	-0.32	0.90**	1.76	5.01	0.00
LRA 5166 x G.Cot.10	3.49	4.09	2.53**	2.76	9.61	0.50**	2.62	1.88	0.82**
LRA 5166 x DHY 286-1	3.07	0.81	1.55**	2.96	1.29	3.54**	3.49	-2.24	0.08
LRK 516 x G.Cot.10	2.73	0.90	4.03**	2.49	-8.47	0.00	2.13	4.47	0.93**
LRK 516 x DHY 286-1	4.00	5.89	0.41**	3.56	-2.69	0.67**	3.49	-3.49	-0.05
G(B) 20 x G.Cot.10	4.09	0.87	-0.06	3.91	1.54	-0.07	3.60	5.88	0.00
G(B) 20 x DHY 286-1	3.60	1.30	-0.06	3.27	-0.69	0.26*	3.60	1.80	1.57**
G.Cot.100 x G.Cot.10	2.98	2.32	1.66**	3.09	0.02	-0.06	3.49	-6.78	-0.06
G.Cot.100 x DHY 286-1	3.60	10.36	0.06	2.56	0.08	0.29*	3.24	-5.77	0.24*
Mean	2.80	-	-	2.73	-	-	2.71	-	-
S.E. \pm	0.60	6.79	-	0.54	4.18	-	0.09	5.58	-

Table 8: Stability parameters of different genotypes for number of sympodia per plant

Genotypes	CON			GMS			CMS		
	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
76 IH 20	18.73	1.41	0.43	18.73	1.18	3.20	18.73	0.98	0.12
LH 900	13.89	0.88	-2.14	13.89	0.84	-3.06	13.89	0.62	-3.11
PH 93	18.56	2.16	-2.21	18.56	2.01	-2.57	18.56	1.53	-3.28
LRA 5166	13.71	1.39	185.56**	13.71	0.98	25.09**	13.71	0.94	19.10**
LRK 516	14.71	1.35	-0.61	14.71	1.14	1.51	14.71	0.94	-1.03
G(B) 20	17.13	0.31	-0.43	17.13	0.38	-1.55	17.13	0.23	-1.39
G.Cot. 100	15.56	0.97	1.97	15.56	0.75	3.92	15.56	0.67	1.58
G.Cot. 10	18.00	1.65	24.55**	18.00	1.83	14.09**	18.00	1.21	21.79**
DHY 286-1	15.24	1.26	3.09	15.24	1.00	6.26	15.24	0.87	2.90
76 IH 20 x G.Cot.10	15.69	-1.08	-2.46	19.64	0.58	35.48**	18.84	1.87	0.21
76 IH 20 x DHY 286-1	19.47	1.33	11.24**	22.07	1.65	75.23**	19.09	0.27	42.01**
LH 900 x G.Cot.10	16.71	1.80	25.76**	18.58	-1.49	-2.07	19.71	0.87	45.01**
LH 900 x DHY 286-1	17.80	1.43	30.87**	21.96	3.67	-1.17	22.56	1.29	19.31**
PH 93 x G.Cot.10	20.00	1.82	1.25	18.67	-1.22	3.85	16.04	-0.24	-3.30
PH 93 x DHY 286-1	23.16	1.89	35.11**	15.47	0.07	15.39**	21.18	-0.38	4.59
LRA 5166 x G.Cot.10	23.51	2.30	64.55**	20.96	2.63	31.84**	19.71	2.66	-3.17
LRA 5166 x DHY 286-1	18.44	-0.87	-0.12	20.09	6.61	-1.61	20.31	2.32	16.72**
LRK 516 x G.Cot.10	20.16	-0.55	-2.51	22.44	1.67	11.05	20.73	1.68	44.79**
LRK 516 x DHY 286-1	24.00	1.90	15.04**	27.33	0.71	-2.38	24.87	0.09	0.26
G(B) 20 x G.Cot.10	25.31	0.56	2.30	23.36	0.57	11.15*	22.00	0.20	5.49
G(B) 20 x DHY 286-1	23.82	2.28	4.88	22.51	1.17	9.69	23.89	2.43	-1.03
G.Cot.100 x G.Cot.10	24.09	-0.16	34.95**	22.71	1.47	10.07	21.33	2.03	-2.14
G.Cot.100 x DHY 286-1	25.20	2.76	15.98**	24.33	-0.14	-0.53	18.40	-1.14	-1.43
Mean	19.25	-	-	19.37	-	-	18.87	-	-
S.E. \pm	2.71	1.30	-	2.61	1.17	-	21.68	0.91	-

Table 9: Stability parameters of different genotypes for number of bolls per plant

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	30.00	0.67	21.87**	30.00	1.69	12.95*	30.00	0.89	16.70**
LH 900	27.90	1.07	7.06	27.90	1.82	15.62**	27.90	1.16	10.59
PH 93	29.76	-0.46	-0.06	29.76	-0.99	-2.55	29.76	-0.56	-2.39
LRA 5166	31.67	-0.35	51.94**	31.67	-0.07	54.97**	31.67	-0.22	53.54**
LRK 516	26.33	0.81	-2.58	26.33	1.54	-1.87	26.33	0.93	-3.08
G(B) 20	31.38	1.70	53.94**	31.38	3.90	24.56**	31.38	2.15	37.52**
G.Cot. 100	28.36	1.49	30.23**	28.36	3.35	11.10	28.36	1.87	19.13**
G.Cot. 10	33.40	1.09	2.98	33.40	2.30	-2.18	33.40	1.32	-0.75
DHY 286-1	26.09	0.94	11.02*	26.09	2.12	2.89	26.09	1.18	5.95
76 IH 20 x G.Cot.10	43.00	0.96	70.58**	44.44	0.55	60.91**	33.78	1.02	8.42
76 IH 20 x DHY 286-1	45.36	1.23	103.49**	45.16	3.32	182.62**	44.18	0.32	21.81**
LH 900 x G.Cot.10	43.11	1.13	36.11**	28.71	2.42	-3.08	33.02	2.64	4.92
LH 900 x DHY 286-1	40.80	3.03	53.23**	42.38	2.50	0.68	35.38	0.91	16.89**
PH 93 x G.Cot.10	45.71	-0.79	10.76*	42.51	0.54	23.12**	41.73	0.56	0.26
PH 93 x DHY 286-1	44.91	-1.53	-0.17	41.64	-5.09	-3.11	48.42	-1.16	-3.09
LRA 5166 x G.Cot.10	48.22	2.45	0.48	44.42	3.97	-2.02	39.11	3.59	1.94
LRA 5166 x DHY 286-1	53.40	1.76	10.11*	42.76	0.00	15.93**	44.33	0.22	36.26**
LRK 516 x G.Cot.10	36.70	-0.17	66.51**	38.80	-2.25	45.48**	39.49	1.26	21.70**
LRK 516 x DHY 286-1	46.64	1.49	-1.05	44.62	-0.70	-0.20	42.45	2.62	6.97
G(B) 20 x G.Cot.10	47.16	1.23	-0.28	48.58	0.67	63.62**	50.36	3.25	1.79
G(B) 20 x DHY 286-1	46.76	1.09	30.58**	45.29	-4.41	5.77	38.49	-0.25	115.89**
G.Cot.100 x G.Cot.10	43.69	2.81	10.41*	40.29	2.94	1.84	40.60	0.68	-3.95
G.Cot.100 x DHY 286-1	42.44	1.36	79.43**	45.38	-1.67	11.46*	48.53	0.69	86.14**
Mean	38.81	-	-	37.38	-	-	36.73	-	-
S.E. ±	3.91	1.01	-	3.58	1.84	-	3.39	1.02	-

Table 10: Stability parameters of different genotypes for boll weight (g)

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	3.58	0.34	0.36**	3.58	0.38	0.35**	3.58	0.15	0.41**
LH 900	3.10	1.43	-0.01	3.10	1.54	-0.02	3.10	1.73	0.03
PH 93	3.07	1.60	0.02	3.07	1.72	0.01	3.07	1.84	0.18**
LRA 5166	2.86	1.07	0.04	2.86	1.15	0.04	2.86	1.38	-0.02
LRK 516	4.00	0.84	-0.01	4.00	0.90	-0.01	4.00	1.04	-0.01
G(B) 20	3.78	0.17	0.02	3.78	0.18	0.02	3.78	0.28	0.01
G.Cot. 100	3.32	0.40	-0.01	3.32	0.43	-0.02	3.32	0.46	-0.01
G.Cot. 10	3.30	0.22	-0.01	3.30	0.24	-0.01	3.30	0.24	-0.01
DHY 286-1	3.60	0.28	0.27**	3.60	0.31	0.27**	3.60	0.11	0.31**
76 IH 20 x G.Cot.10	3.44	1.57	0.34**	3.31	1.70	-0.01	3.15	1.77	0.04
76 IH 20 x DHY 286-1	3.75	2.73	-0.01	3.76	2.29	0.01	3.16	1.97	0.34**
LH 900 x G.Cot.10	3.88	0.15	0.49**	3.83	-0.17	-0.02	3.47	0.07	0.00
LH 900 x DHY 286-1	4.18	1.61	0.02	4.16	1.21	-0.02	3.84	1.73	0.33**
PH 93 x G.Cot.10	3.55	2.57	0.05	3.52	0.45	0.00	3.14	1.86	0.03
PH 93 x DHY 286-1	3.05	1.23	0.00	3.37	2.08	0.00	2.99	1.87	0.11**
LRA 5166 x G.Cot.10	3.64	1.42	0.20**	3.87	1.25	0.09**	3.60	0.33	0.00
LRA 5166 x DHY 286-1	3.20	1.19	0.03	3.44	1.79	0.41**	3.23	1.57	0.24**
LRK 516 x G.Cot.10	4.23	-0.16	0.00	3.97	-0.63	0.15**	3.44	1.46	0.01
LRK 516 x DHY 286-1	4.03	1.39	0.13**	4.26	1.19	0.12**	3.93	0.03	0.14**
G(B) 20 x G.Cot.10	5.30	0.26	0.18**	4.04	0.31	0.12**	3.66	-0.41	-0.02
G(B) 20 x DHY 286-1	5.22	1.24	0.10**	4.00	2.88	0.09**	4.14	1.93	0.05
G.Cot.100 x G.Cot.10	4.34	-0.71	0.21**	4.31	0.05	0.07	4.19	-0.14	-0.01
G.Cot.100 x DHY 286-1	3.78	2.17	0.01	3.41	1.75	0.64	3.67	0.93	0.50**
Mean	3.66	-	-	3.64	-	-	3.48	-	-
S.E. ±	0.24	0.49	-	0.24	0.52	-	0.25	0.64	-

Table 11: Stability parameters of different genotypes for number of seeds per boll

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	21.68	0.80	-2.00	21.68	0.80	-2.12	21.68	0.65	-2.29
LH 900	19.67	2.34	-1.75	19.67	2.29	-1.71	19.67	0.22	-2.65
PH 93	16.84	3.97	3.46	16.84	3.86	4.16	16.84	3.99	-0.86
LRA 5166	21.29	0.56	-1.08	21.29	0.52	-1.13	21.29	0.68	-1.88
LRK 516	20.07	-0.50	23.39**	20.07	-0.65	23.04**	20.07	0.41	22.98**
G(B) 20	20.00	1.78	15.30	20.00	1.89	14.56**	20.00	0.89	17.80**
G.Cot. 100	17.36	1.92	0.35	17.36	1.86	-0.23	17.36	1.97	-1.94
G.Cot. 10	21.33	0.05	7.47	21.33	-0.05	7.37	21.33	0.57	6.47
DHY 286-1	19.43	3.77	-2.16	19.43	3.74	-2.26	19.43	3.40	-1.66
76 IH 20 x G.Cot.10	20.90	-1.27	6.59	19.62	0.25	-2.21	18.16	1.89	-2.56
76 IH 20 x DHY 286-1	24.07	2.44	54.81**	25.54	-7.83	59.82**	20.73	-1.15	3.00
LH 900 x G.Cot.10	21.03	-1.47	0.18	19.10	4.44	28.56**	16.69	0.92	2.73
LH 900 x DHY 286-1	25.32	1.02	31.78**	23.40	-1.27	1.71	21.03	0.54	121.79**
PH 93 x G.Cot.10	16.68	3.40	-1.89	21.77	-6.39	31.84**	17.28	-0.59	3.75
PH 93 x DHY 286-1	18.70	1.96	-2.12	18.61	6.36	-0.50	20.77	0.18	1.89
LRA 5166 x G.Cot.10	24.13	0.20	-1.62	20.23	3.45	-2.21	19.36	2.51	0.73
LRA 5166 x DHY 286-1	25.12	0.22	1.25	21.79	6.36	-0.58	19.73	5.09	7.77
LRK 516 x G.Cot.10	21.02	-4.06	43.29**	25.41	1.08	19.38**	19.52	-3.22	4.66
LRK 516 x DHY 286-1	26.59	4.33	6.99	27.29	-1.90	-1.41	23.38	0.18	21.30**
G(B) 20 x G.Cot.10	25.17	-0.45	10.21**	26.07	0.53	2.12	24.71	3.17	-2.10
G(B) 20 x DHY 286-1	27.17	-0.53	46.12**	28.64	2.66	4.03	29.33	0.70	-0.80
G.Cot.100 x G.Cot.10	21.49	-5.37	-1.38	26.88	-3.05	-1.86	25.76	-3.08	9.53
G.Cot.100 x DHY 286-1	26.26	2.37	-1.98	22.53	4.04	4.28	24.47	1.05	9.16
Mean	21.75	-	-	21.93	-	-	20.80	-	-
S.E. ±	24.8	3.03	-	2.26	2.74	-	2.44	2.76	-

Table 12: Stability parameters of different genotypes for seed index (g)

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	7.44	0.54	-0.04	7.44	0.09	0.10	7.44	-0.18	0.14
LH 900	8.19	3.27	0.06	8.19	4.19	0.05	8.19	9.22	0.59
PH 93	8.00	1.19	-0.36	8.00	1.39	-0.24	8.00	2.97	-0.12
LRA 5166	7.86	0.93	-0.21	7.86	1.37	-0.38	7.86	3.14	-0.33
LRK 516	8.61	-2.30	1.08	8.61	-3.60	-0.34	8.61	-8.33	0.33
G(B) 20	9.90	1.08	-0.24	9.90	1.51	-0.37	9.90	3.39	-0.30
G.Cot. 100	10.59	1.65	3.43**	10.59	3.54	0.77	10.59	8.69	0.28
G.Cot. 10	9.16	-1.14	0.33	9.16	-2.00	-0.29	9.16	-4.73	-0.32
DHY 286-1	8.21	0.25	0.34	8.21	0.15	-0.33	8.21	0.23	-0.29
76 IH 20 x G.Cot.10	9.09	4.27	2.35**	7.51	2.73	-0.22	6.86	8.78	-0.34
76 IH 20 x DHY 286-1	8.17	4.00	3.52**	9.27	-0.66	0.99	8.21	-2.33	0.96
LH 900 x G.Cot.10	6.99	1.02	-0.34	8.58	2.94	-0.22	7.27	5.59	-0.32
LH 900 x DHY 286-1	8.83	-0.27	-0.12	9.07	2.38	0.15	8.87	2.64	-0.29
PH 93 x G.Cot.10	7.19	3.56	-0.12	7.49	0.34	-0.11	7.93	-0.13	0.47
PH 93 x DHY 286-1	7.53	1.20	2.47**	8.97	2.53	4.63**	7.62	0.71	0.19
LRA 5166 x G.Cot.10	7.68	2.43	-0.13	9.06	-2.77	-0.33	8.93	-3.19	0.08
LRA 5166 x DHY 286-1	7.18	1.62	-0.32	7.11	3.11	2.47**	7.84	0.23	0.24
LRK 516 x G.Cot.10	9.97	-2.27	-0.04	9.38	-2.39	0.02	8.32	-5.98	-0.32
LRK 516 x DHY 286-1	9.26	-1.31	-0.06	9.79	0.69	0.72	8.89	-8.01	0.05
G(B) 20 x G.Cot.10	8.81	0.83	-0.28	9.14	2.32	-0.11	9.36	11.47	0.06
G(B) 20 x DHY 286-1	8.82	-1.09	-0.03	8.46	1.65	3.43**	9.96	-3.54	2.90
G.Cot.100 x G.Cot.10	9.20	-0.42	0.36	9.42	-1.68	-0.19	9.23	-2.84	0.86
G.Cot.100 x DHY 286-1	10.02	3.95	3.15**	9.61	5.16	2.24**	10.20	5.21	-0.32
Mean	8.55	-	-	8.73	-	-	8.58	-	-
S.E. ±	0.68	1.33	-	0.67	1.67	-	0.49	2.84	-

Table 13: Stability parameters of different genotypes for ginning percentage (%)

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	31.59	-0.32	-1.83	31.59	-0.64	-1.76	31.59	-0.46	-1.57
LH 900	34.77	-0.73	-1.81	34.77	-0.64	-1.53	34.77	-0.73	-1.58
PH 93	41.26	-0.31	3.03	41.26	-4.25	-1.67	41.26	-1.82	0.95
LRA 5166	35.38	-2.57	-1.78	35.38	1.04	1.30	35.38	-1.32	0.52
LRK 516	37.03	-0.48	-1.38	37.03	1.49	-1.74	37.03	0.25	-0.94
G(B) 20	34.90	-5.69	-0.33	34.90	3.02	13.19**	34.90	-2.64	10.67**
G.Cot. 100	33.67	3.28	-0.15	33.67	-2.91	2.97	33.67	1.08	4.63
G.Cot. 10	36.08	0.31	-1.19	36.08	-1.70	-1.80	36.08	-0.49	-0.92
DHY 286-1	36.33	-0.77	4.46	36.33	4.93	-1.70	36.33	1.36	3.72
76 IH 20 x G.Cot.10	36.86	9.33	16.43**	38.62	0.96	-1.82	33.51	6.03	13.68**
76 IH 20 x DHY 286-1	35.82	4.48	19.84**	35.91	-4.61	12.75**	33.39	2.89	0.22
LH 900 x G.Cot.10	34.96	6.76	0.03	32.79	-4.64	21.42**	31.81	1.29	5.82
LH 900 x DHY 286-1	34.77	-0.19	6.99*	35.78	2.75	0.46	33.11	4.38	17.35**
PH 93 x G.Cot.10	41.57	1.70	-1.02	41.43	1.16	23.14**	39.73	-2.92	14.41**
PH 93 x DHY 286-1	44.50	-0.71	0.83	39.19	1.86	19.55**	39.25	-2.00	5.59
LRA 5166 x G.Cot.10	39.14	0.46	-0.79	36.82	2.82	13.97**	34.42	10.41	9.16**
LRA 5166 x DHY 286-1	33.84	3.97	-0.72	34.98	8.58	10.28**	35.61	-3.94	13.20**
LRK 516 x G.Cot.10	34.14	5.89	52.21**	34.30	0.14	-0.49	37.49	8.68	3.91
LRK 516 x DHY 286-1	36.20	5.61	4.27	33.55	1.29	13.93**	35.51	6.82	8.37**
G(B) 20 x G.Cot.10	34.85	-0.70	-1.82	37.03	7.19	14.09**	31.43	-0.15	4.52
G(B) 20 x DHY 286-1	32.72	1.39	-0.91	33.61	1.18	16.25**	35.24	-2.22	19.31**
G.Cot.100 x G.Cot.10	32.11	-2.22	43.97**	34.26	8.50	11.83**	33.17	2.39	20.24**
G.Cot.100 x DHY 286-1	37.48	-1.40	-1.84	28.67	-4.04	-1.82	35.71	-3.93	-1.48
Mean	36.08	-	-	35.99	-	-	35.23	-	-
S.E. ±	1.98	4.00	-	2.09	5.70	-	2.01	3.28	-

Table 14: Stability parameters of different genotypes for seed cotton yield per plant (g)

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	93.49	0.32	437.71**	93.49	0.44	405.75**	93.49	0.33	468.02**
LH 900	86.50	1.16	-16.39	86.50	1.47	-21.57	86.50	1.32	6.12
PH 93	75.89	0.33	22.34	75.89	0.43	14.64	75.89	0.37	35.42
LRA 5166	81.27	0.30	520.13**	81.27	0.42	487.07**	81.27	0.31	550.77**
LRK 516	96.40	0.77	-18.01	96.40	0.92	-1.63	96.40	0.88	-19.74
G(B) 20	104.78	0.84	129.46**	104.78	1.09	84.59*	104.78	0.94	177.31**
G.Cot. 100	84.03	0.83	48.30	84.03	1.07	20.15	84.03	0.94	82.98*
G.Cot. 10	104.15	0.77	-24.22	104.15	0.91	-20.08	104.15	0.82	-16.72
DHY 286-1	90.93	0.88	10.32	90.93	1.13	-7.90	90.93	1.00	38.03
76 IH 20 x G.Cot.10	113.08	1.37	506.66**	106.35	1.55	863.45**	80.82	0.69	34.61
76 IH 20 x DHY 286-1	118.01	1.80	721.76**	128.08	2.27	2282.77**	104.08	1.71	786.00**
LH 900 x G.Cot.10	115.52	0.80	26.50	83.92	0.69	-20.80	82.03	1.28	359.19**
LH 900 x DHY 286-1	135.04	2.12	23.58	125.18	1.54	3.22	100.56	1.70	972.45**
PH 93 x G.Cot.10	112.37	1.12	-18.27	105.03	0.82	48.37	93.95	1.17	481.60**
PH 93 x DHY 286-1	101.68	0.28	-13.67	104.51	0.26	236.69	111.40	0.08	-4.50
LRA 5166 x G.Cot.10	140.39	2.11	-3.30	127.10	1.96	-10.58	110.12	1.44	162.35**
LRA 5166 x DHY 286-1	126.07	1.29	49.51	107.10	0.78	212.26**	107.65	0.91	-15.37
LRK 516 x G.Cot.10	119.14	0.34	133.37**	117.86	1.02	371.31**	99.28	1.27	179.66**
LRK 516 x DHY 286-1	141.82	0.97	466.90**	146.70	0.44	317.58**	126.86	0.76	522.64**
G(B) 20 x G.Cot.10	161.36	1.17	109.52**	154.05	1.03	267.92**	145.29	1.05	81.10*
G(B) 20 x DHY 286-1	158.44	1.07	116.02**	168.42	0.98	-18.53	130.99	1.09	1997.74**
G.Cot.100 x G.Cot.10	127.89	0.99	55.06	126.46	0.85	53.11	120.82	0.84	315.40**
G.Cot.100 x DHY 286-1	121.21	1.47	747.58**	112.33	0.95	1.53	129.97	0.50	296.51**
Mean	113.35	-	-	108.72	-	-	102.54	-	-
S.E. ±	9.99	0.35	-	11.48	0.51	-	13.16	0.52	-

Table 15: Stability parameters of different genotypes for 2.5 per cent span length (mm)

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	23.15	1.62	-0.99	23.15	1.88	-0.47	23.15	1.48	-0.80
LH 900	23.46	1.00	-1.01	23.46	1.17	-0.74	23.46	0.91	-0.87
PH 93	22.28	1.33	-0.72	22.28	1.51	-0.04	22.28	1.20	-0.47
LRA 5166	24.56	1.49	2.88	24.56	1.58	4.71**	24.56	1.32	3.49*
LRK 516	25.62	-0.18	-2.25	25.62	-0.35	2.21	25.62	-0.19	2.32
G(B) 20	25.14	0.65	-0.52	25.14	0.70	-0.08	25.14	0.57	-0.32
G.Cot. 100	27.30	1.52	1.04	27.30	1.90	0.18	27.30	1.42	0.82
G.Cot. 10	23.23	0.54	2.35	23.23	0.77	1.97	23.23	0.52	2.31
DHY 286-1	24.91	0.50	-0.66	24.91	0.63	-0.63	24.91	0.46	-0.58
76 IH 20 x G.Cot.10	24.39	0.55	-0.03	23.66	0.78	0.79	25.22	1.07	6.78**
76 IH 20 x DHY 286-1	24.11	1.09	-0.23	24.56	1.03	-0.66	24.34	2.54	0.54
LH 900 x G.Cot.10	23.97	-0.01	-1.00	23.55	0.64	1.22	26.08	1.12	3.33*
LH 900 x DHY 286-1	22.54	1.51	-0.66	26.15	1.83	-0.71	26.49	1.10	4.32**
PH 93 x G.Cot.10	23.67	1.09	-0.33	24.40	1.39	0.05	22.05	1.04	1.64
PH 93 x DHY 286-1	24.59	1.40	0.18	23.32	1.38	2.13	24.49	1.17	0.55
LRA 5166 x G.Cot.10	25.99	-0.56	-0.53	24.28	0.83	0.11	25.49	0.44	10.00**
LRA 5166 x DHY 286-1	25.07	1.20	-0.97	23.96	1.80	-0.82	24.23	0.17	2.19
LRK 516 x G.Cot.10	26.34	1.53	2.97	25.06	1.35	-0.56	25.51	1.87	1.71
LRK 516 x DHY 286-1	23.36	1.82	1.63	23.88	0.58	-0.76	24.26	1.93	3.75*
G(B) 20 x G.Cot.10	24.07	0.45	4.62**	24.42	-0.23	4.80**	25.77	0.99	-0.89
G(B) 20 x DHY 286-1	22.88	1.18	3.30	24.47	0.98	4.53**	25.97	-0.02	-0.75
G.Cot.100 x G.Cot.10	27.27	1.91	10.46**	23.50	0.08	5.83**	26.68	0.71	2.20
G.Cot.100 x DHY 286-1	26.83	1.37	18.18**	23.17	0.78	0.56	25.35	1.17	0.80
Mean	24.55	-	-	24.26	-	-	24.84	-	-
S.E. ±	1.19	0.85	-	0.96	0.81	-	1.16	0.75	-

Table 16: Stability parameters of different genotypes for fibre strength (g/tex)

Genotypes	CON			GMS			CMS		
	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i	Mean	b _i	S ² d _i
76 IH 20	17.57	1.87	-0.52	17.57	2.29	-0.61	17.57	2.57	0.13
LH 900	16.48	2.92	-0.32	16.48	3.08	-0.16	16.48	3.47	0.63
PH 93	17.89	0.33	2.05	17.89	2.64	-0.76	17.89	3.11	-0.20
LRA 5166	18.18	-0.64	1.85	18.18	1.65	0.51	18.18	2.02	1.06
LRK 516	19.08	0.84	-0.42	19.08	0.87	-0.73	19.08	0.82	-0.10
G(B) 20	18.91	-0.93	-0.66	18.91	-0.68	-1.03	18.91	-0.74	-0.36
G.Cot. 100	19.59	-0.17	-0.67	19.59	-0.23	-1.45	19.59	-0.26	-0.81
G.Cot. 10	18.36	0.04	0.06	18.36	-1.18	-1.14	18.36	-1.40	-0.52
DHY 286-1	20.17	2.00	0.01	20.17	-3.02	-0.93	20.17	-3.44	-0.19
76 IH 20 x G.Cot.10	18.84	1.71	0.20	18.30	4.21	-1.46	19.56	0.42	-0.67
76 IH 20 x DHY 286-1	17.67	1.42	-0.64	19.36	3.66	-0.54	17.81	2.53	-0.71
LH 900 x G.Cot.10	18.69	0.82	3.07**	18.04	1.54	1.49	20.52	-0.56	-0.77
LH 900 x DHY 286-1	19.13	1.34	-0.66	19.17	1.68	-0.62	20.52	-0.29	-0.64
PH 93 x G.Cot.10	19.08	1.89	-0.67	17.56	-0.82	-0.68	16.77	2.71	-0.78
PH 93 x DHY 286-1	17.92	4.42	9.42**	18.14	1.01	-0.92	19.91	3.10	-0.81
LRA 5166 x G.Cot.10	18.84	1.98	2.22	19.74	-0.11	-1.26	18.58	-0.42	-0.67
LRA 5166 x DHY 286-1	19.99	3.97	-0.61	17.68	2.83	-1.37	20.40	3.05	-0.75
LRK 516 x G.Cot.10	20.82	2.88	-0.67	19.44	2.83	1.88	17.51	2.18	-0.80
LRK 516 x DHY 286-1	18.68	0.76	-0.64	20.17	0.50	-1.44	19.40	2.86	-0.80
G(B) 20 x G.Cot.10	19.83	1.45	-0.27	19.09	-1.70	-1.46	19.52	0.83	-0.67
G(B) 20 x DHY 286-1	19.07	1.11	1.06	19.46	0.77	-1.18	18.56	1.21	-0.55
G.Cot.100 x G.Cot.10	20.38	0.71	0.05	19.46	2.06	-0.13	19.47	1.54	-0.80
G.Cot.100 x DHY 286-1	18.90	0.75	0.68	18.52	2.06	-1.35	19.37	0.91	-0.52
Mean	18.92	-	-	18.71	-	-	18.87	-	-
S.E. ±	0.79	1.40	-	0.62	1.62	-	0.42	1.27	-

Days to 50 per cent flowering

In conventional method, the estimates of stability parameters revealed that, the parents G(B) 20 and LRA 5166 manifested low mean values for days to flowering accompanied by regression co-efficient (b_i) equal to approximately unity (b_i = 1.0) and least deviation from regression. The parent LH 900 had low mean, regression co-efficient equal to unity and non-significant deviation from regression. Among crosses three crosses viz., LRK 516 x G.Cot.10, LRA 5166 x G.Cot.10 and

PH 93 x DHY 286-1 were characterized by having low mean values with b_i near to unity and low S²d_i.

In GMS method, only one parent G.Cot.10 recorded low mean value, b_i value equal to approximately unity (b_i = 1.00) and low deviation from regression (S²d_i). Two crosses viz., PH 93 x G.Cot.10 and 76 IH 20 x DHY 286-1 exhibited low mean value, b_i value equal to approximately unity and low S²d_i.

In CMS-R system, two parents *viz.*, G(B) 20 and G.Cot.10 registered low mean values and S^2di . alongwith bi value nearer to one. Among the crosses, only one cross LRK 516 x G.Cot.10 exhibited low mean value, approximately equal to one bi value and low S^2di value.

Plant height (cm)

In conventional method, the parents LRK 516 and LRA 5166 showed lowest mean and S^2di values having bi values greater than one. The cross LRK 516 x G.Cot.10 showed low mean value, approximately equal to one bi value and low S^2di value. Three crosses *viz.*, LH 900 x DHY 286-1, PH 93 x DHY 286-1 and G.Cot.100 x G.Cot.10 showed nearer to one bi value, high mean and high S^2di values.

In GMS method, the parent DHY 286-1 showed low mean and S^2di value and bi-value nearer to one. Among the crosses, three crosses *viz.*, LH 900 x G.Cot.10, LRK 516 x G.Cot.10, LRK 516 x DHY 286-1 exhibited low mean and S^2di values and bi value nearer to unity.

In CMS method, the parent DHY 286-1 showed low mean and S^2di value and near to one bi value. The cross LRK 516 x G.Cot.10 exhibited lowest mean value, nearer to one bi value and low S^2di value.

Number of monopodia per plant

In conventional method, the parents DHY 286-1 and LRK 516 showed highest mean values, low S^2di values and bi value greater than one. Among the crosses, two crosses *viz.*, G(B) 20 x G.Cot.10 and G(B) 20 x DHY 286-1 showed highest mean values low S^2di values with bi values nearer to one.

In GMS method, two parents *viz.*, LRA 5166 and DHY 286-1 showed highest mean values, regression coefficient greater than one and low deviation from regression. The cross G(B) 20 x G.Cot.10 recorded high mean value, greater than one bi value and low S^2di value.

In CMS method, the parents G.Cot.100 exhibited high mean, nearer to one bi value but significant deviation from regression. The parent LRA 5166 and DHY 286-1 showed highest mean values and lower than one bi values and lower deviation from regression values. Among the crosses, LRA 5166 x G.Cot.10 and G (B) 20 x DHY 286-1 exhibited higher mean values, greater than one regression coefficient and significant S^2di values.

Number of sympodia per plant

The parents 76 IH 20, G.Cot.100, DHY 286-1 recorded high mean values, nearer to one regression coefficient values and low deviation from regression values in all three methods *viz.*, conventional, GMS and CMS method.

In conventional crosses 76 IH 20, DHY 286-1, G(B) 20 x DHY 286-1 and G.Cot.100 x DHY 286-1 exhibited high mean values, greater than one bi values but significant deviation from regression.

In GMS based crosses, LRK 516 x DHY 286-1, G(B) 20 x DHY 286-1 and G.Cot.100 x G.Cot.10 showed high mean values, nearer to one bi values and low S^2di value.

In CMS based crosses, LH 900 x G.Cot.10 and LH 900 x DHY 286-1 recorded high mean values, nearer to one regression coefficient and significant S^2di values.

Number of bolls per plant

In conventional method, the parents *viz.*, LH 900, LRK 516, G.Cot.10 and DHY 286-1 recorded high mean values, approximately unit regression coefficient (bi) and lower

deviation from regression values. Among the crosses, 76 IH 20 x G.Cot.10, 76 IH 20 x DHY 286-1, LH 900 x G.Cot.10, G(B) 20 x G.Cot.10 and G(B) 20 x DHY 286-1 recorded high mean values, nearer to unity bi value and high value of S^2di .

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.

In CMS method, the parents *viz.*, LH 900, LRK 516, G.Cot.10 and DHY 286-1 registered high mean values with approximately unit regression co-efficient (bi) and least deviation from regression. Among the crosses, 76 IH 20 x G.Cot.10, LH 900 x DHY 286-1 and LRK 516 x G.Cot.10 displayed high number of bolls per plant coupled with regression coefficient approximately near unity and significant deviation from regression except 76 IH 20 x DHY 286-1.

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 all the three methods *viz.*, conventional, GMS and CMS method.

In conventional crosses, PH 93 x DHY 286-1, LRA 5166 x DHY 286-1 and G(B) 20 x DHY 286-1 registered high mean values with nearer to unity bi 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.

In CMS based crosses, G.Cot.100 x DHY 286-1 recorded high mean with approximately one bi-values and significant S^2di , whereas crosses *viz.*, LH 900 x DHY 286-1, LRK 516 x G.Cot.10 and G(B) 20 x DHY 286-1 exhibited high mean values and greater than one bi with low deviation from regression.

Number of seeds per boll

In all the three methods *viz.*, conventional, GMS and CMS, the parent 76 IH 20 recorded high mean with nearer to one regression coefficient and low S^2di value, whereas LRA 5166 registered high mean, regression coefficient less than one and least deviation from regression.

In conventional and GMS based crosses, LH 900 x DHY 286-1 and LRK 516 x G.Cot.10 exhibited high mean values with approximately equal to unity regression coefficient and significant deviation from regression. In CMS based crosses, G.Cot.100 x DHY 286-1 recorded high mean, regression coefficient equal to approximately unity and low S^2di values.

Seed index (g)

In conventional method, the parents PH 93 and G(B) 20 showed high mean accompanied by regression coefficient approximately equal to unity with low deviation from regression whereas the parent G.Cot.100 showed highest mean with greater than one bi and significant S^2di . Among the crosses, G(B) 20 x G.Cot.10 exhibited high mean with approximately equal to one bi and low S^2di . The crosses LH 900 x G.Cot.10 and PH 93 x DHY 286-1 recorded moderate mean with approximately equal to one bi and low deviation from regression.

In GMS method, parents *viz.*, PH 93, LRA 5166 and G(B) 20 registered high mean values, nearer to one regression coefficient and low S^2di values. Among the crosses, LRK 516 x DHY 286-1 registered high mean with nearer to one regression coefficient and low deviation from regression.

In CMS method, the parents G(B) 20 and G.Cot.100 showed highest seed index with greater than one regression coefficient and low deviation from regression. Among the crosses, G.Cot.100 x DHY 286-1 and LH 900 x DHY 286-1 registered high mean values with greater than one regression coefficient and low deviation from regression.

Ginning percentage (%)

In conventional method, the parents PH 93 and LRK 516 recorded highest ginning percentage with less than one regression coefficient and low deviation from regression. Among crosses, PH 93 x DHY 286-1 and LRA 5166 x G.Cot.10 showed highest mean with regression coefficient less than one and low deviation from regression.

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.

In CMS method, PH 93 and LRK 516 exhibited highest ginning percentage with lower than one regression coefficient and low deviation from regression. The crosses *viz.*, PH 93 x G.Cot.10, PH 93 x DHY 286-1, G(B) 20 x DHY 286-1 and G.Cot.100 x DHY 286-1 recorded high mean values with less than one regression coefficient and low deviation from regression except the crosses PH 93 x G.Cot.10 and G(B) 20 x DHY 286-1 which showed significant deviation from regression.

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 deviation from regression except G(B) 20 which showed significant deviation from regression, in all the three methods *viz.*, conventional, GMS and CMS methods.

In conventional crosses, the crosses *viz.*, LH 900 x G.Cot.10, PH 93 x G.Cot.10, LRK 516 x DHY 286-1, G(B) 20 x G.Cot.10, G(B) 20 x DHY 286-1, G.Cot.100 x G.Cot.10 showed high mean values with approximately equal to one regression coefficient and low and non significant deviation from regression except the crosses *viz.*; LRK 516 x DHY 286-1, G(B) 20 x G.Cot.10 and G(B) 20 x DHY 286-1 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.

In CMS based crosses, crosses *viz.*, PH 93 x G.Cot.10, LRA 5166 x DHY 286-1, LRK 516 x G.Cot.10, G(B) 20 x G.Cot.10, G(B) 20 x DHY 286-1 and G.Cot.100 x G.Cot.10 exhibited high mean values with regression coefficient approximately equal to one but high S^2di value except cross LRA 5166 x DHY 286-1 which showed low and non significant deviation from regression.

2.5 per cent span length (mm)

In all the three methods, 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 conventional crosses, 76 IH 20 x DHY 286-1, PH 93 x G.Cot.10, LRA 5166 x DHY 286-1 and G.Cot.100 x DHY 286-1 registered high mean with nearer to one regression coefficient and low values of deviation from regression.

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 .

In CMS based crosses, LH 900 x G.Cot.10, LH 900 x DHY 286-1, PH 93 x G.Cot.10, PH 93 x DHY 286-1, G(B) 20 x G.Cot.10 and G.Cot.100 x DHY 286-1 exhibited high mean with nearer to one regression coefficient and low deviation from regression.

Fibre strength (g/tex)

In all the three methods, 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 conventional crosses, LH 900 x G.Cot.10, LRK 516 x DHY 286-1, G(B) 20 x DHY 286-1 and G.Cot.100 x DHY 286-1 crosses recorded high mean values with nearer to one regression coefficient and lower values of deviation from regression coefficient.

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.

In CMS based crosses, G(B) 20 x DHY 286-1 and G.Cot.100 x DHY 286-1 showed high mean values with approximately equal to one regression coefficient and low values of deviation from regression.

Discussion:

Pooled analysis of variance revealed highly significant variation among the genotypes for all the characters and the three environments for all the characters except number of monopodia per plant, seeds per boll and ginning percentage against pooled error. The mean square due to GxE interaction were highly significant for all the characters except days to 50 per cent flowering, 2.5 per cent span length and fibre strength when tested against pooled error suggesting that the genotypes interacted considerably with the environment in the expression of these characters. Mean squares due to environment (linear) were highly significant for all the characters except ginning percentage which indicated considerable differences among environment and their predominant effects on these characters. The variances due to GxE interaction (linear) were significant for all the characters except days to 50 per cent flowering, ginning percentage, 2.5 per cent span length and fibre strength, indicating significant differences among the genotypes for their regression on environmental indices. The non-significant GxE (linear) variances for days to 50 per cent flowering, ginning percentage, 2.5 per cent span length and fibre strength, indicated the need of interpreting the results by considering numerical values of regression co-efficient and giving greater emphasis for deviation from regression parameter for these characters. The prediction of performance based on regression

analysis might not be reliable as observed from the significant pooled deviation for all the characters except days to 50 per cent flowering, plant height, seed index, 2.5 per cent span length and fibre strength. When tested against pooled error indicating their fluctuating performance over environments. The above findings are in confirmation with Jinks and Stevans (1959)^[7], Bucio Alanis (1966)^[2], Perkins and Jinks (1968)^[10], Gupta and Katiyar (1980)^[6], Bhandari (1980)^[1] and Pavasia and Shukla (1997).

According to the model of Eberhart and Russell (1966)^[3], a variety may be said to be stable over different environments, if it shows unit regression co-efficient ($b_i=1$) with lowest deviation (non significant) from the regression ($S^2_{di} = 0$). 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.

In the present investigation when these parameters were studied for each genotype separately, none of the parents/hybrids exhibited average stability for all the characters. Thus any generalization regarding stability of genotype for all the characters is too difficult since the genotype may not simultaneously exhibit uniform responsiveness and stability patterns for these characters (Bhandari 1980; Gill and Singh 1982^[5] and Pavasia and Shukla, 1997) 1999^[1, 5, 9]. It is therefore suggested that in order to produce stable hybrid actual testing of hybrids over a range of environments would be necessary.

In the present investigation, hybrids showed better performance than the corresponding parents. 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 in all the three methods. In conventional crosses, LH-900 x G.Cot.10, PH-93 x G.Cot.10, LRK-516 x DHY 286-1, G(B) 20 x G.Cot.10, G(B) 20 x DHY-286-1, G.Cot.100 x G.Cot.10 showed high mean values with approximately equal to one regression coefficient and low deviation from regression. In GMS based crosses, six *viz.*, PH-93 x G.Cot.10, LRK 516XG.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^2_{di} values. In CMS based crosses, PH-93 x G.Cot.10, LRA-5166 x DHY-286-1, LRK-516 x G.Cot.10, G(B) 20 x G.Cot.10, G(B) 20 x DHY-286-1 and G.Cot.100 x G.Cot.10 exhibited high mean values with regression coefficient approximately equal to one and high S^2_{di} values except LRA-5166 x DHY 286-1. In all the three methods the crosses *viz.*, 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 G.Cot.10 showed high mean values with regression coefficient approximately equal to one and low deviation from regression. Hence these genotypes can be considered as most stable and can be recommended for wider adaptability. Thus parents showing considerable stability for yield produced hybrids having greater productivity and stability. These hybrids were also stable for yield contributing characters *viz.*, number of bolls, boll weight, number of monopodia, number of sympodia and ginning percentage.

The stability parameters *viz.*, mean, regression co-efficient (b_i) and deviation from regression coefficient (S^2_{di}) in conventional, GMS and CMS based crosses for seed cotton yield per plant (Table 2.10) stated that the conventional crosses showed high mean values and approximately unity regression coefficient and low deviation from regression as compared to GMS and CMS based crosses. But the GMS and

CMS based crosses also exhibited nearer to one b_i and low S^2_{di} values, which indicated that the GMS and CMS based crosses could also show stable performance over locations. Almost identical results have been reported by Srinivasan and Gururajan, 1978; Nizama *et al.*, 1988; Shroff *et al.*, 1989; Tuteja *et al.*, 1999^[14, 8, 13, 15].

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