

Genetic Parameters and Variability Analysis in Mungbean [*Vigna radiata* (L.) Wilczek.]

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Abstract

Sixty diverse mungbean [*Vigna radiata* (L.) Wilczek.] genotypes were assessed for genetic variability, heritability, and genetic advance in a randomized block design with three replications, and data were collected on ten morphological characters. Analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating a wide range of variability among them. Higher values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for seed yield per plant, harvest index, tillers per plant, and biological yield per plant. Heritability estimates were highest for initial flowering, followed by yield per plant, number of pods per plant, pod length, plant height, and number of seeds per pod. Genetic advance (GA) estimates were the highest for initial flowering, moderate to low for 50% flowering, number of pods per plant, yield per plant, pod length, and number of seeds weight, number of primary branches per plant, and number of secondary branches per plant. High heritability, along with high genetic advance (as a percentage of the mean) was observed for initial flowering, number of pods per plant.

Key words: Mungbean, Vigna radiata, GCV, PCV, heritability, genetic advance

Introduction

Mungbean (Vigna radiata (L.) R. Wilczek) is a prominent pulse crop extensively cultivated in India, with a history dating back to prehistoric times, establishing its status as a native crop (Vavilov, 1926). Its popularity is attributed to superior digestibility and reduced flatulence issues, owing to lower levels of raffinose, stachyose, and verbascose (Poehlman 1991). Notably, the protein content of mungbean is rich in lysine, an essential amino acid deficient in cereal grains, while cereals are abundant in methionine, cystine, and cysteine, the sulfur-bearing amino acids. With its nutritional value highlighted, 100 grams of green gram seeds contain energy (234 cal.), protein (24.6%), fat (1.0%), fibre (2.2 g), carbohydrates (57.5%), calcium (0.08 g), phosphorus (0.045 g), iron (5.7 mg), vitamin B (300 mg), and thiamine (0.525 mg) (Srivastava and Ali, 2004). It is also recommended as a medicinal diet for individuals experiencing flatulence and for those who are ill. Additionally, it is rich in vitamin B and is considered a remedy for beriberi (Singh, 2001).

Green gram, a self-pollinated diploid grain legume (2n=2x=22) crop with a small genome size of 579 Mb/1C (Arumuganathan *et al.*, 1991), plays a crucial role in crop rotation due to its ability to fix atmospheric nitrogen, thereby improving soil fertility and benefiting subsequent crops. Genetic diversity is pivotal in plant breeding, facilitating the exploitation of heterosis or the generation of productive recombinants. The selection of parents holds paramount importance in breeding programs, necessitating knowledge of genetic diversity and relatedness in the germplasm for crop improvement initiatives. A reduction in genetic variability renders crops increasingly susceptible to diseases and adverse climatic changes.

Therefore, this study aims to assess the extent of variability, heritability, and genetic advancement by leveraging 60 germplasm lines. This investigation serves as a prerequisite for any crop improvement initiative, as understanding the available germplasm's genetic aspects within its specific environmental context is crucial for developing superior mungbean varieties.

Materials and Methods

The present study was conducted at the Agricultural Research Farm, Janta Mahavidyalaya, Ajitmal, Auraiya (U.P.) during the Kharif season of 2022-23 to evaluate sixty diverse mungbean genotypes for their genetic variability, heritability, and genetic advance. These genotypes, obtained from the Indian Institute of Pulse Research, Kanpur, were planted in a randomized block design with three replications. Data were collected on ten morphological characters, with each genotype sown in single-row plots of 2.5 meters in length. Plots were randomly assigned to genotypes within each replication, maintaining a row-to-row distance of 35cm and a plantto-plant distance of 10cm. Thinning was performed in the second week after sowing to ensure a plant-to-plant distance of 10 cm. From each plot, five competitive plants were randomly selected for recording observations on ten yield-related traits, including days to initial flowering, days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), 100-seed weight (g), and yield per plant (g). Statistical analyses, including analysis of variance (Fisher, 1936), coefficient of variation (Burton and Devane, 1953), and genetic advance (Johnson et al., 1955), were performed on the recorded data for these characters.

Results and Discussion

The statistical analysis was conducted using the mean values of quantitative traits derived from five randomly selected plants per genotype. These mean values for the ten traits were subjected to analysis of variance (ANOVA) to evaluate the significance of variation under the experimental design. Table 1 presents the mean sum of squares for the various morphological traits. The analysis of variance indicated significant differences among the germplasm lines for all characters, highlighting the variability within the studied traits. The genotypic coefficients of variation for all studied characters were lower than the phenotypic coefficient of variation, suggesting the influence of environmental factors. Among the traits, the highest phenotypic coefficient of variation was observed for pods per plant (41.04%), followed by yield per plant (33.66%), number of secondary branches

per plant (30.68%), plant height (24.77%), and number of primary branches per plant (24.69%). In contrast, 50% flowering exhibited a very low phenotypic coefficient of variation (12.10%). Pod length (24.21%), 100-seed weight (23.91%), number of seeds per pod (14.11%), and initial flowering (13.99%) showed moderate phenotypic coefficients of variation. The highest genotypic coefficient of variation was found for the number of pods per plant (30.78%), followed by yield per plant (27.16%) and initial flowering (13.68%). Pod length (13.24%), plant height (9.51%), 100-seed weight (6.53%), number of seeds per pod (5.11%), and number of primary branches per plant (5.04%) exhibited moderate to low genotypic coefficients of variation. In comparison, the number of secondary branches per plant (3.64%) and 50% flowering (1.61%) showed very low genotypic coefficients of variation. In certain traits, such as initial flowering, days to 50% flowering, and plant height (cm), the estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were very close, indicating minimal environmental influence. These characteristics may be considered stable, and selection based on their phenotypic values is expected to be effective. However, for traits such as seed yield per plant, number of primary branches per plant, pod length, and 100-seed weight, significant differences between PCV and GCV were observed, suggesting a relatively high environmental influence. Similar findings were reported by Garg et al. (2017). Burton (1952) suggested that considering GCV along with heritability provides the best indication of the potential advance expected from selection.

High broad-sense heritability estimates were observed for initial flowering (0.96%), seed yield per plant (0.65%), number of pods per plant (0.56%), pod length (0.30%), and plant height (0.15%), indicating that selection would be effective in improving these traits. Moderate to low heritability was noted for the number of seeds per pod (0.13%), number of primary branches per plant (0.04%), days to 50% flowering (0.02%), and number of secondary branches per plant (0.01%), suggesting that improvement in these traits could be achieved through selection to some extent. Similar findings have been reported by Katiyar *et al.* (2015), Jagdhane *et al.* (2017), Garg *et al.* (2017), and Asari *et al.* (2019).



The highest genetic advance was observed for initial flowering (7.96), followed by 50% flowering (6.02), number of pods per plant (5.14), and yield per plant (2.31). Genetic advance was moderate for pod length (0.80) and number of seeds per pod (0.47), and 50% flowering (0.20); and low for 100-seed weight (0.15), number of primary branches per plant (0.8), and number of secondary branches per plant (0.02). The genetic advance expressed

as a percentage of the mean was the maximum number of pods per plant (47.57%), yield per plant (45.14%) and initial flowering (27.57%). The values were moderate (14.91%) pod length for plant height (7.52%), number of seeds per pod (3.80%) and 100-seed weight (3.68%). It was low for the number of primary branches per plant (2.12%), the number of secondary branches per plant (0.89%) and 50% flowering (0.44%).

Source of vari- ation	d. f.	Initial flowering	Days to 50% flowering	Plant height (cm)	No. of primary branches /plant	No. of secondary branches /plant	No. of pods /plant	Pod length (cm)	No. of seeds/ pod	100- Seed weight (g)	Yield/ plant (g)
Replications	2	1144.64	49.47	76.13	0.93	15.67	8.86	6.04	1.19	2.98	1.93
Treatments	59	67.15**	1.05**	1.52**	1.13**	1.04**	4.86**	2.28*	1.45**	1.24*	6.60**
Error	118	0.71	31.05	334.86	0.85	0.27	8.60	1.18	2.68	0.87	1.03

Table 1: A	Analysis of va	riance (ANO	VA) for ten	characters of	f Mungbean.
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 Table 2: Mean range, coefficient of variability, heritability (broad sense), genetic advance and genetic advance as per cent of the mean for 10 characters in Mungbean.

S N	Characters	Range		Mean	Coefficient of variation %		Heritability (h²) Broad	Genetic Advance	Genetic Advance	
5.1 (*	Characters	MIN.	MAX	_ witchin	GCV	PCV	sense %		as % of mean	
1	Initial flowering	19.47	35.97	28.88	13.68	13.99	0.96	7.96	27.57	
2	Days to 50% flowering	39.26	54.09	46.45	1.61	12.10	0.02	0.20	0.44	
3	Plant height (cm)	57.69	115.03	80.02	9.51	24.77	0.15	6.02	7.52	
4	No. of primary branches/plant	2.60	5.13	3.82	5.04	24.69	0.04	0.08	2.12	
5	No. of secondary branches/plant	1.00	2.50	1.72	3.64	30.68	0.01	0.02	0.89	
6	No. of pods/plant	5.51	24.41	10.80	30.78	41.03	0.56	5.14	47.57	
7	Pods length (cm)	3.23	7.71	5.35	13.24	24.21	0.30	0.80	14.91	
8	No. of seeds/pod	9.46	14.93	12.44	5.11	14.11	0.13	0.47	3.80	
9	100-seed weight (g)	2.75	5.41	4.05	6.53	23.91	0.08	0.15	3.68	
10	Seed yield/plant (g)	2.40	8.56	5.11	27.16	33.61	0.65	2.31	45.14	

Heritability, when considered alongside genetic advance, provides an accurate estimation of gains in a selection program. In this study, the highest heritability coupled with a high genetic advance as a percentage of the mean was observed for initial flowering (27.57%), followed by seed yield per plant, number of pods per plant, and pod length. Similarly, Mehandi *et al.* (2018), Sandhiya *et al.* (2018), and Susmita *et al.* (2018) reported high heritability coupled with higher genetic advance for secondary branches per plant, indicating the presence of additive gene effects and suggesting that selection for these traits would be more effective for improvement. Conversely, high heritability together with low genetic advance was noticed for the number of seeds per pod, number of primary branches per plant, days to 50% flowering, and number of secondary branches per plant. Similar results were observed by Jagdhane *et al.* (2017), indicating the role of non-additive genes in the inheritance of these characters. The high heritability in the latter case might be attributed to favourable environmental conditions. It is concluded that improvement in these characters is possible only when a hybridization program is initiated and the inheritance of these characters is well established.

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