Assessment of Genetic Variability, Heritability and Genetic Advance in Mungbean (*Vigna radiata* (L) R. Wilczek)

Samidha Walke[1], Dr. Deepak Sapkal[2], Dr. Kevin Gawali[3], Dr. Mukesh Rathod[4], Dr. Ashish Sarda[5]
[1] P.G. Scholar, Department of Genetics and Plant Breeding, GHRU, Saikheda
[2,3,4] Associate Professor, Department of Genetics and Plant Breeding, GHRU, Saikheda
[5] Associate Professor, Department of Statistics and Mathematics, GHRU, Saikheda

Abstract: - The current research study on Assessment of genetic variability, heritability and genetic advance in mungbean (*Vigna radiata* (L.) R Wilczek) was granted to evaluate variability, heritability, genetic advance in eight genotypes of mungbean were sown in randomized block design (RBD) with three replications during kharif season (2024) at School of Agricultural Sciences G H Raisoni University, Saikheda. The observation was recorded for nine characters and the nine characters are days to maturity, days to 50% flowering, plant height (cm), number of pods per plant, number of primary branches per plant, pod length (cm), number of seeds per pod, 100 seed weight (gm) and seed yield per plant (gm). According to the analysis of variance, there was enough variability in the experimental material used because the mean squares resulting from genotypes were highly significant for days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod, and seed yield per plant. The high range coefficient values of the current experimental material indicated a broad range of phenotypic variation for the number of primary branches per plant, number of pods per plant and seed yield per plant. The PCV magnitude was marginally higher than the GCV, indicating that there was enough variability to show that environmental variation had very little effect on any of the characters. There is a modest genotypic coefficient of variation and a high phenotypic coefficient of variation in seed yield per plant.

Index Terms: - Mungbean, genetic variability, genotypic coefficient of variance, phenotypic coefficient of variance, genetic advance, heritability, green gram.

I. INTRODUCTION

In South and Southeast Asia mung bean is one of the crucial legume crops. It constitutes third-most prominent pulse crop in India. The main regions where it is grown in several Indian states. It was extensively cultivated in the prehistoric period. According to Ayurvedic principles, mungbeans are highly recommended for individuals struggling with obesity and excess body fat. Their richness in fiber and protein, combined with low fat content, makes them a healthy dietary choice. Throughout harvest, the crop's cultivation increases the soil's fertility by adding 30 to 40 kg N/ha. The subsequent crop, which often includes a cereal, needs approximately 25% less nitrogen as a result. The "Outlook report from ANGRAU" suggests that 31.5 lakh tonnes of green grams have been produced in 2021–2022, with production rate of 783 kg/ha. Estimation 40.38 million hectares of land, this represents 11% of the total production of pulses. Based on the first predictions for kharif 2022-2023, 17.5 lakh tonnes of green gram were produced on 33.37 lakh hectares. The states of Madhya Pradesh (1.57 lakh ha), Orissa (1.48 lakh ha), Maharashtra (3.94 lakh ha), Karnataka (4.40 lakh ha), and Rajasthan (20.89 lakh ha). Additionally, 2.60 million tons of green gram produced overall in 2020–21. (Anon 2020–21).

Genetic variability forms the foundation of crop improvement, as it defines the potential for selection and genetic gain in desirable traits. Successful plant breeding depends on the availability of adequate heritable variation within a population. This allows identification of superior genotypes for yield and adaptability. Traits like seed yield and its related characters are quantitative, controlled by many genes, and influenced by the environment. Hence, separating genetic effects from environmental ones is essential. Tools such as the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in measuring variability. Heritability estimates indicate the proportion of observable variation that is genetic in origin. Genetic advance provides the expected improvement from selection. A combination of high heritability and high genetic advance suggests predominance of additive gene action. This further implies that direct selection would be effective for crop enhancement. Evaluating these genetic parameters provides guidance in breeding programs. It ensures accurate identification of promising traits and genotypes. In this context, the present study aims to analyze variability, heritability, and genetic advance in soybean. The focus is on key yield traits and their contribution to productivity. The outcomes will help in developing superior and high-yielding soybean varieties. Different researchers discovered genetic parameters for yield components according to heritability, connection between characters, and variability. These parameters are highly variable and inconsistent. Thus, understanding that any crop species contain genetic variability in propagative material believed that necessary for advance enhancement in genetic yield and other economically significant features. An estimate of the potential improvement of the character through selection is provided by the combined effect of heritability, genetic variability and genetic advancement.

II. MATERIAL AND METHODS

The field trial was undertaken during kharif season in the year 2024-2025. The experiment was performed at School of Agricultural Sciences G H Raisoni University, Saikheda. The research study consists of eight mungbean genotypes, including AKM-9911, BM-2002-1, PDM-139, AKM-9904, BM-2003-2, Vaibhav, IPM 205-7, IPM 410-3. Eight genotypes of mungbean sown in randomized block design (RBD). Every variety was kept in single row with the spacing of 30 x 15 cm^2. Data for nine traits was recorded: Days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant, pod length, 100 seed weight, seed yield per plant. Five randomly plants were chosen for each genotype in each replication (except from days to maturity and days to 50% flowering, noted on plot basis). Mean value were later applied for statistical analysis. Statistical analysis included estimation of GCV, PCV, heritability, genetic advance and ANOVA. R studio software and Excel used for analysis of data.

III. RESULTS AND DISCUSSION

1. Analysis of variance (ANOVA): -

This research investigation was performed on eight genotypes for nine traits with three replications in randomised block design. Analysis demonstrated that most of the traits showed highly significant genotypic variation (Table 1), confirming sufficient presence of genetic variability within green gram genotype evaluated. It offers solid support for selection also improvement in hybridization program, particularly for traits directly influencing yield like number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant.

Eight mung bean genotypes were assessed for yield-attributing traits. ANOVA revealed significant variation among genotypes for number of primary branches per plant, days to 50% flowering, pod length, days to maturity, seed weight, plant height, number of pods per plant, number of seeds per pod, and seed yield per plant. This indicates ample genetic variability in the studied material. Comparable observations were also reported by Makeen et al. (2007) and Garg et al. (2017). Such diversity provides opportunities to select superior genotypes for yield improvement.

2. Mean performance and Range: -

The range of days to 50% flowering was 35.00 to 38.00 days, with an average of 36.64 days. The range of days to maturity was 58.00 to 65.3 days, with an average of 61.3 days. With a mean of 46.84 cm, the plant height ranged from 42.60 to 49.60. The average number of primary branches per plant was 5.84, with a range of 4.73 to 7.13. The average number of pods per plant was 24.18, with a range of 18.60 to 28.86. The mean number of seeds per pod 8.12, with a range of 5.30 to 12.00. Pod length ranged between 5.00 to 8.26 cm, with average pod length of 6.58 cm. 100 seed weight ranged between 3.1 to 4.23g, with average 100 seed weight of 3.93g. The range between 3.06 to 10.20g was observed in seed yield per plant with an average of 6.21g. A direct criterion for choosing the most desirable genotypes from the diversified population is the mean performance. Selecting for traits linked to yield is all that is required to increase the population’s yield. The mean performance according to traits (Table 2).

3. Genotypic and Phenotypic Coefficient of Variation:

The genotypic and phenotypic coefficients of variation are the dependable measures that will help us to assess the degree of variability and understand its heritable and non-heritable components. The percentage of environmental influence on the genotypes' variability is shown by the difference between the phenotypic and genotypic coefficients of variation. PCV had marginally greater value compared with GCV in terms of its magnitude for all the characters, hence, it shows that it had very low influence of environmental variation for their expressions. Range of PCV values (3.10–38.29%) were slightly higher than GCV values (2.81–36.69%), showing little environmental influence and it indicates that the extent of PCV and GCV in material studied. Highest GCV (36.69%) and PCV (38.29%) were recorded for seed yield per plant (Table 2).

In the present study, highest PCV was recorded for seed yield per plant (38.2%), similar findings are reported by Makeen et al. (2007), Ruturi et al. (2015), Kate et al. (2017), Yadav et al. (2017), Abbas et al. (2018), and Asari et al. (2019). Moderate PCV and GCV were observed for number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight and plant height, these results are agreement of Asari et al. (2019), Abhisheka & Mogali (2020), and Tabasum et al. (2010). Low variability for days to maturity, days to 50% flowering, and pod length similar results are reported by Dangi et al. (2017), Yadav et al. (2017), Dhunde et al. (2021), and Kumar et al. (2010). Overall, traits with moderate PCV and GCV indicate good potential for effective selection, whereas those with low values provide limited scope for improvement.

4. Heritability (h^2) (Broad sense): -

Heritability is a reliable specification of how parents impart their character into offspring. Heritability examined for nine attributes of mungbean (Table 2). The Days to maturity (96.22%), number of seeds per pod (94.40%), seed yield per plant (91.80%), plant height (90.67%), pod length (87.05%), number of pods per plant (86.11%), days to 50% flowering (82.11%) and number of primary branches per plant (71.90%) had maximum heritability. Whereas, 100 seed weight (48.86%) expressed moderate heritability (Table 2).

High heritability was recorded for days to maturity, number of seeds per pod, seed yield per plant, plant height, pod length, number of pods per plant, days to 50% flowering, number of primary branches, and 100-seed weight. Similar results are reported by Muthuswamy et al. (2019). Abbas et al. (2018) also observed high heritability for plant height, pods per plant, seed yield, and 100-seed weight. Days to 50% flowering, number of primary branches, pod length, number of pods per plant, plant height, seed yield per plant, and number of seeds per pod these results are agreement of Mohammed et al. (2020).

5. Genetic Advance expressed as mean percentage: -

Genetic advance expressed as mean percentage is presented in Table 2 found high value for seed yield per plant (72.42%), number of seeds per pod (57.66%), pod length (32.91%), number primary branches per plant (29.60%), number of pods per plant (23.93%). It was medium for 100 seed weight (12.77%). It was low for plant height (9.25%), day to maturity (7.74%) and day to 50% flowering (5.25%).

Similar findings on high genetic advance for yield and related traits were noted by Makeen et al. (2007) and Dangi et al. (2017). Low values were recorded for days to maturity and days to 50% flowering, in line with Baisakh et al. (2016) and Abbas et al. (2018). Traits showing high genetic advance coupled with heritability, such as number of pods per plant, number of primary branches per plant and seed yield per plant, indicate effective selection potential, as reported by Abhisheka & Mogali (2020) and Wesly et al. (2020).

Table 1. Analysis of Variance (ANOVA) for nine characters in 8 genotypes of Mungbean

Source of variance	Degree of freedom	Dt 50% F	DM	PH (cm)	No. PB/P	No. Po/P	No. Se/P	PL	100 SW (g)	SY/P (g)
MEAN SUM OF SQUARES										
Replication	2	0.04	0.12	1.38	0.15	16.83	3.85	3.07	0.16	1.34
Genotype	7	3.42**	17.02**	15.15**	3.62**	29.12**	16.94**	4.007**	0.49**	16.18**
Error	14	0.23	0.22	0.50	0.41	1.48	0.32	0.18	0.12	0.46

* Significant at 5 percent, **significant at 1 percent

Characters: - 1) Dt 50% F – Days to50% flowering, 2) DM – Days to maturity, 3) PH – plant height, 4)No. PB/P – Number of primary branch / plant, 5) No. Po/P – Number of pod/plant, 6) No. Se/P -Number of seeds / pod, 7) PL – Pod length, 8) 100 SW- 100 Seed weight, 9) SY/P- Seed yield / plant.

Table 2. Parameters for genetic variability for yield and yield contributing characters in Mungbean

Sr.no.	Characters	Phenotypic Range		Mean	Coefficient of Variance (%)		Heritability (broad sense) (%)	GA	Genetics advance in percent of mean
		Minimum	Maximum		GCV	PCV			
1	Days to 50% flowering	35.00	38.00	36.64	2.81	3.10	82.11	1.92	5.25
2	Days to maturity	58.00	65.3	61.3	3.83	3.90	96.22	4.78	7.74
3	Height of plant(cm)	42.60	49.60	46.84	4.71	4.95	90.67	4.33	9.25
4	No. of primary branch per plant	4.73	7.13	5.84	16.84	19.8	71.90	1.80	29.60
5	No. of pods per plant	18.60	28.86	24.18	12.52	13.49	86.11	5.80	23.93
6	No. of seeds per pod	5.30	12.00	8.12	28.81	29.65	94.40	4.70	57.66
7	Length of pod (cm)	5.00	8.26	6.58	17.12	18.35	87.05	2.16	32.91
8	100 seed weight (g)	3.1	4.23	3.93	8.87	12.69	48.86	0.50	12.77
9	Seed yield per plant (g)	3.06	10.20	6.21	36.69	38.29	91.80	4.51	72.42

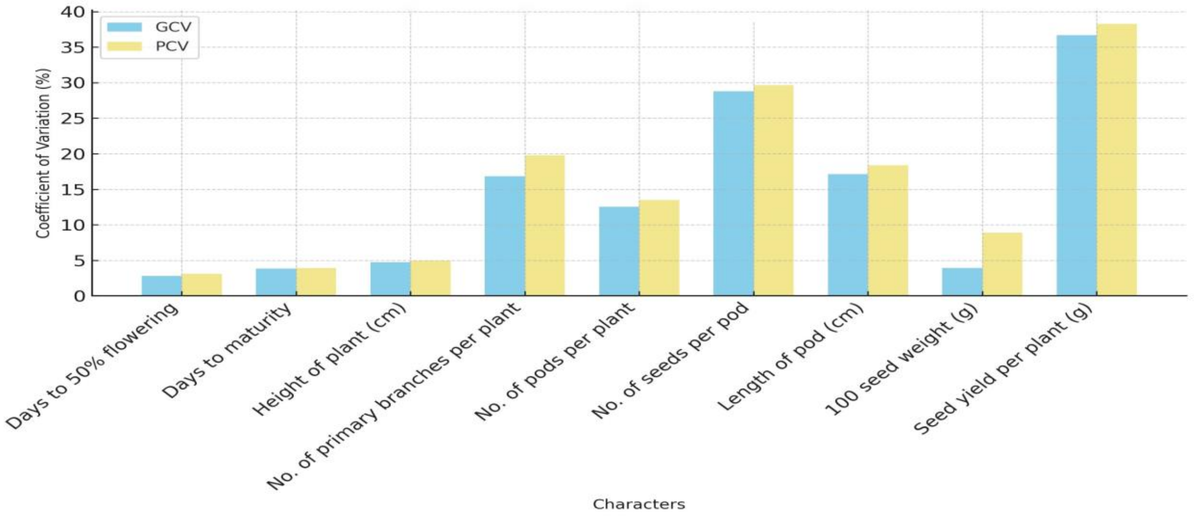

Figure 1. Graphical representation of genotypic and phenotypic coefficients of variation for various characters in mungbean

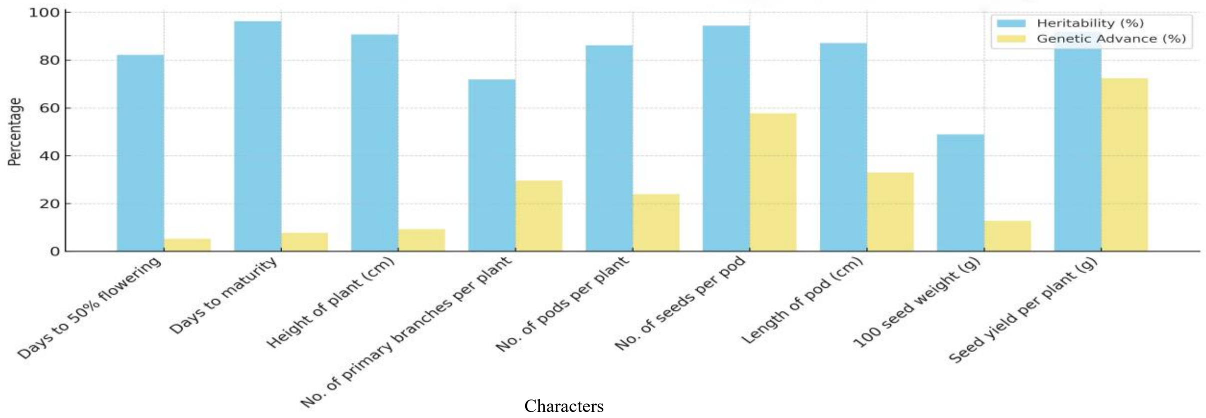

Figure 2. Graphical representation of heritability and genetic advance for various characters in mungbean

IV. CONCLUSION

The analysis of variance revealed significant differences among genotypes for all studied traits, indicating sufficient genetic variability in the experimental material. The widest range of variation was observed for seed yield per plant, followed by number of pods per plant, number of branches per plant, number of seeds per pod, 100-seed weight, plant height, pod length, days to 50% flowering, and days to maturity. Among genotypes, BM-2003-2 showed the highest seed yield (10.20 g), while IPM-205-7 recorded the maximum number of pods per plant (28.86). BM-2003-2 also excelled in number of seeds per pod, and several genotypes showed superiority in 100-seed weight. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all traits, suggesting limited environmental influence. High GCV and PCV were observed for seed yield per plant, while moderate values were noted for number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length and 100-seed weight. Heritability estimates were generally high for traits such as days to maturity, number of seeds per pod, seed yield per plant, plant height, number of pods per plant and pod length, indicating strong genetic control. Genetic advance as a percentage of mean was highest for seed yield per plant (72.42%), followed by number of seeds per pod, pod length, number of primary branches per plant, and number of pods per plant, while moderate to low values were recorded for 100-seed weight, plant height and days to 50% flowering. Overall, the study highlights that additive gene action plays a major role in traits like number of pods per plant, number of primary branches per plant, seed yield per plant and 100-seed weight, making them key targets for selection in breeding programs.

REFERENCE

[1] Abbas G.; Asghar, M. J.; Rizwan M.; Akram M.; Hussain, J. and Ahmad, F. (2018). Genetic analysis of yield and yield components for the improvement of mungbean germplasm. *Pak. J. Agric. Res.*, 31(2): 158-165.

[2] Abhisheka, L. S. and Mogali, S. C. (2020). Genetic variability, correlation and path coefficient analysis for yield and yield attributing traits in advanced breeding lines (ABLs) of green gram [*Vigna radiata* (L.) Wilczek] in F6 generation. *Int. J. Curr. Microbiol. App. Sci.*, 9(6): 314-321.

[3] ANONYMOUS, (2021). Indian Institute of Pulses Research, Kanpur., 105-108.

[4] Asari, T.; Patel, B. N.; Patel, R.; Patil, G. B. and Solanki, C. (2019). Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mung bean [*Vigna radiata* (L.) Wilczek]. *Int. J. Chem. Stud.,* 7(4): 383-387.

[5] BAISAKH, B.; SWAIN, S. C.; PANIGRAHI, K. K.; DAS, T. R. AND MOHANTY, A. (2016). Estimation of genetic variability and character association in micro mutant lines of green gram [*Vigna radiata* (L.) Wilczek] for yield attributes and cold tolerance. *Legume Genomics Genet*., 7(2): 1-9.

[6] BURTON, G. W. (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.*, held at Pennsylvania State College, 1: 277-283.

[7] Dangi, R.K.; Gurjar, D.; Singh P. B. and Lavanya, G. R. (2017). Correlation studies on morphological and yield characters of mungbean (*Vigna radiata* L. Wilczek). *J. Multidiscip. Adv. Res.,* 6(1): 6-9.

[8] DHUNDE, B. B.; DEVMORE, J. P.; PALSHETKAR, M. G.; JAGTAP, D. N.; DHEKALE, J. S. AND BURONDKAR, M. M. (2021). Genetic variability studies in F2 generation for yield and yield component traits in green gram (*Vigna radiata* L. Wilczek). *Int. J. Curr. Microbiol. App. Sci.*, 10(1): 321-327.

[9] Garg, G. K.; Verma, P. K. and Kesh, H. (2017). Genetic variability, correlation and path analysis in mungbean (*Vigna radiata* L. Wilczek). *Int. J. Curr. Microbiol. App. Sci.,* 6(11): 2166-2173.

[10] KATE, A. M.; DAHAT, D. V. AND CHAVAN, B. H. (2017). Genetic variability, heritability, correlation and path analysis studies in green gram [*Vigna radiata* (L.) Wilczek]. *Int. J. Dev. Res*., 7(11): 16704-16707.

[11] MAKEEN, K.; ABRAHIM, G.; JAN, A. AND SINGH A. K. (2007). Genetic variability and correlation studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *J. Agron.,* 6(1): 216-218.

[12] MOHAMMED, R. J.; PRASANTHI, L.; VEMIREDDY, L. R. AND LATHA, P. (2020). Studies on genetic variability and character association for yield and its attributes in greengram [*Vigna radiata* (L.) Wilczek]. *Electron. J. Plant Breed*., 11(02): 392-398.

[13] Muthuswamy, A.; Jamunarani M. and Ramakrishnan, P. (2019). Genetic variability, character association and path analysis studies in green gram [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.,* 8(4): 1136-1146.

[14] RUTURI, A.; SINGH, S. K.; SHARMA, V. AND PATHAK, R. (2015). Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Res*., 38(2): 157-163.

[15] Tabasum, A.; Saleem, M. and Aziz, I. (2010). Genetic variability, trait association and path analysis of yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *Pak. J. Bot.,* 42(6): 3915-3924.

[16] WESLY, K. C.; NAGARAJU, M. AND LAVANYA, G. R. (2020). Estimation of genetic variability and divergence in green gram *Vigna radiata* (L.) *germplasm. J. pharmacogn. phytochem.,* 9(2): 1890-1893.

[17] YADAV, R.; RAM, B. L.; SURESH, B. G. AND LAVANYA, G. R. (2017). Studies on genetic variability, character association for yield and yield components in greengram (*Vigna radiata* L. Wilczek). *J. Pharmaco. & Phytochem.,* 6(4): 1988-1991.