Evaluation of Genetic parameters for yield and its Attributing traits in Greengram [*Vigna radiata* (L.) Wilczek]

ABSTRACT

A prominent pulse crop in India is the greengram, commonly referred to as the mungbean or *Vigna radiata* L. Wilczek. The majority of its cultivation occurs in subsistence agricultural systems across India. It is grown in three different seasons throughout India, although the average production is incredibly poor. The crop has grown in a wide range of environmental conditions, resulting in a large genetic heterogeneity in the local germplasm. A study employing twelve quantitative traits was undertaken out on 40 green gram genotypes with the intent to uncover the genetic variability, heritability and genetic advance. Significant variance was found for each characteristic when using simple descriptive statistics.High PCV and GCV estimates was noticed for number of pods per plant, seed yield per plant, number of cluster per plant and number of pods per cluster. Days to 50% flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, biological yield per plant and seed yield per plant showed high heritability with high genetic advancement based on a study of genetic variability, suggesting that additive gene action predominates. It will be beneficial to select for these traits.

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

1. INTRODUCTION

A notable pulse crop of the Vigna genus, green gram [*Vigna radiata* (L.) Wilczek] also gets referred to as mungbean in South Asia. Green gram has a relatively small genome size of 543 Mb and a chromosome number (2n) of 22 thus making it a desirable and useful model for improving our comprehension of the diversity and evolution of legume genomes. (**Mathivathana *et al.,*2019**). In India, major states having green gram cultivation includes Maharashtra, Gujarat, Tamil Nadu, Andhra Pradesh, Bihar, Uttar Pradesh, Rajasthan, Karnataka and Orissa (**Dharajiya*et al.*, 2018**). Due to its high protein content, it significantly reduces malnutrition from a nutritional standpoint. Additionally, by fixing atmospheric nitrogen in the soil, it increases soil fertility. Thus, a fourth less supply of nitrogen will be needed for the cereal crops that follow. This crop is grown in dry settings as a rainfed, intercrop, and rice fallow because to its tough nature and short growing season.To boost green gram productivity, a breeding program must be started with a deeper comprehension of the elements governing genetic variability. Forty green gram germplasm accessions were assessed for twelve quantitative features in the current study. This publication presents the findings of the calculation of the genetic variability parameters, namely, mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance.

2. MATERIALS AND METHODS

The present investigation was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, during summer 2022. Forty germplasm were raised in randomized block design with three replications and the seeds were raised with a spacing of 30×10 cm. Recommended agronomic practices and need based plant protection measures were taken. The data was collected on twelve yield and yield contributing characters viz., 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). Among different genotypes, five plants were randomly selected and tagged for taking observations and the mean value was calculated for analysis on three replications.The analysis of variance was performed in accordance with **Burton (1952).**Heritability and genetic advance estimates were estimated using heritability formula given by **Hanson*etal.*(1956)** and **Johnson *et al.* (1955)**, respectively.**Johnson et al. (1955)** proposed that genetic genetic advance, measured as a percentage, showed values ranging from lower (<10%) to moderate (10–20%) and high (>20%).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The analysis of variance showed significant variations for all the traits under study(Table 1). The presence of these variations is sufficient to start the selection process.

3.2. Per se Performance and Range

Days to 50% flowering varied from 27 to 42 days with mean of 36 days. Days to maturity varied from 58 to 73 days with the average value of 65 days. The degree of dispersion for the plant height ranged between 22.07 to 45 cm with an average performance of 32.82 cm. Number of branches had a mean value 1.86 and varied from 1.23 to 3.64. Number of clusters per plant was recorded in the range of 2.67 to 9.62 with an average of 5.09. Number of pods per plant varied from 6.73 to 24.09 with a mean of 15.1. Pod length had an average 7.78 and varied from 5.8 to 9.63. Number of seeds per pod ranged from 4.43 to 12.17 with a mean of 9.59. Hundred seed weight had an average of 3.57g with a minimum ranged of 1.85g and maximum of 5.68g. Biological yield per plant ranged from 5.72g to 26.56g with an average performance of 16.76g. Harvest index varied from 20.10% to 43.38% with mean of 31.79%. Seed yield per plant had an average performance of 5.27g with a range of 1.95g to 9.03g.The direct criterion for choosing the best genotypes from the heterogeneous population is the mean performance. The population's yield may be increased simply by selecting for features linked to yield. Table 2 provides the mean performance based on traits.

3.3. Coefficient of Variation

Phenotypic and genotypic coefficient of variations are the trustworthy metrics that will give us an understanding of the heritable and non-heritable components of the variability and allow us to assess the magnitude of variability. The percentage of environmental influence on the variability displayed by the genotypes is indicated by the difference between the phenotypic and genotypic coefficient of variations. The fact that PCV values in this study are greater than GCV values indicates that the environment has an impact on all biometrical features. In Table 2, the coefficients of variation were provided.The high PCV values (Table 2) were observed for seed yield per plant (33.62%), biological yield per plant (32.22%), number of branches per plant (31.95%), number of clusters per plant (29.32%), number of pods per plant (27.19%) and 100 seed weight (24.44%). Moderate PCV values observed for number of seeds per pod (17.07%), harvest index (16.69%), plant height (15.37%), pod length (11.54%) and days to 50% flowering (10.42%), while low GCV values were observed days to maturity (5.54%).

The high GCV valueswere noted for seed yield per plant (31.86%), biological yield per plant (30.91%), number of branches per plant (29.45%), number of clusters per plant (28.11%) number of pods per plant (26.84%) and 100 seed weight (24.33%). Moderate GCV values observed for number of seeds per pod (16.12%), plant height (14.8%), harvest index (14.08%), pod length (11.33%) and days to 50% flowering (10.11%), while low GCV values were observed days to maturity (5.41%). 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)**.

Seed yield per plant, biological yield per plant, number of branches per plant, number of clusters per plant, number of pods per plant and 100 seed weight were found to have high coefficients of variation, which suggests that these features may be improved by effective selection. Therefore, in order to improve yield, these features might be taken into account throughout the selection process.

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

Estimates of heritability provide an explanation for the features that are inherited and determine how similar parents and offsprings are to each other. Heritability is a prerequisite for any selection program in order for the traits to exhibit a similar phenotypic expression in the offspring of the chosen individuals. However, heritability by itself is insufficient to modify features genetically. Additionally, it should possess a significant degree of genetic advance, which is a measure of how well a certain feature has improved through appropriate selection. Therefore, high heritability combined with strong genetic advance as a percentage of mean for the genetic development of the traits is a prerequisite for selection to be effective. Table 2 included values for heritability and genetic advancement.

Highest heritability (bs) (Table 2) was recorded for 100 seed weight (99.08%) followed by number of pods per plant (97.42%), pod length (96.39%), days to maturity (95.24%), days to 50% flowering (93.99%), plant height (92.7%), biological yield per plant (92.04%), number of clusters per plant (91.92%), seed yield per plant (89.82%), number of seeds per pod (89.17%) number of branches per plant (84.99%) and harvest index (71.11%).

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

The expected genetic advance as percentage of mean was high for the character seed yield per plant (62.2%), biological yield per plant (61.09%), number of branches per plant (55.93%), number of clusters per plant (55.52%), number of pods per plant (54.57%), 100 seed weight (49.89%), number of seeds per plant (31.36%), plant height (29.36%), harvest index (24.45%), pod length (22.92%) days to 50% flowering (20.18%) while, days to maturity (10.87%) recorded medium estimates of genetic advance.

Broad heritability and genetic advance as a percentage of mean are direct selection criteria that yield a transmissibility index for characters, indicating how well the selection process has improved the individual characters. 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. The similar kind of results were also reported by **Muthuswamy et al. (2022), Parsaniya*et al.* (2022) and Prajapati *et al.* (2022).**

4. CONCLUSION

All of the traits included in this investigation's analysis of variance were found to have significant results, indicating that there is enough genetic variation for each trait. For the majority of the traits, high heritability (bs) was shown to be correlated with the highest genetic advancement. In order to maximize the crop's genetic yield potential, high yielding breeding traits may be chosen based on traits that have been found to have higher heritability and high genetic advance as a percentage of mean. A systematic hybridization program may also be constructed, taking into account traits with higher heritability and high genetic progress as a percentage of mean for the selection of transgressive segregants in the segregating generations. The future yield, productivity, and higher breeding value of the greengram will all be greatly enhanced by the segregants.

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
Replication	2	2.86	0.98	3.33	0.02	0.04	0.03
Treatments	39	41.15**	37.60**	72.65**	0.95**	6.33**	49.71**
Error	78	0.86	0.62	1.86	0.05	0.18	0.44

Source of variations	df	Mean sum of square					
		Pod length	No. of seeds per pod	100 seed weight	Biological yield per plant	Harvest index	Seed yield per plant
Replication	2	0.02	0.09	0.03	2.40	2.18	0.09
Treatments	39	2.36**	7.46**	2.27**	82.79**	68.20**	8.78**
Error	78	0.03	0.29	0.01	2.32	8.14	0.32

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

S. No.	Traits	Range			Coefficient of variation		h^2 (bs) %	Genetic Advance as % of mean
		Mean	**Min**	**Max**	**GCV %**	**PCV %**		
1	**Days to 50% flowering (DT50%F)**	**36**	27	42	10.11	10.42	93.99	20.18
2	**Days to maturity (DM)**	**65**	58	73	5.41	5.54	95.24	10.87
3	**Plant height (PH)**	**32.82**	22.07	45	14.80	15.37	92.70	29.36
4	**Number of branches per plant (NBPP)**	**1.86**	1.23	3.64	29.45	31.95	84.99	55.93
5	**Number of clusters per plant (NCPP)**	**5.09**	2.67	9.62	28.11	29.32	91.92	55.52
6	**Number of pods per plant (NPPP)**	**15.10**	6.73	24.09	26.84	27.19	97.42	54.57

7	**Pod length (PL)**	**7.78**	5.8	9.63	11.33	11.54	96.39	22.92
8	**Number of seeds per pod (NSPP)**	**9.59**	4.43	12.17	16.12	17.07	89.17	31.36
9	**100 seed weight (100 SW)**	**3.57**	1.85	5.68	24.33	24.44	99.08	49.89
10	**Biological yield per plant (BYPP)**	**16.76**	5.72	26.56	30.91	32.22	92.04	61.09
11	**Harvest index (HI)**	**31.79**	20.10	43.38	14.08	16.69	71.11	24.45
12	**Seed yield per plant (SYPP)**	**5.27**	1.95	9.03	31.86	33.62	89.82	62.20

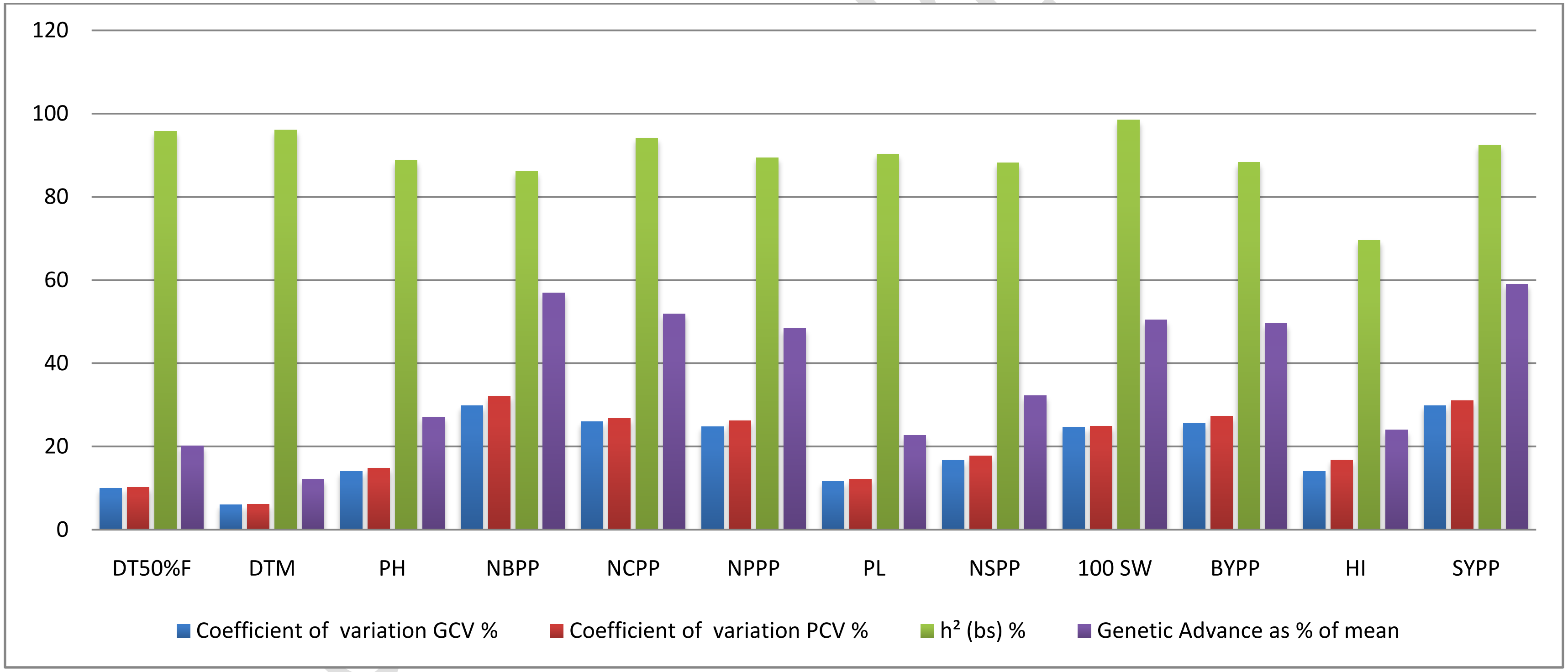

Fig 1:Genetic variability parameters of different quantitative traits

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