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Genetic variability, heritability and genetic advance in diverse panel of mungbean [*Vigna radiata* (L.) Wilczek] genotypes for seed yield and other agronomic traits

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Abstract

An experiment was conducted with 106 diverse mungbean genotypes during *Kharif* 2021 to assess the variation spectrum for yield traits and to realize the associations among them at the Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana. The result of genetic parameters revealed that trait namely, the number of branches /plant showed high genotypic (GCV) and phenotypic coefficients of variations (PCV). High heritability coupled with high genetic advance was found for the traits *viz*., plant height, number of branches/plant and clusters/plant, number of seeds/pod, biological yield, harvest index, 100-seed weight, and seed yield /plant indicated additive gene effects. Character association revealed significant positive association of seed yield with the number of clusters, pods/plant, harvest index, number of seeds/pod, biological yield/plant and 100-seed weight. Based on yield and other morphological traits studied, the genotypes ML 1628, ML 2037, SML 1023, MH 521, MH 560, MH 565, IPM 312-394, IPM 410-3 and EC 581523 were found superior and exhibited sufficient diversity and can be utilized for future mungbean improvement programs.

Keywords: Correlation, genetic variability, mungbean

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek.; 2n=22) is a native crop of the Indo-Burma region of the Hindustan centre (Vavilov, 1935) [25]. Area wise mungbean is second most important legume crop after chickpea (*Cicer arietinum*) in Indian agriculture (Anonymous, 2022) [3]. In North India, it is grown in spring, summer and *Kharif* seasons while in South India mungbean is grown in the *Kharif* and *Rabi* seasons, only. Being a short duration crop it can be grown as a sole crop or as an intercrop with cotton, pigeon pea, maize, sorghum and many minor millets for maintaining soil fertility and enhanced crop production (Maitra *et al*., 2021) [17]. India is the largest producer and consumer of mungbean, accounting for about 65% of the world's acreage and about 54% of the world's production (Anonymous, 2019) [4]. In the annual year of 2020-21, India produced about 3.09 million tonnes of mungbean from about 5.13 million hectares with average productivity of ~601 kg/ha (Anonymous, 2022) [3]. It is a cheap source of easily digestible high-quality protein (22-28%), total amino acids (21-25%), lipids (1.53-2.63%), fat (1.0-1.5%), fibre (3.5-4.5%), ash (4-5%) and carbohydrates (59-65%) on a dry weight basis and provides 334-344 k/cal energy (Rohilla *et al*., 2022) [20]. Moreover, mungbean seeds are free from anti-nutritional factors such as trypsin inhibitor, phytohaemagglutinin and tannin (Chen *et al*., 2003) [9]. Most of the natural variation for yield traits has unintentionally been lost in mungbean mainly due to the fact that mungbean was a crop grown on unproductive and marginal areas. As a result, only the features that increase the likelihood of survival have accumulated over the process of domestication. Such a reduced level of preexisting variation has hampered mungbean improvement breeding programs based on hybridization. Hence, under such circumstances mungbean research for genetic diversity and variability along with the identification of resistant sources became prominently important for all kind of breeding procedures. The knowledge of genetic advance along with heritability is useful in selective breeding programs and the correlation coefficient is very important to conceive the association between the yield and its contributing traits for the better selection of quantitative traits in mungbean.

Materials and Methods

The experimental material comprised of one hundred and six mungbean genotypes evaluated in Randomized Block Design with two replications at Pulses Research Farm, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Kharif* 2021. Each genotype was grown in a row of 4-meter length with row to row spacing of 30 cm and plant to plant spacing of 10 cm. All the recommended agronomic measures were adopted to raise a healthy crop. Observations on different quantitative characters *viz*. days to 50% flowering, days to maturity, plant height, number of branches/plant, number of pods/plant, number of clusters/plant, number of seeds/pod, biological yield/plant, harvest index, 100-seed weight, seed yield/plant were recorded on five randomly selected competitive plants except for days to 50% flowering and days to maturity where data were recorded on plot basis.

Analysis of variance was carried out as suggested by Fisher (1930) [10]. Variability parameters (Range, PCV, GCV, h^2, GA) were computed according to Hanson *et al. (*1956). Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.* (1955) [14]. For calculation of correlation coefficient, variance and covariance components were used at genotypic and phenotypic levels. Phenotypic and genotypic correlations between all the selected traits were estimated using the method described by Al-Jibouri *et al.* (1958) [2]. Statistical analyses were done using R studio.

Results and Discussion

The highly significant differences among genotypes for all these traits revealed presence of high magnitude of variability among the genotypes studied for all the traits. The results are presented in Table 1. Results regarding all the variability parameters *viz*., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percent of mean (GAM) for all the eleven quantitative traits have been furnished in Table 2 indicated that there is almost perfect relation between PCV and GCV of each character. High genotypic (GCV) and phenotypic coefficient of variance (PCV) were observed for the number of branches/plant (21.39 and 20.05%) and number of clusters/plant (19.92 and 17.79%) suggesting that these characters were under the influence of genetic control. So, the characters can be relied upon and simple selection can be practiced for further improvement. While moderate for all the remaining yield attributing traits except days to 50% flowering and days to maturity where these were low. Heritability refers to how much genetic variation contributes to phenotypic variability. Estimates of broad sense heritability was recorded almost high for all the traits & it ranged from 71.00 percent (Harvest Index) to 95.10 percent (100 seed weight) indicating less effect of environment on these traits. However, selection for the traits showing high heritability is not significant because broad sense heritability is calculated from total genetic variance which include additive, dominant and epistatic variances. A high value of genetic advance show that the trait is regulated by additive gene action. Thus, the effective selection came from the combination of traits having high heritability coupled with high genetic advance. Characters *viz*., plant height, number of branches/plant, number of clusters/plant, number of seeds/pod, biological yield/plant, harvest index, 100-seed weight and seed yield/plant shows high heritability coupled with high genetic advance indicating that selection is quite effective and fruitful for these traits. Lokesh and Lavanya (2019) [16] and Muthuswamy *et al*. (2019) [18] also reported high heritability with high genetic advance for the trait number of branches/plant.

Table 1: Analysis of variance for various quantitative traits of mungbean genotypes (*Vigna radiata* L.)

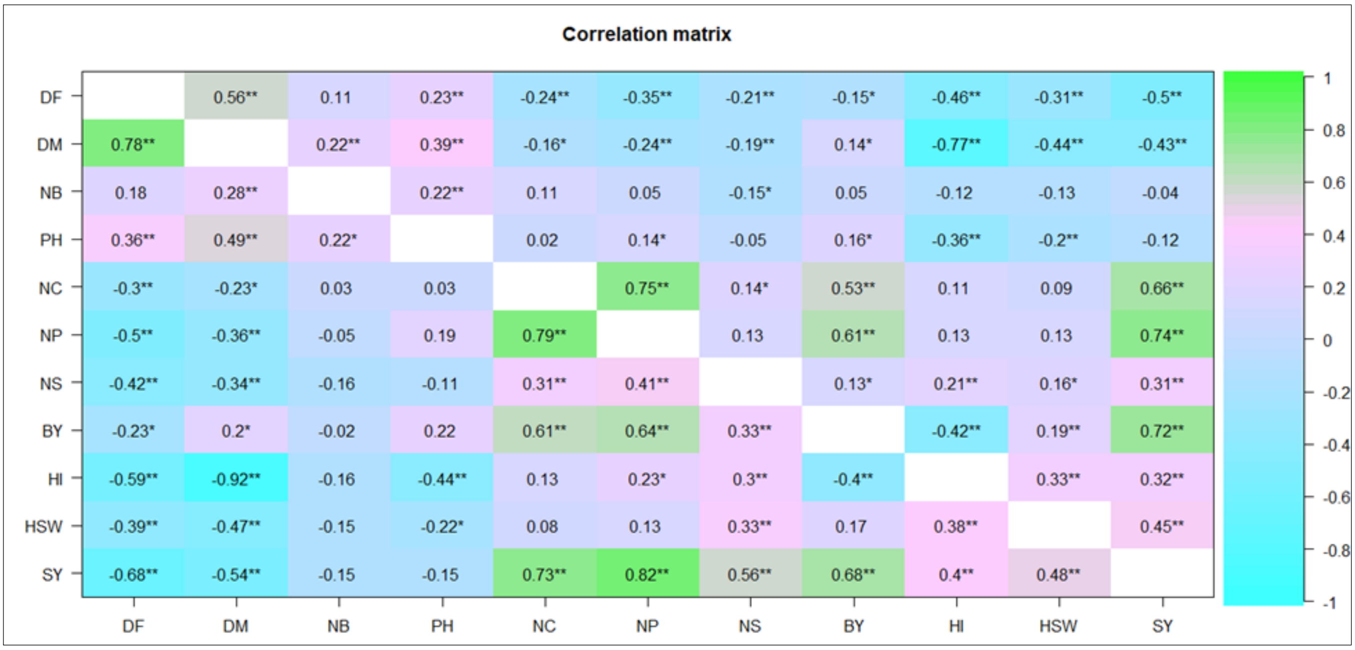
	Mean Sum of Squares		
Characters	**Replication (df= 1)**	**Genotype (df= 105)**	**Error (df= 105)**
Days to 50% flowering	5.15	18.22**	3.79
Days to maturity	0.11	30.36**	2.18
Number of branches per plant	4.59	1.10*	0.13
Plant height (cm)	296.70	191.84**	20.9
Number of clusters per plant	27.82	8.65 **	1.74
Number of pods per plant	60.55	14.20**	4.24
Number of seeds per pod	0.032	5.11*	0.32
Biological yield per plant (g)	120.70	119.29**	33.97
Harvest Index (%)	5.69	14.47**	4.19
100 Seed weight (g)	0.23	0.49**	0.02
Seed yield per plant (g)	1.13	4.97**	0.87

**Significant (p=0.01), *Significant (p=0.05)

Table 2: Estimates for genetic parameters for different traits in mungbean genotypes (*Vignaradiata* L.)

Sr. No.	**Trait**	**PCV (%)**	**GCV (%)**	**Heritability (h^2 bs) (%)**	**Genetic advance as percent of mean (%)**
1	Days to 50% flowering	7.58	6.75	79.18	12.37
2	Days to maturity	5.58	5.38	92.80	10.67
3	Number of branches per plant	21.39	20.05	87.90	38.72
4	Plant height (cm)	15.25	14.40	89.09	27.99
5	Number of clusters per plant	19.92	17.79	79.80	32.74
6	Number of pods per plant	11.76	9.84	70.05	16.96
7	Number of seeds per pod	16.03	15.53	93.73	30.95
8	Seed yield per plant (g)	16.89	15.33	82.34	28.65
9	Biological yield per plant (g)	15.49	13.10	71.52	22.82
10	Harvest Index (%)	14.22	11.98	71.00	20.97
11	100 Seed weight (g)	14.46	14.10	95.10	28.32

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation



Correlation matrix

	DF	DM	NB	PH	NC	NP	NS	BY	HI	HSW	SY
DF		0.56**	0.11	0.23**	-0.24**	-0.35**	-0.21**	-0.15*	-0.46**	-0.31**	-0.5**
DM	0.78**		0.22**	0.39**	-0.16*	-0.24**	-0.19**	0.14*	-0.77**	-0.44**	-0.43**
NB	0.18	0.28**		0.22**	0.11	0.05	-0.15*	0.05	-0.12	-0.13	-0.04
PH	0.36**	0.49**	0.22*		0.02	0.14*	-0.05	0.16*	-0.36**	-0.2**	-0.12
NC	-0.3**	-0.23*	0.03	0.03		0.75**	0.14*	0.53**	0.11	0.09	0.66**
NP	-0.5**	-0.36**	-0.05	0.19	0.79**		0.13	0.61**	0.13	0.13	0.74**
NS	-0.42**	-0.34**	-0.16	-0.11	0.31**	0.41**		0.13*	0.21**	0.16*	0.31**
BY	-0.23*	0.2*	-0.02	0.22	0.61**	0.64**	0.33**		-0.42**	0.19**	0.72**
HI	-0.59**	-0.92**	-0.16	-0.44**	0.13	0.23*	0.3**	-0.4**		0.33**	0.32**
HSW	-0.39**	-0.47**	-0.15	-0.22*	0.08	0.13	0.33**	0.17	0.38**		0.45**
SY	-0.68**	-0.54**	-0.15	-0.15	0.73**	0.82**	0.56**	0.68**	0.4**	0.48**	

Fig 1: Correlogram: Estimation for phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients for different traits in mungbean (*Vigna radiata*) genotypes

DF: Days to 50% flowering, DM: Days to maturity, NB: Number of branches/plant, PH: Plant height (cm), NC: Number of clusters/plant, NP: Number of pods/plant, NS: Number of seeds/pod, BY: Biological yield/plant (g), HI: Harvest index (%), HSW: 100 seed weight (g), SY: Seed yield/plant (g)

Direct selection for seed yield is a tough task due to its complexity, dependence on multiple traits, and strong influence of environment. Many plant traits that are highly heritable and significantly associated with seed yield provide an opportunity for indirect and effective yield selection. To choose high yielding genotypes in a breeding program, it is critical to analyze the phenotypic and genotypic correlation for yield-related traits.

Character association studies (Fig.1 & Table 3) revealed that at both the genotypic and phenotypic levels, number of clusters/plant (0.73G, 0.66P), number of pods/plant (0.82G, 0.74P), 100 seed weight (0.48G, 0.45P), harvest index (0.40G, 0.32P), biological yield/plant (0.68G, 0.72P) and number of seeds/pod (0.56G, 0.31P) were found to be significant and positively linked with seed yield/plant. 100-seed weight was positively correlated with number of seeds per pod (0.155), biological yield/plant (0.193), harvest index (0.326) and seed yield/plant (0.446). (G and P represents genotypic and phenotypic correlations, respectively). Findings of our research were in agreement with the results obtained by Baisakh *et al*. (2016) [7], Garg *et al*. (2017) [11], Sunayana *et al*. (2017) [24], Azam *et al*. (2018) [6], Kumar *et al*. (2018) [15], Asari *et al*. (2019) [5], Muthuswamy *et al*. (2019) [18], Ahmad and Belwal (2020) [1] and Singh *et al*. (2021) [23].

For the enhancement of the yielding capacity of mungbean, component analysis of seed yield per plant and harvest index revealed that superior ideotypes can be developed by choosing the traits *viz*., number of clusters/plant, number of pods/plant and number of seeds/pod.

Table 3: Type of correlations among different traits of mungbean genotypes (*Vigna radiata* L.)

Sr No.	Traits	Positive correlation	Negative correlation
1	DF	Days to maturity, plant height	Number of clusters per plant, number of pods per plant, number of seeds per pod, seed yield per plant, harvest index, 100 seed weight
2	DM	Number of branches per plant, plant height, biological yield per plant	Number of clusters per plant, number of pods per plant, seed yield per plant, number of seeds per pod, harvest index, 100 seed weight
3	NB	Days to maturity, plant height, days to 50% flowering	Number of seeds per pod
4	PH	No. of pods per plant, biological yield per plant	Harvest index, 100 seed weight
5	NC	Number of pods per plant, seed yield per plant, biological yield per plant, number of seeds per pod	
6	NP	Seed yield per plant, harvest index, 100-seed weight (g)	
7	NS	Seed yield per plant, biological yield per plant, harvest index	Plant height, number of clusters per plant, MYMV
8	BY	100-seed weight (g), seed yield per plant	Harvest index
9	HI	Number of seeds per pod, seed yield per plant, 100-seed weight (g)	Days to 50% flowering, days to maturity, Plant height
10	HSW	Seed yield per plant, biological yield per plant, harvest index	Days to 50% flowering, days to maturity, number of branches per plant, Plant height
12	SY	Number of clusters per plant, number of pods per plant, seed yield per plant, number of seeds per pod, biological yields per plant, 100 seed weight	Days to 50% flowering, days to maturity

Conclusion

Based on the above discussions, it is reasonable to conclude that biological yield/plant, harvest index, number of clusters/plant, number of pods/plant and 100-seed weight should be considered as important traits when selecting for high seed yield producing genotypes. As a result, these characteristics may be regarded significant for developing selection criteria for improving seed yield in mungbean. The present study's findings on genetic advance, heritability, and variability showed potential for increasing mungbean yield through selection using variables like the genetic coefficient of variation, heritability, and GA. These results have significance when creating an effective breeding programme because breeders may employ additive gene effects, transgressive segregation, and heterosis to increase yield when there is enough genetic variability.

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