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Estimate the magnitude of genotype, environment and genotype by environment interaction for seed yield and its component traits in mungbean

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Abstract
Crop varieties developed should exhibit stable performance under various environmental conditions, especially in a diverse country like India, where a wide range of environments exist. Developing genotypes with a potency of adjustability across a broad spectrum of environmental conditions is essential for effectively realizing their inherent potential. Therefore, research aimed to estimate the magnitude of genotype, environment, and genotype-by-environment interaction for seed yield and its component traits in mungbean. Fourteen genotypes of mungbean were evaluated from four different environments in Madhya Pradesh. The experiment was regulated in the experimental areas of the All India Co-ordinated Research Project on MULLaRP, R.A.K. College of Agriculture in Sehore, Krishi Vigyan Kendra Barwani, Krishi Vigyan Kendra Jhabua, and the College of Agriculture in Gwalior, during *kharif* 2021. The mungbean was grown using a Randomized block design with three replications, and the data were subjected to stability analysis following the model suggested by Eberhart and Russell (1966). The stability performance of genotypes RVSM 22-6 and IPM 205-7 (Virat) exhibited average stability for major yield-contributing traits. Hence, these genotypes may be fitted for cultivation in different environments. Stability analysis is a crucial tool in plant breeding for predicting the performance of various genotypes across changing environments.

Keywords: Stability, environments, Eberhart and Russell, mungbean

Introduction

Mungbean, an integral pulse crop in India, holds significant importance for its nutritional value and contribution to soil fertility. Its high protein content, rich nutrient profile, and ability to fix nitrogen make it a crucial element in the largely vegetarian Indian diet. The UN's acknowledgment of pulses in 2016 highlighted their nutritional benefits, further emphasizing the importance of crops like mungbean.

Over the years, mungbean production has steadily risen, hitting 3.17 million tonnes in 2021-22. States like Rajasthan, Maharashtra, Karnataka, Andhra Pradesh, and notably Madhya Pradesh have been key contributors due to their conducive environments and production efficiency.

Agricultural stability in mungbean cultivation is pivotal, given India's diverse environmental conditions. Genotypes that consistently perform well across varied environments are essential for ensuring reliable production. Research focused on understanding how genotypes interact with the environment aids in identifying stable varieties adaptable to diverse conditions.

Ongoing studies aim to evaluate how genotype, environment, and their interaction impact mungbean seed yield and its traits. Pinpointing adaptable genotypes tailored to specific environments is crucial in averting crop failures. These varieties should demonstrate resilience to changing practices like sowing times and fertilizer doses while maintaining stability and high yield potential.

The need for mungbean varieties resilient to unpredictable environmental changes is urgent. This study strives to identify consistent genotypes exhibiting stability in yield and its component traits across diverse locations. By doing so, it aims to provide tailored recommendations that can mitigate uncertainties and enhance mungbean cultivation,

ensuring sustained productivity in India's agricultural landscape.

Materials and Methods

In the Kharif season of 2021, the current study was conducted in four distinct locations within Madhya Pradesh. The experiment was carried out in the research areas of the All India Co-ordinated Research Project on MULLaRP, situated at R.A.K. College of Agriculture in Sehore, Krishi Vigyan Kendra Barwani, Krishi Vigyan Kendra Jhabhua, and the College of Agriculture in Gwalior, during *Kharif* 2021. These fields exhibited uniform characteristics, including a slight slope, adequate drainage, and normal soil fertility. The planting material was arranged in a randomized block design with three replications. Each genotype was assigned to a single-row plot, measuring 4 meters in length, with a spacing of 30 cm between rows and 10 cm between individual plants. Data were collected for ten different traits from five randomly selected plants within each plot, and subsequently, stability analysis was conducted following the model developed by Eberhart and Russell in 1966 [5].

Results and Discussion

In our current study, a group of fourteen genotypes of greengram were assessed in four distinct environments to evaluate the stability (Akbari, K.M. *et al*., 2022) [1]. To understand variations among genotypes, environments, and genotype-environment interactions, we performed a pooled analysis of variance following the Eberhart and Russell

(1966) [5] model.

Our results unveiled significant differences among the genotypes for all the traits, with the exception of days to maturity, indicating a substantial amount of genetic variability. The mean squares attributed to environmental factors were highly significant for all traits, except for days to maturity, implying the considerable diversity among the environments (Table 1).

Genotypes displayed varying performance, as evidenced by the significant mean squares linked to genotype-environment interactions, particularly in the case of plant height at maturity and 100-seed weight. Additionally, the mean squares associated with environmental factors (linear) were significant for all traits, indicating that the environments had varying effects on the traits due to environmental variations across the four environments. Similarly, the mean squares for genotype-environment interactions (linear) were significant for traits such as plant height, biological yield per plant, and 100-seed weight, suggesting the presence of a predictable genotype-environment interaction. It's noteworthy that a significant portion of the genotype-environment interaction was attributed to linear effects. Furthermore, when tested against the pooled error, pooled deviation effects were significant for traits like days to 50% flowering, days to maturity, number of pods per plant, biological yield per plant, 100-seed weight, and seed yield per plant. These findings align with the results of previous studies conducted by Kuchanur *et al*. (2017) [8], Islam *et al*. (2021) [7], and Payasi (2015) [2], Rana *et al*. (2023) [14].

Table 1: Analysis of variance (Pooled) for stability in Mungbean genotype

Sr. No.	source	DF	Days to 50% flowering	Days to maturity	No. of pods/plant	No. of primary branches.	Plant height	No. of seeds/pod	Biological yield per plant	Harvest index	100 seed weight	Seed yield per plant
1	Rep within Env.	8	0.950	2.881	2.675	0.137	0.968	0.117	1.107	7.850	0.018	0.054
2	Varieties	13	6.113 **	8.067 **	12.852 *	0.506	26.029 ***	0.742 ***	37.136 **	17.599 **	0.126 **	2.395 **
3	Env.+ (Var.* Env.)	42	1.860	2.469	12.197 *	0.756 **	12.187 ***	0.547 ***	4.938 **	9.581 *	0.192 **	0.609 **
4	Environments	3	6.892 *	5.372	66.405 **	5.817 ***	46.949 ***	5.314 ***	27.334 **	53.858 **	1.998 **	5.022 **
5	Var.* Env.	39	1.473	2.246	8.027	0.367	9.513 ***	0.180	3.216	6.175	0.053 *	0.269
6	Environments (Lin.)	1	20.675 **	16.117 *	199.214 **	17.450 ***	140.847 ***	15.942 ***	82.001 **	161.573 **	5.995 **	15.065 **
7	Var.* Env.(Lin.)	13	0.985	1.402	11.075	0.429	23.304 ***	0.225	5.272 *	7.165	0.109 **	0.289
8	Pooled Deviation	28	1.594 **	2.477 *	6.039 **	0.311	2.431	0.147	2.032 **	5.275	0.024 *	0.241 **
9	Pooled Error	104	0.705	1.317	1.568	0.259	4.509	0.209	0.923	4.007	0.013	0.046
10	Total	55	2.865	3.792	12.352	0.697	15.459	0.593	12.549	11.476	0.177	1.031

According to Eberhart and Russell's stability criteria, a stable genotype should have a higher mean than the population mean, a regression coefficient equal to 1, and a squared deviation equal to 0. In our study, no single genotype displayed stability for every trait. However, we grouped together the genotypes that exhibited desirable mean values and non-significant squared deviations, indicating desirable mean performance, regression coefficients close to unity, and deviations from regression approaching zero. These genotypes were considered stable. Genotypes that exhibited stability and suitability for all environments included RVSM 22-6, RVSM 22-8, and MI 750-1 for 50% flowering, which aligns with the findings of Desai *et al*. (2020) [4] and Aparna *et al*. (2015) [2]. RVSM 22-6, MI 98-64, and IPM 205-7 (Virat) were stable for days to maturity, in agreement with Baraki *et al*. (2020) [3] and Desai *et al*. (2020) [4]. For the number of pods per plant, RVSM 22-5, MI 181-1, and IPM 205-7 (Virat) showed stability, and this corresponds to Naidu and Satyanarayana's

(1991a) [16] report on significant linear and non-linear components of genotype-by-environment interaction.

IPM 205-7 (Virat), RVSM 18-1, and RVSM 22-8 were stable for the number of primary branches per plant, which is consistent with Karale's (2010) [11] report of a significant non-linear component of genotype-by-environment interaction for this trait. RVSM 22-6 exhibited stability for plant height, in agreement with Karale (2010) [11], and for the number of seeds per pod, which corresponds to Kumar *et al*.'s (2020) [9] findings. RVSTM 22-2 and RVSM 22-5 were stable for biological yield per plant, in line with Nath's (2013) [13] results. MI 181-1 exhibited stability for harvest index, and IPM 410-3 (Shikha) was stable for 100-seed weight, consistent with Karale (2010) [11] and Naidu and Satyanarayana's (1991 a) [16] report of significant linear and non-linear components of genotype-by-environment interaction for seed weight. MI 181-1 was stable for seed yield per plant, consistent with earlier reports by Singh *et al*. (2013) [15], Kuchanur *et al*. (2017) [12], Kumar *et al*. (2020) [9], and Katiyar *et al*. (2021) [10].

Genotypes RVSM 22-6 and IPM 205-7 (Virat) demonstrated average stability for major yield-contributing traits, making them suitable for different environments. (Table 3). The use of stability analysis is a vital tool in plant breeding to predict how various genotypes will perform in changing environments.

Table 2: Estimation of stability parameters in Mungbean genotype

Sr. No	Genotype	Days to 50% flowering			Days to maturity			No. of pods per plant		
		Mean	bi	S²di	Mean	bi	S²di	Mean	bi	S²di
1	RVSTM 22-1	40.333	0.46	0.45	62.000	0.14	-0.44	18.250	0.72	4.10*
2	RVSTM 22-2	41.167	2.60	2.34*	63.750	0.02	2.06	19.333	1.51	13.72**
3	RVSM 22-3	41.500	0.34	-0.53	65.167	0.12	0.40	22.333	0.94	-0.32
4	RVSM 22-4	43.750	1.02	-0.12	68.250	0.63	0.16	23.750	0.06	2.48
5	RVSM 22-5	41.500	2.80*	-0.68	65.500	1.27	-1.19	20.083	0.89	2.48
6	RVSM 22-6	42.500	0.69	0.87	65.583	0.83	0.55	22.583	-0.40	8.82**
7	RVSM 22-7	41.750	0.45*	-0.72	65.333	3.05	1.56	23.083	0.83	6.98**
8	RVSM 22-8	40.250	0.65	1.45	65.583	0.80	3.35*	23.250	2.97	1.74
9	RVSM 18-1	43.083	1.45	-0.69	66.583	2.26	2.23	21.583	0.85	10.05**
10	MI 98-64	39.750	0.67	-0.68	65.167	1.13	4.56*	19.833	0.22	-1.06
11	MI 181-1	42.500	0.91	2.49*	65.417	0.53	0.34	21.333	1.67	3.71*
12	MI 750-1	40.083	0.66	0.33	65.750	3.01	-0.84	23.083	2.26	8.66**
13	IPM 410-(Shikha)	41.917	1.32	1.36	65.000	0.37	-0.39	20.250	0.41*	-1.46
14	IPM 205-7 (Virat)	40.083	-0.03	6.32**	63.833	1.13	2.33	19.083	1.06	1.59
	Population Mean	41.440			65.208			21.274		

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

Table 3: Estimation of stability parameters in Mungbean genotype

Sr. No	Genotype	No of primary branches			Plant height			Number of seeds per pod		
		Mean	bi	S²di	Mean	bi	S²di	Mean	bi	S²di
1	RVSTM 22-1	6.583	1.68	0.04	53.917	1.88	-1.77	9.167	1.33	-0.16
2	RVSTM 22-2	6.750	0.14	1.11**	54.917	3.18	-3.00	9.250	1.41	0.05
3	RVSM 22-3	6.417	0.86	-0.01	61.083	-0.62	-0.28	10.250	0.63	-0.06
4	RVSM 22-4	7.250	1.31	0.05	61.667	-0.80	-0.68	9.750	0.39	-0.03
5	RVSM 22-5	6.750	1.21	0.22	59.833	-1.18	2.54	9.083	0.55	0.34
6	RVSM 22-6	6.333	0.05	0.08	62.083	-0.19	0.27	9.500	0.60	0.10
7	RVSM 22-7	7.000	1.26	-0.24	62.083	-0.78**	-4.13	9.667	1.58	-0.17
8	RVSM 22-8	6.500	0.62	0.01	61.000	0.82	-3.95	9.750	1.13	-0.11
9	RVSM 18-1	6.500	0.62	0.01	58.667	2.71	0.23	9.000	1.06	-0.06
10	MI 98-64	5.917	0.64*	-0.25	58.333	1.67	-3.00	9.250	0.41	-0.15
11	MI 181-1	6.250	2.09	-0.15	57.000	2.66	-1.96	9.917	1.36	-0.11
12	MI 750-1	6.167	1.05	-0.22	59.167	1.02	-3.88	9.583	0.63	-0.06
13	IPM 410-(Shikha)	6.750	1.70*	-0.23	59.333	0.84	-3.27	10.333	1.58	-0.17
14	IPM 205-7 (Virat)	6.917	0.76	0.43	57.500	2.79*	-2.69	10.083	1.35	-0.19
	Population Mean	6.577			59.042			9.613		

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

Table 4: Estimation of stability parameters in Mungbean genotype

Sr. No.	Genotype	Biological yield per plant.			Harvest index		
		Mean	bi	S²di	Mean	bi	S²di
1	RVSTM 22-1	12.983	1.19	-0.05	20.050	1.22	3.19
2	RVSTM 22-2	13.125	1.29	0.90	18.967	-0.41*	-3.60
3	RVSM 22-3	17.467	0.33	-0.78	22.725	1.02	-3.39
4	RVSM 22-4	20.158	0.64	5.93**	22.333	1.32	-4.08
5	RVSM 22-5	15.500	1.15	0.47	26.042	0.29	4.60
6	RVSM 22-6	22.233	0.50	1.15	21.892	2.15	-2.31
7	RVSM 22-7	19.717	-0.43	3.02*	21.742	1.22	-0.85
8	RVSM 22-8	15.892	3.25	1.56	26.317	-0.51	-0.82
9	RVSM 18-1	15.558	1.56	-0.62	22.333	1.71	-2.70
10	MI 98-64	12.400	0.29	-0.55	22.350	0.62	16.09*
11	MI 181-1	12.933	0.64	-0.21	22.933	0.96	2.36
12	MI 750-1	15.983	2.48	0.07	24.125	0.97	-2.92
13	IPM 410-3 Shikha)	14.733	0.79	2.10*	21.408	1.52	10.80*
14	IPM 205-7 (Virat)	13.342	0.34	2.34*	19.900	1.93	-2.46
	Population Mean	15.859			22.365		

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

Table 5: Estimation of stability parameters in Mungbean genotype

Sr. No.	Genotype	100 seed weight			Seed yield per plant		
		Mean	bi	S²di	Mean	bi	S²di
1	RVSTM 22-1	3.208	0.75	0.13**	2.633	1.19	0.26**
2	RVSTM 22-2	3.200	0.56*	-0.01	2.475	0.36	0.14*
3	RVSM 22-3	3.108	1.15	-0.01	3.925	0.56	0.06
4	RVSM 22-4	2.717	1.36	-0.01	4.500	1.46	0.31**
5	RVSM 22-5	2.725	1.82	0.04*	4.008	0.75	0.59**
6	RVSM 22-6	3.083	1.51	0.01	4.825	1.44	0.13*
7	RVSM 22-7	2.825	0.97	-0.01	4.258	0.42	0.41**
8	RVSM 22-8	3.000	1.79	-0.01	4.108	1.72	0.21**
9	RVSM 18-1	2.925	0.76	-0.01	3.483	1.65**	-0.05
10	MI 98-64	3.200	0.34	0.02	2.783	0.51	0.36**
11	MI 181-1	2.975	0.53	0.01	2.967	0.59	0.16
12	MI 750-1	3.258	0.36	0.01	3.850	1.77	0.03
13	IPM 410-3 (Shikha)	3.025	1.36*	-0.01	3.117	0.82	0.11*
14	IPM 205-7 (Virat)	2.908	0.73	0.00	2.608	0.75	-0.02
	Population Mean	3.011			3.539		

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

Table 6: Stable genotypes for different characters in Mungbean genotype

Sr. No.	Character	Genotypes showing average stability (suitable for all four types of environments)
1	Days to 50% flowering	RVSM 22-6, RVSM 22-8, MI 750-1
2	Days to maturity	RVSM 22-6, MI 98-64, IPM 205-7
3	Number of pods per plant	RVSM 22-5, MI 181-1, IPM 205-7
4	Number of primary branches per plant	IPM 205-7, RVSM 18-1, RVSM 22-8
5	Plant height	RVSM 22-6
6	Number of seeds per pod	RVSM 22-6
7	Biological yield per plant(gm)	RVSTM 22-2, RVSM 22-5
8	Harvest index (%)	MI 181-1
9	100 seed weight (gm.)	IPM 410-3
10	Seed yield per plant (gm)	MI 181-1

Table 7: Pedigree of genotype used in research

Sr. No.	Genotype	Parentage
1	RVSTM 22-1 (TGM 130)	Samrat × Kopergoan
2	RVSTM 22-2 (TGM 140)	TM98-80 × SML-68
3	RVSM 22-3	ML 131×TMB 37
4	RVSM 22-4	JM 721×CZMK 1-1
5	RVSM 22-5	BM4×TMB 37
6	RVSM 22-6	HUM 1×TMB 37
7	RVSM 22-7	ML131×PKVAKM4
8	RVSM 22-8	JM721× PKVAKM4
9	RVSM 18-1	TJM 3 × HUM 1
10	MI 98-64	JM 45 × ML 131
11	MI 181-1	JM – 721 × ML-422
12	MI 750-1	J-45 × ML-131
13	IPM 410-(Shikha)	IPM 03-1 × NM 1
14	IPM 205-7 (Virat)	IPM 02-1 × EC 398889

Conclusion

Stability performance of genotypes RVSM 22-6, IPM 205-7 (virat) gave average stability for major yield contributing characters, thus could be suitable for different environment. Stability analysis is an imperative tool for plant breeding in anticipating the effect of various genotypes over changing environment.

Reference

1. Akbari KM, Patel MP, Borkhatariya TH, Sondarava PM, Delvadiya JB. Interpreting genotype×environment interaction in greengram (*Vigna radiata* L. Wilczek) using Eberhart and Russell Model. Electron J Plant Breed. 2022;13(4):1326-1333.

2. Aparna R, Singh SK, Sharma V, Pathak R. Genetic variability, heritability, genetic advance and path analysis in mungbean (*Vigna radiata* (L.) Wilczek). Legume Res. 2015;38(2):157-163.

3. Baraki F, Gebregergis Z, Belay Y, Berhe M, Zibelo H, Moral MJ. Genotype x environment interaction and yield stability analysis of mungbean (*Vigna radiata* (L.) Wilczek) genotypes in Northern Ethiopia. Cogent Food Agric. 2020, 6(1).

4. Desai VK, Parmar LD, Chaudhary AR, Chaudhary NB. Genetic variability, correlation, path coefficient and stability analysis for yield and its attributing traits in summer Green gram [*Vigna radiata* (L.) Wilczek] accessions. Int J Curr Microbiol App Sci. 2020;9(6):2942-2955.

5. Eberhart ST, Russell W. Stability parameters for comparing varieties. Crop Sci. 1966;6:36-40.
6. Gupta D, Muralia S, Gupta NK, Gupta S, Jakhar ML, Sandhu JS. Genetic Diversity and Principal Component Analysis in Mungbean [*Vigna radiata* (L.) Wilczek] under Rainfed Condition. Legume Res. 2023;46(3):265-272.
7. Islam MR, Sarker BC, Alam MA, Javed T, Alam MJ, Zaman MSU, *et al*. Yield stability and genotype environment interaction of water deficit stress tolerant Mungbean (*Vigna radiata* L. Wilczak) Genotypes of Bangladesh. Agronomy. 2021;11(11):2136.
8. Kuchanur PK, Konda CR, Hiremath C, Vijayakumar AG. Stability of mungbean [*Vigna radiata* (L.) Wilczek] genotypes for seed yield during summer. Legume Res. 2017;(41):602-605.
9. Kumar S, Choudhary H, Sharma J, Kumar A, Sandhu R, Gupta R, *et al*. Study on genotype × environment interactions and AMMI analysis for agronomic traits in mungbean (*Vigna radiata* L. Wilczek.) under rainfed conditions. Indian J Genet Plant Breed. 2020;80:354-358.
10. Katiyar M, Nitesh SD, Kumar S, Singh M, Singh L, Bajpai VP, *et al*. Yield Stability Analysis of Mungbean (*Vigna radiata* L. Wilczek) Hybrids Using AMMI Method. IJAEB. 2021;14(03):307-311.
11. Karale SN. Stability for yield and its components in Mungbean (*Vigna radiata* (L.) Wilczek.). M.Sc. (Agric) Thesis submitted to MPKV, Rahuri, Dist. Ahmednagar, Maharashtra; c2010.
12. Kuchanur PK, Konda CR, Hiremath C, Vijayakumar AG. Stability of mungbean [*Vigna radiata* (L.) Wilczek] genotypes for seed yield during summer. Legume Res. 2017;(41):602-605.
13. Nath A, Harer NP, Pal UD. Stability analysis and GE interaction in Mungbean (*Vigna radiata* L. Wilczek). Afr J Agric Res. 2013;8(26):3340-3347.
14. Rana S, Sharma S, Pathania A, Sharma A. Evaluation of four Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes for yield and yield contributing Traits under Different Environmental Conditions. 2023;7(02):1-23.
15. Singh V, Yadav RK, Yadav R, Malik RS, Yadav NR, Singh J. Stability analysis in Mungbean [*Vigna radiata* (L.) Wilczek)] for nutritional quality and seed yield. Legume Res. 2013;36(1):56-61.
16. Naidu NV, Satyanarayana A. Studies on genetic divergence over environments in mungbean (*Vigna radiata* (L.) Wilczek). Indian Journal of Genetics and Plant Breeding. 1991;51(04):454-460.