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Stability analysis on elite genotypes of Indian Mustard (*Brassica Juncea* L.) in Terai Agro-Climatic Region

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Abstract

Among the oilseed crops, mustard has gained precedence in the human diet due to its superior oil quality. Genotype × environment interactions have a significant effect on plant breeding because it reduces the stability of the genotypes in diverse environments. In order to assess the impact of environments on genotypes and determine the stable genotypes in terms of seed yield and yield attributing characters in the terai agro-climatic zone, seventy-one Indian mustard genotypes were evaluated during two consecutive years,namely, 2017-18 and 2018-19, focusing on nine quantitative characters across six environments. Eberhart and Russell model (1966) of stability analysis revealed that various genotypes exhibited adaptability to favourable and unfavourable environments for different characters, influenced by the different sowing dates over the two years. However, Rohini (SC) and KMR-15-14 to be well adapted in terai agro-climatic zone in respect to seed yield and plant height, while Pusa mustard 27 (EJ 17) were adapted to specifically favorable (rich) environment for the seed yield. In terms of secondary branches per plant and number of siliquae on branches, Pusa mustard 27 (EJ 17) showed adaptability across all types of environments. Therefore, Rohini (SC) and KMR-15-14 were identified as stable genotypes for optimum seed yield across different environmental conditions.

Keyword: Mustard, G × E interaction, stability, Regression, Deviation from regression, Brassica juncea

INTRODUCTION

Indian Mustard (*Brassica juncea L. Czern & Coss.*), is also known as brown mustard or sarson and belongs to the family Cruciferae. After China, European Union and Canada, India stands in fourth position with a contribution of 10.37% to world mustard production (Anonymous 2021). India produced rapeseed-mustard 72.41 million metric tons out of the total global oilseed production of 597.27 million metric tons, which is equivalent to India's contribution of 12.1% of global oilseed production (Anonymous, 2020). Mustard is cultivated for various commercial products such as edible oil, spices and vegetables. Among these, edible oil is particularly important for cooking as it consists of both saturated and unsaturated fats that provide high energy to the human body (Carr and McDonald, 1991). India has the fourthlargest oil economy in the world, after the United States, China, and Brazil, and is the third-largest producer of oilseeds globally (Hegde and Kiresur, 1999). Mustard holds a prominent place in the human diet because of its superior oil quality. The global demand and importance for Indian mustard are rising continuously.

In this scenario, many research methodologies have been combined with plant breeding to enhance the performance of mustard genotypes, which is necessary to meet the growing need and to find out superior genotypes

that are capable of producing consistent performance in a wide range of varied environments. The performance of genotypes can vary tremendously due to the influence of the environment on genotypes. The genotype × environment (G × E) interaction has a significant impact on plant breeding mainly on quantitative characters as it reduces the stability of genotypic value under a wide range of environments. The G × E interaction affects the relative rank of a genotype due to the alteration of environments and also the magnitude of the genotypes changes. Certain genotypes function exceptionally well in a particular environment but poor in others environment. Stability analysis is a crucial method for identifying superior varieties that are more adaptable to fluctuating environmental conditions and that are suggested as useful genotypes for breeding programme and cultivation. If a genotype has a high mean yield with minimal yield fluctuation when grown in several seasons, it will be deemed more stable or adaptive (Amin et al., 2005). Plant breeders can identify superior stable genotypes across a range of environments depending on multi-environment trials (MET) over the years or locations. Stability can be measured by calculating the residual mean square obtained from the regression of each genotype yield on environmental variable (Eberhart and Russell, 1966). In order to select genotypes for a plant breeding program, it is crucial to evaluate stable genotypes to a wide range of environments (Manjubala et al., 2018; Sahana et al., 2023). With this approach, both stable and adaptable regions were indicated by the regression's slope. Due to simplicity, the Eberhart and Russell (1966) model allows for more precise evaluations of genotypes for performance and adaptation across a range of years or locations. Therefore, the objective of this analysis was to identify stable genotypes that are generally adapted to all environments or specifically stable to favorable or unfavourable environments and can be utilized in advance breeding programme.

MATERIALS AND METHODS

The present study was conducted at Cooch Behar during two consecutive seasons of 2017-2018 and 2018-2019 to reveal information on the stability of performance of 71 Indian mustard genotypes [Brassica juncea (L)] for nine quantitative characters across six environments. These genotypes were collected from the germplasm collection center, BHU., Uttar Pradesh; the Directorate of Rapeseed - Mustard Research, Bharatpur (Rajasthan); and the Pulse and Oilseed Research Station, Berhampore, Murshidabad (West Bengal). The experiment was laid out during Rabi seasons of 2017-18 and 2018-19 with three distinct sowing dates for each year, namely 14th November, 21st November and 28th November 2017 during 2017-18 and 1st November, 10th November, and 19th November during 2018-2019. In each of the environments, the experiment was laid out in randomized block design with three replications, with a spacing of 30 cm between rows and 10 cm between plants and a plot size of 5 m×1.5 m. Observation regarding the character days to 50% flowering was collected on the plot basis. Observations on the characters like plant height, number of primary branches per plant, and number of secondary branches per plant were collected from five randomly chosen plants of each replication. Seed based characters like number of siliquae on main shoot, number of siliquae on branches, number of seeds per siliquae and seed yield, the data were collected from ten randomly selected plants from each replication. The seed yield was calculated on a plot-by-plot basis. The statistical analysis of genotype × environment interaction and stability parameters was performed by Eberhart and Russell model (1966) for the various characters using software GENRES (1994, version 3.11) and Windowstat (version 9.1). According to the Eberhart and Russell model (1966), a stable variety is defined as having genotypic mean value higher than the population mean, a regression coefficient of bi = 1, and deviation from the regression of $S^2di = 0$.

RESULTS AND DISCUSSION

The pooled analysis of variance (ANOVA) (Table 1) revealed that the variance due to genotype, environment and the genotype × environment component differed significantly for all the eight characters viz., days to 50% flowering, plant height (cm), primary branches per plant, secondary branches per plant, number of siliquae on main shoot length, number of siliquae on branches, number of seeds per siliquae, and seed yield (q/ha). These findings indicate that further stability analysis and estimation of stability parameters can be carried out for the aforementioned eight characters. The results of this experiment on mustard are further supported by few more scientists (Henry and Daulay, 1990; Dhillon et al., 1999; Chaudhary et al., 2004; Brar et al., 2007; Gupta and Pratap, 2007; and Yadava et al., 2010, Asima et al., 2013). To confirm the existence of variance caused by the G×E interaction components, stability analysis was performed for all the observable characters using the Eberhart and Russell model (1966) (Table 2). The ANOVA for stability, based on Eberhart and Russell model (1966) (Table 2) reflected that the genotypes, environments (linear) and genotype × environment (linear) [G × E (linear)] components and the pooled deviation differed significantly for all the characters. The significant difference among the genotypes for all the characters indicated that sufficient amount of diversity was present in the selected genotypes. The environment (linear) component differed significantly indicating that environments affect significantly the phenotypic expression of genotypes. The G × E (linear) component also differed significantly for all the characters except days to 50% flowering, which implied that genotypes varied over the environments due to the cause of G × E interaction and for the character days to 50% flowering, the variability is unpredictable in nature (Dhillon et al., 2001; Brar et al., 2007 and Yadava et al., 2010). Hence, the stability parameters as per Ebarhart and Russell (1966) was not carried out for this character but the same was done for the remaining seven characters viz., plant height, number of primary

Table 1. Pooled ANOVA

Source Of Variation	Days to 50% flowering	Plant Height (cm)	No. of Primary Branches per Plant	No.of Secondary Branches per Plant	No. of siliquae on main shoot length	No. of siliquae on branches	No. of Seeds per Siliquae	Seed Yield (q/ha)
Genotype	254.7**	4615.6**	22.4**	102.1**	368.5**	6638.7**	25.8**	101.8**
Environment	3728.3**	28403.4**	78.3**	940.4**	8576.9**	896399.9**	216.4**	5906.9**
Genotype × Environment	44.6**	767.3**	3.9**	22.3**	114.7**	3251.2**	9.6**	65.0**
Pooled error	4.9	172.5	2.2	9.8	47.0	1754.3	2.9	2.7

* & ** indicates 5% and 1% level of significance respectively

Table 2. ANOVA for Stability as per Eberhart and Russell Model (1966)

Source	DF	Days of 50% flowering	Plant Height (cm)	No. of Primary Branches/ Plant	No.of Secondary Branches/ Plant	No. of siliquae on main shoot length	No. of siliquae on branches	No. of Seeds/ Siliquae	Total Yield (q/ha)
Rep within Env.	12	0.9	384.0*	4.4**	35.8**	14.6	4063.6**	1.0	15.2
Genotypes	70	84.9**	1538.5**	7.5**	34.0**	122.8**	2212.9**	8.6**	33.9**
E+(G×E)	355	32.2**	385.5**	1.7**	11.7**	78.0**	5276.9**	4.2**	49.1**
Environments	5	1242.7**	94.7**	26.1**	313.5**	359.0**	298799.9**	72.1**	1969.0**
G×E	350	14.9	255.8**	1.3	7.4	38.2	1083.7*	3.2*	21.6**
Environments (Linear)	1	6213.8**	47338.4**	130.5**	1567.3**	14294.8**	1494000.0**	360.7**	9844.8**
Genotypes × Environments (Linear)	70	9.5	519.9**	1.7*	9.7*	54.6**	1828.3**	5.8**	55.2**
Pooled deviation	284	16.0**	187.0**	1.2**	6.8**	33.7**	885.0**	2.5**	13.1**
Pooled Error	840	1.6	57.5	0.7	3.2	15.7	584.7	1.0	0.9
Total	425	40.8	575.4	2.6	15.4	85.4	4772.2	4.9	46.6

"*" and "**" for 5% and 1% Level of Significance

E= Environment, G=Genotype

branches per plant, number of secondary branches per plant, number of siliquae on main shoot length, number of seeds per siliquae and seed yield.

According to Eberhart and Russell model (1966), all the 71 genotypes were evaluated for three stability parameters i.e., mean, b_i , and S²di, in order to categorize the genotypes into different groups based on stability and adaptability to specific environments (**Table 3**). The stable genotypes over the six environments created over two years were identified based on their mean, which was greater than the population mean, along with $b_i = 1$ and S²di=0; The genotypes which were specifically adapted to favourable (rich) environment due to their genotypes which were adapted specifically to unfavourable (poor) environment due to their genotypes which were adapted specifically to unfavourable (poor) environment due to their genotypic mean and $b_i < 1$, mean and $b_i < 1$ and S²di=0; The genotypic mean and $b_i < 1$, mean and $b_i < 1$ and S²di=0; the genotypes which were adapted specifically to unfavourable (poor) environment due to their genotypic mean and $b_i < 1$, mean and $b_i < 1$, mean and $b_i < 1$.

S²di =0. The genotypes exhibiting stability and superiority in these three categories for different characters were presented in **Table 4**. The current findings, which revealed that different genotypes were exhibiting stability for one or more characters, are consistent with previous reports of genotype stability for multiple characters based on these three parameters by Dhillon *et al.*, 2001; Brar *et al.*, 2007; Yadava *et al.*, 2010; Srivastava and Srivastava, 2020; Patil *et al.*, 2020 and Nagrale *et al.*, 2023.

In terms of plant height, it was found that 19 genotypes *viz.*, TM-276, Rohini(SC), KMR-15-4, PR-2012-9, Kranti-NC, DRMRIJ-15-85, KM-126, KMR-53-3, RH-1209, SVJ-64, RH-0923, RGN-389, RAURD-214, DRMR-4001, RB-81, PRD-2013-9, DRMRIJ-15-66, RH-406, RH-749 were found to be stable over the six environments created over two years. Likewise, five genotypes *viz.*, NPJ-198,

Table 3. Stability parameters for 71 Mustard genotypes over 6 environments

S No.	Genotype	F	Plant Heig	ht	No. of	Primary Br Plant	anches/	No.of Se	condary E Plant	ranches/
		Mean	b _i	S²di	Mean	b _i	S²di	Mean	b _i	S ² di
1.	B-85(Seeta)	137.43	-0.27*	52.04	4.17	-0.17	-0.16	4.41	0.2	1.2
2.	RW-351(Bhagarathi)	141.76	0.35	-25.05	3.78	-0.39*	-0.68	4.11	0.03	2.81
3.	RW-85-59(Sarna)	141.87	0.27*	-16.1	4.09	-1.11*	-0.6	3.69	-0.14*	-2.36
4.	RW-4C-6-3(Sanjukta Asech)	154.85	0.12	209.07**	4.13	-0.19*	-0.46	6.04	0.7	-1.31
5.	NPJ-194	132.02	0.08	423.41**	4.26	-0.28*	-0.62	5.02	-0.06*	-2.46
6.	TM-276	180.85	-0.18	94.60*	4.89	1.17	-0.36	6.18	0.3	-0.22
7.	Rohini(SC)	185.11	0.68	-4.27	4.87	0.81	0.49	7.31	-0.62*	-1.49
8.	KMR-15-4	183.48	-0.09	58.29	4.61	1.23	-0.1	5.96	0.27	3.89
9.	PR-2012-9	189.96	0.48	-12.45	6.09	2.35	1.63*	4.65	0.25*	-2.21
10.	Divya-88	181.5	-0.25*	40.42	7.8	4.16	8.72**	6.59	0.45	6.96*
11.	RL-JEB-52	191.11	0.38	423.53**	5.85	2.64	0.55	7.26	0.35	0.43
12.	Kranti-NC	191.28	0.55	-13.4	12.17	4.43	17.18**	4.3	0.34	-0.81
13.	DRMRIJ-15-85	187.22	0.29	58.4	5.54	0.56	-0.08	6.81	-0.03	6.81*
14.	RH-1202	189.52	-0.15*	2.54	5.43	0.15	1.65*	4.96	-0.02*	-3
15.	NPJ-196	184.04	-0.43	282.48**	7.24	1.19	2.88**	10.22	0.86	50.68**
16.	RMM-09-10	176.02	0.18	106.27*	5.72	1.44	0.61	6.82	0.83	-2.28
17.	JMM-927-RC	169.98	0.63	270.29**	5.96	1.71	2.36**	8.7	-0.05	24.54**
18.	RRN-871	174.5	-0.23	568.06**	5.28	0.78	0.28	7.5	0.43	16.53*
19.	KM-126	178.67	0.07	102.47*	4.85	0.66	-0.52	6.78	0.53	-0.46
20.	SKM-1313	189.13	0.87	351.07**	5.57	0.68	-0.34	8.41	0.77	4.41
21.	RB-77	167.74	0.29	263.39**	4.81	0.34	-0.51	5.39	0.56	-2.74
22.	DRMR-15-5	174.52	0.02*	-29.72	4.72	0.27	-0.62	5.89	1.47	-2.49
23.	KMR-53-3	175.24	0.25	18.39	4.93	-0.49*	-0.74	4.76	1.12	0.93
24.	RL-JEB-84	164.87	-0.62	457.45**	4.22	-0.34*	-0.71	3.82	0.19	1.43
25.	Ganga	183.81	-0.35*	32.37	4.28	0.49	-0.43	5.09	0.98	-1.58
26.	RGN-73-JC	180.87	0.46	155.66**	4.37	0.17*	-0.74	4.89	1.26	-2.64
27.	RH-1209	177.8	1.09	77.3	4.63	0.7	-0.45	5.83	1.28	9.30**
28.	PR-2012-12	173.35	1.69	169.62**	5.19	1.28	-0.47	8.17	0.86	-0.85
29.	RGN-385	163.78	1.2	-21.99	4.61	0.22*	-0.75	6.76	0.59	-1.71
	NPJ-195	174.76	1.13	169.42**	5.24	1.03	-0.55	8.09	1.35	17.61**
	Maya-C	171.48	0.03	116.54*	5.65	1.2	0.23	6.52	0.77	0.1
32.	SKJM-05	170.33	0.96	260.77**	4.98	0.95	-0.44	9.65	0.64	-0.96
33.	SVJ-64	188.89	0.14	6.26	5.07	0.5	-0.58	7.18	1.05	-2.01
34.	Sitara-Sreenagar	202.22	0.55	175.25**	5.76	1.51	-0.72	11.07	1.21	0.02
	RH-0923	187.26	1.53	9.55	5.2	0.89	-0.61	10.37	1.89*	-2.08
36.		158.07	2.02	387.97**	6.89	2.7	4.17**	11.41	0.53	6.16*
37.		180.35	3.02*	-58.07	6.31	0.62	-0.42	12.46	1.07	10.39*
38.	JMM-927-RC	187.15	1.98	206.98**	5.63	1.39	-0.67	10.26	2.09	1.26
39.		176.11	2.59*	40.34	5.28	1.09	-0.68	7.91	1.53	2.55
40.		182.44	1.74	22.92	5.37	0.98	-0.02	8.39	1.68	0.05
41.		192.43	1.37	-14.29	5.32	1.12	-0.17	8.81	1.31	5.56*
42.	DRMR-15-14	192.43	1.8	260.75**	5.96	0.74	1.03	8.83	1.01	17.80*
43.	DRMR-4001	174.87	2.15	81.41	5.33	1.18	-0.37	9.41	1.46	-1.89
	RGN-384	194.54	1.62*	-51.62	6.04	1.63	-0.23	11.43	1.57*	-3.56
	1 "**" for 5% and 1% Lev			-01.02	0.04	1.00	-0.23	11.40	1.07	-0.00

Table 3. Continued

S. No	Genotype	Р	lant Heig	lht	No. of F	Primary Br Plant	anches/	No.of Se	condary E Plant	Branches/
	·	Mean	b _i	S²di	Mean	b _i	S²di	Mean	b _i	S²di
45.	NPJ-197	178.89	1.1	475.97**	5.17	1.11	0.34	9.81	1.76	9.83**
46.	RB-81	174.96	2.27	199.03**	5.85	0.71	0.06	11.07	1.01	2.37
47.	NPJ-200	153.67	1.04	125.52*	5.89	1.21	-0.42	10.87	1.65*	-3.02
48.	DRMR-15-9	168.15	2.01*	22.63	5.17	1.3	-0.36	10.65	2.13*	-1.3
49.	KMR-L-15-6	164.17	1.09	63.03	5.59	1.68	0.47	10.89	1.95	3.58
50.	PRD-2013-9	202.07	1.03	14.98	5	0.16	0.51	7.32	1.15	14.36**
51.	DRMRIJ-15-66	185.11	1.57	3.02	4.56	1.42	-0.37	7.39	1.86	5.51*
52.	RH-1368	164.02	0.66	280.05**	4.46	0.11	-0.23	4.67	0.45	-0.58
53.	RH-1325	171.5	1.97	213.25**	5.52	0.7	0.13	8.19	1.92*	-1.92
54.	RGN-386	178.28	1.75*	-52.16	5.24	1.27	-0.06	8.5	1.72	5.11
55.	RNWR-09-3	181.11	2.13*	19.63	5.22	1.1	-0.64	7.93	1.62	9.79**
56.	PRD-2013-2	160.28	1.15	0.35	5.26	1.37	-0.53	7.91	1.54	-0.17
57.	GIRIRAJ	163.04	1.23	172.97**	4.83	0.78	0.49	6.93	1.42	0.36
58.	NRCHB-101	158.82	1.44	78.15	4.37	1.29	-0.53	7.22	1.71	6.22*
59.	RGIN-73	168.61	1.81	27.89	7.04	3.73	3.77**	16.3	-0.11	4.9
60.	DRMR-IJ-31	161.02	1.02	8.45	6.26	3.14*	-0.06	9.32	1.36	-0.24
61.	NRCHB-101	160.14	1.24	237.01**	5.49	0.87	1.43*	8.81	1.52	5.16*
62.	DRMR-150-35	156.72	1.58	121.10*	4.59	0.94	-0.38	8.06	1.41	-0.82
63.	RH-406	177.52	1.32	67.78	5.3	1.19	-0.17	8.98	2.08	1.93
64.	RH-749	189.96	1.07	58.91	5.44	0.58	-0.24	8.04	1.92	-0.93
65.	Pusa mustard-25(NPJ 112)	133.37	1.21	-54.87	4.98	0.55	-0.43	8.15	1.29	3.12
66.	Pusa mustard 26(NPJ 113)	143.56	1.26	143.98*	5.63	0.73	-0.2	10.87	0.88	-1.55
67.	Pusa mustard 27(EJ 17)	160.65	0.82	51.27	5.02	0.82	0	9.63	1.06	-3.2
68.	CS 54	187.96	1.91	100.78*	5.24	0.56	0.1	10.33	0.95	-2.72
69.	PHR -2	191.63	3.22	400.21**	5.8	0.68	-0.56	7.72	1.81	14.51**
70.	RL 1359	188.37	2.97*	169.29**	5.98	0.86	-0.51	9.32	1.50*	-3.18
71.	KRANTI	150.59	1.15	251.31**	4.11	0.14	-0.6	5.31	0.57	-1.67
Av	erage Population Mean	173.68			5.37			7.86		

"*" and "**" for 5% and 1% Level of Significance

Table 3. Continued

S. No.	Genotype	No. of siliq	uae on main	shoot length	No. of s	siliquae on br	anches
		Mean	b _i	S²di	Mean	b _i	S²di
1.	B-85(Seeta)	37.41	1.13	82.89**	145.5	1.25	-223.87
2.	RW-351(Bhagarathi)	38.24	0.4	12.37	186.59	1.45	830.34
3.	RW-85-59(Sarna)	37.94	0.64	-1.53	166.32	1.32	-341.4
4.	RW-4C-6-3(Sanjukta Asech)	39.26	0.4	92.72**	169.26	1.28	561.34
5.	NPJ-194	29	0.57	19.17	162.24	1.03	-63.01
6.	TM-276	41.3	0.83	-6.46	164.87	1.05	-600.62
7.	Rohini(SC)	35.31	1.06	-14.88	158.44	1	-198.32
8.	KMR-15-4	35.83	0.64	-11.1	158.46	1.29*	-539.72
9.	PR-2012-9	35.43	0.33	14.65	153.11	1.09	-7.35
10.	Divya-88	34.91	0.51	2.25	167	0.71*	-454.97

Table 3. Continued

S. No.	Genotype	No. of siliq	uae on main s	hoot length	No. of	siliquae on b	ranches
		Mean	b _i	S²di	Mean	b _i	S²di
11.	RL-JEB-52	34.89	0.52	0.76	136.06	0.71	453.62
12.	Kranti-NC	35.3	1.29	0.33	190.87	0.42	1428.40*
13.	DRMRIJ-15-85	37.39	0.29*	-11.31	118.51	0.49*	-478.72
14.	RH-1202	35.02	0.22	11.15	122.97	0.78*	-563.69
15.	NPJ-196	33.46	0.73	0.11	160.7	0.84	-290.04
16.	RMM-09-10	30.61	0.67*	-14.43	146.28	1.05	-75.56
17.	JMM-927-RC	29.19	0.86	-7.44	154.04	0.87	760.92
18.	RRN-871	33.24	0.39	129.15**	150.54	0.41	1779.77*
19.	KM-126	39.19	0.55	17.65	162.72	0.58	1230.85
20.	SKM-1313	35.26	0.16	50.41**	168.26	0.72	-142.99
21.	RB-77	35.11	0.91	6.88	135.46	1.08	152.6
22.	DRMR-15-5	33.46	0.39	1.69	124.78	0.95	-417.7
23.	KMR-53-3	33.04	0.66	-8.01	127.95	1.15	653.62
24.	RL-JEB-84	35.87	0.66*	-13.42	122.37	1.3	495.73
25.	Ganga	37.17	1.02	-2.57	140.96	1.43	-67.29
26.	RGN-73-JC	36.59	1.03	-10.77	116.87	1.14	-484.34
27.	RH-1209	31.37	0.76	-12.92	127.72	1.14	-12.27
28.	PR-2012-12	31.54	0.81	9.04	118.17	0.81	-479.98
29.	RGN-385	33.69	0.92	-0.71	142.11	1.01	-149.57
30.	NPJ-195	37.83	1.26	4.71	181.39	1.1	2231.06**
31.	Maya-C	34.45	1.03	0.74	163.61	1.11	-573.14
32.	SKJM-05	36.87	0.9	51.56**	156.52	0.76*	-484.04
33.	SVJ-64	43.91	0.75	34.58*	148.78	1.01	-284.7
34.	Sitara-Sreenagar	44.82	0.23	41.00**	150.13	1	-403.88
35.	RH-0923	42.59	0.51*	-9.56	156.74	0.77	-363.9
36.	DRMR-15-16	37.56	0.92	12.37	164.87	0.5	77.43
37.	NPJ-198	40.87	1.65	33.70*	175.89	0.75	667.18
38.	JMM-927-RC	36.5	1.42	44.11**	175.07	1.13	976.01*
39.	DRMR-15-47	35.09	1.74*	-5.44	151.81	1.04	29.09
40.	RGN-389	40.13	1.43	-6.2	170.93	1.46*	-506.14
41.	RAURD-214	41.37	1.06	80.39**	164.35	1.17	-92.03
42.	DRMR-15-14	44.91	0.97	26.45*	185.7	1.04	4993.94**
43.	DRMR-4001	34.04	1.33	18.1	154.19	0.99	-308.73
44.	RGN-384	39.35	1.54	37.80**	178.48	1.51*	-295.47
45.	NPJ-197	40.46	-0.1	36.60*	156.91	1.42*	-553.45
46.	RB-81	39.83	1.13	-5.02	189.22	1.22	1000.55*
47.	NPJ-200	35.93	1.36	-6.65	173.76	0.84	266.12
48.	DRMR-15-9	37.44	1.13	-9.64	187.24	1.05	877.14*
49.	KMR-L-15-6	36.65	0.73	-5.09	168.72	1.11	-540.85
50.	PRD-2013-9	47.24	1.84	4.77	183.13	1.24	2261.39**
51.	DRMRIJ-15-66	45.39	1.5	32.09*	175.54	1.46*	-153.41
52.	RH-1368	38.82	1.37	21.67*	153.43	1.65*	376.68
53.	RH-1325	39.43	2.38*	10.51	168.87	1.3	40.79
54.	RGN-386	40.95	1.21	14.88	178.37	0.93	-145.58
55.	RNWR-09-3	44.78	1.53	49.96**	191.13	0.88	1661.35**
56.	PRD-2013-2	37.8	1.54	28.12*	157.67	1.17	25.2
57.	GIRIRAJ	36.95	1.71	2.69	164.67	1.47*	-493.65

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Table 3. Continued..

S. No.	Genotype	No. of siliq	uae on main s	shoot length	No. of	siliquae on l	oranches
		Mean	b _i	S²di	Mean	b _i	S²di
58.	NRCHB-101	32.31	2.33*	19.42	152.11	1.31	190.95
59.	RGIN-73	33.96	2.03	16.26	190.59	0.27	1192.74*
60.	DRMR-IJ-31	35.04	1.73	8.54	177.44	0.63*	-288.97
61.	NRCHB-101	29.68	1.91	31.75*	151.08	1.07	-401.33
62.	DRMR-150-35	31.17	1.31	27.13*	136.3	0.82*	-570.41
63.	RH-406	35.7	1.35*	-15.08	145.74	0.98	-414.9
64.	RH-749	39.91	0.96	12.8	157.35	0.84	326.85
65.	Pusa mustard-25(NPJ 112)	33.44	1.07	-6.85	149.7	0.86	2161.01**
66.	Pusa mustard 26(NPJ 113)	40.22	0.41	57.00**	179.02	0.5	391.12
67.	Pusa mustard 27(EJ 17)	45.63	0.54	42.84**	166.39	0.63	316.54
68.	CS 54	42.65	0.73	80.34**	160.31	0.81	-535.94
69.	PHR -2	47.32	0.9	59.16**	157.2	0.66	1101.07*
70.	RL 1359	50.02	1.02	25.48*	178.98	1	1654.40**
71.	KRANTI	39.28	1.31	45.01**	136.61	1.19	-328.29
Average I	Population Mean	37.52			158.66		

"*" and "**" for 5% and 1% Level of Significance

Table 3. Continued..

S. No.	Genotype	No. of	Seeds / Siliqu	uae	Se	ed Yield(Q/	ha)
		Mean	b	S²di	Mean	b _i	S²di
1.	B-85(Seeta)	10.44	1.2	4.08**	8.91	0.51	9.13**
2.	RW-351(Bhagarathi)	11	1.41	3.33**	9.47	0.78	4.65**
3.	RW-85-59(Sarna)	9.89	1.6	0.12	7.36	0.63	6.75**
4.	RW-4C-6-3(Sanjukta Asech)	9.99	2	2.86**	10.15	1.04	11.83*
5.	NPJ-194	12.17	1.19	2.91**	13.9	2.01	19.47*
6.	TM-276	11.05	-0.34	0.87	7.56	0.81	14.33*
7.	Rohini(SC)	10	2.07	0.33	10.71	0.66	1.42
8.	KMR-15-4	9.16	1.75	0.07	10.75	0.86	0.77
9.	PR-2012-9	11	-1.25*	0.67	9.62	0.32	16.51*
10.	Divya-88	11.06	-1.20*	1.90*	9.96	0.71	10.22*
11.	RL-JEB-52	9.47	-0.35*	-0.18	9.71	0.73	11.97*
12.	Kranti-NC	10.37	0.62	1.86*	12.6	0.87	13.45*
13.	DRMRIJ-15-85	10.91	1.39	0.44	10.12	0.7	5.43**
14.	RH-1202	9.35	0.14	0.29	8.29	0.42*	-0.39
15.	NPJ-196	10.75	0.9	-0.42	9.56	0.34*	-0.99
16.	RMM-09-10	12.44	-0.26*	-0.44	9.49	0.66	4.70**
17.	JMM-927-RC	12.42	1.09	13.47**	9.56	0.09	25.47*
18.	RRN-871	9.95	2.48	2.97**	8.68	0.41	21.21*
19.	KM-126	13.03	-0.58	1.89*	7.53	0.18*	9.76**
20.	SKM-1313	11.12	2.50*	0.09	9.05	0.24	14.13*
21.	RB-77	11.62	1.15	3.77**	6.43	-0.24*	6.08**
22.	DRMR-15-5	11.2	-0.03	-0.18	11.09	0.49	31.57*
23.	KMR-53-3	8.85	1.34	0.36	6.74	-0.02*	4.66**
24.	RL-JEB-84	9.27	0.23	-0.44	8.16	0.24*	9.29**

"*" and "**" for 5% and 1% Level of Significance

Table 3. Continued..

S. No.	Genotype	No. c	of Seeds / Sil	iquae	Se	ed Yield(Q	/ha)
		Mean	b	S²di	Mean	b _i	S²di
25.	Ganga	10.58	0.16	2.68**	9.06	0.39*	3.62**
26.	RGN-73-JC	13.29	0.3	1.56*	7.56	0.62	3.67**
27.	RH-1209	10.9	0.49	3.06**	9.02	0.83	6.58**
28.	PR-2012-12	10.19	1.73	1.2	7.17	0.8	5.02**
29.	RGN-385	9.9	2.76*	0.32	9.35	0.89	9.39**
30.	NPJ-195	11.04	0.81	0.52	11.29	1.02	17.33**
31.	Maya-C	12.47	1.16	-0.66	9.09	0.94	9.56**
32.	SKJM-05	12.27	0.09	0.22	15.11	1.69	10.48**
33.	SVJ-64	9.95	0.4	-0.32	9.67	0.34*	2.44*
34.	Sitara-Sreenagar	11.31	0.29	-0.4	13.02	1.33	2.67**
35.	RH-0923	12.31	0.83	0.59	9.46	1.04	6.79**
36.	DRMR-15-16	12.93	-2.39	23.99**	9.48	0.86	21.09*
37.	NPJ-198	9.28	0.58	1.40*	9.19	1.05	6.47**
38.	JMM-927-RC	9.49	1.65	0.24	8.64	1.05	12.35*
39.	DRMR-15-47	9.68	1.49	0.28	11.06	1.27	2.25*
40.	RGN-389	8.07	1.76	-0.19	9.31	0.9	4.72**
41.	RAURD-214	9.44	0.59	0.2	9.25	0.98	16.84*
42.	DRMR-15-14	9.52	0.51	1.91*	11.63	1.43	13.66*
43.	DRMR-4001	9.24	0.49	0.16	7.94	0.63	4.44**
44.	RGN-384	9.46	-0.08	1.65*	9.13	1.05	11.44*
45.	NPJ-197	10.57	1.64	1.58*	11.16	1.46	7.46**
46.	RB-81	9.13	0.6	-0.62	12.96	1.75	26.74*
47.	NPJ-200	8.36	1.19	-0.38	11.22	1.35	12.20*
48.	DRMR-15-9	10.59	1.28	4.10**	11.38	1.01	10.26*
49.	KMR-L-15-6	10.09	1.91	0.73	9.91	0.74	3.97**
50.	PRD-2013-9	10.99	0.32*	-0.81	9.58	0.9	19.60*
51.	DRMRIJ-15-66	9.76	1.05	3.30**	10.04	1.28	4.73**
52.	RH-1368	9.51	0.51	1.71*	9.34	0.53	3.60**
53.	RH-1325	10.07	0.55	6.01**	9.28	0.88	13.50*
54.	RGN-386	10.63	1.01	2.84**	9.96	1.09	8.03**
55.	RNWR-09-3	8.81	1.74	0.48	11.43	1.35	14.55*
56.	PRD-2013-2	9.69	2.32*	-0.87	9.44	0.92	13.37*
57.	GIRIRAJ	10.69	3.37*	-0.62	10.01	1.02	30.63*
58.	NRCHB-101	10.45	2.85*	-0.31	10.03	1.48	5.05**
59.	RGIN-73	9.19	2.24	1.87*	22.24	3.66*	104.48'
60.	DRMR-IJ-31	9.65	1.67	1.12	15.69	3.09*	31.71*
61.	NRCHB-101	9.44	2.13	1.72*	13.56	1.77	13.26*
62.	DRMR-150-35	10.21	1.17	-0.34	11.05	1.37	12.39*
63.	RH-406	9.04	2.13	0.83	8.99	1.2	2.55**
64.	RH-749	10.25	1.89	3.41**	12.98	2.05	22.01*
65.	Pusa mustard-25(NPJ 112)	10.57	2.36*	-0.04	7.87	0.77	6.43**
66.	Pusa mustard 26(NPJ 113)	8.11	1.35	-0.41	9.88	1.58	16.77*
67.	Pusa mustard 27(EJ 17)	10.86	-1.06*	0.61	10.66	1.35*	1.08
68.	CS 54	9.55	1.22	1.97*	11.49	1.51	18.70*
69.	PHR -2	7.77	-0.71*	-0.72	6.12	1.21	14.60*
70.	RL 1359	9.36	1.76	1.80*	12.65	1.92*	5.43**
71.	KRANTI	10.03	1.8	4.75**	9.61	1.22	5.76**
	Average Population Mean	10.30			10.13		

"*" and "**" for 5% and 1% Level of Significance

Stability	2	Plant Height (cm)	Number of primary branches per plant	No.of secondary branches per plant	Number of siliquae on main shoot	Number of siliquae on branches	Number of seeds per siliquae	Seed Yield(Q/ha)
a) We Popu b _i =1, S²di =0]	a) Well adapted to all environments; [Mean > Population Mean, b _i =1, S ² di =0]	TM-276, Rohini(SC), KMR- 15-4, PR-2012- 9, Kranti-NC, DRMRIJ-15-85, KM-126, KMR- 53-3, RH-1209, 53-3, RH-1209, SVJ-64, RH- 0923, RGN-389, RAURD- 0923, RGN-389, RAURD- 214, DRMR- 214, DRMR	RL-JEB-52, DRMRIJ-15-85, RMM-09-10, SKM-1313, Maya-C, Sitara -Sreenagar, NPJ-198, JMM- 927-RC, RGN- 389,DRMR-15- 14, RGN-384, RB-81, NPJ-200, KMR-L-15-6, RH-1325, RH-1325, RH-1325, RH-749, Pusa mustard 26(NPJ 113), PHR-2, RL	SKM- 1313, PR-2012-12, SKJM-05, Sitara – Sreenagar, JMM-927- RC, DRMR-15-47, RGN-389, DRMR- 4001, RB-81, KMR-L-15-6, RGN- 386, PRD-2013- 2, RGIN-73, DRMR- 1J-31, DRMR-150-35, RH-406, RH-749, Pusa mustard- 25(NPJ 112), Pusa mustard 26(NPJ 113), Pusa mustard 27(EJ 17), CS 54	RW- 351(Bhagarathi), RW-85-59(Sarna) , TM-276, KM-126, NPJ- 195,DRMR-15-16, NPJ-198, RGN- 389, DRMR-15- 14,RB-81, PRD- 2013-9, RGN-386, RH-749	RW- 351(Bhagarathi),RW- 85-59(Sarna),RW-4C-6- 3(Sanjukta Asech),NPJ- 194, TM-276, NPJ-196,Maya-C, DRMR-15-16,NPJ- 198,RAURD-214, NPJ- 200, RH-1325,RGN-386, Pusa mustard 26(NPJ 113),Pusa mustard 27(EJ 17),CS 54	TM-276,DRMRIJ- 15-85,NPJ- 196,DRMR-15- 5,NPJ-195,Maya- C,SKJM-05,Sitara- Sreenagar, RH- 0923,NPJ-197	Rohini(SC), KMR- 15-4
(q	Specifically adapted to favorable (rich) environment; [Mean > Population Mean, b_1^1, S²di =0]	NPJ-198, DRMR- 15-47,RGN-384, RGN- 386,RNWR-09-3	DRMR-IJ-31	RH-0923, RGN-384, DRMR-15-9 RH-1325, RL 1359	RH-1325	RGN-389,RGN- 384,DRMRIJ-15- 66,GIRIRAJ	SKM-1313, GIRIRAJ,PBR-540- 6,Pusa mustard- 25(NPJ 112)	Pusa mustard 27(EJ 17)
ΰ	Specifically adapted to unfavorable (poor) environment; [Mean > Population Mean, b ₁ <1, S ² di	Divya-88, RH- 1202,DRMR-15-5, Ganga	I	I	RH-0923	DRMR-IJ-31	PR-2012- 9,RMM-09-10, PRD-2013-9,Pusa mustard 27(EJ 17),PHR -2	I

DRMR-15-47, RGN-384, RGN-386, RNWR-09-3 were found to be specifically adapted to the favorable (rich) environment. Four genotypes *viz.*, Divya-88, RH-1202, DRMR-15-5, Ganga were found to be specifically adapted to unfavorable (poor) environment for plant height (**Table 4**).

Nineteen genotypes *viz.*,RL-JEB-52, DRMRIJ-15-85, RMM-09-10, SKM-1313, Maya-C, Sitara –Sreenagar, NPJ-198, JMM-927-RC, RGN-389, DRMR-15-14, RGN-384, RB-81, NPJ-200, KMR-L-15-6, RH-1325, RH-749, Pusa mustard 26(NPJ 113), PHR-2, RL 1359 were found to be stable over six environments created over two years for the character number of primary branches per plant. Only one genotype DRMR-IJ-31 was found to be specifically adapted to favorable (rich) environment. No genotype was found to be specifically adapted to unfavorable (poor) environments (**Table 4**).

In terms of the number of secondary branches per plant, it was found that 21 genotypes *viz.*, SKM-1313,PR-2012-12, SKJM-05, Sitara -Sreenagar, JMM-927-RC, DRMR-15-47, RGN-389, DRMR-4001, RB-81, KMR-L-15-6, RGN-386, PRD-2013-2, RGIN-73, DRMR-IJ-31, DRMR-150-35, RH-406, RH-749, Pusa mustard-25 (NPJ 112), Pusa mustard 26 (NPJ 113), Pusa mustard 27 (EJ 17), CS 54 were stable over six environments. Five genotypes *viz.*, RH-0923, RGN-384, DRMR-15-9, RH-1325, RL 1359 were found to be specifically adapted to the favorable (rich) environment. No genotype found to be specifically adapted unfavorable (poor) environment (**Table 4**).

Thirteen genotypes *viz.*, RW-351 (Bhagarathi), RW-85-59 (Sarna), TM-276, KM-126, NPJ-195, DRMR-15-16, RGN-389, DRMR-15-14, RB-81, PRD-2013-9, RGN-386, RH-749 were found to be stable over the six environments for the character number of siliquae on main shoot. Only one genotype RH-1325 were found to be specifically adapted to the favorable (rich) environment and one genotype RH-0923 was found to be specifically adapted to unfavorable (poor) environments for the character number of siliquae on main shoot (**Table 4**).

In terms of the number of siliquae on branches 16 genotypes *viz.*, RW-351 (Bhagarathi), RW-85-59(Sarna), RW-4C-6-3(SanjuktaAsech), NPJ-194, TM-276, NPJ-196, Maya-C, DRMR-15-16, NPJ-198, RAURD-214, NPJ-200, RH-1325, RGN-386, Pusa mustard 26 (NPJ113), Pusa mustard 27(EJ 17), CS 54 were found to be stable over the six environments. Four genotypes *viz.*, RGN-389, RGN-384, DRMRIJ-15-66, GIRIRAJ were found to be adapted to specifically favorable (rich) environment. Only one genotype DRMR-IJ-31 was found to be specifically adapted to the unfavorable (poor) environment for the character number of siliquae on main shoot (**Table 4**).

Ten genotypes *viz.*, TM-276, DRMRIJ-15-85, NPJ-196, DRMR-15-5, NPJ-195, Maya-C, SKJM-05, Sitara-Sreenagar, RH-0923, NPJ-197 were found to be stable over six environments. Four genotypes *viz.*, SKM-1313, GIRIRAJ, BPR-540-6, Pusa mustard-25 (NPJ 112) were found to be specifically adapted to the favorable (rich) environment. Five genotypes *viz.*, PR-2012-9, RMM-09-10, PRD-2013-9, Pusa mustard 27 (EJ 17), PHR -2 were found to be specifically adapted to unfavorable (poor) environment (**Table 4**).

In terms of seed yield (q/ha), two genotypes viz., Rohini (SC), KMR-15-4 were found to be stable in all environments. Pusa mustard 27 (EJ 17) was found to be specifically adapted to the favorable (rich) environment and no genotype was found to be the specifically adapted unfavourable (poor) environment for the seed yield. The genotype Rohini(SC) and KMR-15-4 also found to have superior stable performance for plant height along with stable superior yield performance. The genotype Pusa mustard 27 (EJ 17) in addition to being specifically adapted to the favourable (rich) environments for yield performance, also had stability in the number of secondary branches per plant and number of siliquae on branchesin all types of environments. However, the number of seeds per siliquae was found to be stable specifically adapted to unfavorable (poor) environment (Table 4) (Karale et al., 1997; Yadav et al., 1997; Ahamed, 2001; and Dewi et al., 2014).

The pooled ANOVA revealed significant differences among genotype, environment, and genotype × environment interactions for all eight characters under study. This indicated the need for stability analysis using the Eberhart and Russell (1966) model, which confirmed significant differences among genotypes, environments, and their interactions for all the characters except days to 50% flowering. Stability parameters (mean, b,, and S²di) were evaluated for seventy-one genotypes to categorize them based on stability and adaptability. The stable genotypes across the six environments over two years were Rohini (SC) and KMR-15-14 for seed yield. Pusa mustard 27 (EJ 17) was specifically adapted to the favourable (rich) environment for the seed yield, but this was also well adapted in all environments for the secondary branches per plant and the number of siliquae on branches. Hence, these genotypes can be included in systematic breeding programme for the development of high vielding stable and superior genotypes over environments or locations. The present study concluded that these genotypes can be used as parents for hybridization programme to improve specific targeted characters.

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