GENOTYPE-ENVIRONMENT INTERACTION FOR YIELD AND ITS ATTRIBUTES IN MAIZE (*ZEA MAYS* L.)

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Abstract

Genotype-environment interaction and phenotypic stability of the present-day 8 maize inbred lines and their 28 hybrids was assessed as against 4 checks during *Kharif* 2012-2013 at 3 different agro-climatic locations: Gwalior, Indore and Delhi. Significant results were observed for all the traits studied related to grain yield. Pooled deviations were found significant for most of the traits studied except for the 3 characters, days to maturity, grain yield per plant and shelling percent. Genotype – environment interaction of the test hybrid CML132 × LM16 is best suited for Delhi agro-climate followed by at Indore. This test hybrid performed better than the best standard check PMH 1, insofar, as the stability criteria of Eberhart and Russel (1966) is concerned.

Key words : Stability, genotype, environment, G × E, yield components.

Introduction

Maize is one of the leading world cereals both in terms of production and productivity. It possesses great genetic diversity and can be grown across varied agro-ecological zones (Ferdu *et al.*, 2002). The improved genotypes should have good adaptability across a range of diverse environments because unstable varieties are major source of risks (Javed *et al.*, 2006). The phenotypic performance is not the same under diverse agro ecological conditions. Phenotypic stability is most important for the selection of a variety. Since maize is a highly cross pollinated crop, it offers a scope for exploitation of heterosis by development of hybrids. However, the performance of hybrids is not the same at all the places and is dependent on the environment of that place. This is studied under the topic 'genotype × environment interaction'. Hence, it becomes obvious for a plant breeder to select hybrids which perform consistently superior across most of the environments and this is known as stability. The cause of yield stability is unclear, but, the mechanisms of stability fall into four general categories, genetic heterogeneity, yield component compensation, stress tolerance and capacity to recover rapidly from stress. Since the phenotype of a hybrid is the resultant of Genotype (G) × Environment (E), a large G × E interaction effect causes problem to the breeder in selecting a genotype with consistent performance across environments. This is statistically detected as a different response pattern among the genotypes across the environments, and biologically this will occur when the contributions of genes regulating the trait differ among environments (Basford and Cooper, 1998). Analysis of variance is useful in estimating the existence, significance and magnitude of G × E interaction, but doesn't explain the importance and implications, therefore regression analysis is an important biometrical approach of measuring G × E effect (Showemimo, 2007). Therefore, the present investigation was carried out in order to understand changes in the relative performance of maize inbred lines and their single crosses across different environments and their stability which could be further used in breeding programme.

Materials and Methods

The experimental material consisted of half diallel of 8 present day inbred lines and their 32 test hybrids tested against 4 national checks hybrids (table 2). The experiment was carried out during *Kharif*, 2013 by raising the crop at three locations *viz.* College of Agriculture, Gwalior, Indian Agriculture Research Institute, Delhi and College of Agriculture, Indore, India. The experiment was laid out in RCBD in three replications. The plot size for each genotype was 3.0 m × 0.75 m. The sample size constituted

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Table 1: Pooled analysis of variance for different traits among forty genotypes of maize

Source of variance	Df	Grain yield per plant (gm)	Days to 50% tasselling	Days to 50% silking	Days to 75% dry husk	Plant height (cm)	Ear height placement (cm)	cob length	Cob girth	No.of kernel rows per cob	No.of Kernels per row	100 seeds weight	Shelling %
Genotypes	39	1779.23**	21.75**	18.96**	25.51**	1974.61**	1101.68**	9.06**	0.50**	5.35**	65.06**	31.40**	39.01**
Environments	2	26533.09**	1352.76**	1033.36**	913.88**	28551.27**	16745.51**	71.55**	3.81**	19.93**	861.83**	348.75**	5231.70**
Genotype ×	78	215.49**	1.68**	5.58**	5.15**	175.96**	128.53**	0.98**	0.24*	0.60**	7.77**	6.35**	26.58**
Environment (GXE) E+(G×E)	80	873.43**	35.46**	31.3**	27.87**	885.35**	543.96**	2.75**	0.33**	1.09**	29.11**	14.91**	156.71**
Environment Linear	1	53066.18**	2705.54**	2066.72**	1827.77**	57102.55**	33491.02**	143.11**	7.63**	39.87**	1723.67**	697.50**	10463.40**
(GXE) linear	39	210.51	2.12**	9.34**	3.57	241.63**	202.80**	0.85	0.37**	0.48	6.95	7.31	48.80**
Pooled deviation	40	214.97	1.22**	1.78**	6.57	107.55**	52.90**	1.08**	0.11**	0.70**	8.37**	5.26**	4.25
Pooled error	234	66.21	1.03	1.28	2.52	34.09	25.97	0.54	0.15	0.21	3.18	3.66	7.07

* and ** significant at 5% and 1% level of significance, respectively.

5 randomly selected plants of each genotype in each replication and data were collected on all 13 characters (table 2). Stability analysis for all different characters over the 3 environments was done as per the model of Eberhart and Russel (1966) detailed by Singh and Chaudhury (1979). According to this model, a desirable & stable genotype is one which has (i) high mean, (ii) a regression coefficient (bi) around unity and (iii) a mean square deviation from regression (S^2di) near to zero.

Results and Discussion

Table 1 shows statistically highly significant mean sum of squares for genotypes and environments for all the traits under study indicating the presence of substantial variation among the genotypes over environments and the environmental means over test genotypes. Similar results had been reported earlier (Akanda *et al.*, 2007; Guillen-Portal *et al.*, 2003; Carvalho *et al.*, 2000; Cardoso *et al.*, 2000). Significant G × E interaction indicated that genotypes under different environments behaved differently for the expression of characters of interest. This means a particular genotype may not exhibit the same phenotypic performance under different environments or different genotype may respond differently to a specific environment. The environment + G × E interactions were highly significant when tested against pooled deviation for all the characters which satisfied the requirement of stability analysis *i.e.*, the genotypes interacted considerably with environments in the expression of the characters. Highly significant mean sum of squares due to environment (linear) for the traits indicated considerable differences among the environments and their predominant effects on the characters due to variations in weather conditions of different locations. Pixley and Bjamson (2002) reported similar significant environmental effects (linear) for grain yield in maize. Variance due to G × E (linear) was non-significant for some of the traits, such as, days to 75% dry husk, cob length, no. of kernel rows per cob, no. of kernels per row, 100 seed weight, grain yield per plant. Rest of the traits were found to be significant. Roy *et al.* (1999) observed similar result, that is, non-significant G × E (linear) component for days to maturity and grain yield in maize. Variance due to pooled deviation was significant for all the characters except days to dry husk, grain yield per plant and shelling percent indicating the major components of differences in stability due to the deviation from linearity and not the linear regression.

Table 2 presents the estimates of mean performance, and stability criteria *viz.*, regression coefficient (bi) and deviation from regression (S^2di) of 40 genotypes studied

Table 2 : Pooled analysis of mean performances *per se* and stability analysis of different traits studied in forty genotypes of maize.

S. no.	Genotypes	Grain yield per plant (gm)			Days to 50% tasselling			Days to 50% silking			Days to 75% dry husk			Plant height (cm)			Ear height		
		Mean	bi	S²di	Mean	bi	S²di	Mean	bi	S²di	Mean	bi	S²di	Mean	bi	S²di	Mean	bi	S²di
1.	HKI163XHKI1105	113.1	1.67	449.02*	54	1.03	-0.30	55.8	1.26	0.45	97.4	1.10	9.99*	162.8	1.16	35.8	78.5	1.18	4.24
2.	HKI163XHKI1128	107.3	1.44	52.08	55	1.18	-0.29	57.6	1.34	-0.41	99.4	1.01	14.08*	183.1	0.97	9.1	88.31	1.30	-7.51
3.	HKI163XDMRPE6	99.5	1.16	437.91**	52	1.07	-0.07	54.1	1.28	-0.18	98.6	0.85	10.04*	165.0	1.01	122.77*	73.61	1.15	-8.65
4.	HKI163XCML285	104.1	1.45	-13.14	54	1.19	-0.30	56.7	1.37*	-0.37	101.1	0.86	8.37	183.1	1.21	11.7	91.14	1.42	42.84
5.	HKI163XCML292	111.2	1.11	31.38	55	1.08	0.27	57.4	1.26	0.45	101.6	0.75	14.94*	172.8	1.30	117.3	95.94	1.67	-6.71
6.	HKI163XCML132	111.0	0.93	-21.54	54	1.01	1.57	56.7	1.09	4.71*	99.7	0.70	10.23*	176.1	1.55*	325.99**	86.00	1.76**	109.97
7.	HKI163XLM16	122.5	1.66	71.69	51	0.81	-0.34	52.8	0.96	0.43	95.4	0.93	-0.80	162.6	1.25	158.29*	76.58	1.23**	323.46**
8.	HKI1105XHKI1128	92.1	0.94	93.39	52	1.15	-0.05	54.2	1.25	0.02	97.7	1.16	-0.28	143.8	0.92	8.6	59.48	0.94	-2.78
9.	HKI1105XDMRPE6	111.5	1.49	-8.43	49	0.68*	1.03	51.2	0.91	0.47	94.3	0.90	0.09	163.1	1.30	3.6	70.99	1.32	28.62
10.	HKI1105XCML285	98.2	0.77	-15.64	52	1.01	2.74	53.9	1.27	0.62	96.4	1.00	6.01	169.5	1.18	52.6	80.33	1.47	137.28*
11.	HKI1105XCML292	111.7	0.93	438.67**	53	0.96	-0.34	54.4	1.22	-0.09	97.0	0.84	-0.46	160.9	1.28	119.5	69.02	1.18	-1.12
12.	HKI1105XCML132	105.7	1.38	40.31	55	1.08	0.27	56.9	1.29	0.63	99.6	1.10	-0.70	165.0	1.33	6.9	76.97	1.16	4.16
13.	HKI1105XLM16	106.5	0.69	-13.15	51	0.76	-0.06	53.1	0.98	-0.19	94.8	0.97	2.50	145.3	1.03	-7.8	67.88	1.02	8.65
14.	HKI1128XDMREPE6	99.7	1.30	93.15	51	1.06	1.72	53.3	1.31	0.45	95.7	0.93	2.24	171.0	0.85	54.6	76.81	1.24	133.93*
15.	HKI1128XCML285	91.9	1.20	21.37	51	1.10	0.90	53.2	1.38*	0.14	95.3	1.04	12.64*	172.6	1.11	-10.2	78.78	0.99	-8.45
16.	HKI1128XCML292	103.9	1.13	52.41	54	1.17	0.15	56.4	1.39*	0.16	100.3	1.14	-0.75	170.7	1.09	53.7	83.57	1.17	-7.64
17.	HKI1128XCML132	108.4	1.11	97.73	54	1.10	0.00	55.8	1.26	0.45	99.1	0.91	6.44	184.9	1.41	50.7	88.31	1.17	3.39
18.	HKI1128XLM16	114.4	1.44	211.10	50	1.05	0.17	51.7	1.40	-0.38	94.3	1.07	1.47	158.0	0.96	12.5	70.48	0.90	37.63
19.	DMRPE6XCML285	71.7	0.81	305.96*	54	1.01	0.73	55.9	1.23	-0.41	98.7	1.04	-0.31	161.9	0.96	68.7	73.31	0.88	57.03
20.	DMRPE6XCML292	117.7	1.48	88.50	52	0.97	-0.23	54.1	1.19	0.62	96.2	1.07	0.51	173.3	1.03	-11.4	80.36	1.04	8.45
21.	DMRPE6XCML132	128.5	0.52	149.91	52	0.76	-0.06	54.1	1.04	-0.27	96.1	0.94	0.23	180.2	1.25	20.7	92.70	1.41	44.83
22.	DMRPE6XLM16	107.7	1.21	482.68**	47	0.85	-0.21	49.0	1.22	3.95**	91.8	0.74	-0.74	159.3	1.36	36.7	74.10	1.16	-4.98
23.	CML285XCML292	111.5	0.64	-4.33	53	0.77	-0.27	54.3	0.92	-0.26	97.4	1.03	-0.62	176.7	1.22	-1.4	93.10	1.38	8.73
24.	CML285XCML132	115.3	0.91	-6.05	54	0.97	-0.23	55.6	1.36	0.46	98.6	0.94	0.02	194.2	1.35	104.3	96.33	1.28	11.79
25.	CML285XLM16	110.3	1.69	-21.39	51	0.79	12.69**	53.1	1.07	13.96	96.4	0.67	18.95**	172.2	1.28	-1.6	83.09	1.33	97.17*
26.	CML292XCML132	106.4	0.91	3.32	54	0.92	0.86	55.7	0.82	0.32	100.2	0.57	16.60*	172.1	1.13	154.22*	92.02	1.08	103.28*
27.	CML292XLM16	118.8	0.93	235.78*	52	1.37**	-0.32	54.2	1.44	2.31	97.3	1.29	0.13	162.5	1.14	-7.2	88.42	1.05	-3.78
28.	CML132XLM16	118.1	1.09	1.57	52	1.03	0.51	54.2	1.32	2.92	99.0	1.07	35.98**	176.3	1.30	0.33	95.63	1.41	8.20
29.	BIO 9637 (C)	120.4	0.95	119.08	53	1.06	0.62	54.4	1.24	1.48	97.9	0.69	30.00**	185.4	1.19	-5.46	83.30	1.08	121.92*
30.	PMH 1 (C)	132.6	1.42	-0.14	53	0.85	0.03	54.9	1.02	0.03	98.7	0.56	1.10	194.6	1.60*	49.9	100.22	1.73**	6.81
31.	PRAKASH (C)	104.6	0.73	160.46	47	0.92	-0.29	48.7	1.10	-0.10	91.7	1.04	-0.31	157.6	1.30	130.64*	78.37	1.20	60.18
32.	VIVEK HYBRID9(C)	88.6	1.06	-18.00	45	0.82	0.11	46.9	0.95	-0.08	88.8	0.29	-0.84	151.1	0.70	42.1	60.83	0.67	2.13
33.	HKI163	75.9	0.76	-14.65	54	1.27	3.11	51.9	0.11**	0.08	98.7	1.79*	-0.38	121.3	0.30*	234.95**	33.86	0.04**	119.86*
34.	HKI 1105	49.3	0.51	-6.92	55	0.99	0.40	54.4	0.23**	1.58	98.6	1.47	-0.81	108.9	0.45*	448.43**	31.08	0.05**	133.08*
35.	HKI1128	64.8	0.75	1321.21**	57	1.23	4.76	55.7	0.26**	2.12	101.0	1.20	17.03	111.4	0.01**	124.46*	38.52	0.10**	56.11
36.	DMRPE6	48.1	0.49	69.73	53	0.78	-0.34	53.4	0.32**	3.37	98.3	0.92	11.08	112.3	0.19**	208.62*	38.03	0.18**	-3.78
37.	CML285	53.6	0.45	-7.07	57	1.38**	-0.32	55.3	0.52**	9.74**	99.2	1.49	4.55	115.8	0.10**	285.87**	46.39	0.32**	21.85
38.	CML292	52.4	0.15*	2635.42**	56	1.09	0.09	57.1	0.14**	0.36	101.9	1.19	3.17	91.8	0.49	4.6	37.61	0.08**	155.15*
39.	CML132	28.6	0.14*	145.94	59	1.05	5.53*	57.8	-0.11*	0.08	102.8	1.38	-0.51	112.1	0.56	694.86**	42.67	0.26**	-8.55
40.	LM16	69.0	0.61	78.66	56	0.88	1.28	59.4	0.37**	4.88**	102.5	1.37	-0.82	116.5	0.15**	150.54*	62.3	0.00**	-8.08
	Mean	98.6			52.62			54.1			97.5			158.5			73.4		
	SE(m)	14.09			1.76			1.96			2.75			10.1			8.83		
	CD .5%	28.7			3.58			3.99			5.60			20.6			17.97		
	CV%	14.3			3.34			3.62			2.82			2.13			12.03		

Table 2 continued...

Table 2 : Pooled analysis of mean performances *per se* and stability analysis of different traits studied in forty genotypes of maize.

S. no.	Genotypes	Cob length			Cob girth			No. of Kernel rows per cob			No. of Kernels per row			100 seeds weight			Shelling %		
		Mean	bi	S²di	mean	bi	S²di	mean	bi	S²di	mean	bi	S²di	mean	bi	S²di	mean	bi	S²di
1.	HKI163XHKI1105	18.82	1.07	-0.17	4.4	1.36	-0.01	14.6	1.49	0.29	31.96	1.56	-0.04	26.7	0.62	-1.21	73	1.30*	12.29
2.	HKI163XHKI1128	18.3	0.61	0.09	4.3	1.17	-0.04	15.5	2.18	0.75*	29.83	1.06	-0.19	26.2	1.27	1.21	74	0.91	1.08
3.	HKI163XDMRPE6	17.0	0.91	0.21	4.6	1.99	-0.02	12.8	-0.01	-0.05	27.19	0.85	-0.78	31.8	0.61	13.06*	70	1.63**	-0.23
4.	HKI163XCML285	19.1	1.52	-0.03	4.2	1.18	0.02	13.2	1.59	-0.03	30.17	0.84	3.66	30.1	1.65	8.83	69	1.17	-2.12
5.	HKI 163XCML292	17.5	1.13	0.25	4.1	1.58	-0.05	13.0	0.91	-0.03	36.08	1.07	2.85	26.3	1.24	0.26	75	1.05	-2.32
6.	HKI163XCML132	18.8	1.45	3.33*	4.4	1.30	0.13	13.2	0.10	2.53**	35.54	0.79	19.56*	25.0	0.50	0.66	74	1.17	-0.99
7.	HKI163XLM16	18.5	1.20	-0.06	4.6	1.97	0.02	14.4	0.89	0.98*	30.99	1.37	-0.78	30.3	1.54	0.53	74	1.44**	-1.38
8.	HKI1105XHKI1128	18.1	1.62	0.84	4.1	1.47	-0.05	13.2	0.57	0.08	26.32	0.86	7.17	30.2	1.98	6.63	73	1.35**	10.54
9.	HKI1105XDMRPE6	18.0	1.76	0.19	4.4	1.03	-0.01	12.5	0.93	0.31	29.29	1.29	-0.07	32.4	2.32*	-0.62	73	1.17	0.33
10.	HKI1105XCML285	18.0	0.93	-0.18	4.2	1.24	-0.05	11.7	0.44	-0.03	26.22	0.69	19.36**	30.6	1.37	16.92*	70	1.05	2.34
11.	HKI1105XCML292	19.4	0.30	-0.16	4.1	1.18	-0.05	12.5	1.18	0.35	35.57	0.87	7.87	28.6	0.53	-0.51	75	1.51**	-2.27
12.	HKI1105XCML132	18.1	1.72	-0.14	4.0	1.53	-0.02	12.2	1.98	0.91*	34.94	1.18	0.64	28.1	-0.12*	-0.53	76	1.00	-1.35
13.	HKI1105XLM16	18.4	0.50	0.02	4.2	1.46	-0.05	13.3	0.46	-0.06	29.34	1.22	3.09	29.7	0.95	-1.16	76	0.87	-1.89
14.	HKI1128XDMREP6	16.5	0.45	1.92	4.2	1.04	-0.05	12.8	1.55	0.77*	26.03	1.39	17.26*	32.7	1.70	5.77	76	0.65**	-1.99
15.	HKI1128XCML285	17.9	0.71	2.46*	5.1	-2.69**	1.88**	12.7	0.99	0.01	28.31	1.22	3.81	31.8	1.73	-0.94	72	1.03	-2.13
16.	HKI1128XCML292	17.5	1.25	0.10	3.9	1.17	0.03	12.3	1.68	-0.07	32.74	1.46	-0.16	27.7	0.80	-1.09	80	0.63**	-2.05
17.	HKI1128XCML132	17.8	1.59	0.22	4.1	1.82	-0.04	12.2	1.61	1.80**	33.71	1.15	-0.26	28.9	1.28	-1.22	76	1.00	-0.48
18.	HKI1128XLM16	17.5	0.88	0.03	4.5	0.81	0.40	14.0	1.85	1.96**	28.72	1.59	7.25	34.0	1.28	13.83*	79	0.85	-2.08
19.	DMRPE6XCML285	15.1	0.73	-0.18	3.8	0.95	-0.04	10.6	0.55	0.99*	24.74	0.64	8.70	30.4	1.22	2.52	71	1.17	7.09
20.	DMRPE6XCML292	18.1	1.49	-0.15	4.1	1.37	-0.05	12.0	1.12	0.10	33.88	0.92	6.51	30.9	1.45	-0.27	79	0.89	-0.36
21.	DMRPE6XCML132	17.3	1.28	0.08	4.1	0.64	-0.05	11.2	1.10	-0.02	35.29	1.42	-0.81	30.3	0.16	-0.76	72	1.43**	-1.07
22.	DMRPE6XLM16	16.9	0.36	5.13**	4.0	0.21	0.01	12.0	1.14	0.19	31.06	1.26	35.19**	30.6	0.01	14.19*	73	1.30	-1.39
23.	CML285XCML292	18.6	0.35	-0.14	4.0	1.46	-0.02	11.0	0.22	1.15*	36.33	0.74	9.52	29.4	-0.38*	19.03**	76	0.76	-1.80
24.	CML285XCML132	17.5	0.62	-0.18	5.1	6.24	1.02**	10.6	0.18	0.07	31.14	0.59	-0.86	34.1	0.99	-0.37	77	0.49**	-1.97
25.	CML285XLM16	18.3	1.13	2.1*	4.2	1.41	0.00	11.9	2.01	-0.07	31.87	1.54	10.94	33.7	2.24*	1.10	73	0.82	7.72
26.	CML292XCML132	17.5	1.20	1.89	4.2	1.52	0.00	11.3	0.14	0.26	36.89	0.88	16.17**	29.4	0.08	0.93	75	1.32*	2.00
27.	CML292XLM16	18.8	0.47	-0.18	4.2	0.77	-0.03	12.2	0.52	0.03	34.78	0.64	11.19	29.9	0.54	3.04	74	0.92	1.45
28.	CML132XLM16	18.1	1.18	0.23	4.2	1.29	-0.03	12.0	0.27	0.69	36.30	1.37	-0.66	30.5	1.41	-0.98	81	0.49**	-0.56
29.	BIO 9637 (C)	18.9	1.31	0.10	4.6	-0.82**	-0.05	13.1	0.45	0.07	31.88	1.52	2.46	32.8	1.09	-0.51	73	1.45**	5.56
30.	PMH 1 (C)	18.1	1.31	0.41	4.7	-1.48**	-0.05	13.6	0.65	-0.05	31.16	1.16	-0.63	34.1	1.68	2.35	77	0.84	0.64
31.	PRAKASH (C)	17.2	1.04	0.57	3.9	-1.95**	-0.05	12.4	2.09	-0.07	31.19	0.45	-0.78	31.1	0.70	-0.44	80	0.77	-0.18
32.	VIVEK HYBRID9(C)	14.8	1.65	-0.11	4.4	-1.39**	0.07	14.5	1.36	0.17	28.94	1.17	8.73	25.8	0.41	-0.80	77	1.24	-2.35
33.	HKI 163	15.5	0.87	0.02	4.1	1.24	-0.03	13.4	0.73	0.09	26.96	1.17	0.26	26.1	0.77	-0.34	73	0.46**	-1.90
34.	HKI 1105	14.6	0.98	0.28	3.8	1.29	-0.05	11.0	0.46	0.09	23.72	1.02	0.98	23.4	0.36	-1.04	69	1.79**	0.53
35.	HKI1128	14.9	1.49	-0.18	3.9	1.34	-0.05	12.1	1.06	2.26**	23.50	0.80	8.61	24.1	1.68	9.08	81	-0.20*	53.00**
36.	DMRPE6	13.6	0.94	-0.08	3.3	0.47	-0.04	10.1	0.42	5.71**	20.74	0.51	3.20	28.0	0.17	6.45	71	1.55**	-1.99
37.	CML285	14.9	0.34	0.11	3.5	0.26	0.02	10.1	0.76	0.01	23.54	-0.01*	-0.09	28.0	0.64	30.23**	68	1.14	6.76
38.	CML292	14.6	1.37	7.04**	3.3	2.82*	0.00	10.5	2.64	0.08	24.58	-0.04*	55.09**	20.9	1.19	12.25	80	0.06**	-1.62
39.	CML132	11.5	0.79	2.53*	3.1	1.14	-0.05	9.6	1.87	2.67**	17.79	0.46	-0.81	22.1	1.05	-1.04	69	1.36**	5.38
40.	LM16	17.2	-0.53**	8.06**	3.5	0.60	-0.05	10.5	-0.16	0.30	28.3	1.35	30.28**	27.0	1.29	7.99	79	0.16**	-2.36
	Mean	17.2			4.2			12.4			30.1			29.1			74.7		
	SE(m)	1.28			0.7			0.79			3.09			3.3			4.6		
	CD5%	2.60			1.4			1.60			6.29			6.7			9.4		
	CV%	7.41			16.4			6.36			10.28			11.4			6.2		

for grain yield per plant (gm), days to 50% tasselling, days to 50% silking, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, 100-grain weight (g), shelling %. Eberhart and Russel (1966) suggested an ideal genotype is one having high mean performance, regression coefficient (bi) near unity and deviation from regression (S^2di) near zero. Accordingly, in this study, these three criteria were considered simultaneously for identifying stable genotypes.

As per the values depicted in table 2 for grain yield /plant only two test entries have statistically significant values from bi = 1 and only 7 test entries show statistically significant values from (S^2d = 0). Therefore, most of the test entries meet the stability criteria of Eberhart and Russel (1966). However, amongst all these stable test entries the test hybrid CML132 × LM16 stands out as best because it has(bi=1.09) being closest to one and its (S^2d = 1.57) is nearest to zero. As regard to the grain yield performance this test hybrid has obtained an average value of (118.1g/plant) over the three locations. Since, the grain yield/plant is the outcome of the various artefacts of the seed yield studied and depicted in tables 1 and 2, these artefacts as a whole shows mostly a similar trend as shown by their individual yield performances of individual test entries with a few exceptions.

G × E shows that test hybrid CML132 × LM16 is best suited for Delhi agro-climate (145.78g/plant) followed by at Indore (119.48g/plant) and performs better over the best standard check PMH 1 as regard to stability having (bi = 1.42, S^2d = -0.14, average grain yield = 132.6g/ plant).

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