The Pharma Innovation Journal 2022; 11(9): 2883-2886

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(9): 2883-2886

www.thepharmajournal.com
Received: 01-06-2022
Accepted: 10-08-2022

GS Dandale
Pulses Research Unit, Dr. PDKV, Akola, Maharashtra, India

SS Lande
Pulses Research Unit, Dr. PDKV, Akola, Maharashtra, India

Archana W Thorat
Pulses Research Unit, Dr. PDKV, Akola, Maharashtra, India

MN Ingole
Pulses Research Unit, Dr. PDKV, Akola, Maharashtra, India

Corresponding Author:
GS Dandale
Pulses Research Unit, Dr. PDKV, Akola, Maharashtra, India

Genetic variability studies in mungbean (*Vigna radiata* (L.) Wilckzek)

GS Dandale, SS Lande, Archana W Thorat and MN Ingole

Abstract
Forty Nine divergent genotypes of mungbean were evaluated to study genetic variability. Analysis of variance indicated significant differences among the genotypes for all the traits under study. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The high values of GCV and PCV observed for seed yield per plant.
All the characters studied exhibited high heritability except the number of pods per plant. High heritability coupled with high genetic advance expressed as percentage of mean was observed for pod length, (cm). Plant height (cm), seed yield per plant, (g), number of primary branches per plant, which may attribute to the preponderance of additive gene action and possessed high selective value.

Keywords: Mungbean, genetic variability, heritability, genetic advance

Introduction
Mungbean (*Vigna radiata* L. Wilczek) 2n=22 is one of the most widely adapted; drought-tolerant, versatile, green manuring and nutritious grain legumes or pulse crop. Mung bean (*Vigna radiata* var. *radiata)* is believed to have originated in Indian subcontinent (deCandolle, 1884; Vavilov, 1926; Zukovskij, 1962) [5, 17]. Since India has a wide range of genetic diversity of cultivated, as well as of weedy wild types of mung bean, it is considered as the region of its first domestication (Baudoin and Marechal, 1988) [2]. It is one of the most important pulse crops in many Asian countries including India, China and Pakistan as well as many tropical and sub-tropical parts of the world since it can be grown in a wide range of environment (Wilczek, 1950; Verdcourt, 1970; Roychowdhury, Datta, Gupta, & Tah, 2012) [20, 15].
The success of any plant breeding programme depends on the extent of heritable variability existing in breeding material. Therefore, it is necessary to assess the extent of variation, which can be assessed by estimating different genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance. The improvement in yield is the basic criteria for any crop which a plant breeder always has to keep in view while evolving the new plant variety.

Material and Methods
The experimental material under present study comprised of forty nine genotypes of mungbean which were at Pules Research Station, Dr. P. D. K. V., Akola during *kharif* 2020 following the randomized block design with two replications. Recommended package of practices was followed to raise the crop. Five plants per genotype in each replication were randomly selected for recording the observations on different characters *viz*., days to 50% flowering, days to maturity, plant height (cm)., number of primary branches per plant, pod length(cm)., number of pods per plant, number of seeds per pod, 100 seed weight (g)., seed yield per plant (g). Each genotype was grown in two rows plot of four meters length with 45 cm 10 cm. Data recorded on various traits were statistically analysed using software WINDOSTAT version 8.6.

Results and Discussion
Analysis of variance indicated significant differences among the genotypes for all the traits under study indicating the presence of substantial genetic variation among the genotypes selected for study. In the present study the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all the characters. It indicated that expression of character mainly governed by genotype itself along with meager effect of environment.

Similar results were obtained by Hemavathy *et al.,* (2015) [8], Bhanu *et al*., (2016) [3] Garg *et al.*,(2017) [6].

The high values of GCV and PCV were recorded for seed yield per plant similar trends of estimates for GCV and PCV in mungbean have been observed by Rohman *et al.,* (2003) [14], Pandey *et al.*,(2007) [11], Garg *et al.*,(2017) [6]. For the characters number of primary branches per plant and number of pods per plant, high PCV and moderate GCV estimated. These results are in agreement with the findings of Ramakrishanan *et al.,* (2018) [13] for number of primary branches per plant, Ghimire *et al.,* (2018) [7] for number of pods per plant. The moderate values of GCV and PCV were observed for the characters plant height, pod length, number of seeds per pods similar result were reported by Garg *et al.*,(2017) [6], Ramakrishanan *et al.*,(2018) [13] for pod length and number of seeds per pod. Chaudhari *et al.,* (2016) [4] for plant height and number of seeds per pod. The value low of GCV and moderate of PCV were recorded for days to 50% flowering and 100 seed weight. Similar result are very close to the finding of Ramakrishanan *et al.,* (2018) [13] for days to 50% flowering. Narasimhulu *et al.,* (2013) [10] for 100 seed weight. The characters days to maturity observed the low values of GCV and PCV. Similar finding were reported by Garg *et al.,* (2017) [6], Hemavathy *et al.,* (2015) [8], Chaudhari *et al.*,(2016) [4].

The high heritability (broad sense) was observed for pod length followed by days to 50% flowering, plant height, seed yield per plant, 100 seed weight, days to maturity, number of primary branches per plant, number of seeds per pod. Similar result was reported by Sinha *et al.,* (2018) [16], Mohammed *et al.*,(2020) [9], Payasi *et al.*,(2015) [12]. The character number of pods per plant observed the moderate magnitude of heritability similar result reported by Ghimire *et al.,* (2018) [7].

High estimate of genetic advance as per cent of mean was observed for seed yield per plant followed by plant height, number of primary branches per plant, pod length, number of pods per plant. It indicated that maximum genetic gain can be received by using these characters are transmitted from parent to their offspring. Similar result have been reported in mungbean by Bhanu *et al.,* (2016) [3], Ramakrishanan *et al.,* (2018) [13] for plant height, pod length, number of pods per plant. Asari *et al.,* (2016) [1] for number of primary branches per plant. Moderate values of genetic advance expressed as per cent of mean for days to 50% flowering, 100 seed weight, number of seeds per pod, days to maturity. It indicated that partial genetic gain by selection. Similar result by Payasi *et al.,* (2015) [12] for days to 50% flowering, 100 seed weight, days to maturity and Rohman *et al.*,(2003) [14] for days to 50% flowering, day to maturity, number of seeds per pod. Asari *et al.*,(2019) [1] and Suresh *et al.*,(2010) for number of seeds per pod.

High estimate of heritability coupled with high genetic advance as percent of mean was observed for pod length, plant height, seed yield per plant, number of primary branches per plant. It indicated that additive gene action was predominantly operated in transmission of these characters. Similar kind of result were also reported by Muthuswamy *et al.,* (2019), Bhanu *et al.*,(2016) [3] for pod length, plant height, seed yield per plant. Sinha *et al.,* (2018) [16] and Asari *et al.,* (2019) [1] for number of primary per plant.

Higher estimate of heritability coupled with moderate genetic advance was observed for days to 50% flowering, days to maturity, number of seeds per pod, 100 seed weight. It is indicative of non additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than the genotypes. Similar kinds of result were also reported by Payasi *et al.,* (2015) [12] for days to 50% flowering, days to maturity, 100 seed weight. Rohman *et al.,* (2003) [14] and Asari *et al.,* (2019) [1] for days to 50% flowering, days to maturity, number of seeds per pod. Narasimhulu *et al.,* (2013) [10] for number of seeds per pod and 100 seed weight. Where as, moderate heritability coupled with high genetic advance expressed as percent of mean for number of pods per plant. Similar result in mungbean have been reported by Ramakrishanan *et al.,* (2018) [13] and very close to the finding of Ghimire *et al.,* (2018) [7].

Table 1: Analysis of variance for mean sum of squares for nine characters in forty nine mungbean genotypes

Sr. No.	Characters	Mean Sum of Squares		
		Replications	Genotypes	Error
	Degree of freedom	1	48	48
1	Days to 50% flowering	0.25	31.38**	0.90
2	Days to maturity	0.04	40.87**	5.16
3	Plant height (cm)	9.99	174.50**	10.62
4	Number of primary branches per plant	0.05	0.74**	0.10
5	Pod Length(cm)	0.13	1.73**	0.03
6	Number of pods per plant	0.04	15.11**	3.88
7	Number of seeds per pod	0.40	3.18**	0.68
8	100 seed weight (g)	0.0004	0.27**	0.02
9	Seed yield per plant (g)	0.08	7.17**	0.53

*Significance at 5% level, **Significance at 1% level

Table 2: Parameters of genetic variability for seed yield and yield contributing characters in mungbean genotypes

Sr. No.	Characters	Range		Mean	GCV (%)	PCV (%)	Heritability (bs) (%)	Genetic Advance (GA)	Genetic Advance as per cent of mean
		Min.	Max.						
1	Days to 50% flowering	33.00	51.00	39.17	9.97	10.26	94.4	7.82	19.95
2	Days to maturity	58.00	78.50	67.24	6.28	7.14	77.6	7.67	11.40
3	Plant height (cm)	21.50	76.30	50.66	17.88	18.99	88.5	17.55	34.63
4	Number of primary branches per plant	2.20	5.10	3.08	18.39	21.19	75.4	1.01	32.89
5	Pod Length (cm)	3.80	9.90	7.17	12.84	13.11	95.9	1.86	25.89
6	Number of pods per plant	11.80	24.60	15.29	15.49	20.15	59.1	3.75	24.53
7	Number of seeds per pod	6.50	13.20	10.45	10.70	13.31	64.6	1.85	17.71
8	100 seed weight (g)	3.00	4.55	5.85	9.57	10.39	84.9	0.68	18.18
9	Seed yield per plant (g)	2.80	11.50	3.72	31.15	33.56	86.1	3.84	59.54

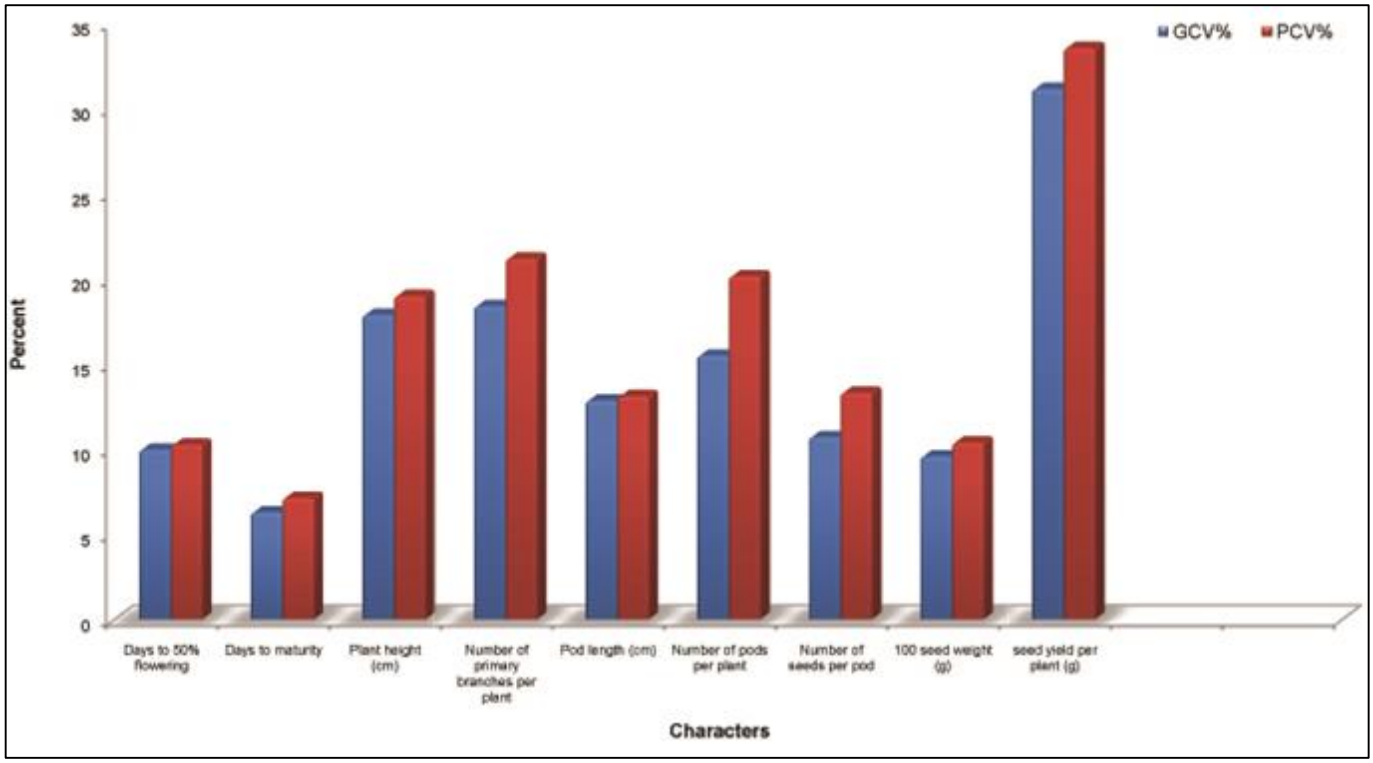

Fig 1: GCV and PCV estimates for various characters in Mungbeen

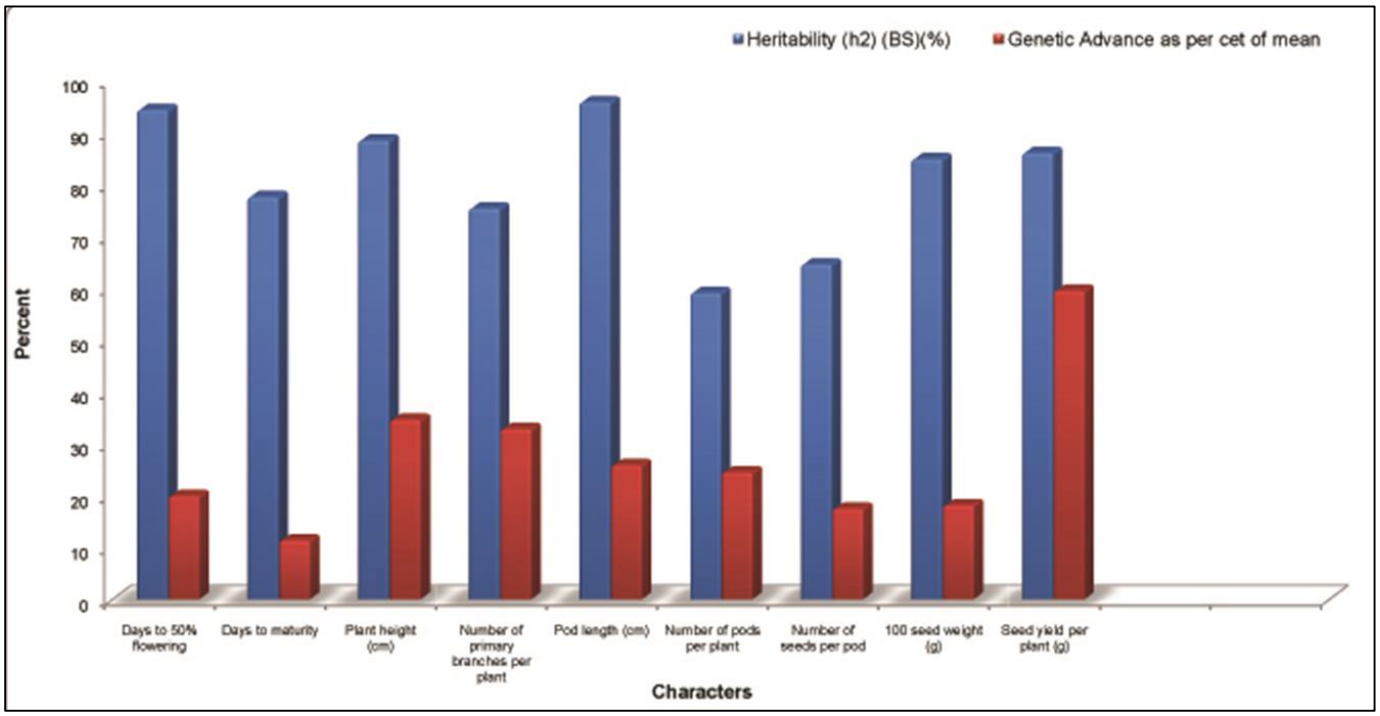

Fig 1: Heritability and genetic advance estimates for various characters in Mungbeen

References

1. Asari T, Patel BN, Patel R, Patil GB, Solanki C. Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mungbean. International Journal of Chemical Studies. 2019;7(4):383-387.
2. Baudoin JP, Marechal R. Taxonomy and evolution of the genus Vigna: Mungbean. In: Proceedings of second international symposium. AVRDC, Bangkok, Shanhua, Taiwan; c1988.
3. Bhanu AN, Singh MN, Singh M. Genetic variability, correlation and path coefficient analysis for quantitative traits in mungbean genotypes. Journal of Food Legumes. 2016;29(3&4):199-205.
4. Chaudhari P, Payasi SK, Urmaliya Karishma. Genetic association and path analysis for yield contributing traits in mungbean (*Vigna radiata* L. Wilczek). International Journal of Agriculture Sciences, c2016, p. 2465-2468.
5. De Candolle A. Origine des plantes cultives. Nabu Press, USA, c1884, p. 424.

6. Garg GK, Verma PK, Kesh H. Genetic variability, correlation and path analysis in mungbean. International Journal of Current Microbiology and Applied Sciences. 2017;6(11):2166-2173.
7. Ghimire S, Khanal A, Kohar GR, Acharya B, Basnet A, Kandel P. Variability and path coefficient analysis for yield attributing traits of mungbean. Azarian Journal of Agriculture. 2018;5:7-11.
8. Hemavathy AT, Shunmugavalli N, Anand G. Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilezek]. Legume Research. 2015;38(4):442-446.
9. Mohammed R, Prasanthi J, Lakshminarayana L, Vemireddy R, Latha P. Studies on genetic variability and character association for yield and its attributes in greengram [*Vigna radiata* (L.) Wilczek]. Electronic Journal of Plant Breeding; c2019.
10. Narasimhulu R, Naidu NV, Shanthi Priya M, Rajarajeswari V, Reddy KHP. Genetic variability and association studies for yield attributes in mungbean (*Vigna radiata* L. Wilczek). Indian Journal of Plant Sciences, 2013, 2319-3824.
11. Pandey MK, Srivastava N, Kole CR. Selection strategy for augmentation of seed yield in mungbean (*Vigna radiate* (L.)Wilczek). Legume Research. 2007;30(4):243-249.
12. Payasi DK. Genetic Variability Analysis for Seed Yield and its Components in mungbean (*Vigna radiata* L. Wilczek). International Journal of Plant Breeding and Genetics. 2015;9(3):177-188.
13. Ramakrishan CK, Savithramma DL, Vijayabharathi V. Studies on genetic variability, correlation and path analysis for yield and yield related traits in greengram. International Journal of Current Microbiology and Applied Sciences. 2018;7(3):2753-2761.
14. Rohman Md, Iqbal Hussain ASM, Md. Saykhul Arifin, Zerin Akhter, Mirza Hasanuzzaman. Genetic variability, correlation and path analysis in mungbean. Asian Journal of plant sciences. 2003;2:1209-1211.
15. Roychowdhury R, Datta S, Gupta P, Tah J. Analysis of Genetic Parameters on Mutant Populations of Mungbean (*Vigna radiata* L.) after Ethyl Methane Sulphonate Treatment Notulae Scientia Biologicae. 2012;4(1):137-143.
16. Sinha S, Mishra SB, Kishore C, Pandey SS. Genetic variability, correlation and path analysis in Intra- and inter-specific hybrids of *Vigna*. Journal of Pharmacognosy and Phytochemistry, 2018, 180-184.
17. Vavilov NI. Studies on the origin of cultivated plants. Leningrad; c1926a.
18. Verdcourt B. Studies in the Leguminosae-Papilionoideae for the Flora of Tropical East. Africa: IV. Kew Bulletin. 1970;24:507-569. http://dx.doi.org/10.2307/4102859.
19. Wilczek R Vigna. In: Fiore du Congo Beige. 1954;6:343-393.
20. Verdcourt B. Studies in the Leguminosae-Papilionoideae for the Flora of Tropical East. Africa: IV. Kew Bulletin. 1970;24:507-569. http://dx.doi.org/10.2307/4102859.