Assessment of Genetic Variability,Heritability and Genetic Advance for seed yield and its contributing traits in Greengram[*Vigna radiata* (L.) Wilczek]

ABSTRACT

Vigna radiata L. Wilczek, sometimes known as greengram or mungbean, is a popular pulse crop in India. Most of its cultivation takes place in India's subsistence farming systems. It is cultivated in three distinct seasons in India, despite the extremely low average productivity. Due to the crop's extensive growth in a variety of environmental circumstances, the local germplasm exhibits a high degree of genetic variation. In order to determine the genetic variability, heritability, and genetic advancement of 40 green gram genotypes, a study utilizing twelve quantitative variables was conducted. For every traits, significant variance was discovered using basic descriptive statistics.High PCV and GCV estimates High coefficients of variation (GCV) were identified for seed yield per plant, number of branches per plant, number of clusters per plant, biological yield per plant, number of pods per plant and 100 seed weight.. Moderate PCV and GCV values observed for number of seeds per pod, plant height, harvest index, pod length and days to 50% flowering, whereas low PCV and GCV values were observed days to maturity. Most of the characters studied in the current study had high estimates of heritability coupled with high to moderate genetic advance as a percentage of mean. This may be attributed to the preponderance of additive gene action and their high selective value, meaning that selection pressure can be applied profitably to these characters to improve them rationally.

Keywords: Green gram; genetic advance; genetic variability; heritability; genetic advance *mungbean.*

1. INTRODUCTION

Native to India and Southeast Asia, the green gram, or *Vigna radiata* (L.) Wilczek, is a legume crop that is widely grown. Usually, it is grown in the rainy season . Because of its brief growing season, it is also cultivated in the wheat-rice cropping system in the spring and summer to increase pulse production and crop intensity. Despite having the capacity to be cultivated in three seasons, the crop's average productivity worldwide is a pitiful 0.5 t ha^{-1}, far less than the 2.5 to 3.0 tonnes per hectare estimated yield potential (**Thakur *et al.,*** 2022) Due to ongoing limitations on pulse availability, pulse costs have increased, rendering them unaffordable for individuals who are depressed.Germplasm accessions have accumulated several advantageous characteristics, like tolerance to a variety of weather conditions such as a preponderance of infections, temperature stress, or drought, among others. Thus, the evolution of the crop is still greatly influenced by natural selection. The crop has developed a diversity of agronomic features, such as yield and its determinants, pod number, biological yield, maturity time, and so forth.Assessing germplasm accessions is the most important step towards utilizing the variety that is available. Within this research, the significant yield-related traits of the green gram germplasm were evaluated. The results, which include the spectrum of genetic variability and genetic advancement appropriate for specific qualities, could support initiatives for agricultural improvement.

2. MATERIALS AND METHODS

The current study was conducted in the summer of 2022 at the College of Agriculture's Department of Plant Breeding and Genetics. 30 x 10 cm seed spacing was used to grow 40 germplasm units in a randomized block design with three replications. Plant protection measures that were based on need and recommended agronomic procedures were implemented. Data were gathered on twelve yield and yield contributing characters, which included days to 50% flowering, days to maturity, plant height(cm), number of branches per plant, number of clusters per plant, number of pods per cluster, pod length(cm), number of seeds per pod, 100 seed weight(g), harvest index, biological yield per plant and seed yield per plant (g). Five plants of various genotypes were chosen at random, tagged, and observed. The mean value was then computed for analysis over three replications. Burton's recommendations for doing an analysis of variance were followed (1952). The heritability formula provided by Hanson et al. (1956) and Johnson et al. (1955) was used to estimate heritability and genetic advance estimates, respectively. According to Johnson et al. (1955), the percentages of genetic advance ranged from lower (<10%) to high (>20%) and moderate (10–20%).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

For every variable under investigation, the analysis of variance revealed substantial variances (Table 1). To begin the selecting process, these differences alone are adequate.

3.2. Per se Performance and Range

With a mean of 36 days, the days to 50% flowering ranged from 26 to 41 days. The range of days to maturity was 57 to 73 days, with an average of 65 days. With an average performance of 33.20 cm, the plant height's degree of dispersion varied from 21.13 to 44.57 cm. The mean number of branches was 2.02, with a range of 1.25 to 3.95. The average number of clusters per plant was 5.24, with a range of 2.67 to 8.93.Plants had an average of 15.55 pods, ranging from 6.43 to 21.93. Between 5.8 and 9.67 inches, the average pod length was 7.82. Number of seeds per pod ranged from 4.82 to 12.80 with a mean of 9.69. With a minimum range of 1.84g and a maximum range of 5.61g, the average weight of 100 seeds was 3.57g. Plants produced an average of 17.64g of biological output, ranging from 6.08g to 27.8g respectively. Between 17.41% and 38.87%, with a mean of 30%, was the harvest index. The range of 1.58g to 8.55g was observed in the average seed yield per plant, 5.28g.The mean performance serves as a direct criterion for selecting the best genotypes from the diverse population. All it takes to raise the population's yield is to choose for traits associated with yield. The mean performance according to attributes is shown in Table 2.

3.3. Coefficient of Variation

The reliable measures that will enable us to evaluate the amount of variability and comprehend its heritable and non-heritable components are the genotypic and phenotypic coefficient of variations. The difference between the phenotypic and genotypic coefficient of variations indicates the percentage of environmental effect on the variability presented by the genotypes. The environment affects all biometrical aspects, as evidenced by the fact that PCV levels in this study are higher than GCV values. Table 2 presented the coefficients of variation. The high PCV values (Table 2) were number of branches per plant (32.11%), seed yield per plant (30.99%), biological yield per plant (27.25%), number of clusters per plant (26.75%), number of pods per plant (26.22%) and 100 seed weight (24.85%). Moderate PCV values observed for number of seeds per pod (17.74%), harvest index (16.74%), plant height (14.83%), pod length (12.19%) and days to 50% flowering (10.22%), whereas low PCV values were observed days to maturity (6.13%). In general, phenotypic coefficients of variation (PCV) values were higher than the genotypic coefficients of variation (GCV) for the respected characters. The high GCV values (Table 2) were reported for seed yield per plant (29.8%), number of branches per plant (29.78%), number ofclusters per plant (25.96%), biological yield per plant (25.6%), number of pods per plant (24.8%) and 100 seed weight (24.66%). Moderate GCV values observed for number of seeds per pod (16.66%), plant height (13.96%), harvest index (13.96%), pod length (11.58%) and days to 50% flowering (10%), whereas low GCV values were observed days to maturity (6%). These observations are in agreement with the findings of **Wesly *et al.* (2020), Sineka *et al.* (2021), Parsaniya*et al.* (2022) and Prajapati *et al.* (2022)**.

High coefficients of variation were identified for seed yield per plant, number of branches per plant, number of clusters per plant, biological yield per plant, number of pods per plant and 100 seed weight. This shows that these parameters may be enhanced by efficient selection. Therefore, these qualities may be considered throughout the selection process to increase yield.

3.4. Heritability (h^2) and genetic advance as per cent of mean (GAM)

Heritability estimates tell us how similar parents and children are to one another and explain the traits that are inherited. Any selection program must be heritable for the features to manifest in a comparable phenotypic way in the progeny of the selected individuals. Heritability alone, however, is not enough to genetically alter characteristics. It should also have a high level of genetic advancement, which is a gauge of how effectively a certain trait has evolved by suitable selection. Thus, for selection to be effective, there must be both high heritability and a significant genetic progress as a percentage of mean for the genetic development of the traits. Genetic advance and heritability values were shown in Table 2.

Highest heritability (bs) (Table 2) was recorded for 100 seed weight (98.48%) followed by days to maturity (96.03%), days to 50% flowering (95.72%), number of clusters per plant (94.14%), seed yield per plant (92.47%), pod length (90.29%), number of pods per plant (89.43%), plant height (88.71%), biological yield per plant (88.25%), number of seeds per pod (88.23%) and number of branches per plant (86.04%), while harvest index (69.56%) recorded medium heritability respectively.

The similar kind of results were also reported by **Wesly *et al.* (2020), Parsaniya*et al.* (2022) and Prajapati *et al.* (2022).**

For the traits namely, seed yield per plant (59.03%), number of branches per plant (56.91%), number of clusters per plant (51.88%), 100 seed weight (50.42%), biological yield per plant (49.54%), number of pods per plant (48.3%), number of seeds per plant (32.24%), plant height (27.09%), harvest index (23.98%), pod length (22.67%), days to 50% flowering (20.16%), and harvest index (23.98%), there was a high expected genetic advance as a percentage of mean while, days to maturity (12.12%).recorded medium estimates of genetic advance.

A transmissibility index is produced for each character based on direct selection criteria, namely broad heritability and genetic advancement as a percentage of mean. This index shows how well the selection process has enhanced each particular character. The majority of the features examined in this study demonstrated high to moderate genetic progress as a percentage of mean together with high estimates of heritability. This may be explained by the high selective value and preponderance of additive gene action, which means that selection pressure can be profitably applied to certain features to improve them logically. The similar kind of results were also reported by **Muthuswamy et al. (2022), Parsaniya*et al.* (2022) and Prajapati *et al.* (2022).**

4. CONCLUSION

There is sufficient genetic diversity for each characteristic, as evidenced by the substantial results of the analysis of variance for every trait included in this inquiry. High heritability (bs) was shown to be connected with the highest genetic advancement for most of the characteristics. High yielding breeding traits may be selected based on features that have been determined to have higher heritability and high genetic advance as a percentage of mean in order to optimize the crop's genetic yield potential.In order to choose transgressive segregants in the segregating generations, a methodical hybridization program may also be built, accounting for features with higher heritability and high genetic advancement as a percentage of mean. The segregants will significantly increase the greengram's future yield, productivity, and higher breeding value.

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Table 1:ANOVA for various quantitative traits of green gram.

Source of variations	df	Mean sum of square											
		Days to 50% flowering	Days to maturity	Plant height	No. of branches per plant	No. of clusters per plant	No. of pods per plant	Pod length	No. of seeds per pod	100 seed weight	Biological yield per plant	Harvest index	Seed yield per plant
Replication	2	3.475	1.308	6.476	0.017	0.299	1.058	0.059	0.295	0.03	18.109	3.859	2.633
Treatments	39	39.86**	46.53**	67.20**	1.14**	5.65**	46.38**	2.55**	8.17**	2.33**	63.90**	60.27**	7.62**
Error	78	0.586	0.633	2.734	0.059	0.115	1.758	0.088	0.348	0.012	2.715	7.672	0.201

Table 2: Genetic variability parameters for yield and its constituent traits

S. No.	Traits	Range			Coefficient of variation		h² (bs) %	Genetic Advance as % of mean
		Mean	Min	Max	GCV %	PCV %		
1	**Days to 50% flowering**	**36**	26	41	10.00	10.22	95.72	20.16
2	**Days to maturity**	**65**	57	73	6.00	6.13	96.03	12.12
3	**Plant height**	**33.20**	21.13	44.57	13.96	14.83	88.71	27.09
4	**Number of branches per plant**	**2.02**	1.25	3.95	29.78	32.11	86.04	56.91
5	**Number of clusters per plant**	**5.24**	2.67	8.93	25.96	26.75	94.14	51.88
6	**Number of pods per plant**	**15.55**	6.43	21.93	24.80	26.22	89.43	48.30
7	**Pod length**	**7.82**	5.80	9.67	11.58	12.19	90.29	22.67
8	**Number of seeds per pod**	**9.69**	4.82	12.80	16.66	17.74	88.23	32.24
9	**100 seed weight**	**3.57**	1.84	5.61	24.66	24.85	98.48	50.42
10	**Biological yield per plant**	**17.64**	6.08	27.80	25.60	27.25	88.25	49.54
11	**Harvest index**	**30**	17.41	38.87	13.96	16.74	69.56	23.98
12	**Seed yield per plant**	**5.28**	1.58	8.55	29.80	30.99	92.47	59.03

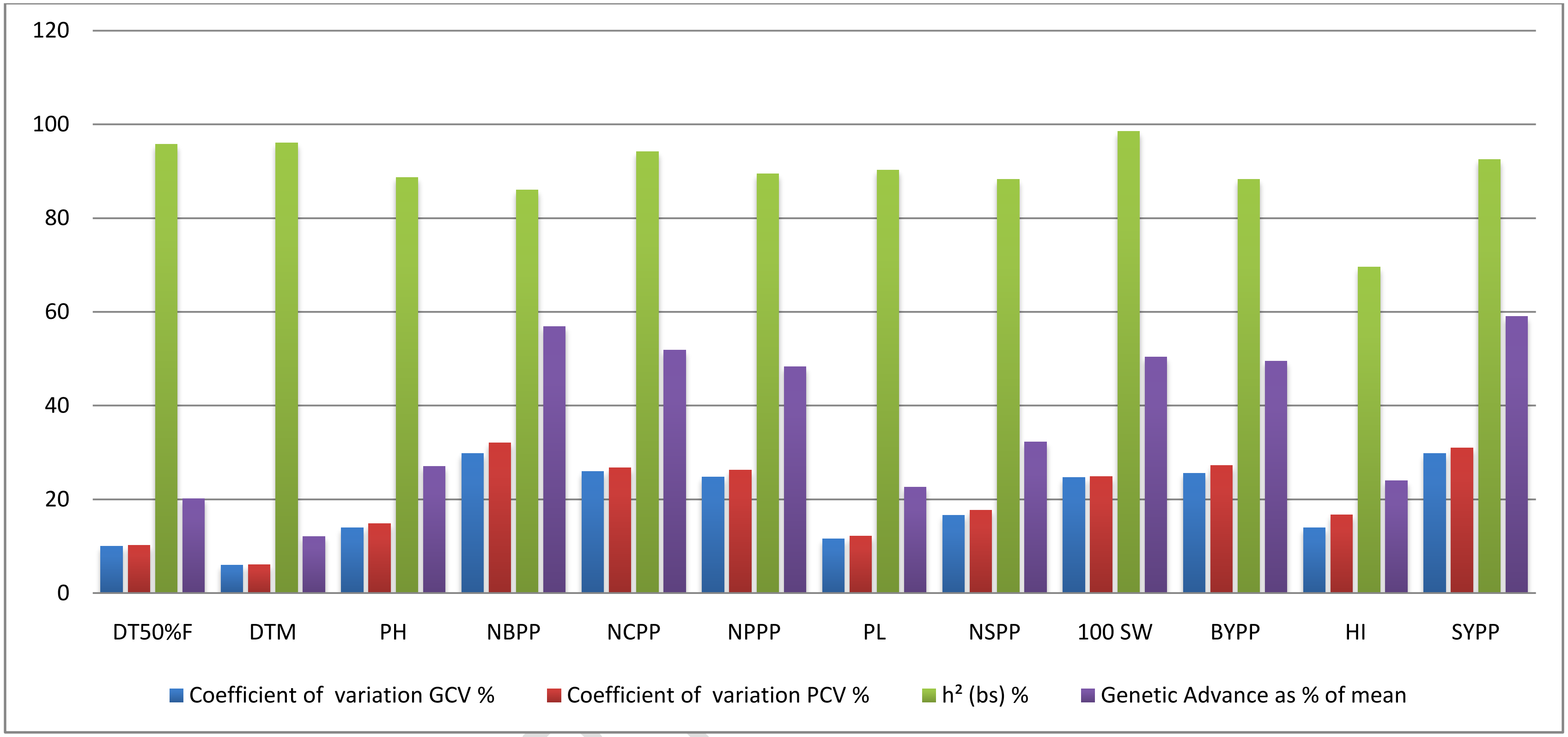

Fig 1:Genetic variability parameters of different quantitative traits