Original Research Article

Assessment of variability for yield attributing traits and seed quality parameters ~~on~~ in mung bean *(Vigna radiata* L. Wilczek) ~~for yield attributing traits and seed quality parameters~~

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Abstract

The present investigation was undertaken to evaluate ten germplasm of mung bean, used to estimate genetic variability, heritability and genetic advance for 16 characters. ~~All t~~The results showed significant differences among the mung bean genotypes in all characters~~ are shown as significant~~. All the character~~istic~~s had a larger PCV,~~, GCV,~~ showing the enfluence of the environmental variable ~~influence of~~on their expression. In the present study, PCV is higher than GCV for all the characters under study. High heritability coupled with high genetic advance indicates additive gene action. Heritability for broad sense was estimated for all the studied characters observed range from 33.6 to 98.175 %. Genetic advance as percentage of mean is observed range from 2.484% to 26.315%. All these characters coupled with hhigh heritability coupled with high genetic advance can be used for the selection of lines as a parents for further breeding programme, where as in breeding programme these traits were more important for selection.

Keywords: *Mung bean, Green gram, Genetic variability, Heritability, Genetic advance*

INTRODUCTION

Mung bean or green gram is a legume crop with chromosome number 2n= 2x= 22. It is belonging to the Fabaceae family, genus *Vigna*, species *radiata*~~.~~, which is mostly grown for its edible seeds and sprouts. It is the third most significant pulse crop farmed in India, behind only red gram and chick pea.

India, which accounts for over 70% of the world's manual production of green grams, is the world's largest producer, followed by China and Myanmar (reference). According to the source Ministry of agriculture and farmers welfare, govt of India, (2021-2022~~).~~), ~~The~~ the area of production of green gram in both kharif and rabi season ~~are~~ were 51.3 million hectares, and the production ~~is~~ was 30.85 million tonnes, with the productivity of 601kg per hectare in 2020-2021. In Madya Pradesh, total area under green gram production ~~is~~ was 5.4 million hectares with the production of 6.41 million tonnes and with the productivity of 1179 kg per hectare in the crop year 2021-2022. Its seed contains 23-28 per cent protein, 3.5-4.5 per cent fiber, 60-65 per cent carbohydrate and1.0-1.5 per cent fat (reference). Green gram is rich in essential amino acids like lysine, leucine, phenylalanine and isoleucine (Lambrides and Godwin, 2007).

Green gram is a legume crop and fixes atmospheric nitrogen with the symbiotic association with *Rhizobium* bacteria and improves soil texture and fertility. It is a short duration crop and it is an outstanding crop to use as an inter crop with major crops like cereals. It can also be grown as green manure crop to enrich the soil. Inter cropping green gram in rice-wheat and rice-rice systems ~~rises~~raises the ~~produce~~ production of these cereal crops and decreases pest incidence.

Genetic variability in a cultivar is the key factor for the further improvement in the yield and also other traits. In green gram large amount of genetic variability has been reported (Moulick *et al.*, 2020), which indicates the potential for genetic improvement. The knowledge of genetic variability present in a breeding material is very important for the selection of superior parents for the initiation of very effective breeding programme (Sakthivel *et al.*, 2019) Yield depends on many characters. It is a result of combined effect of many quantitative characters. The evaluation of association between the yield and these quantitative characters gives the minimum knowledge for the selection of characters which influence the yield. Heritability and genetic advance as per cent of mean is an effective method in the selection programme to determine the extent to which various characters can be improved through the selection. The identification of Mung bean genotypes with high yield helps breeder in identifying donors for future breeding programme. With this in view, the current study was conducted with the goal of determining the level of genetic variability in 10 Mung bean genotypes.

MATERIALS AND METHODS

The present research on green gram was conducted at the Crop Research Centre, School of Agriculture, Sithouli Campus, ITM University Gwalior, Madhya Pradesh during the *Zaid* season 2022, following the detailed plan of work. The coordinates are 26.140° N, 78.196° E, and the average elevation is 197 meters above sea level. It is part of the Grid Region of Madhya Pradesh.

The materials used for this experimental trial consists of 10 genetically diverse genotypes obtained from the source ICAR - Indian Institute of Pluses Research, Kanpur (U.P.), India viz., IPM-2-3, IPM-2-14, Meha, Soorya, Virat, Varsha, Kanika, Varshudha, Heena and Shikha (Table of Pedigree and sources). The germplasms accessions and checking varieties were ~~sowed~~ sown during *Zaid* 2022. The field experiment was conducted in Randomized Block Design with three replications. Every genotype was space planted with row to row spacing of 30 cm and plant to plant spacing of 5 cm in a plot size of 30x10 (350 cm). Observations were made from the ten competitive plants from each replication that had been marked with tags at various growth phases of the crop plants. 13 characters were used to record the following information: days to 50% flowering, days to maturity, number of primary and secondary branches per plant, height of plant, number of pods per plant, number of clusters per plant, length of pods, number of seeds per pod, 1000 seed weight (g), biological yield per plant, harvest index, and seed yield per plant (g). The lab experiment was conducted in Complete

Randomized Block with three replications. Three characters were used to record data viz., seed germination, vigour index length & vigour index mass. (How they were measured?)

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By using the formula proposed by Burton and De Vane (1953), the levels of genotypic and phenotypic genetic variability were estimated for each feature. With the use of percentage values derived by dividing genotypic variation by total phenotypic variance, broad sense heritability was determined (Hanson *et al.*, 1956). Based on Johnson's (1995) (it is not found in the reference list) formula, the predicted genetic advance for the chosen characters ~~is~~ was estimated.

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RESULTS AND DISCUSSION

The results indicated significant differences among the genotypes for 16 characters studied in the present investigation. For each of the 16 characters under study, estimates of Analysis of Variance, Genotypic Coefficient of Variation, Phenotypic Coefficient of Variation, Heritability in a broad sense and Genetic advance as a percentage of mean have been provided.

Analysis of variance

The analysis of variance was carried out to partition the total variance into all characters show variance due to genotype and other sources. For the following traits: number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight, harvest index, vigour index length, and vigour index mass, the mean sum of squares due to genotypes were found to be highly significant ($P>0.05$ and $P>0.01$). Days to 50% flowering, days to maturity, plant height, number of clusters plant^{-1}, pod length, biological yield plant^{-1}, and seed germination, on the other hand, were only significant (P 0.05) and showed that the genotypes had a lot of variation (Table1). There is no significant variation for replication which shows that error due to environmental error was ~~less~~low. These findings are consistent with those reported by **Kate *et al.*, (2017)**; **Jedidah *et al.*, (2021).** (it is not found in the reference list)

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Phenotypic and Genotypic coefficients of Variability

Table 2 & Fig 1 lists the phenotypic and genotypic coefficients of variation for the yield and characteristics under consideration. For all the qualities included in each analysis, the phenotypic coefficient of variation was noticeably larger in size than the genotypic coefficient of variance. To make inferences regarding these characteristics, PCV and GCV were ~~categorised~~categorized as low (below 10%), medium (10%–20%), and high (beyond 20%) (reference).

The estimations of genotypic (GCV) and phenotypic (PCV) coefficients of variation revealed that PCV was greater than GCV for all characteristics, perhaps owing to genotype-environment combination or other environmental variables impacting the appearance of these features. Narrow differences in all variables identified between PCV and GCV showed a larger importance for hereditary components and less effect from the environment. Similar results were obtained by **Garg *et al.*, (2017); Yadav *et al.*, (2017); Ramakrishnan *et al.*, (2018)** for seed yield and its components in green gram.

~~Higher~~ Medium value of GCV and PCV were recorded for number of primary branches plant^{-1} (12.795, 18.58), number of secondary branches plant^{-1} (14.926, 17.418) and harvest index (11.576, 15.22). Low GCV and Moderate PCV ~~and~~ ~~Low GCV~~ recorded for plant height (9.876, 14.918), 1000 seed weight (8.615, 11.806), number of seeds pod^{-1} (9.303, 12.59), and seed yield plant^{-1} (6.947, 11.984). Low values of GCV and PCV were recorded for days to 50% flowering (2.395, 3.389), days to maturity (1.822, 2.755), number of pods plant^{-1} (6.069, 7.284), number of clusters plant^{-1} (6.532, 9.79), pod length (5.274, 8.407), biological yield plant^{-1} (5.066, 8.018), seed germination (1.532, 1.825), vigour index length (8.782, 8.863) and vigour index mass (6.099, 6.863). Similar findings were reported by **Sana *et al.*, (2017) and Shiv *et al.*, (2017).**

Heritability

The extent of phenotypic variation relied on ~~by~~ the additive gene action is measured by heritability. Heritability for broad sense was estimated for all the characters under study and presented in Table 2 ~~&~~ and Fig. 2, with observed range from 33.6 to 98.175 %. High heritability (above 60%) was observed for number of secondary branches plant^{-1} (73.44), number of pods plant^{-1} (69.422), seed germination (70.69), vigour index length (98.175) and vigour index mass (78.991). Moderate heritability (30-60%) was observed for traits like days to 50% flowering (38.924), days to maturity (43.765), plant height (43.826), number of primary branches plant^{-1} (47.422), number of clusters plant^{-1} (44.514), pod length (39.355), number of seeds pod^{-1} (54.605), 1000 seed weight (53.245), biological yield plant^{-1} (39.913), harvest index (57.846) and seed yield plant^{-1} (33.6). Low heritability (below 30%) haven't observed for any of the traits in the study. Similar results were obtained by **Jedidah *et al.*, (2021).**

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Genetic Advance as Percentage of Mean

Table 2 and Fig. 2 exhibit genetic progress as a percentage of the mean, with the observed range being between 2.484% and 26.315%. The number of secondary branches per plant showed the largest genetic advance as a percentage of mean (above 20%) ~~(~~at 5% selection intensity~~)~~ (26.351). Moderate genetic advance as percentage of mean (10-20%) was recorded for plant height (13.468), number of primary branches per plant (18.151), number of pods per plant (10.416), number of seeds per pod (14.162), 1000 seed weight (12.95), harvest index (18.136), vigour index length (17.925) and vigour index mass (11.167). Low genetic advance as percentage of mean (below 10%) was recorded for days to 50% flowering (3.078), days to maturity (2.484), number of clusters per plant (8.978), pod length (6.816), biological yield plant^{-1} (6.593), seed germination % (2.658) and seed yield per plant (8.296). These results are in agreement with those reported by **Garg *et al.*, (2017); Yadav *et al.*, (2017); Ramakrishnan *et al.*, (2018); Jedidah *et al.*, (2021).**

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CONCLUSION

Analysis of variability (PCV, GCV) raveled comparable differences between phenotypic and genotypic ~~cofficiant~~coefficients of variation indicating less influcence of envinorment on the phenotypic expression of the character. Higher value of GCV and PCV were recorded for number of primary branches per plant, number of secondary branches per plant and harvest index. Moderate PCV and Low GCV recorded for plant height, 1000 seed weight, number of seeds per pod, and seed yield per plant. Low values of GCV and PCV were recorded for days to 50% flowering, days to maturity, number of pods per plant, number of clusters per plant, pod length, biological yield per plant, seed germination, vigour index length and vigour index mass. High heritability ~~copuled~~coupled with high genetic advance indicates additive gene action~~.~~, which is beneficial for crop improvement. ~~the~~ The characters, no. of secondary branches per plant, no. of pods per plant, seed germination, vigour index length, and vigour index mass show high heritability ~~copuled~~coupled with high genetic advance. Meha and shikha varieties are high in heritability and genetic advance (not mentioned in the results and discussion), can be select as a parents for further breeding program.

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Table1. Analysis of variance for seed yield and its components in green gram

		Mean sum of squares

No.		Replication	Genotypes	Error
	Degree of freedom	**2**	**9**	**18**
1	**Days to 50% flowering**	0.10	5.15*	1.77
2	**Days to maturity**	0.70	5.79*	1.74
3	**Plant height (cm)**	17.96	76.21*	22.81
4	**No. of primary branches plant^{-1}**	0.15	0.68**	0.18
5	**No. of secondary branches plant^{-1}**	0.24	0.67**	0.07
6	**No. of pods plant^{-1}**	0.15	3.06**	0.39
7	**No. of clusters plant^{-1}**	0.00	0.23*	0.07
8	**Pod length**	0.07	0.56*	0.19
9	**Number of seeds pod^{-1}**	0.23	1.37**	0.30
10	**1000 seed weight (g)**	17.59	81.98**	18.56
11	**Biological yield plant^{-1} (g)**	0.23	8.83*	2.95
12	**Harvest index (%)**	1.77	39.89**	7.80
13	**Seed germination (%)**	0.40	7.26**	0.88
14	**Vigour index length**	540.15	56424.63**	347.55
15	**Vigour index mass**	0.10	56.30**	4.58
16	**Seed yield plant^{-1} (g)**	0.019	2.00*	0.79

***=significant at 5% and **=significant at ~~5% and~~ 1% level of probability**

Table 2. Estimates of variability components for 16 quantitative traits of 10 green gram genotypes

Characters	**Coefficient of Variation**		**Heritabilty (bs) (%)**	**Genetic Advance ~~ment~~ 5%**	**Gen. Adv As % of Mean 5%**
	GCV	**PCV**			
Days to 50% flowering	2.395	3.839	38.924	1.364	3.078
Days to maturity	1.822	2.755	43.765	1.585	2.484
Plant height (cm)	9.876	14.918	43.826	5.754	13.468
No. of primary branches plant^{-1}	12.795	18.58	47.422	0.579	18.151
No. of secondary branches plant^{-1}	14.926	17.418	73.44	0.791	26.351
No. of pods plant^{-1}	6.069	7.284	69.422	1.619	10.416
No. of clusters plant^{-1}	6.532	9.79	44.514	0.323	8.978
Pod length	5.274	8.407	39.355	0.452	6.816
Number of seeds pod^{-1}	9.303	12.59	54.605	0.909	14.162
1000 seed weight (g)	8.615	11.806	53.245	6.911	12.95
Biological yield plant^{-1} (g)	5.066	8.018	39.913	1.822	6.593
Harvest index (%)	11.576	15.22	57.846	5.125	18.136

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Seed germination (%)	1.535	1.825	70.69	2.525	2.658
Vigour index length	8.782	8.863	98.175	9.061	17.925
Vigour index mass	6.099	6.863	78.991	7.601	11.167
Seed yield plant^{-1} (g)	6.947	11.984	33.6	0.75	8.296

GCV: Genotypic Coefficient of Variation; **PCV:** Phenotypic Coefficient of Variation

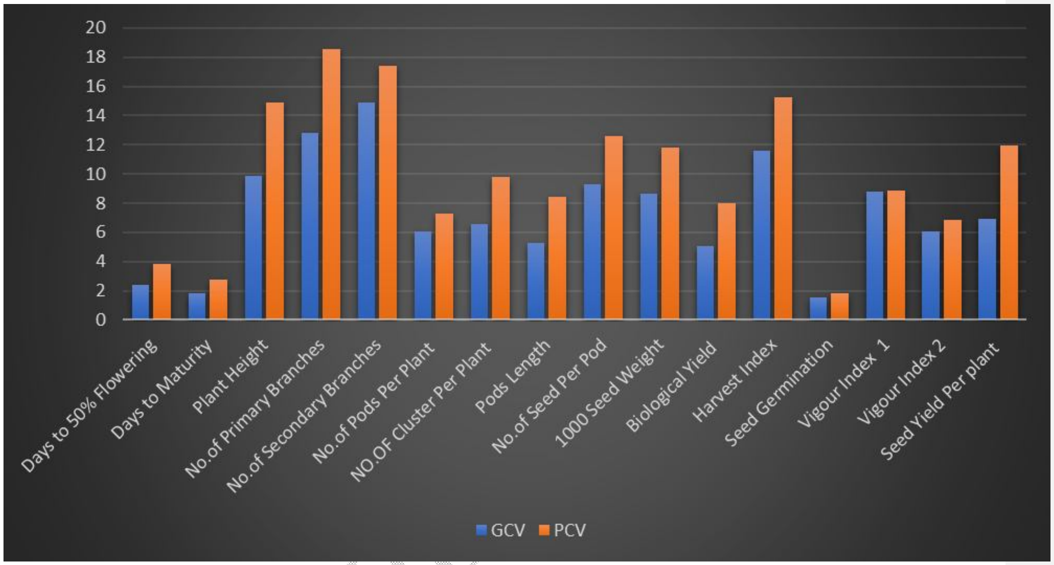

Fig. 1: *Genotypic and Phenotypic coefficient of variation estimates of 10 genotypes of Mung bean*

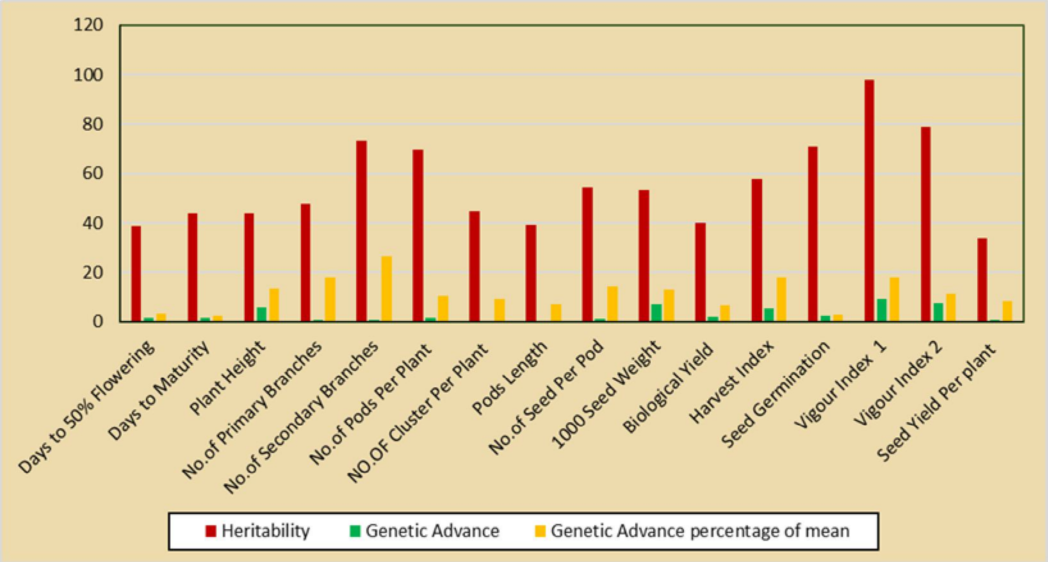

Fig. 2: *Heritability, genetic advance and genetic advance as per cent mean estimates of 10 genotypes of Mung bean*