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Understanding Genetic Variability Parameters of Greengram (*Vigna radiata* L. Wilczek) Germplasm for Agro-Morphological Traits

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Authors' contributions

All authors contributed to the completion of this research. The final manuscript was read and approved by all authors.

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ABSTRACT

The greengram, also known as mungbean or *Vigna radiata* L. Wilczek, is a significant pulse crop in India. Throughout India, it is mostly cultivated in subsistence agricultural systems. Even though it may be cultivated in three seasons across India, the average production is unbelievably low. The local germplasm has a significant genetic variation since the crop has developed in a wide variety of environmental settings. To comprehend the genetic variability and identification of distinct germplasm lines, a study was conducted on 300 green gram accessions utilising 14 quantitative traits. For pods per plant, pod clusters per plant, branches per plant, biological yield per plant, 100 seed weight, nodes per plant, harvest index, and seeds per pod, relatively high PCV and GCV were found. Additionally, an evaluation of the genetic advance (GA) and broad-sense heritability (h^2) was done to select the most significant quantitative variables. Due to their high broad sense heritability (h^2) and genetic advance, biological yield per plant, pods per plant, plant height, and harvest index were shown to be highly suited for mungbean breeding programmes. The breeder must typically utilise an appropriate breeding strategy to use these traits in subsequent breeding programmes.

Keywords: Greengram; genetic advance; genetic variability; heritability; mungbean; germplasm.

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1. INTRODUCTION

The mungbean, or *Vigna radiata* (L.) Wilczek is an extensively produced legume crop native to India and South-East Asia. It is usually grown during the Kharif (rainy) season. Due to its short duration, it is also grown in the spring and summer in the wheat-rice cropping system to elevate crop intensity and boost pulse production. Although it may be grown in three seasons, the worldwide average productivity is appallingly low at 0.5 t ha^{-1}, which is significantly lower than the crop's forecasted yield potential of 2.5 to 3.0 tonnes per hectare [1]. Persistent restrictions on pulse availability have caused the pulse prices to increase, making them unaffordable for those in despair [2]. Germplasm accessions have acquired an array of desirable traits such as resistance to a wide range of climatic circumstances like drought, temperature stress, a predominance of pathogens etc. Thus, natural selection continues to have a significant impact on the crop's evolution. The crop has built up diversity in agronomic traits including yield and factors that contribute to yield, the number of seeds per pod, biological yield, maturity duration, and so on. Mungbean diversity has reportedly been declining at an increasing pace. The acreage of improved mungbean cultivars has increased throughout the last 20 years of mungbean research and breeding programmes, mostly due to the substitution of conventional cultivars. The majority of the time, mungbean genetic improvement is restricted to assessment and screening from segregating progenies involving a small number of frequently used parental lines. As a result, this crop has a relatively low genetic variability. Thus, the necessity for the collection, preservation, and use of mungbean germplasm in contemporary breeding programmes has grown significantly. The most crucial task in making effective use of the available diversity is the evaluation of germplasm accessions. In this study, the mungbean germplasm used was assessed for significant agro-morphological and yield-related characteristics. The findings including the range of genetic variability, genetic advance, and germplasm lines suitable for particular traits, may aid in crop improvement strategies.

2. MATERIALS AND METHODS

The study was performed during the Summer of 2022 in an Augmented Block Design (ABD) with 300 accessions collected from IIPR, Kanpur, Uttar Pradesh, PAU, Ludhiana, Punjab and JNKVV, Jabalpur, Madhya Pradesh along with three checks, namely Virat, Shikha and MH-421 to estimate phenotype variation for the population being analysed. There was a total of 6 blocks and each comprised 50 accessions. A row length of 4 m with a 35 cm row spacing was used to grow each accession. In each block, all three checks were repeated once. Data on quantitative traits were analysed as suggested by Federer [3] and further utilized to estimate indicators of genetic variability of breeders' interest including mean, range, skewness, kurtosis, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) as per Burton [4], to guarantee effective use of the promising accessions found for various qualities. According to Lush [5], the broad sense heritability (h^2) was computed and it was further divided into low (30%), medium (30-60%), and high (>60%) categories by Robinson [6]. The augmented RCBD package (https://CRAN.R-project.org/package=augmentedRCBD) was used to analyse the data in R studio version 4.2.1.

3. RESULTS AND DISCUSSION

The outcome of the analysis of variance (ANOVA) are presented in Table 1. The ANOVA was seen for all attributes across all sources of variance. For all of the traits, both the Block effect (ignoring treatments) and the Treatment effect (ignoring blocks) are significant. The effects of the test germplasm lines and checks are likewise significant, except for the harvest index, which is not significant in the case of checks (treatment adjusted and block adjusted). Except for days to 50% flowering, harvest index, and seed yield per plant, block effects (eliminating treatments) are non-significant for all traits, demonstrating the homogeneity of blocks for evaluation. For all traits except the harvest index, the mean square due to test vs. check is significant, showing that test entries differ considerably from checks other than the harvest index. Similarly, while the harvest index is non-significant in the context of checks, the effects caused by varieties are of significance (Table 1).

The majority of the examined characteristics exhibited a reasonable range of variability; nevertheless, the values for skewness and kurtosis show deviation of some quantitative traits from normal distribution patterns. Statistical parameters were also examined using the established methodology. Statistical metrics like GCV, PCV, h^2 and GA may be used to understand the scope of variation as well as its use. Table 2 shows that PCV and GCV were found to be relatively high for the traits such as pods per plant, pod clusters per plant, branches per plant, biological yield, 100 seed weight, nodes per plant, harvest index, and seeds per pod, while PCV and GCV were found to be moderate to low for the other traits. Estimates of PCV were often greater than the corresponding GCV. However, very minor differences were found for parameters like days to 50% flowering, 100 seed weight, pod clusters per plant, and biological yield, indicating that a larger amount of the variance shown for these variables is controlled by genetic factors. Gayacharan et al., [7] and Govardhan et al., [8] revealed similar results. Greater differences between PCV and GCV were seen for the characteristics of seed yield per plant and harvest index, which suggests the influence of the environment on phenotypic development. Any breeding material must exhibit genetic variation since it not only serves as a foundation for selection but also offers important insights into the choice of varied parents to be employed in hybrid programmes [9].

The percentage of variation that may be attributable to hereditary variables is known as heritability (h^2). When choosing superior lines from accessions for use in crop improvement programmes, this indicator is helpful. The h^2 statistic shows how well polygenic attributes are passed down to the progeny. Given the complexity of quantitative traits, it is important to consider mean, range, distribution, h^2, and GA when choosing genotypes for crop improvement. For selection based on phenotypic performance, traits with greater h^2 and higher GCV and GA are regarded as beneficial [10]. Genetic advance (GA) is a helpful indicator of the development that may be anticipated as a result of the selection of the relevant population [11].

Days to 50% flowering, flowering period, days to maturity, pod length, seeds per pod and as well as 100-seed weight, were determined to be very desirable features for mungbean breeding programmes. Research and breeding operations in mungbean can be significantly impacted by germplasm chosen for trait improvement. On the other side, hybridization programmes can be used to enhance promising germplasm accessions for attributes with poor heritability and genetic advance. Days to 50% flowering (99.76), 100 seed weight (99.73), pod clusters per plant (99.63), and biological yield (99.44) all had excellent broad sense heritability (h^2). Days to maturity exhibited a relatively low h^2 value (71.83). The biological yield per plant (24.12) and pods per plant (23.69) were assessed with the highest genetic advance. Plant height (17.7) and harvest index (11.7) were moderate, however, 100 seed weight (2.4) had a dramatic decrease similar to the studies of Azam et al., [12].

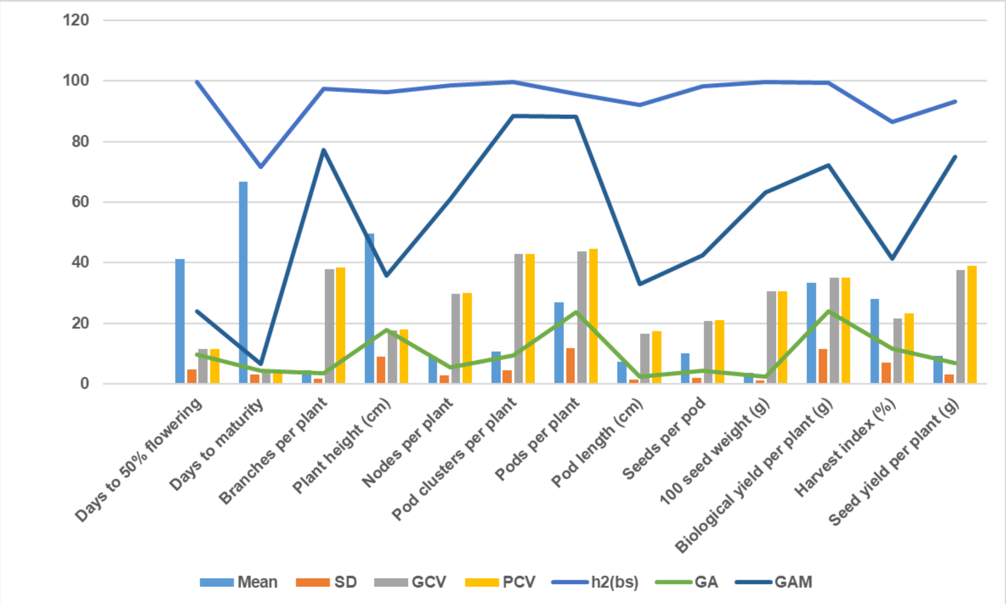

Fig. 1. Genetic variability parameters of different quantitative agro-morphological traits

Where, SD- standard deviation, GCV- genotypic coefficient of variation, PCV- phenotypic coefficient of variation, h2(bs)- heritability in broad sense, GA- genetic advance, GAM- genetic advance as percentage of mean

Table 1. Augmented block design ANOVA (block and treatment adjusted) for 13 traits of 300 genotypes of mungbean

Source	**df**	**dtf**	**dtm**	**bpp**	**ph**	**nnpp**	**npcp**	**npp**	**pl**	**spp**	**100 sw**	**by**	**hi**	**syp**
Block (Ignoring Treatments)	5	185.96 **	35.1 **	61.87 **	680.63 **	99.1 **	667.98 **	4749.75 **	2.6 **	13.69 **	6.15 **	4707.24 **	87.77 **	443.17 **
Treatment (ignoring Blocks)	302	28.92 **	12.8 **	2.82 **	87.69 **	7.71 **	20.84 **	144.48 **	1.57 **	4.66 **	1.38 **	140.59 **	42.09 **	13.28 **
Block (eliminating Treatments)	5	0.99 **	1.3 ns	0.02 ns	0.91 ns	0.08 ns	0.02 ns	10.85 ns	0.13 ns	0.09 ns	0.01 ns	1 ns	26.73 *	4.76 *
Treatment (Eliminating Blocks)	302	25.86 **	12.24 **	1.8 **	76.43 **	6.07 **	9.78 **	66.02 **	1.53 **	4.44 **	1.28 **	62.67 **	41.07 **	6.02 **
Test	299	22.8 **	9.11 *	2.8 **	79.71 **	7.25 **	20.72 **	143.86 **	1.55 **	4.45 **	1.37 **	138.2 **	42.46 **	13.13 **
Checks	2	6.06 **	40.17 **	3.63 **	211.22 **	5.71 **	8.82 **	57.54 **	5.14 **	12.98 **	0.26 **	137.76 **	2 ns	14.13 **
Test and Test vs. Check	300	25.99 **	12.05 **	1.79 **	75.54 **	6.07 **	9.79 **	66.08 **	1.51 **	4.38 **	1.28 **	62.17 **	41.34 **	5.96 **
Test vs. Check	1	1904 **	1059.79 **	7.57 **	2224.83 **	150.04 **	82.24 **	504.73 **	1.29 **	53.15 **	6.43 **	862.28 **	9.78 ns	56.05 **
Residuals	10	0.06	2.57	0.07	2.94	0.1	0.08	6.1	0.12	0.08	0.0037	0.77	5.67	0.88

** P= 0.05; ** P= 0.01*

Where, dtf- days to 50% flowering, dtm- days to maturity, bpp- branches per plant, ph-plant height (cm), nnpp- nodes per plant, npcp- pod clusters per plant, npp- pods per plant, pl- pod length (cm), spp- seeds per pod, 100 sw-100 seed weight (g), by- biological yield per plant (g), hi- harvest index (%), syp- seed yield per plant (g)

Table 2. Measures of genetic variability parameters of different quantitative agro-morphological traits

Trait	Range		Mean	SD	GCV	PCV	h2(bs)	GA	GAM	Skewness	kurtosis
	Minimum	Maximum									
Days to 50% flowering	20.7	51.7	41.2	4.7	11.6	11.6	99.8	9.8	23.9	-0.28 *	3.12 ns
Days to maturity	56.2	77.5	66.7	3.2	3.8	4.5	71.8	4.5	6.7	0.7 **	4.08 **
Branches per plant	1.9	7.2	4.4	1.7	38.0	38.5	97.4	3.4	77.3	0.01 ns	1.75 **
Plant height (cm)	26.9	69.7	49.7	8.9	17.6	18.0	96.3	17.7	35.7	-0.52 **	2.41 **
Nodes per plant	4.0	13.9	9.0	2.7	29.7	29.9	98.6	5.5	60.9	-0.07 ns	1.95 **
Pod clusters per plant	2.6	18.5	10.6	4.5	42.9	43.0	99.6	9.4	88.4	-0.03 ns	1.94 **
Pods per plant	4.7	48.3	26.9	11.7	43.7	44.6	95.8	23.7	88.2	0.11 ns	1.86 **
Pod length (cm)	4.9	9.6	7.2	1.3	16.6	17.3	92.2	2.4	32.9	0.07 ns	1.82 **
Seeds per pod	6.3	14.0	10.0	2.1	20.9	21.1	98.2	4.3	42.6	0.01 ns	1.9 **
100 seed weight (g)	1.6	5.8	3.8	1.2	30.7	30.7	99.7	2.4	63.3	-0.1 ns	1.87 **
Biological yield per plant (g)	13.6	61.0	33.4	11.5	35.1	35.2	99.4	24.1	72.2	0.04 ns	1.82 **
Harvest index (%)	6.7	47.7	28.1	6.9	21.6	23.2	86.6	11.7	41.4	-0.1 ns	3.34 ns
Seed yield per plant (g)	1.5	15.6	9.3	3.2	37.7	39.0	93.3	7.0	75.1	-0.2 ns	2.4 **

** P= 0.05; ** P= 0.01 and P > 0.05 ns= non-significant*

The traits that have a direct application in crop improvement programmes include days to 50% flowering, days to maturity, pod length, seeds per pod, pods per plant, and 100 seed weight (Fig. 1). Early maturing lines like RMG-1028, TMB 37, and SML 2160 that blossom 35 days after planting can play a crucial role in sustaining mungbean produce in tropical and subtropical countries amidst climate changes and declining monsoon precipitation. Mungbean production in rice-wheat crop agricultural systems throughout the spring and summer months can benefit from the development of short-duration variants [13]. The creation of short-duration mungbean variants will be essential in this situation for maintaining mungbean production. It is possible to test promising lines with high 100 seed weight (e.g., MH 1703, TMB163, and EC 520026), high seeds per pod (e.g., IPM 06-5, EC 396399, SML 1932) and larger pods size (e.g., PUSA 1501 and SML 2088) in multilocation trials to assess their viability as a credible source for trait introgression in current elite varieties. Early and synchronous type cultivars might improve and increase the productivity of summer mungbean. The research will be beneficial for choosing genotypes with traits of importance including maturity, pod features, and seed size. This analysis demonstrated that germplasm represents a rich source of undiscovered variability. Its use in breeding programmes has the potential to significantly improve mungbean productivity.

4. CONCLUSION

GCV, h^2 and GA can all be valuable indicators to determine possible advancements in mungbean genetic improvement. The genetic variation of 300 germplasm lines was sufficiently high to be used in breeding initiatives. The germplasm collection comprised traits such as pods per plant, seeds per pod, pod length, 100 seed weight, and early maturity that help increase productivity. For biological yield per plant, pods per plant, plant height, and harvest index, heritability and genetic advance estimates were high to moderate, providing scope for the characteristics for development by the selection, making these characters more amenable to improvement than the other characters. To use these features in future breeding programmes, the breeder needs generally employ an appropriate breeding approach.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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