

Original Research Article

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Assessment of Genotype × Environment Interaction and Stability Analysis in Indian Mustard (*Brassica juncea* L.)

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ABSTRACT

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Fifty-five Indian mustard genotypes comprising forty-five hybrids and ten parental genotypes along with a two checks viz., NRCHB-506 and DMH-1 were evaluated for stability parameters of morphological and biochemical characters over the three different environments. Pooled analysis of variance over three environments showed that the genotypic variance when tested against $G \times E$ were significant for all the eight characters when tested against pooled error. Pooled deviation effect was significant for all the traits except protein content. The parents, parents Pusa Vijay and Bio-902 showed their suitability for unfavourable environment for 1000 seed weight. Two crosses Pusa Vijay × Bio-902 and Pusa Vijay × RB-50 had suitability for unfavourable environment while cross Pusa Vijay × RB-50 exhibited its suitability for favourable environment for seed yield per plant. For protein content, only one cross Pusa Vijay × PM-30 showed its suitability for unfavourable environment, thereby this cross would have specific adaptability to poor yielding environments. These genotypes can be recommended for varied environments to exploit their high yield potential with morphological traits.

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss] is an important oilseed crop of Brassicaceae family which accounts more than 70 % under rapeseed and mustard. The Brassicaceae, contains about 3500 species and

350 genera, is one of the 10 most economically important plant families. Rapeseed-mustard comprising eight different species viz. Indian mustard, toria, yellow sarson, brown sarson, gobhisarson, karan rai, black mustard and taramira are being cultivated in 53 countries spreading all over

the world. In India, mustard and rape seed are being grown largely in states like Uttar Pradesh, Rajasthan, Haryana, Assam, Gujarat, Punjab, West Bengal and Madhya Pradesh. Mustard seed is largely crushed for oil, which is perhaps the cheapest source of oil in our daily diet. Mustard seeds contain about 38-42% oil, which is golden yellow, fragrant and considered among the healthiest and most nutritional cooking medium. In addition to this, it is also utilized as condiment, for medicinal uses and in preparation of soaps, hair oil, lubricants, paints, plasticizers and as a condiment in pickles.

Stability in performance of genotype for economic characters is one of the desirable properties for selection or recommendation of new genotypes in plant breeding program. For this purpose, growing of breeding lines over time and space has become an integral part of any crop improvement programme. Despite such vigorous evaluation and subsequent selection, genotypes x environments interaction have been a major problem for consistent performance of selected genotypes. It is commonly observed that many varieties of different crops do not exhibit consistent performance, when tested under different environments. Such interaction, result in change of relative ranking of different genotypes and also alters magnitude of difference between genotypes, which create problem for plant breeders in making proper assessment of genotypes, when the same are tested over varied environments. The progress resulting from selection is also reduced due to effect of large genotypes x environments interaction. It may be noted that genotypes x environments interaction exists regardless of genetic material with which a breeder is working.

A knowledge regarding nature and relative magnitude of genotypes x environments interaction is important in making decisions

concerning breeding methods, selection programme and testing procedures in crop plants (Baker, 1969). In order to minimize genotypes x environments interactions, and to increase precision in selection, stratification of environments has been employed; however, even with refinement of technique, an interaction of genotypes with environments within same year remains very large (Bradshaw, 1965). Sprague (1966) opined that the possibility of reducing genotypes x environments (G x E) interaction in field experiments is questionable despite knowledge of the factors responsible for such interactions.

Materials and Methods

Fifty-five Indian mustard genotypes comprising forty-five crosses and ten parental genotypes along with a two checks *viz.*, NRCHB-506 and DMH-1 were evaluated in randomized block design with three replications during *Rabi* 2015-2016 at three locations *viz.*, Instructional Farm RCA, Udaipur (E₁), Instructional Farm CTAE, Udaipur (E₂) and Instructional Farm, KVK Chittorgarh (E₃). A single row plot of four meter length was planted with crop geometry of 30 cm x 10 cm. The recommended agronomical practices were adopted to raise a healthy crop.

Observations were recorded on five randomly selected competitive plants in each genotype in each replication for various characters *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, length of main branch, number of silique per plant, length of silique, number of seeds per plant, 1000 seed weight, seed yield per plant, harvest index, biological yield per plant, oil content and protein content. Mean data obtained was statistically analysed and the genotypes were assessed for their stability of

performance across environments following the method described by Eberhart and Russell (1966).

Results and Discussion

Plant breeder attempts to produce progressively better-adapted populations to the existing or altered environments. Stability parameters have proved to be valuable for assessing the response of various genotypes under changing environmental conditions.

The quantitative characters are highly influenced by the environment. The magnitude of this influence is reflected by $G \times E$ interaction. This interaction generally remains confounded with variance and leads to biased estimates of genetic parameters. This bias can be minimized by growing the breeding materials over the environments. The study of $G \times E$ interactions was made as per the procedure outlined by Eberhart and Russell (1966).

Analysis of Variance

Pooled analysis of variance over three environments showed that the genotypic variance when tested against $G \times E$ were significant for all the eight characters (Table 1). Partitioning of $G \times E$ interaction showed that Environment linear interaction effects were non-significant for all the eight traits and ($G \times E$) linear interactions were highly significant for all the traits. Pooled deviation effect was significant for all the traits except protein content. Further, partitioning of variance i.e. Environment + (Genotype \times Environment) interaction was observed to be significant all the traits. The Magnitude of mean square due to Environment + (Genotype \times Environment) was also recorded higher as compared to Genotype \times Environment (linear) for all the characters except protein content.

Stability parameter

Since, bartlet test was detected non-significant for days to 50 % flowering, plant height, number of primary branches per plant, length of main branch, seed yield per plant, 1000 seed weight, harvest index and protein content and the stability parameters in respect of these eight traits were compared to evaluate relative stability of fifty-seven different genotypes (ten parents, forty-five crosses and two checks) as per Eberhart and Russell' 1966. The results are presented in Table 2 to 5.

The genotypes with higher mean values, regression coefficient value of unity ($b_i=1$) and non-significant deviations from linear regression deviation ($\bar{S}^2_{di}=0$) were considered as stable for the traits and adaptable to varied environmental conditions studied in the present investigation. However, genotypes with a higher mean value with non-significant deviations from linear regression and regression coefficient near to unity were considered to be responsive and suitable for favorable environmental conditions.

Further, the genotypes with higher mean values and regression coefficient less than one (unity) or negative and non-significant deviations from linear regression were considered to be responsive and suitable for poor environmental conditions. Accordingly, the genotypes were classified into different classes as suitable for varied environmental condition.

For the trait days to 50 % flowering, none of the parent showed significant regression coefficient while among the crosses, one cross RB-50 \times RGN-48 exhibited non-significant deviation from regression, lower mean (50.44) than mean of crosses (50.12 days) with regression coefficient less than unity.

Thus, this cross showed its suitability for favorable environment. For plant height, two crosses viz., Bio-902 × DRMR-IJ-31 and RGN-229 × RGN-48 showed non-significant deviation from regression with mean value (189.11 and 186.78 cm, respectively), higher than the mean of crosses (181.98 cm). Out of these, one cross Bio-902 × DRMR-IJ-31 exhibited regression coefficient more than unity with mean plant height of 189.11 cm expressed its suitability for favorable environment. While another cross RGN-229 × RGN-48 expressed higher mean (186.78 cm) and regression coefficient less than unity, therefore expressed its suitability for unfavorable environment.

Parent Bio-902 exhibited higher mean (7.53) than parental mean (6.41). Likewise, cross Pusa Vijay × RGN-229 also showed higher mean (6.16) than mean of the crosses (6.10). Parent Bio-902 and cross Pusa Vijay × RGN-229 both exhibited non-significant deviation from regression, regression coefficient about unity, showed their suitability for average environment. For the trait length of main branch, only one cross Bio-902 × Laxmi

exhibited higher mean (6.76) than mean of crosses (6.58) with non-significant deviation from regression and regression coefficient more than one. Thus, this cross exhibited its suitability for favourable environment.

Two crosses Pusa Vijay × Bio-902 and Pusa Vijay × RB-50 showed higher mean than the parental mean (31.84 g) for seed yield per plant. Both these crosses exhibited non-significant deviation from regression. Cross Pusa Vijay × Bio-902 depicted higher mean (39.99 g) regression coefficient less than unity thereby showed its suitability for unfavourable environment.

Further, cross Pusa Vijay × RB-50 exhibited higher mean (34.10 g) with regression coefficient more than unity which expressed its suitability for favourable environment. Among parents, two parents Pusa Vijay and Bio-902 showed their mean for 1000 seed weight higher than parental mean (5.06 g). Both the parents showed non-significant deviation from regression, regression coefficient less than unity and showed their suitability for unfavorable environment.

Table.1 Analysis of variance Eberhart and Russel (1966)

SN	Characters	Genotype	E+(G x E)	E (L)	G x E (L)	Pool dev.	Pool Err
		[56]	[114]	[1]	[56]	[57]	[336]
1	Days to 50% flowering	44.6870**	4.8623**	0.0017	3.7530**	6.0374**	0.9741
2	Plant height (cm)	149.2952**	36.2346**	0.0668	36.4870*	36.6211*	24.98
3	No. of primary branches Per plant	0.6143**	0.5437**	0.0034	0.5331**	0.5636**	0.1364
4	Length of main branch (cm)	86.1009**	25.5599**	0.0336	27.1162**	24.4787**	4.532
5	Seed yield per plant (g)	64.5820**	9.3606**	0.0029	6.2233**	12.6071**	2.895
6	1000 seed weight(g.)	0.6494**	0.1747**	0.0001	0.1260**	0.2256**	0.03501
7	Harvest index	60.3987**	43.4796**	0.0436	34.2310**	53.3278**	7.256
8	Protein content (%)	7.5084**	0.6339**	0.0005	0.7651**	0.5161	0.3948

Table.2 Stability parameters for days to 50% flowering and plant height [Eberhart and Russel (1966)]

SN	Genotype	Days to 50% flowering			Plant height		
		μ	bi	s^2d_i	μ	bi	s^2d_i
1	P1	55.67	4.76	1.078	181.11	3.83	75.704*
2	P2	49.22	4.93	5.877**	183.33	-0.82	-14.886
3	P3	54.67	-0.94	-0.391	181.00	-2.70	-23.224
4	P4	44.22	5.38	-0.121	201.22	1.69	-24.893
5	P5	50.11	-16.24	0.699	197.22	-0.04	-21.798
6	P6	52.89	18.19	4.925*	182.78	3.35	1.352
7	P7	56.11	2.18	2.199	182.78	-2.13	151.524**
8	P8	47.78	-3.27	2.965*	180.44	4.17	-24.980
9	P9	47.22	-1.57	21.085**	174.56	3.79	-6.378
10	P10	54.44	3.65	0.048	190.22	2.44	132.800*
11	P1 x P2	52.67	0.49	-0.108	181.78	2.11*	-24.914
12	P1 x P3	54.22	-4.79	2.682	176.56	1.33	-9.215
13	P1 x P4	49.56	2.33	6.579**	198.22	0.40	76.704*
14	P1 x P5	51.33	0.49	-0.108	188.89	1.39	11.286
15	P1 x P6	54.67	0.73	0.975	177.67	-0.85	7.180
16	P1 x P7	55.56	0.58	8.845**	178.67	0.38	20.684
17	P1 x P8	53.33	0.69	0.536	175.33	4.00	-11.840
18	P1 x P9	52.44	-1.52	14.212**	173.33	-3.25	-24.515
19	P1 x P10	55.67	5.69	-0.526	184.67	5.09	149.261**
20	P2 x P3	52.78	5.31	1.726	179.56	0.13	-17.860
21	P2 x P4	41.44	-2.01	7.825**	178.89	3.76	192.698**
22	P2 x P5	51.33	-12.28	3.229*	190.56	4.09	-2.911
23	P2 x P6	51.22	6.56	-0.582	177.67	2.70	-23.227
24	P2 x P7	53.56	1.60	0.855	179.67	-0.71+	-24.921
25	P2 x P8	47.78	6.94	-0.852	175.89	3.26	-24.283
26	P2 x P9	48.33	-8.30	-0.685	174.67	-4.74	-24.185
27	P2 x P10	51.11	8.16	2.938*	186.44	-1.76	35.472
28	P3 x P4	44.11	0.11	2.654	179.67	1.01	17.997
29	P3 x P5	49.78	5.31	1.726	185.00	1.11*	-24.977
30	P3 x P6	53.78	0.60	7.066**	180.22	-2.60	-23.655
31	P3 x P7	53.78	5.97	3.912*	172.44	3.35	1.354
32	P3 x P8	49.56	-1.29	1.607	182.22	2.07	24.730
33	P3 x P9	49.44	0.03	10.211**	174.44	-0.71	-18.619
34	P3 x P10	52.89	-6.70	-0.312	169.67	3.56**++	-24.979
35	P4 x P5	40.78	4.13	2.795*	199.44	2.63	-13.450
36	P4 x P6	44.78	5.07	0.414	199.33	1.27	-24.268
37	P4 x P7	49.22	0.58	8.845**	185.33	-0.13	4.510
38	P4 x P8	44.22	6.81	0.216	189.11	3.21*+	-24.891

39	P4 x P9	43.89	-6.01	-0.803	179.56	3.44	-23.299
40	P4 x P10	47.22	6.36	6.781**	188.89	5.75	4.002
41	P5 x P6	51.67	12.85	16.081**	186.56	-1.39	52.185
42	P5 x P7	51.89	-4.54	4.678*	183.44	6.11	-5.583
43	P5 x P8	46.00	-3.13	10.752**	178.11	6.81	-13.436
44	P5 x P9	47.33	5.37	24.486**	184.67	-4.21	-19.926
45	P5 x P10	48.22	-2.22	-0.263	180.00	1.00	-16.112
46	P6 x P7	53.33	-4.76	1.077	182.33	2.74	0.677
47	P6 x P8	50.67	-11.39	0.814	181.78	1.75	-10.799
48	P6 x P9	51.00	-7.89	22.612**	186.78	-5.09*+	-24.604
49	P6 x P10	55.33	4.27	-0.722	185.11	2.16	144.469**
50	P7 x P8	49.89	4.16	0.995	174.56	-1.02	-19.789
51	P7 x P9	50.44	8.37*	-0.940	178.67	-1.63	-14.868
52	P7 x P10	55.22	0.46	17.302**	185.56	0.83	263.605**
53	P8 x P9	47.22	-5.84	26.049**	178.89	-7.58	-22.459
54	P8 x P10	47.22	-0.15	19.542**	179.56	1.81	-4.942
55	P9 x P10	49.33	11.80	7.913**	179.33	-2.06*+	-24.900
56	NRCHB 506	46.44	2.91	-0.825	189.56	-0.27	-22.078
57	DMH 1	43.56	-2.02	8.042**	192.11	2.20	-22.928

Table.3 Stability parameters for number of primary branches per plant and length of main branch [Eberhart and Russel (1966)]

SN	Genotype	No. of primary branches per plant			Length of main branch		
		μ	bi	s^2d_i	μ	bi	s^2d_i
1	P1	6.53	-0.91	-0.131	84.36	1.88	-4.379
2	P2	6.44	1.88	0.294	86.00	0.30	64.846**
3	P3	6.19	0.10	-0.009	79.56	-4.53	41.533**
4	P4	7.53	1.93*	-0.135	94.33	-3.57	37.972**
5	P5	7.27	0.55	-0.133	98.89	-1.56	69.543**
6	P6	6.58	1.16	0.458*	86.67	1.65	47.807**
7	P7	6.18	2.41	-0.102	83.56	-8.55	-0.951
8	P8	5.94	3.39	-0.091	87.11	2.21	13.056*
9	P9	5.73	2.40	1.333**	80.56	1.47	-1.939
10	P10	5.76	0.91	3.351**	93.33	7.36	4.508
11	P1 x P2	5.84	-0.78	0.135	83.67	0.28	11.539
12	P1 x P3	5.34	1.10	0.725*	78.33	-2.34	39.832**
13	P1 x P4	6.08	2.96	0.566*	95.00	0.29	35.533**
14	P1 x P5	5.86	0.53	-0.133	94.22	-1.26	30.296**
15	P1 x P6	5.91	1.80	-0.087	84.67	-4.04	80.377**
16	P1 x P7	5.79	0.46	-0.105	85.11	4.38*	-4.314
17	P1 x P8	6.29	0.93	2.029**	81.67	3.51	18.716*

18	P1 x P9	6.47	0.28	1.655**	77.44	-1.47	-1.939
19	P1 x P10	5.69	0.89	0.211	89.67	-2.63	92.435**
20	P2 x P3	6.40	1.35	-0.074	85.89	2.43	79.753**
21	P2 x P4	6.66	3.44	-0.095	86.78	-2.17	49.224**
22	P2 x P5	6.47	1.90	-0.039	95.00	0.35	29.896**
23	P2 x P6	6.16	2.19*	-0.131	84.33	2.96	-4.416
24	P2 x P7	5.70	0.48	-0.113	85.33	1.25	15.372*
25	P2 x P8	5.86	1.03	0.746*	82.89	2.26	-1.379
26	P2 x P9	5.94	-2.03	0.053	81.78	-2.36	9.759
27	P2 x P10	5.93	-2.20	1.912**	93.33	-5.29	-3.147
28	P3 x P4	7.00	0.85	0.258	89.67	4.34	20.922*
29	P3 x P5	6.68	2.16	0.287	91.78	2.33	4.218
30	P3 x P6	6.53	-0.49	-0.124	87.00	-1.11	7.978
31	P3 x P7	6.24	1.80	-0.128	79.00	5.22	-4.020
32	P3 x P8	6.54	0.52	-0.087	88.11	6.56	-3.322
33	P3 x P9	5.66	0.07	3.530**	81.67	1.18	11.461
34	P3 x P10	6.56	1.40	-0.022	80.89	5.19	20.925*
35	P4 x P5	6.33	2.10	0.527*	99.78	6.76*+	-4.449
36	P4 x P6	5.91	2.63	0.215	99.78	-2.45	-3.529
37	P4 x P7	6.27	1.78	1.208**	85.89	1.98	0.455
38	P4 x P8	6.56	3.34	-0.028	93.22	2.43	6.479
39	P4 x P9	6.79	0.23	-0.115	87.22	3.45	16.296*
40	P4 x P10	6.06	1.38	0.101	90.00	6.21	44.624**
41	P5 x P6	6.61	2.21	0.783**	92.56	0.04	47.316**
42	P5 x P7	6.28	2.69	-0.108	89.78	6.88	-3.631
43	P5 x P8	5.22	2.15	2.712**	85.78	7.05	31.986**
44	P5 x P9	6.00	0.08	-0.131	90.89	-5.39	4.103
45	P5 x P10	6.17	2.04	0.320	86.00	2.30	3.322
46	P6 x P7	5.87	1.05	0.029	93.11	-0.89	74.479**
47	P6 x P8	6.07	0.78	-0.068	91.67	5.29	-3.146
48	P6 x P9	6.23	1.16	-0.017	92.56	-3.43	62.119**
49	P6 x P10	6.19	-2.23	1.847**	88.78	1.96	29.498**
50	P7 x P8	5.58	-1.06	-0.126	83.11	-2.33	0.476
51	P7 x P9	5.60	-0.01	0.212	90.78	4.85	9.176
52	P7 x P10	6.18	0.26	-0.047	90.11	4.13	-3.926
53	P8 x P9	5.68	0.47	1.119**	90.00	-1.89	18.154*
54	P8 x P10	5.72	1.06	0.480*	86.22	1.73	-0.839
55	P9 x P10	5.61	-0.27	-0.118	87.11	-0.06	-3.576
56	NRCHB 506	6.77	0.37*+	-0.136	94.56	-2.72	8.219
57	DMH 1	6.39	0.36	-0.112	92.33	4.57*	-4.360

Table.4 Stability parameters for seed yield per plant and 1000-seed weight [Eberhart and Russel (1966)]

SN	Genotype	Seed yield per plant			1000-Seed weight		
		μ	bi	s^2d_i	μ	bi	s^2d_i
1	P1	30.61	6.29	-2.794	4.64	1.23	0.054
2	P2	34.32	1.94	-1.590	5.69	-6.14+	-0.034
3	P3	36.39	-0.65	5.239	5.27	2.68	0.145*
4	P4	39.44	2.03	11.995*	6.13	-2.00*+	-0.035
5	P5	32.81	7.60	19.540**	5.35	-3.36	-0.025
6	P6	29.03	-3.17	4.089	4.51	2.37	-0.032
7	P7	28.10	-0.00	32.450**	4.51	3.38	-0.030
8	P8	29.86	1.11	7.964	4.71	6.41	0.292**
9	P9	32.49	4.05	29.194**	4.46	-3.40	0.067
10	P10	25.39	-3.55	1.752	5.33	-2.05	0.039
11	P1 x P2	31.97	-6.36	3.093	4.57	-1.20	0.217**
12	P1 x P3	32.70	1.89	11.930*	4.74	-8.12	0.539**
13	P1 x P4	36.88	0.26	6.243	5.32	-2.66	0.078
14	P1 x P5	31.44	0.57	20.802**	4.79	2.00	1.083**
15	P1 x P6	31.94	5.81	16.506**	3.89	1.47	-0.014
16	P1 x P7	31.02	1.44	8.862*	4.10	9.49	0.366**
17	P1 x P8	26.53	-0.62	-2.035	4.14	2.24	0.121*
18	P1 x P9	32.51	-1.10	-1.747	4.89	0.47	0.128*
19	P1 x P10	35.58	2.85	-1.369	4.96	10.23	0.236**
20	P2 x P3	33.89	-3.42	6.506	4.82	6.71	0.334**
21	P2 x P4	39.99	-11.41**++	-2.893	5.36	-3.89	1.174**
22	P2 x P5	37.87	-0.64	45.529**	4.84	2.71	0.435**
23	P2 x P6	27.47	0.77	5.966	4.35	1.34	0.584**
24	P2 x P7	34.10	11.74*+	-2.866	4.89	1.43	0.248**
25	P2 x P8	36.62	0.67	9.712*	4.77	9.92	-0.022
26	P2 x P9	35.99	14.74	-1.428	4.05	-2.80	0.020
27	P2 x P10	38.74	3.46	5.552	4.88	5.17	0.185*
28	P3 x P4	42.78	-1.77	-1.375	4.87	-2.68	-0.020
29	P3 x P5	37.46	0.11	-2.718	4.94	0.53	0.088
30	P3 x P6	33.61	-4.00	14.581*	4.69	-0.01	0.253**
31	P3 x P7	34.76	11.65	15.939*	5.06	-1.23	0.083
32	P3 x P8	26.65	0.50	9.143*	4.64	12.14	0.124*
33	P3 x P9	27.39	-3.86	6.372	4.03	-3.13	1.088**
34	P3 x P10	35.34	-9.81	-0.703	4.58	0.43	0.005
35	P4 x P5	38.32	-9.51	23.515**	4.77	-8.14	0.006
36	P4 x P6	34.21	4.36	96.860**	4.83	-7.71	0.218**
37	P4 x P7	33.36	-3.02	4.331	5.32	-1.86	0.039
38	P4 x P8	36.01	-10.13	28.415**	5.08	7.19*+	-0.035

39	P4 x P9	43.64	-0.87	0.672	5.11	1.65	0.453**
40	P4 x P10	41.63	1.30	7.484	4.58	-7.35	-0.013
41	P5 x P6	32.34	-9.26	10.760*	4.88	4.45	0.014
42	P5 x P7	28.03	-0.86	1.336	4.45	2.67	-0.004
43	P5 x P8	26.15	10.57	10.339*	4.69	5.98	-0.017
44	P5 x P9	27.67	6.10	-1.168	4.16	4.33	0.115*
45	P5 x P10	30.77	-9.75	22.527**	3.86	-3.61	0.129*
46	P6 x P7	28.05	4.37	3.911	4.10	-2.83	0.042
47	P6 x P8	28.88	7.00	-1.352	4.43	-4.41**++	-0.035
48	P6 x P9	34.34	-0.20	5.518	4.94	4.62	0.118*
49	P6 x P10	26.94	8.89	14.748*	4.42	-1.30	0.883**
50	P7 x P8	33.43	11.21	19.341**	3.95	13.33	0.055
51	P7 x P9	35.13	3.52	9.526*	4.25	3.69	0.155*
52	P7 x P10	36.55	3.29	5.078	4.18	9.82	0.322**
53	P8 x P9	27.81	11.73	0.500	4.17	2.01	0.131*
54	P8 x P10	25.10	7.06	4.606	4.11	-6.53	0.286**
55	P9 x P10	33.22	-3.84	8.432*	4.46	-0.77	0.033
56	NRCHB 506	40.40	-0.36	0.272	4.94	7.50	0.079
57	DMH 1	39.03	-3.72	0.491	4.91	-5.36	0.117*

Table.5 Stability parameters for harvest index and protein content [Eberhart and Russel (1966)]

SN	Genotype	Harvest index			Protein content		
		μ	bi	s^2d_i	μ	bi	s^2d_i
1	P1	39.36	3.49	-6.038	30.30	-0.47	-0.066
2	P2	44.13	2.54	6.263	31.07	4.63	-0.364
3	P3	48.63	-1.44	-2.157	30.48	5.78	-0.361
4	P4	46.18	2.24	2.435	32.54	-0.07	-0.289
5	P5	40.04	10.39	16.179	30.59	-6.43	0.688
6	P6	38.80	-1.51	-5.058	30.79	-5.00	-0.179
7	P7	38.23	0.86	45.444**	29.94	-5.83	0.244
8	P8	35.48	6.12	8.376	29.51	-4.27	-0.109
9	P9	46.14	6.14	175.459**	30.26	0.58	-0.213
10	P10	33.59	-3.00	-1.037	30.70	0.51	-0.395
11	P1 x P2	43.45	-1.82	-2.340	29.81	-5.82	0.140
12	P1 x P3	40.47	-4.29	321.555**	30.45	1.93	0.087
13	P1 x P4	54.28	4.43	34.161*	30.95	6.05	-0.173
14	P1 x P5	39.57	3.03	17.220	30.40	-5.92	-0.179
15	P1 x P6	38.84	1.68	59.018**	30.20	-2.09	-0.288
16	P1 x P7	39.36	-3.46	-6.934	29.13	-3.30	0.642

17	P1 x P8	37.10	2.56	114.907**	28.03	-1.59	-0.295
18	P1 x P9	38.80	-1.33	85.710**	29.74	-2.07	0.214
19	P1 x P10	45.94	-6.03	350.689**	27.00	4.09	-0.357
20	P2 x P3	41.11	-2.63	27.050*	30.54	-0.50+	-0.395
21	P2 x P4	45.51	-2.47	29.617*	27.12	5.50	-0.192
22	P2 x P5	52.09	1.29	67.587**	31.32	-0.07	-0.046
23	P2 x P6	34.14	0.15	11.620	26.50	-0.64	-0.388
24	P2 x P7	40.79	5.71	-3.408	27.00	7.28	0.465
25	P2 x P8	49.47	-0.36	-4.931	26.10	-0.50	-0.185
26	P2 x P9	50.82	9.77	6.958	30.22	-4.75	-0.277
27	P2 x P10	42.65	-0.63	41.232**	30.31	0.92	0.140
28	P3 x P4	42.90	-1.47	-5.957	31.42	9.28	-0.365
29	P3 x P5	39.56	0.06	-4.521	30.14	10.12	-0.292
30	P3 x P6	44.37	-1.43	4.616	30.11	5.94	2.846**
31	P3 x P7	41.06	3.44	-1.736	30.16	0.49	0.351
32	P3 x P8	36.61	-1.18	-7.176	27.09	0.99	-0.368
33	P3 x P9	41.76	-0.77	-4.524	30.49	4.84	0.883
34	P3 x P10	40.54	-2.21	-2.142	30.76	-2.96	-0.391
35	P4 x P5	40.31	-0.86+	-7.220	29.56	8.79	-0.120
36	P4 x P6	38.95	2.91	83.391**	29.91	9.85	0.279
37	P4 x P7	42.16	-3.14	-5.738	28.98	9.56	-0.088
38	P4 x P8	43.86	-4.65	245.289**	28.52	10.31	0.112
39	P4 x P9	47.08	4.79	-6.475	30.79	1.49	-0.212
40	P4 x P10	45.56	1.26	7.526	30.40	-1.31	0.433
41	P5 x P6	42.35	5.48	5.346	27.17	-2.83	-0.334
42	P5 x P7	38.88	3.06	76.672**	30.05	0.58	-0.381
43	P5 x P8	43.31	7.66	123.345**	28.70	-5.66	0.342
44	P5 x P9	41.68	0.80	1.605	27.17	8.97	-0.091
45	P5 x P10	39.01	-3.57	101.567**	28.55	4.39	0.707
46	P6 x P7	40.64	0.65	37.269*	25.71	-2.02	-0.185
47	P6 x P8	36.71	1.50	91.555**	27.72	-7.43	-0.227
48	P6 x P9	43.48	-5.30	64.948**	29.23	-3.96	-0.230
49	P6 x P10	33.42	4.73	44.586**	29.46	5.70	-0.176
50	P7 x P8	36.07	4.46	19.360	27.50	-4.78	-0.300
51	P7 x P9	40.07	-0.09	-5.661	27.15	4.61	-0.276
52	P7 x P10	44.31	1.05	90.851**	28.64	1.06	-0.394
53	P8 x P9	40.58	3.02	14.165	29.96	2.89	-0.279
54	P8 x P10	40.58	2.86	11.934	27.09	2.69	-0.214
55	P9 x P10	45.33	-0.81	265.620**	26.46	-7.30	-0.040
56	NRCHB 506	47.52	1.67	-2.935	28.57	-7.72	5.472**
57	DMH 1	48.42	1.65	0.970	29.70	12.41	2.587**

While among crosses, cross Bio-902 × DRMR-IJ-31 showed higher mean (5.08 g) than mean of crosses (4.60 g), non-significant deviation from regression and regression coefficient more than unity so that it showed suitability for favorable environment.

None of the parent and none of the cross showed significant regression coefficient. For protein content, only one cross Pusa Vijay × PM-30 showed higher mean (30.54 %) for protein content over the mean of crosses (28.97 %). It showed non-significant deviation from regression with regression coefficient less than one and showed its suitability for unfavourable environment.

The similar results for seed yield and its components and quality traits were found by Yadava *et al.*, (2010), Mahto and Haider (2012), Gazal *et al.*, (2013), Sagolsem *et al.*, (2013) and Sah *et al.*, (2015).

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