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Assessment of genetic variability and trait association in mungbean (*Vigna radiata* L.) genotypes during summer season

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ABSTRACT

Twenty four genotypes of mungbean (*Vigna radiata* L.) were studied to assess the parameters of genotypic variability, correlation and path coefficients among the yield and its contributing traits. Analysis of variance revealed significant differences between the genotypes for seed yield and its attributing traits except for the number of seeds per pod. Traits like harvest index, days to maturity, 100-seed weight, biological yield per plot, days to flowering and seed yield per plot exhibited high heritability estimates. High heritability coupled with high genetic advance was observed for biological yield per plot, harvest index, 100-seed weight and seed yield per plot, indicating the preponderance of additive gene action. Biological yield per plot, the number of pods per plant, the number of seeds per pod and the number of branches per plant exhibited highly significant positive correlation with seed yield. Biological yield per plot and harvest index had high positive direct effects on seed yield per plot.

***Key words:** Correlation, Genetic advance, Heritability, Path analysis, Variation*

INTRODUCTION

The simplest way to achieve the world's mounting nutritious food requirement lies in diversifying agriculture with crops having better yields and nutritional quality. Mungbean [*Vigna radiata* (L.) Wilczek], popularly known as green gram, moong or mungi, green bean, golden gram, is one of the most desirable options for defeating protein malnutrition as it has got numerous nutritional advantages and fits well in different cropping systems due to its short duration nature (Anuragi *et al*. 2022). It is a wide-spreading herbaceous, annual, self-pollinated crop with 2n=2x=22, (Karpechenko, 1925). It is grown as sole as well as inter and multiple crop in different crop seasons (Sunayana *et al*. 2017). In North India, it is cultivated during spring/summer and rainy season; however, in South India, it is also grown in the *Rabi* season after rice on the residual soil moisture. Mungbean is utilized in various ways, where seeds and young pods are consumed as sources of protein, vitamins, and minerals, while plant parts are used as fodder. It is a good source of low flatulence easily digestible protein, vitamins, and minerals with amino acid profiles complementary to cereals (Khattak *et al*., 2001). Besides high-quality protein, mungbean seeds contain carbohydrates, folate and iron (Keatinge *et al*., 2011) and have no anti-nutritional factors such as trypsin inhibitors, phytohemagglutinin, and tannin (Chen *et al*. 2003).

Disease resistant short-duration mungbean varieties with varying maturity groups have opened new niches for various cropping systems and bringing an additional area under its cultivation. However, the realized average productivity of mungbean is well below the economic level. The major reasons for stagnancy in its productivity are limited genetic variability, negative impact of high genotype x environment interaction, and susceptibility of the existing cultivars to various biotic and abiotic stresses, ultimately leading to yield instability (Pratap *et al*. 2019). Genetic variability is prerequisite for selection, while correlation and path coefficient analysis is essential to find out the desired traits which could be included in the selection criteria. For the improvement of plant genotype with a desirable combination of traits, complete information regarding the association of these traits with yield as well as detailed information on the genetic mechanism controlling various traits is important (Rohilla *et al*. 2022). Therefore, the present study was undertaken to assess the genetic parameters and trait associations in advanced mungbean genotypes for use in crop improvement programmes.

MATERIAL AND METHODS

The plant materials comprising of 24 advanced mungbean genotypes were sown during summer season during 2020 and 2021 at three locations *i.e.* Chaudhary Charan Singh Haryana Agriculture University (CCS HAU), Hisar; CCS HAU, Cotton Research Station, Sirsa and CCS HAU Regional Research Station, Uchani, Karnal in Randomized Block Design with three replications. The plot size was kept 4m × 0.3m × 8 rows (9.6 m^2) with plant to plant spacing 8-10 cm. The recommended agronomic and plant protection practices were followed to maintain healthy plants stands. The phenotypic observations recorded were days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of seeds per pod, number of pods per plant, 100 seed weight (g), biological yield per plot (g), harvest index (%) and seed yield per plot (g). The observations on metric traits were recorded on five randomly selected plants in each genotype in all replications and averaged whereas, for days to 50% flowering, days to maturity, biological yield and seed yield, data were recorded on plot basis.

Genetic parameters i.e. variance, genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated according to the methods suggested by Burton and Devane (1953), whereas estimation of heritability and expected genetic advance were computed using the formula suggested by Hanson *et al*. (1956) and Johnson *et al*. (1955), respectively. Genotypic and phenotypic of correlations were calculated as per method of Al-Jibouri *et al*. (1958). Path analysis was carried out as per method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance and mean performance

Analysis of variance revealed significant differences among the genotypes of mungbean for seed yield per plot and its contributing traits under study except for the number of seeds per pod, indicating the prevalence of sufficient genetic variation among the mungbean genotypes for these traits (Table 1).

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

Phenotypic and Genotypic Coefficients of Variation

The morphological variation observed in the field is the phenotypic effect of both genetic and environmental variation. The phenotypic variation is partitioned into heritable and non-heritable components with the help of specific genetic parameters such as heritability and genetic advance, Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV). In the present study high PCV (>20 %) was recorded for

Table 1. Analysis of variance for different traits in mungbean over six environments during summer

Source of variation	df	MSS									
		DF	DM	PH	NB	NS	NP	SW	BY	HI	SY
Replication	2	27.18**	1.29	21.91	0.06	0.55	3.62	0.02	199588	1.81	6019
Genotypes	23	42.49**	104.92**	142.26*	0.64**	1.18	33.01**	1.37**	1148189**	77.27**	31739**
Error	838	4.61	7.87	79.30	0.21	1.35	7.88	0.13	111238	3.99	4662

Table 2. Estimates of phenotypic and genotypic coefficients of variation, heritability and genetic advance for different traits in mungbean over six environments during summer

	DF	DM	PH	NB	NS	NP	SW	BY	HI	SY
MEAN	38.16	62.76	48.31	3.06	9.51	24.02	4.06	2391.26	24.24	572.73
GCV	9.31	9.06	9.48	12.37	2.45	12.05	15.85	24.59	20.39	16.59
PCV	10.88	10.10	20.73	19.46	11.95	16.78	18.12	28.27	21.99	20.43
h^2(%)	73.00	80.00	21.00	40.00	4.00	52.00	77.00	76.00	86.00	66.00
GAM	16.41	16.74	8.93	16.20	1.04	17.82	28.57	44.05	38.94	27.75

(GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h^2: Broad sense heritability (%), GAM: Genetic advance as per cent of mean) biological yield per plot, harvest index, plant height and seed yield per plot (Table 2) whereas, moderate PCV was observed for number of branches per plant, 100-seed weight, number of pods per plant, number of seeds per pod, days to flowering. High GCV recorded for biological yield per plot, harvest index and 100-seed weight while moderate PCV was observed for seed yield per plot, 100-seed weight, number of branches per plant and number of pods per plant. It was observed that magnitude of PCV was higher than that of GCV for all the traits under investigation indicating role of environment on expression of these traits. However, in traits like days to flowering, days to maturity, plant height and harvest index the differences were very narrow implying that the variation is primarily attributable to genetic reasons. These observations are relatable to the findings of Choudhary *et al*. (2016), Garg *et al.* (2017), Kumar *et al.* (2019), Manjhi *et al.* (2020) and Singh *et al*. (2021).

Heritability and genetic advance

The knowledge of heritability coupled with genetic advance aids in selecting the breeding program. High broad sense heritability was recorded for traits like harvest index, days to maturity, 100-seed weight, biological yield per plot, days to flowering and seed yield per plot. Moderate heritability was recorded for traits like the number of pods per plant and the number of branches per plant and low heritability was recorded for traits, plant height and the number of seeds per pod. The plant height and number of seeds per pod had low heritability indicating the effect of the environment on the expression of these traits. The high genetic advance was recorded for biological yield per plot, followed by harvest index, 100-seed weight and seed yield per plot. High heritability coupled with high genetic advance was observed for biological yield per plot, harvest index, 100-seed weight and seed yield per plot which indicated the predominance of additive gene action in the expression of these traits and these are likely to respond effectively to phenotypic selection. Whereas, days to flowering and maturity exhibited high heritability and low genetic advance revealing control of non additive gene action and high GXE interaction and therefore, intermating in early generations of the hybridization programme can be helpful. Low to moderate heritability and genetic advance estimates were observed for plant height, number of branches per plant, number of seeds per pod and number of pods per plant, which indicated that these characters are highly influenced by environment and can be improved by rigorous selections in large segregating populations, especially early generations. These results are in partial agreement with those reported by Muthuswamy *et al.* (2019), Kumar *et al.* (2019), Manjhi *et al.* (2020), and Singh *et al*. (2021).

Correlation coefficient analysis

The genetic architecture of seed yield in mungbean is the complex interaction of different yield attributes. Therefore, understanding these associations is a prerequisite before planning any selection and crop improvement program. Correlation coefficient analysis is a simple technique that provides the magnitude and direction of the association among different traits and forms the basis for the selection for seed yield and its contributing traits. The correlation analysis revealed, increased seed yield was significantly contributed by biological yield per plot, the number of pods per plant, the number of seeds per pod and the number of branches per plant (Fig. 1). This suggests that these traits should be kept in mind while selection is to be practiced for high seed yield. Similar significant correlation of seed yield with yield attributes in mungbean were also observed by Choudhary *et al*. (2016), Keerthiga *et al*. (2018), Asari *et al.* (2019) and Manjhi *et al*. (2020).

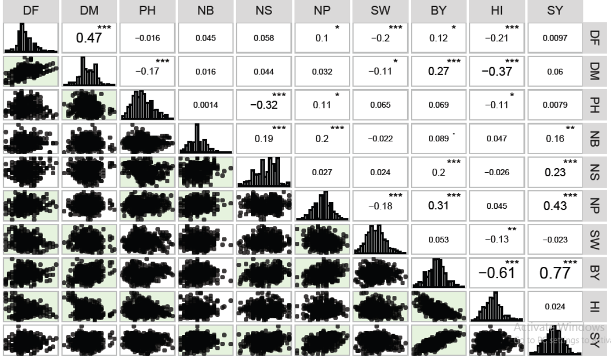

Figure 1. Phenotypic correlation coefficients among various traits of mungbean over six environments during summer

Days to flowering and maturity exhibited significant positive correlation with each other and biological yield per plot while negative with100-seed weight and harvest index. Biological yield per plot was showed a positive correlation with days to flowering, days to maturity, number of branches per plant, number of seeds per pod, number of pods per plant, seed yield per plot and showed a negative correlation with harvest index. Harvest index was found negatively correlated with days to flowering, days to maturity, plant height, 100-

Table 3. Direct (diagonal values) and indirect effects of contributing traits on seed yield per plot of mungbean genotypes across six environment

	DF	**DM**	**PH**	**NB**	**NS**	**SW**	**BY**	**HI**
DF	0.0192	0.0076	-0.0002	0.0003	0.0005	-0.0041	0.1521	-0.1667
DM	0.0090	0.0162	-0.0025	0.0001	0.0003	-0.0023	0.3294	-0.2904
PH	-0.0003	-0.0028	0.0148	0.0000	-0.0025	0.0013	0.0847	-0.0885
NB	0.0009	0.0003	0.0000	0.0073	0.0015	-0.0005	0.1091	0.0368
NS	0.0011	0.0007	-0.0047	0.0014	0.0077	0.0005	0.2479	-0.0206
NP	0.0020	0.0005	0.0016	0.0014	0.0002	-0.0038	0.3807	0.0357
SW	-0.0039	-0.0018	0.0010	-0.0002	0.0002	0.0204	0.0654	-0.1019
BY	0.0024	0.0043	0.0010	0.0007	0.0016	0.0011	1.2313	-0.4786
HI	-0.0041	-0.0060	-0.0017	0.0003	-0.0002	-0.0027	-0.7489	0.7868

seed weight and biological yield per plot.Number of branches per plant revealed positive correlation with the number of pods per plant, the number of seeds per pod, seed yield per plot and biological yield per plot. Number of pods per plant was found positively and significantly correlated with seed yield per plot, biological yield per plot, number of branches per plant, plant height, days to flowering and showed negative association with 100-seed weight. Choudhary *et al*. (2016) and Rohilla *et al.* (2022) reported the similar trend in their studies on yield attributes of mungbean.

Path coefficient analysis

Path coefficient analysis is another efficient statistical technique specially designed to quantify the interrelationship of different components via, their direct and indirect effects on grain yield per plant. Results (Table 3) revealed that biological yield per plot and harvest index had the highest direct positive effect on seed yield per plot which are in consonance with the findings of Choudhary *et al*. (2016). The traits, *viz*. 100-seed weight, days to flowering, days to maturity, plant height, and number of pods per plant also exhibited positive direct effects on seed yield per plot, however, their causal effects were minor. Similar results were also recorded for these traits by Choudhary *et al*. (2016), Keerthiga *et al*. (2018) and Parihar *et al.* (2018). Seed yield was contributed by biological yield per plot *via* number of pods per plant, days to maturity, number of seeds per pod and number of branches per plant. The contribution of harvest index in seed yield per plot was through the positive indirect effects of the number of branches per plant and the number of pods per plant. Similar results for these traits were in concurrence with Takele *et al.* (2022). Biological yield and harvest index were the most contributing traits to seed yield per plot as they have maximum direct as well as indirect effect *via* different yield attributes.

CONCLUSION

The present study revealed high magnitude of PCV and GCV for biological yield, harvest index and seed yield indicating presence of ample genetic variability for these traits. High heritability coupled with high genetic advance for harvest index, biological yield, 100-seed weight and seed yield indicated the predominance of additive gene action and scope of fruitful selection. Traits like biological yield, number of pods, number of seeds and number of branches were found to have high positive association with seed yield per plot. Biological yield and harvest index exhibited the highest direct positive effect on seed yield. Seed yield was contributed by biological yield *via* days to maturity, number of branches, number of seeds and number of pods. The information generated on genetic parameter and character associations would effectively be utilized to improve seed yield and its contributing traits in mungbean.

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