Assess the magnitude of variability in advance breeding line of Mungbean with respecttoseedyield andcomponenttraits.

Abstract

The study was conducted across four distinct environments in Madhya Pradesh during the 2021 kharif season, utilizing a Randomized Complete Block Design involving fourteen mungbean genotypes with three replications. Examination of genetic parameters unveiled a notable pattern: the phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) across all observed traits.Of particular interest were the traits demonstrating the highest PCV and GCV values, notably seed yield per plant in E2 (31.36, 28.58) followed by biological yield per plant in E1 (27.41, 24.80). These findings strongly suggest the prevalence of additive gene action influencing these traits, as indicated by their high heritability estimates.The traits with the highest heritability values were seed yield per plant (97.32) in E3 and E4 (92.95), biological yield per plant (88.66) in E2 and E4 (87.91), and number of pods per plant in E1 (63.66). These results underscore the genetic basis underlying these traits and their potential for targeted breeding efforts.

Keywords: PCV, GCV, Heritability, Genetic advance, Randomized Complete Block Design, Environment.

Introduction

Mungbean, scientifically known as *Vigna radiata* (L.) R. Wilczek var radiata, is a legume from the Fabaceae family. With a chromosome count of 2n = 22 and a compact 579 Mb genome, it goes by various names like green gram, moong, green soy, green bean, mash bean, and golden gram (Rahangdale et al., 2023). This crop, thriving in tropical and subtropical regions, stands as a significant food and cash crop. Its seeds offer easily digestible dietary protein, with an ideal daily intake of about 40 grams per person or 14.6 kg annually (Afroz et al., 2022).

The protein content in green gram surpasses that of cereals by two to three times, comprising 51 percent carbohydrates, 26 percent protein, and 4 percent each of minerals and essential vitamins like A, B1, B2, C, niacin, folate, iron, calcium, and zinc. This nutrient profile complements and diversifies cereal-based diets effectively.

Mungbean has gained importance in double and intercropping systems due to its short growing cycle and nitrogen-fixing capabilities (58–109 kg−1 ha−1), which significantly enhance soil fertility (Haeften et al., 2023). Its agronomic, nutritional, and economic advantages have led to a substantial surge in both production and consumer demand worldwide over the last two decades.

Globally, Mungbean cultivation spans various latitudes and seasons, occupying over 6 million hectares. In the context of pulses in India, which covers 28.79 million hectares with a production of 25.46 million tonnes and a productivity rate of 885 Kg per hectare, Mungbean covers 5.55 million hectares, yielding 3.17 million tonnes at a productivity rate of 570 Kg per hectare (Anonymous, 2022-23). Notably, its production has escalated from 1.60 million tonnes in 2015-16 to 3.17 million tonnes in 2021-22. Rajasthan, Maharashtra, Karnataka, Andhra Pradesh, and Madhya Pradesh stand out as key Mungbean cultivating states. Among these, Madhya Pradesh contributes 938.10 hectares, 1134.52 tonnes, and 1209 Kg per hectare in terms of area, production, and productivity, respectively.

Enhancing the genetic traits of this crop primarily relies on understanding genetic variability and heritability factors. Analyzing parameters like phenotypic and genotypic coefficients of variability, genetic advance, and heritability (Afroz et al., 2022) becomes imperative. This knowledge aids in pinpointing the most favorable yield attributes for selection or hybridization, laying the foundation for effective crop improvement.

Material and Methods

The study took place in the experimental areas of the All India Coordinated Research Project on MULLaRP across four diverse environments in Madhya Pradesh (R.A.K. College of Agriculture, Sehore; K.V.K, Barwani; K.V.K, Jhabhua; and College of Agriculture, Gwalior) during the 2021 Kharif season. Fourteen different mungbean genotypes were cultivated using a Randomized Complete Block Design with three replications. The crop rows spanned 4 meters in length, with a spacing of 30 cm between rows and 10 cm between plants. The fields exhibited uniformity, gentle slopes, proper drainage, and normal fertility levels, where all recommended agronomic practices were implemented to foster a robust crop.

Data collection involved observing five randomly selected plants within each plot. These observations encompassed various characteristics such as days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant, and harvest index.

Analysis of variance followed the methodology outlined by Burton (1952), while the estimation of range was conducted based on Johnson et al.'s method (1955). The Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were calculated using Burton's formula (1952). Heritability was determined using Allard's formula (1960), and genetic advance was calculated as a percentage using Johnson et al.'s formula (1955).

Results and Discussion

Results of the present study on fourteen genotypes were done to understand the genetic variability. The experimental results of the present investigation have been mentioned under following

Analysis of variance:

The analysis of variance highlighted significant differences among genotypes across most traits, with exceptions noted in specific environments for traits like days to maturity in E3, plant height in E3 and E4, and the number of primary branches and seeds per pod across all environments. When pooling data across environments, significant differences among genotypes were observed for most traits, except for the number of primary branches and seeds per pod, where highly significant differences in mean sum of squares were evident, likely due to minimal genotype × environment interaction for these specific traits within the studied material. These findings align with previous research by Sopan et al. (2018) and Mwangi et al. (2021). For detailed results, please refer to Table 1.

Table1:-**Analysis of variance for ten various characters in mungbean**

SourceofVariations	df	Mean Squares									
		Days to 50% flowering					Days to maturity				
		E1	E2	E3	E4	POE	E1	E2	E3	E4	POE
Replicate	2	1.88	1.45	3.50	4.57	8.73	6.02	13.02	0.73	7.73	7.06
Genotypes	13	9.83*	6.85*	8.11*	6.79*	20.67*	8.60*	13.42*	10.30	12.08*	16.11

Error	26	3.31	2.01	1.55	1.57	0.88	2.94	4.15	6.02	2.68	2.23

SourceofVariations	df	Mean Squares									
		No. of pods/plant					No. of primary branches.				
		E1	E2	E3	E4	POE	E1	E2	E3	E4	POE
Replicate	2	0.16	8.00	18.50	5.42	8.32	0.73	0.28	0.30	0.30	0.18
Genotypes	13	36.19*	25.57*	41.15*	7.87*	199.21*	0.71	1.51	0.72	1.86	17.45
Error	26	5.80	4.25	6.98	1.76	7.92	0.50	0.90	0.54	1.15	0.48

SourceofVariations	df	Mean Squares									
		Plant height					No. of seeds per pod				
		E1	E2	E3	E4	POE	E1	E2	E3	E4	POE
Replicate	2	1.59	0.28	1.73	8.00	7.52	0.73	0.21	0.28	0.16	0.25
Genotypes	13	58.45*	83.03*	14.79	7.42	140.84*	1.12	0.58	1.06	1.06	15.9
Error	26	22.26	18.33	7.96	5.53	1.36	0.66	0.39	0.61	0.83	0.38

SourceofVariations	Df	Mean Squares									
		Biological yield per plant					Harvest index				
		E1	E2	E3	E4	POE	E1	E2	E3	E4	POE
Replicate	2	1.28	3.50	5.07	3.42	1.30	26.84	7.94	18.93	28.48	18.72
Genotypes	13	38.85*	43.40*	28.61*	29.47*	82.00*	30.42*	31.65*	141.5	32.14*	161.57
Error	26	2.67	2.65	2.49	3.24	3.99	11.23	14.54	12.22	10.08	25.16

SourceofVariations	Df	Mean Squares									
		100 seed weight					Seed yield per plant				
		E1	E2	E3	E4	POE	E1	E2	E3	E4	POE
Replicate	2	0.02	0.38	0.10	0.04	0.06	0.39	0.009	0.08	0.17	0.11
Genotypes	13	0.18*	0.16*	0.20*	0.24*	5.99*	2.02*	3.90*	2.64*	1.02*	15.06
Error	26	0.02	0.04	0.05	0.02	0.05	0.12	0.24	0.12	0.06	0.17

Parameters of genetic variability :

The genetic variability parameters namely phenotypic coefficient of variation (PCV),genetic coefficient of variation (GCV) , heritability in broad sense (%), genetic advance and expected genetic advance (as per cent of mean) for all ten traits were Estimated and have been presented in Table 2.

Phenotypic coefficient of variation (PCV),genetic coefficient of variation (GCV)

In this study, the phenotypic coefficient of variation (PCV) consistently surpassed the genotypic coefficient of variation (GCV) across all traits analyzed. The traits with the highest PCV and GCV were seed yield per plant in E2 (31.36, 28.58) followed by biological yield per plant in E1 (27.41, 24.80). Moderate PCV and GCV values were observed for biological yield per plant in E4 (19.35 for PCV) followed by number of primary branches in E4 (16.15) and harvest index in E3 (14.61). For GCV, notable values were recorded for seed yield per plant in E4 (18.29), biological yield per plant in E3 (17.06), and number of pods per plant in E1 (16.42).

The traits with the lowest PCV were number of pods per plant in E4 (9.64), followed by 100 seed weight (8.39), and days to maturity in E1 (3.41). As for GCV, the lowest values were observed for plant height in E4 (1.31), number of primary branches in E1 (3.93), and plant height in E2 (8.02).

These results suggest that selecting traits with higher PCV and GCV for further breeding efforts could be more effective. These findings align with previous research by Nitesh et al. (2017) for seed yield per plant, harvest index, and number of pods per plant, Tusharkumar et al. (2019) and Mariyammal et al. (2019) for seed yield per plant, Ramakrishnan et al. (2018), Zida et al. (2021), and Sineka et al. (2021) for number of pods per plant.

Heritability (broad sense) and genetic advance.

Heritability, indicating the inheritance of traits from parents to offspring, aids breeders in selecting superior genotypes. Higher heritability suggests traits less influenced by the environment and primarily controlled by additive genetic effects. Robinson et al. (1949) categorized heritability into high (>60%), moderate (30-60%), and low (<30%). In this study, seed yield per plant displayed the highest heritability in E3 (97.32) and E4 (92.95), followed by biological yield per plant in E2 (88.66) and E4 (87.91), and number of pods per plant in E1 (63.66). Moderate heritability was noted for days to 50% flowering in E1 (59.59) and plant height in E3 (47.21).

Genetic advance, influenced by selection intensity, heritability, and phenotypic standard deviation, ranged from 0.12 to 4.98 across environments. The highest genetic advance was seen in biological yield per plant in E2 (10.52) and number of pods per plant in E3 (11.55), while the lowest was observed in 100 seed weight in E2 (0.65). Other traits had genetic advance values around 7.19 (biological yield per plant in E4), 9.59 (plant height in E1), 7.35 (harvest index in E4), 4.77 (days to 50% flowering in E3), 1.70 (seed yield per plant in E4), and 0.95 (number of primary branches in E4).

These findings align with previous research by Aparna et al. (2015) highlighting high heritability and low genetic advance for days to 50% flowering and traits like biological yield per plant and number of pods per plant, as observed by Malli et al. (2018) and Sineka et al. (2021).

Table 2:- Estimates of genetic parameters for 10 different characters of mungbean genotypes.

Sr. No	Characters	Environ ment	Mean	Range		PCV (%)	GCV (%)	^{h2}(broad	Genet ic	Gen.A dv as
				Mini	Maxi					

.								sense)	advance	% of Mean
1	Daysto50%flowering	E1	41.95	39.00	45.00	5.58	3.52	59.59	3.93	9.37
		E2	40.45	38.66	43.00	4.70	3.14	67.43	3.59	8.88
		E3	41.92	39.00	44.00	4.61	3.53	78.51	4.77	11.38
		E4	41.42	39.00	43.66	4.39	3.18	72.55	4.05	9.78
		POE	41.44	39.75	43.75	4.85	2.75	65.16	2.77	6.68
2	Daystomaturity	E1	64.28	62.00	69.00	3.41	2.14	59.07	3.65	5.68
		E2	65.47	62.00	68.33	4.11	2.69	62.67	4.83	7.38
		E3	65.61	63.00	69.33	4.15	1.82	59.16	2.25	3.43
		E4	65.45	61.00	67.66	3.68	2.70	73.82	5.45	8.33
		POE	65.20	62.00	68.25	3.86	1.95	60.64	2.75	4.22
3	No.ofpodsperplant	E1	19.38	13.00	25.00	20.59	16.42	63.56	10.55	54.44
		E2	21.14	17.33	26.00	15.94	12.61	62.54	8.79	41.58
		E3	24.35	20.00	31.66	17.59	13.86	61.98	11.05	45.38
		E4	20.21	16.00	22.66	9.64	7.06	53.63	4.41	21.82
		POE	21.27	18.25	23.75	16.53	7.25	55.64	2.89	13.59
4	No.ofprimarybranchesper plant	E1	6.62	6.00	7.00	11.45	3.93	56.83	0.47	7.10
		E2	6.64	6.00	8.00	15.82	6.79	63.39	0.91	13.70
		E3	5.74	4.66	6.66	13.52	4.35	50.28	0.45	7.84
		E4	7.31	6.00	8.00	16.15	6.68	62.07	0.95	13.00
		POE	6.58	5.91	7.25	14.57	3.55	66.98	0.35	5.32
5	Plantheight(cm)	E1	57.05	49.33	63.33	10.27	6.09	60.15	8.59	15.06
		E2	57.93	50.33	64.66	10.90	8.02	79.05	14.17	24.46
		E3	60.69	55.33	65.00	5.27	2.49	47.21	3.03	4.99
		E4	60.50	56.00	62.66	4.10	1.31	40.18	1.15	1.90
		POE	59.04	53.91	62.08	8.06	3.80	57.24	4.47	7.57
6	No.ofseedsperpod	E1	10.33	9.00	11.33	8.74	3.82	49.09	0.83	8.03
		E2	9.57	9.00	10.33	7.07	2.65	43.97	0.51	5.33
		E3	9.71	8.66	10.66	9.02	3.99	49.51	0.81	8.34
		E4	8.83	8.00	10.00	10.80	3.14	43.46	0.45	5.10
		POE	9.61	9.00	10.33	8.94	3.83	48.27	0.75	7.80
7	Biologicalyieldperplant(gm)	E1	14.00	10.73	20.60	27.41	24.80	86.83	9.82	70.11
		E2	16.42	12.00	23.66	24.52	22.44	88.66	10.52	64.07
		E3	17.29	12.66	21.83	19.35	17.06	82.73	8.14	47.05
		E4	15.71	12.00	23.00	22.03	18.82	87.91	7.91	50.35
		POE	15.85	12.40	22.23	23.20	18.81	84.62	10.07	63.53
8	Harvest index (%)	E1	21.48	17.40	28.50	19.54	11.77	71.28	6.37	29.66
		E2	23.31	17.83	29.70	19.29	10.24	63.18	5.33	22.87
		E3	24.54	18.73	26.96	14.61	3.27	40.05	0.83	3.38
		E4	20.10	15.96	26.73	20.76	13.49	77.16	7.35	36.57
		POE	22.36	18.96	26.31	18.46	8.06	60.07	3.35	14.98
9	100seedweight(gm)	E1	2.96	2.56	3.36	9.66	7.74.	74.63	0.85	28.72
		E2	3.51	3.26	3.93	8.39	5.64	55.83	0.65	18.52
		E3	2.95	2.40	3.53	11.68	8.86	67.98	0.93	31.53
		E4	2.60	2.16	3.00	12.20	10.43	83.27	1.05	40.38
		POE	3.01	2.71	3.25	10.36	5.30	67.22	0.43	14.29

10	Seedyieldperplant(gm)	E1	2.97	1.93	4.40	29.19	26.77	94.13	2.36	79.46
		E2	3.86	2.20	5.40	31.36	28.58	93.05	3.22	83.29
		E3	4.21	2.96	5.76	23.26	21.74	97.32	2.75	65.32
		E4	3.09	2.26	4.00	20.08	18.29	92.95	1.70	55.02
		POE	3.53	2.47	4.82	26.71	21.37	81.05	1.97	55.81

Conclusions

The pooled analysis of variance shows significance across all genotypes, except for the number of primary branches, signifying ample genetic variability within the population. Traits such as seed yield per plant and biological yield per plant exhibited the highest phenotypic and genetic coefficient of variation, suggesting a strong influence of genetic variability on their expression.

The combination of high heritability and substantial genetic advance as a percentage of the mean was observed prominently in biological yield per plant, followed by seed yield per plant and the number of pods per plant. This suggests that these traits are predominantly governed by additive gene action, making them suitable candidates for direct selection in breeding programs

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