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Research Article

Genotype by environment interaction in mustard (*Brassica juncea*) under Terai Agro-Climatic zone using the AMMI model and GGE biplot

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Abstract

In the present experiment, 71 Indian mustard (*Brassica juncea*) genotypes were evaluated in six environments for two successive years (three environments in each year) to identify the influence of environment over the genotypes and to identify the stable, better-performing genotypes in respect to yield in Terai region of West Bengal. Statistical analysis was carried out to evaluate genotype × environment interaction using two different approaches, namely, additive main effect, and their multiplicative interaction model (AMMI) and genotype plus genotype by environment interaction (GGE) biplot for seed yield of mustard genotypes. AMMI ANOVA showed that genotype and environment accounted for 11.46% and 47.50% of the variation respectively, where GEI captured 36.57% of the variation for seed yield. The AMMI model and GGE biplots showed that genotype RGIN-73 was the highest yielding genotype to a specific environment but DRWR-15-9 was found to be well stable with good yielding in all environments.

Keywords: AMMI, GGE biplot, GSI, stability, GE interaction, *Brassica juncea*

INTRODUCTION

India is the 3rd largest producer of oilseed in the world and is the fourth largest oil economy after the U.S.A, China, and Brazil (Hegde, 2006). Due to the high quality of oil, mustard has become the top priority in the human diet. Over the past few decades, mustard oil has been used as edible vegetable oil, while mustard seeds are used as condiments and for preparing pickles, sauces, sandwiches, salad dressing and green leaves

as vegetables. Mustard is an important nutritious food, containing higher quality of protein and the mustard cake is used for animal feed. The importance and demand for Indian mustard are growing day by day throughout the world. In this context, different research approaches on stability aspects have been integrated with the varietal development programme to improve mustard germplasm and satisfy the future worldwide increasing demand for

this crop. Due to the high demand for Indian mustard, numerous varieties with good yield potential in specific regions have been released from various parts of India, particularly from the Northern regions. However, it is important to evaluate the performance of these superior genotypes in the terai agro-climatic zone. Therefore, the stability of seed yield was assessed under different environmental conditions and genotype performance was evaluated in genotype \times environment interactions.

Genotype \times environment interaction is a valuable concept in plant breeding programme because it aids in the selection and improvement of genotypes that perform well across various environments (Hill, 1975). A specific genotype does not exhibit the same phenotypic performance in all different environments or conversely, the response of different genotypes varies from environment to environment due to genetic and non-genetic interaction, known as genotype \times environment (G \times E) Interaction (Moll and Stuber, 1974; Subudhi *et al.*, 2012). Due to the presence of G \times E interaction, the environmental factor plays an important role in discriminating crop performance, aiding in the selection of appropriate breeding strategies. (Kang and Martin, 1987). Changes in ranking of the same variety in different environments make it difficult for the plant breeders to decide which genotype should be selected. There are several statistical approaches to measure genotypic stability. However, no single method is sufficient to measure the performance of genotypes across different environments.

A genotype is considered more adaptive or stable if its yield fluctuation is less when cultivated over different seasons (Amin *et al.*, 2005). There are two models, AMMI and GGE biplot, used to visualize (Gauch and Zobel, 1988; Gauch and Zobel, 1997; Yan *et al.*, 2000) and analyse genotype \times environment interaction (Abay and Bjornstad 2009; Akcura *et al.*, 2011; Mitrovic *et al.*, 2012) with greater accuracy in many crops (Bradru and Gabriel, 1978 and Crossa *et al.*, 1991). AMMI analysis combines the additive main effect of a model for G \times E interaction with their multiplicative component of the interactions into an integrated least square analysis. The AMMI model is efficient and suited for selecting stable genotypes (McLaren and Chaudhary, 1994). It can calculate the total genotype \times environment (G \times E) interaction of genotypes and partition the interactions to each environment (Zobel *et al.*, 1988). To understand genotype \times environment interaction (GEI), the GGE biplot (Yan *et al.*, 2000; Yan and Kang, 2003) is the most commonly used. The GGE (Genotype and Genotype-by-Environment) biplot analysis provides a graphical presentation of estimated interactions (Abay and Bjornstad, 2009; Miranda *et al.*, 2009; Akcura *et al.*, 2011; Mitrovic *et al.*, 2012). This method integrates ANOVA and PCA, partitioning the sum of the square of genotypes and genotype \times environment interaction (GEI) using the PCA method. It is also used

to present and estimate genotype performance in different environments. (Miranda *et al.*, 2009). For the simultaneous evaluation of genotypes, both genotype (G) and genotype \times environment (GE) interaction must be considered (Yan and Tinker, 2006; Sabaghnia *et al.*, 2008). The G and GE (GGE) biplot excludes environments (E) and incorporates G with GE interaction (Yan *et al.*, 2000). Moreover, it detects genotype \times environment interaction patterns and can identify "which-won-where" (Yan *et al.*, 2007). In this context, the objectives of the present study were to identify the high-yielding and stable genotype in terai agro-climatic region.

MATERIALS AND METHODS

The present investigation was carried out to reveal information about the stability performance of national and regional cultivars. The experiment was conducted in Terai-Agro Climatic Zone (Cooch Behar) over two consecutive seasons of 2017-2018 and 2018-2019, at Uttar Banga Krishi Vishwavidyalaya Instructional Farm Field (26°40' N & 89°39' E). In crop season 2017-2018, the sowing was done in three different dates at seven days interval, i.e., 14-11-2017(E₁), 21-11-2017(E₂) and 28-11-2017 (E₃) consecutively as well as in crop season 2018-2019, the sowing was done in three different dates at 10 days interval, i.e., 01-11-2018 (E₄), 10-11-2018 (E₅), 19-11-2018 (E₆) (Sagolsem *et al.*, 2013; Sahana *et al.*, 2024). The experimental material consisted of 71 genotypes of Indian mustard (**Table 1**) collected from germplasm collection centre, B.H.U, Uttar Pradesh; Directorate of Rapeseed – Mustard Research, Bharatpur (Rajasthan); and Pulse and Oilseed Research Station, Berhampore, Murshidabad, West Bengal.

The experiment was carried out in Randomized Block Design with three replications. The size of each plot was 1 m \times 1 m with three rows for each genotype. The plant-to-plant distance was kept at 10 cm and the row-to-row spacing was maintained at 30 cm. The recommended cultural practices were followed to ensure the optimum growth and development of the crops. Seed yield was determined by collecting seeds from ten tagged plants in each plot and converting it into q/ha.

Statistical analysis: Stability analysis was conducted in R software version 3.6.1 using the agricolae package (Mendiburu, 2014, Sood *et al.*, 2016, Singh *et al.*, 2024) for AMMI analysis and the GUI package was utilized for GGE biplot analysis (Singh *et al.*, 2024).

RESULTS AND DISCUSSION

The Pooled ANOVA (**Table 2**) revealed that the genotype, environment and the genotype \times environment components differed significantly for the character seed yield (q/ha). This indicated that further stability analysis and estimation of stability parameters can be carried out for the aforesaid trait.

Table 1. Mean performance of 71 Mustard genotypes over six environments

No.	Genotype	Seed Yield (q/ha)						Mean
		E 1	E 2	E 3	E 4	E 5	E 6	
1.	B-85(Seeta)	16.2	7.7	5.2	8.32	6.23	9.8	8.91
2.	RW-351(Bhagarathi)	17.4	9.4	5.8	11.93	5.2	7.1	9.47
3.	RW-85-59(Sarna)	14.2	6.3	3.1	10.47	4.8	5.3	7.36
4.	RW-4C-6-3(Sanjukta Asech)	22.8	10.4	6.3	7.07	7.77	6.57	10.15
5.	NPJ-194	35.9	15.3	7.4	11.83	7.3	5.67	13.9
6.	TM-276	17.9	4.4	2.9	9.61	5.17	5.37	7.56
7.	Rohini(SC)	15.4	14.5	10.2	10.9	5.97	7.27	10.71
8.	KMR-15-4	17.7	13.1	11.1	11.63	4.8	6.17	10.75
9.	PR-2012-9	8.9	17.2	6.7	11.17	6.5	7.23	9.62
10.	Divya-88	18.4	7.1	8.8	12	4.47	9	9.96
11.	RL-JEB-52	16.9	12.8	2.7	11.23	6.2	8.43	9.71
12.	Kranti-NC	19.4	13.7	18.5	11.33	6.77	5.9	12.6
13.	DRMRIJ-15-85	17.1	7.9	12.2	11.47	5.9	6.17	10.12
14.	RH-1202	12.5	7.8	8.1	8.73	6.9	5.73	8.29
15.	NPJ-196	12.6	10.6	8.9	9.37	8.2	7.7	9.56
16.	RMM-09-10	14.5	14.3	5.4	9.6	7.2	5.97	9.49
17.	JMM-927-RC	6.6	10	15.4	14.47	3.67	7.23	9.56
18.	RRN-871	8.1	15.3	6.5	13.2	2.53	6.43	8.68
19.	KM-126	5.7	11.4	7.5	11.17	4.33	5.1	7.53
20.	SKM-1313	7.1	12.7	10.5	12.83	7.93	3.23	9.05
21.	RB-77	2.9	4.7	7.3	10.07	8.7	4.9	6.43
22.	DRMR-15-5	11.2	22.1	8.6	10.37	5.63	8.63	11.09
23.	KMR-53-3	5.1	6.4	5.9	11.03	6.13	5.87	6.74
24.	RL-JEB-84	10.7	6.8	3.6	12.53	8.23	7.1	8.16
25.	Ganga	12.7	8.5	6.1	12.43	7.2	7.4	9.06
26.	RGN-73-JC	13.3	8.5	3.5	9.67	6.93	3.47	7.56
27.	RH-1209	14.6	14.2	4.5	11.47	6.1	3.23	9.02
28.	PR-2012-12	14.4	7.2	3.9	10.37	6.2	0.93	7.17
29.	RGN-385	15.9	8.7	12.3	12.87	5.4	0.93	9.35
30.	NPJ-195	15.9	19.8	12.1	12.07	6.57	1.3	11.29
31.	Maya-C	18.5	5.8	9.7	12.37	5.67	2.53	9.09
32.	SKJM-05	29.7	19.2	18.3	13.07	4.63	5.73	15.11
33.	SVJ-64	11.5	9.7	9.8	12.9	8.23	5.87	9.67
34.	Sitara-Sreenagar	25.2	17.3	12.1	10.4	7.97	5.13	13.02
35.	RH-0923	18.2	14.5	9.1	6.13	7.23	1.57	9.46
36.	DRMR-15-16	13.2	17	13.6	7.8	4.47	0.8	9.48
37.	NPJ-198	17.6	9.2	7.9	14.47	4.83	1.13	9.19
38.	JMM-927-RC	19.8	4.9	7.9	11.53	6.37	1.33	8.64
39.	DRMR-15-47	20.6	15.9	8	13.9	5.6	2.33	11.06
40.	RGN-389	15.1	15.3	7.6	9.67	6.07	2.1	9.31
41.	RAURD-214	21.6	5.2	9.2	7.7	8.23	3.57	9.25
42.	DRMR-15-14	25.7	8.8	9.6	16.77	6.07	2.87	11.63
43.	DRMR-4001	11	11.8	9	9.83	3.43	2.6	7.94
44.	RGN-384	20.4	5.4	9.9	10.97	5.9	2.2	9.13

Table 1. Continued..

No.	Genotype	Seed Yield (q/ha)						Mean
		E 1	E 2	E 3	E 4	E 5	E 6	
45.	NPJ-197	25.6	9.7	12.1	12.2	5.5	1.83	11.16
46.	RB-81	30.7	8.6	16.6	15.07	4.23	2.53	12.96
47.	NPJ-200	25.3	8.2	12.7	12.13	6.03	2.93	11.22
48.	DRMR-15-9	18.6	12.4	15.8	13.2	5.9	2.4	11.38
49.	KMR-L-15-6	15.3	12.8	12.4	8.73	6.8	3.4	9.91
50.	PRD-2013-9	19.9	4	8.1	14.1	6.97	4.4	9.58
51.	DRMRIJ-15-66	20.9	14.9	4.5	11.6	5.97	2.4	10.04
52.	RH-1368	12.2	10.8	11.1	11.6	6.8	3.57	9.34
53.	RH-1325	14.5	15.8	3.5	12.9	5.67	3.33	9.28
54.	RGN-386	20.2	13.1	4.6	10.13	9.33	2.37	9.96
55.	RNWR-09-3	21.3	20.2	4.9	12.63	6.93	2.63	11.43
56.	PRD-2013-2	20.4	6.7	9.4	7.83	9.63	2.67	9.44
57.	GIRIRAJ	15	22.3	6.5	8.4	5.77	2.1	10.01
58.	BPR-540-6	24.4	12.7	4.4	11.47	3.83	3.37	10.03
59.	RGIN-73	53.4	43.7	19	9.47	3.8	4.07	22.24
60.	DRMR-IJ-31	47.1	22.3	11.3	8.93	2.1	2.43	15.69
61.	NRCHB-101	27.1	22.3	14.4	11.63	2.07	3.87	13.56
62.	DRMR-150-35	21.3	19.7	10.9	8.03	3.1	3.27	11.05
63.	RH-406	19.7	10.2	10.4	9.57	1.77	2.3	8.99
64.	RH-749	30.2	24.7	8.3	8.97	2.53	3.17	12.98
65.	Pusa mustard-25(NPJ 112)	11.9	13.7	7.9	9	2.23	2.5	7.87
66.	Pusa mustard26(NPJ 113)	27	8.9	11.9	6.37	3.23	1.9	9.88
67.	Pusa mustard27(EJ 17)	23.2	13.9	7.6	10.23	6.7	2.3	10.66
68.	CS 54	28	8.4	11.2	11.03	9.17	1.13	11.49
69.	PHR -2	20.8	3.8	3.9	4.13	2.8	1.27	6.12
70.	RL 1359	30	19.1	10.1	9.7	6.17	0.83	12.65
71.	KRANTI	20.1	12.3	12.6	7.83	3.03	1.8	9.61
	Environmental Mean	18.79	12.45	9	10.78	5.74	4.02	
	C.V(%)	9.24	11.18	12.94	22.77	25.12	30.67	
	SE(m)	1	0.8	0.67	1.42	0.83	0.71	
	CD(p=0.05)	2.8	2.25	1.88	3.96	2.33	1.99	

Table 2. Pooled ANOVA of genotypes for yield over six environments

Source Of Variation	Seed Yield (q/ha)
Genotype	101.81**
Envo.	5906.90**
Genotype × Envo.	64.96**
Pooled error	2.66

The pooled mean of performance of mustard genotypes over environment revealed that RGIN-73 was the highest-yielding genotype (22.24 q/ha) among the 71 (Table 1).

The effect of genotype, environment and their interaction (GEI) on mustard were highly significant ($P < 0.01$). Genotype and environment accounted for 11.46% and 47.50% of the variation respectively, while GEI captured 36.57% of the variation (**Table 3**). This interaction was partitioned between six principal component axes (IPCA). The IPCA 1 was highly significant and captured 26.08% of the total variation of genotype by environment interaction. The IPCA2, IPCA3, and IPCA4 were also highly significant and accounted for 8.21%, 3.94% and 2.71% of the total variation, respectively, of genotype by environment interaction. Therefore, the four IPCA axes jointly captured 40.94% of the sum of square (SS) of the total variation in the genotype by environment interaction (GEI).

The best performance is not always indicative of the most stable genotype; however, there is a method that combines both stability and high performance. Therefore, the rank of Additive Main effects and multiplicative interactions (AMMI) Stability Value (ASV) and the rank of the mean of genotypes are integrated into a single selection index, termed as Genotype Selection Index (GSI). An ideal genotype with high mean as well as the least ASV score is selected as the most stable genotype (Farshadfar, 2008; Sood *et al.*, 2016; Bibi *et al.*, 2018).

The analysis of ASV for yield indicated that RGN-386 (0.18) followed by DRMR-15-9 (0.20), RH-0923 (0.37), KRANTI (0.39) were the genotypes having lower ASV values, suggesting that these genotypes were relatively more stable than the other genotypes. The genotypes

RGIN-73 (16.51) followed by DRMR-IJ-31(10.50), RB-77(6.26), NPJ-194(6.06) showed the higher ASV values, indicating that these genotypes were considered as the least stable genotypes (**Table 4**). The genotypes such as KMR-53-3, KM-126, RL-JEB-84 with high GSI value, were considered as unstable and not adaptable genotypes. Meanwhile, the genotype RGIN-73 had the highest mean yield of 22.24 q/ha, followed by DRMR-IJ-31(15.69), SKJM-05(15.11), NPJ-194 (13.90). However, stability is not the sole determinant for selecting of ideal genotypes, because the most stable genotypes not necessarily give maximum yield. So, the genotype selection index indicated that DRMR-15-9 was the best and top-ranking genotype followed by KMR-15-4, Rohini (SC), RGN-386 (**Table 4**), exhibiting better stability and mean yield performance. This revealed that these genotypes had comparatively lower ASV with a higher genotype yield. Therefore, based on the AMMI model, DRMR-15-9 could be potential and stable genotypes.

The AMMI model and GGE biplot provide extensive information on the genotype \times environment interaction (GEI) in mustard. However, GGE biplots offer more comprehensive insights than AMMI due to their representativeness and discriminating ability. The concept behind the GGE biplot is to use a graphical presentation to display the two important factors, G and GE, which are sources of variance (Yan *et al.*, 2000; Badu-Apraku *et al.*, 2012). The GGE analysis revealed that the PC1 and PC2 captured 64.06% and 18.46% of the interaction, respectively. In **Fig.1** genotypes G54 (RGN-386), G48 (DRMR-15-9) were close to the origin, which indicated

Table 3. Analysis of variance for additive main effects and multiplicative interaction model for seed yield across six environments for 2017 to 2018 and 2018 to 2019 seasons.

Source	Yield (q/ha)				
	DF	SS	MS	%Total SS	% Interaction
Total		62174.8			
Environment	5	29534.5	5906.9**	47.50	
Replications within environment	12	546.3	45.5**	0.88	
Genotype	70	7126.9	101.8**	11.46	
G \times E	350	22735.6	65.0**	36.57	
IPCA1	74	5929.5	80.1**		26.08
IPCA2	72	1866.1	25.9**		8.21
IPCA3	70	896.1	12.8**		3.94
IPCA4	68	615.7	9.1**		2.71
IPCA5	66	283.3	4.3		1.25
IPCA6	64	209.5	3.3		0.92
Residual	840	2231.5	2.7		

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

† DF = degrees of freedom; SS = sum of squares; MS = mean square; G \times E = genotype by environment; IIPCA = interaction principal component analysis.

Table 4. AMMI Stability Value (ASV) and Genotype Selection Index (GSI) for 71 mustard genotypes

S. No.	Genotype	Seed Yield (q/ha)					Rank(ASV)	Rank (MEAN)	GSI
		Mean (q/ha)	IPCA-1	IPCA-2	ASV				
G1	B-85(Seeta)	8.91	-0.47	0.28	1.53	33	57	90	
G2	RW-351(Bhagarathi)	9.47	-0.24	0.18	0.79	10	42	52	
G3	RW-85-59(Sarna)	7.36	-0.75	0.44	2.42	47	67	114	
G4	RW-4C-6-3(Sanjukta Asech)	10.15	0.35	0.48	1.2	20	24	44	
G5	NPJ-194	13.9	1.89	0.76	6.06	68	4	72	
G6	TM-276	7.56	-0.51	0.97	1.88	37	65	102	
G7	Rohini(SC)	10.71	-0.11	-0.68	0.76	8	22	30	
G8	KMR-15-4	10.75	0.08	-0.32	0.4	5	21	26	
G9	PR-2012-9	9.62	-0.68	-1.45	2.61	53	35	88	
G10	Divya-88	9.96	-0.25	0.49	0.94	13	29	42	
G11	RL-JEB-52	9.71	-0.23	-0.26	0.77	9	33	42	
G12	Kranti-NC	12.6	0.39	-0.35	1.28	25	10	35	
G13	DRMRIJ-15-85	10.12	-0.27	0.32	0.91	11	25	36	
G14	RH-1202	8.29	-0.8	0.09	2.55	51	60	111	
G15	NPJ-196	9.56	-0.67	-0.32	2.14	43	38	81	
G16	RMM-09-10	9.49	-0.33	-0.59	1.21	21	40	61	
G17	JMM-927-RC	9.56	-1.14	-0.79	3.72	60	38	98	
G18	RRN-871	8.68	-0.87	-1.24	3.03	57	58	115	
G19	KM-126	7.53	-1.29	-0.86	4.2	62	66	128	
G20	SKM-1313	9.05	-1.06	-0.93	3.48	58	54	112	
G21	RB-77	6.43	-1.97	-0.15	6.26	69	70	139	
G22	DRMR-15-5	11.09	-0.22	-1.94	2.06	42	18	60	
G23	KMR-53-3	6.74	-1.69	-0.22	5.37	66	69	135	
G24	RL-JEB-84	8.16	-1.21	0.14	3.84	61	61	122	
G25	Ganga	9.06	-0.87	0.02	2.76	54	53	107	
G26	RGN-73-JC	7.56	-0.81	0.19	2.59	52	64	116	
G27	RH-1209	9.02	-0.37	-0.48	1.26	23	55	78	
G28	PR-2012-12	7.17	-0.75	0.49	2.43	48	68	116	
G29	RGN-385	9.35	-0.37	0.27	1.19	19	45	64	
G30	NPJ-195	11.29	0.2	-1.18	1.35	27	15	42	
G31	Maya-C	9.09	-0.34	0.85	1.38	29	52	81	
G32	SKJM-05	15.11	1.61	-0.29	5.12	65	3	68	
G33	SVJ-64	9.67	-0.88	-0.22	2.81	55	34	89	
G34	Sitara-Sreenagar	13.02	0.93	-0.24	2.95	56	6	62	
G35	RH-0923	9.46	0.09	-0.24	0.37	3	43	46	
G36	DRMR-15-16	9.48	-0.16	-0.99	1.11	17	41	58	
G37	NPJ-198	9.19	-0.3	0.4	1.03	15	50	65	
G38	JMM-927-RC	8.64	-0.32	1.14	1.52	32	59	91	
G39	DRMR-15-47	11.06	0.33	-0.28	1.08	16	19	35	
G40	RGN-389	9.31	-0.24	-0.56	0.94	12	47	59	
G41	RAURD-214	9.25	-0.13	1.2	1.27	24	49	73	
G42	DRMR-15-14	11.63	0.45	0.99	1.73	35	11	46	
G43	DRMR-4001	7.94	-0.79	-0.43	2.54	50	62	112	

Table 4. Continued..

S No.	Genotype	Seed Yield (q/ha)					Rank(ASV)	Rank (MEAN)	GSI
		Mean (q/ha)	IPCA-1	IPCA-2	ASV				
G44	RGN-384	9.13	-0.22	1.09	1.29	26	51	77	
G45	NPJ-197	11.16	0.56	0.87	1.98	39	17	56	
G46	RB-81	12.96	1.08	1.3	3.65	59	8	67	
G47	NPJ-200	11.22	0.44	1.03	1.73	36	16	52	
G48	DRMR-15-9	11.38	0.06	-0.04	0.2	2	14	16	
G49	KMR-L-15-6	9.91	-0.31	-0.28	1.01	14	31	45	
G50	PRD-2013-9	9.58	-0.45	1.22	1.88	38	37	75	
G51	DRMRIJ-15-66	10.04	0.19	-0.04	0.61	7	26	33	
G52	RH-1368	9.34	-0.77	-0.23	2.46	49	46	95	
G53	RH-1325	9.28	-0.43	-0.62	1.5	31	48	79	
G54	RGN-386	9.96	-0.01	0.18	0.18	1	30	31	
G55	RNWR-09-3	11.43	0.49	-0.71	1.7	34	13	47	
G56	PRD-2013-2	9.44	-0.24	0.98	1.23	22	44	66	
G57	GIRIRAJ	10.01	0.04	-1.43	1.43	30	28	58	
G58	BPR-540-6	10.03	0.4	0.5	1.36	28	27	55	
G59	RGIN-73	22.24	5.17	-1.69	16.51	71	1	72	
G60	DRMR-IJ-31	15.69	3.29	0.81	10.5	70	2	72	
G61	NRCHB-101	13.56	1.37	-0.71	4.4	64	5	69	
G62	DRMR-150-35	11.05	0.6	-0.71	2.04	41	20	61	
G63	RH-406	8.99	-0.06	0.44	0.48	6	56	62	
G64	RH-749	12.98	1.68	-0.69	5.38	67	7	74	
G65	Pusa mustard-25(NPJ 112)	7.87	-0.7	-0.54	2.29	46	63	109	
G66	Pusa mustard26(NPJ 113)	9.88	0.61	1.16	2.25	44	32	76	
G67	Pusa mustard27(EJ 17)	10.66	0.36	0.27	1.17	18	23	41	
G68	CS 54	11.49	0.58	1.33	2.28	45	12	57	
G69	PHR -2	6.12	-0.42	1.52	2.02	40	71	111	
G70	RL 1359	12.65	1.36	0.09	4.31	63	9	72	
G71	KRANTI	9.61	0.1	0.21	0.39	4	36	40	

their greater stability. An interesting observation from the GGE biplot vector point of view was that the length of the environment vector. Each environment vector approximates the standard deviation, which is a measure of discriminating ability. Thus, in **Fig.1** environment E1 was identified as the most discriminative environment.

In the present study, the correlation among environments was determined by the angle between them in the GGE biplot. Angle between vectors less than 90° indicated a positive correlation. An angle of 90° between the vectors reflected an independent environment, while angle greater than 90° between the vectors indicated a negative correlation between the environments.

There was a positive correlation between environments E1 and E3, E2 and E3 due to the small angle between them (**Fig. 1**), reflecting the similar responses of the genotypes in these locations. It also can be inferred that genotypes with had high yield in E1, might also perform well in E3 and those genotypes which had high yield in E2 they might also perform well in E3 as well. However, the angles between environment vectors E1 and E6, E2 and E6 indicated a negative correlation. This means that those genotypes were high yielding in E1, might give low yield in E6 or vice versa. To understand genotype × environment interaction (GEI), two approaches namely AMMI and GGE were used in this study to clarify the GEI of the genotypes across environments.

The GGE biplot helps to identify both the “ideal environment” and the “ideal genotype” (Gauch and Zobel, 1997). The AMMI model cannot accurately identify ‘which-won-where,’ but the GGE biplot can determine the superiority of genotypes across different test environments (Yan *et al.*, 2007). The Which-Won-Where/What’ biplot (Fig. 3) partitioned the 71 genotypes into seven sectors (I, II, III, IV, V, VI, VII), where six locations were divided into only three groups (Group IV, Group VI, Group VII). The genotypes located on the vertices of each group illustrated the best performer at sites included in the corresponding group (Alwala *et al.*, 2010). In this study, the genotype located on the vertices of the polygon was G69 (PHR-2), G46 (RB-81), G60 (DRMR-150-35), G59 (RGIN-73), G22 (DRMR-15-5) and G21(RB-77). Groups I, II, III, and V did not include any environments, which indicated that these genotypes in these groups did not have specific environmental recommendations (Fig. 3). Furthermore, it was found that six environments might be partitioned into three separate mega-environments i.e., Group IV consisted of mega-environment of E2 and E3; Group VI consisted of mega-environment of E6 and Group VII consisted of mega-environment E4 and E5. For Group IV, G59 (RGIN 73) and G60 (DRMR-IJ-31) were winning in E2 and E3 mega-environment while for group VII, G21(RB-77) were winning in mega-environment E4 and E5. Similar study was also done by Kumar *et al.* 2023; Singh *et al.* 2024.

Average Environment Axis (AEA) is a line that passes through the average environment and the biplot origin whereas a perpendicular axis is also overlaid on biplot is termed as Average Coordination Axis (AEC). The data consist of genotype (G) along with AEA and rest genotype-environment (GE) along with AEC. More projection of genotypes on AEA means more yield in the trial while more projection in AEC mean more interaction which implies more instability. The genotypes towards the target environment from the origin and close to the AEA axis would be selected as stable high yielding genotypes.

Therefore, the genotype G48 (DRMR-15-9), G8(KMR-15-4) were favourable for further trials considering both average yield and stability compared to G46 (RB-81) and G57 (GIRIRAJ) (Fig. 4) (Cooper *et al.*, 1997). GGE analysis enables to identify the highest yielding stable genotypes. (Akcura *et al.*, 2011).

The intention of test environments evaluation is to find out the superior genotypes. An “ideal environment” clearly discriminates the genotypes and reflects all other environments under the experiment. So, it should be able to identify the best genotype under the terai agro-climatic region. The environments that make smaller angles relative to the AEA are the most representative of the average test environments.

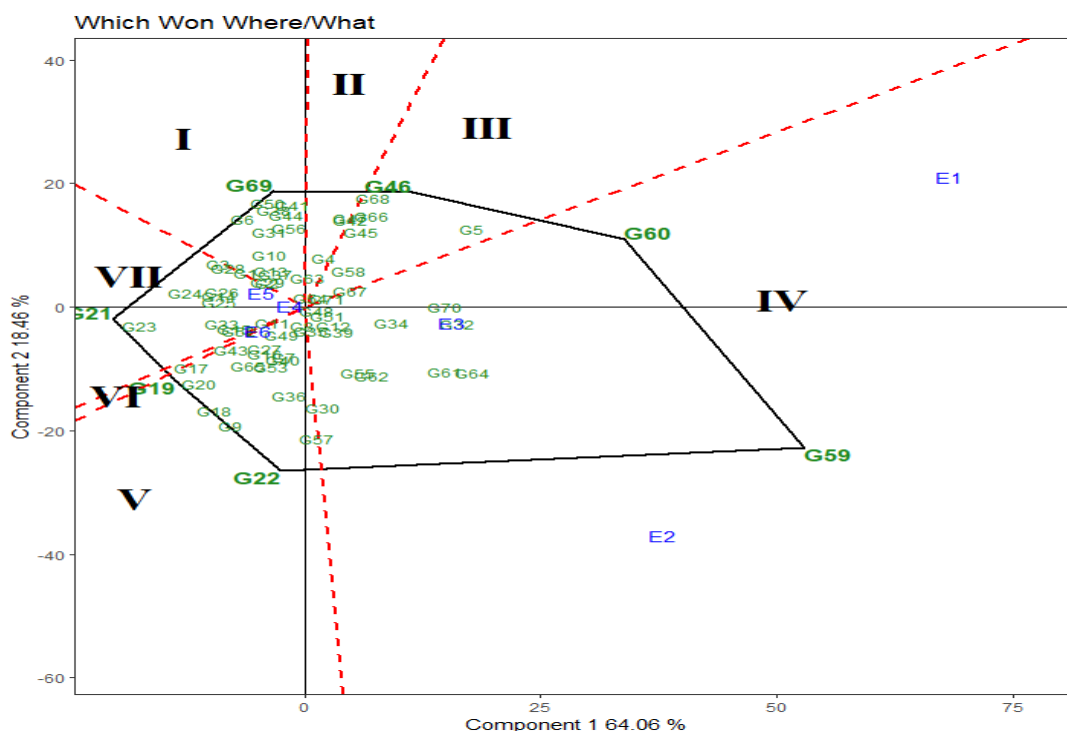


Fig. 3. ‘Which-Won-Where/What’ figure of 71 mustard genotypes yields on six environments

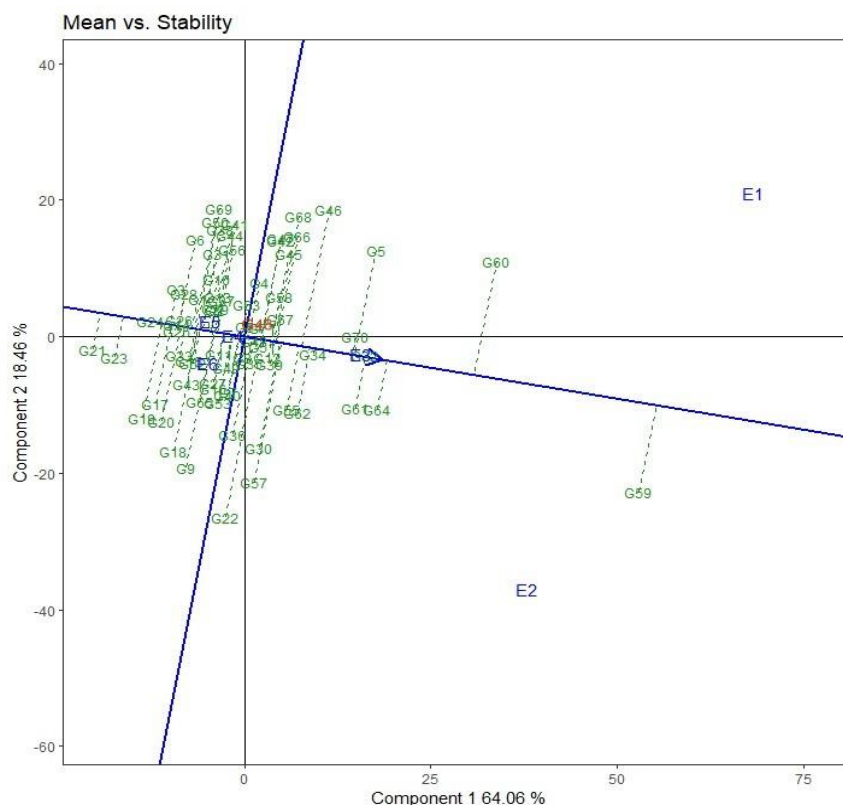


Fig. 4. Mean Vs. Stability of 71 mustard genotypes yields on six environments

Among the environments, E3 could be considered the most representative (Fig.5) because it had a smaller angle with "Average Environment Axis"(AEA) (Yan, 2001) (AEA is the line that crossed through the average environment and the biplot origin) whereas E5 and E6 were the least representative. The cosine of the angles generated between any environment vectors from the origin signifies that the magnitude and direction of correlation among the vectors. An acute angle represents a positive correlation whereas the obtuse angle represents negative correlation. The concentric rings represent the environmental standard deviations, which are helpful in evaluating the discriminating ability of a particular environment. The environment located close to the origin represents low variation. The test environment that had a small angle to the AEA has more representative power than those forming a larger angle with the AEA. Test environment with longer vectors are considered to have relatively more discriminating power. If the test environment has a short vector, it implies that the genotypes in it will perform similarly. It would provide little or no information about genotype variation. Therefore, the separation among the genotypes will be low. In the present study, environment E3 could be considered a good test environments for selecting generally adapted genotypes because it had the highest representativeness of the trial and had the highest

discriminating ability as observed in Fig 3. Therefore, the environment E3 was the most fruitful trial (Yan, 2001).

The mean performance of the 71 mustard genotypes showed that RGIN-73 was the highest yielding genotype but AMMI analysis showed that DRMR-15-9 was stable and had good yield. According to the GGE biplot (which-won-where), it was found that RGIN-73 and DRMR-IJ-31 performed best in the E2 and E3 mega-environments, while RB-77 excelled in the E4 and E5 mega-environments. The GGE 'biplot also indicated that DRMR-15-9 was favourable for further trials due to its stability and high-yielding potential. The tested environments were highly distinct, with E3 being the most fruitful. The GGE biplot study confirmed the findings of the AMMI analysis. The stable and high-yielding genotypes identified in this study could be evaluated in larger areas across multiple locations. This might help to determine their suitability for commercial cultivation in multiple locations. The genotypes can be used as parents in hybridization programme for the development of high-yielding hybrids with consistent stability.

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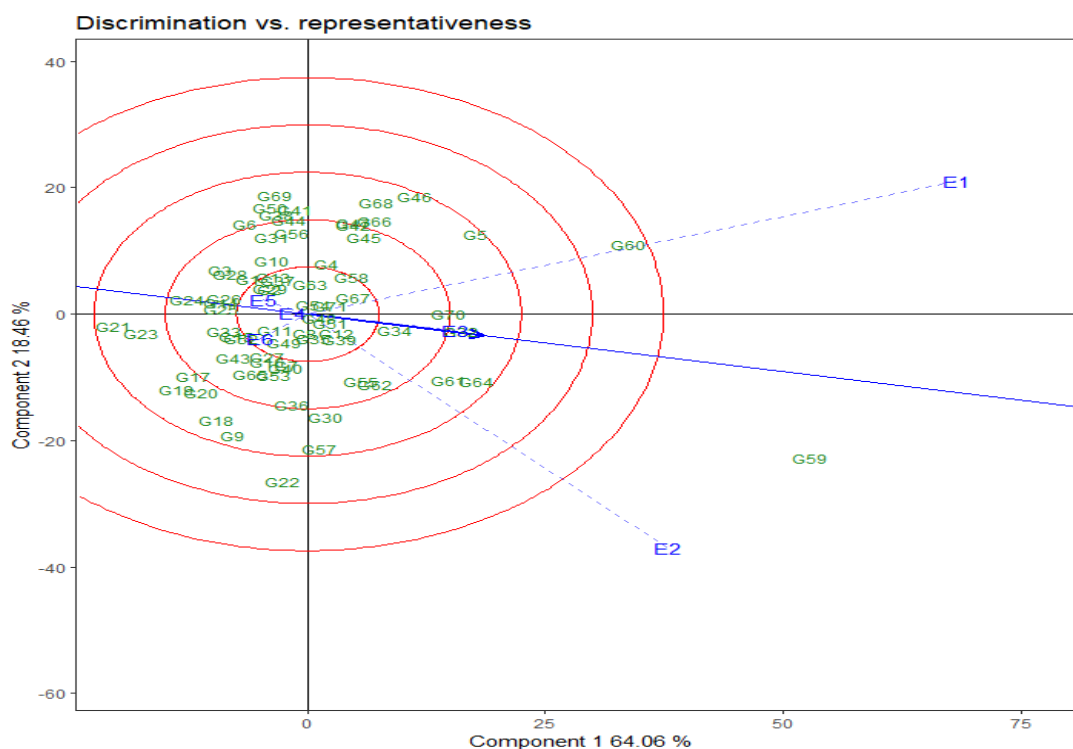


Fig. 5. Discrimination Vs. Representativeness of 71 mustard genotypes yields on six environments

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