

Study of Selection Criteria and Genetic Variability in Mungbean (*Vigna radiata* L. Wilczek) Genotypes for Seed Yield and its Contributing Traits

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Received 11 September 2022, Accepted 24 October 2022, Published on 27 January 2023

ABSTRACT

In this study, forty mungbean genotypes were evaluated for fourteen quantitative agro-morphological traits, planted in RCBD design with three replication during summer season of 2021. Observations were recorded for seed yield and its related traits at specific crop growth stage to study genetic variability parameter and correlation coefficient. The results of ANOVA revealed that all the genotypes differ significantly for all the traits studied indicating significant amount of variability present among genotypes. The values of PCV for all the traits were found to be more than GCV and small difference was present in between GCV

and PCV revealing little influence of environment for their expression. High heritability accompanied with high genetic advance was recorded for traits viz., seed index, plant height, number of pods per plant, leaf length, seed yield per plant, biological yield per plant and number of clusters per plant indicating the preponderance of additive gene action for the expression of this characters and selection may be effective for improving this character. Based on the results of correlation and path coefficient analysis, it is concluded that the characters number of seeds per plant, harvest index, leaf length and number of pods per cluster showing high positive direct effect and significant association with seed yield per plant. Therefore, these traits could be important for the direct selection to improve seed yield.

Keywords Correlation, GCV, Genetic advance, Heritability, Path.

INTRODUCTION

After chickpea and pigeonpea, the mungbean (*Vigna radiata* (L.) Wilczek), which is native to India or the Indo-Burman region, is the third-most significant self-pollinated, short-duration grain legume crop. It is thought that the primary source of mungbean genetic diversity is in central Asia (Kumar and Kumar 2014). Mungbean has a relatively small (579 Mb) genome with 22 chromosomes in the 2n set (Parida *et al.* 1990, Kang *et al.* 2014). It is also referred to as greensoy,

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greengram, greenbean, mashbean and goldengram (Markam *et al.* 2018). Mungbean is a crucial and affordable source of food protein throughout Asia, especially for the underprivileged, and is crucial in reducing protein deficiency, especially in emerging nations (Selvi *et al.* 2006). It has excellent place for balanced diets since it has a relatively high proportion of easily digestible good quality protein (24%) with less flatulence and a high iron content (40-70 ppm) (Selvi *et al.* 2006, Vairam *et al.* 2016).

Central Asia is thought to be the main source of mungbean genetic diversity. The majority of the world's greengram comes from India, and it is grown in almost every states of India. According to 3rd advance estimates- 2021-2022, the overall production of pulses in India to be 27.75 million tonnes. In India, total 2.85mt mungbean productions including 1.48mt in *kharif* and 1.37mt in *rabi*, accounting for 10% of all pulse production (Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare 2022). The mungbean crop grows quickly in warm weather, requires little water, and nitrogen fixation provides good soil fertility enhancement (Yagoob and Yagoob 2014).

Genetic parameters such as genetic coefficient of variation (GCV), phenotypic coefficient of variance (PCV), heritability, genetic advance are biometric tools that are useful for measuring genetic variability. Data on coefficient of variety is helpful in estimating the scope of changeability present in the characters. Similarly, heritability is the measures of transmission of characters from generation to generation. The information about heritability along with genetic advance can provide a glaring picture for selection of desired traits. Correlation studies can be used to determine the relative importance of different variables.

MATERIALS AND METHODS

This study was carried out at Breeder Seed Production Unit, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (MP) during summer season of 2021. Regarding geography and fertility, the trial region was quite uniform. The experimental material consists of 40 genotypes of mungbean obtained from BARC Project- Mutation

breeding for mung and urd improvement, were planted in Randomized Complete Block Design with three replications. Each plot was consisted of four rows of two meter length with a spacing 30 cm row to row and 10 cm plant to plant. To record quantitative traits, middle five competitive plants from each plot were randomly selected and recorded the data at specific growth stage. Days to 50% flowering and days to maturity were recorded on whole plot basis.

Statistical analysis

Statistical analysis was done by using mean values. The methods recommended by Panse and Sukhatme (1985), Burton (1952), Burton and Devane (1953), and Johnson *et al.* (1955) were used to estimate analysis of variance, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability, and genetic advance respectively. Correlation coefficients were calculated as described by Miller *et al.* (1958) and direct and indirect contribution of various characters to yield were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Genetic variability parameters

As per analysis of variance, the mean sum of squares owing to genotypes was highly significant for all measures, indicating that there was substantial variation among genotypes for these traits. The magnitude of variation between genotypes was reflected by high values of mean and range for genotypic traits studied (Table 1).

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

The magnitude of GCV and PCV were recorded high (>20%) for traits such as number of primary branch, biological yield per plant, seed yield per plant, number of pods per plant and harvest index (Table 1). Therefore, these characters should be considered during selection of desired mungbean genotypes in crop improvement program. This finding was in con-

Table 1. Parameters of genetic variability for yield, yield attributing traits in mungbean genotypes.

Sl. No.	Traits	Mean \pm SE	Range		Coefficient of variation		h ² (bs) %	Genetic advance as 5% of mean
			Min	Max	GCV (%)	PCV (%)		
1	DF	42.75 \pm 0.57	39.33	45.67	3.21	3.47	0.85	6.09
2	DM	71.94 \pm 0.63	67.33	79.00	3.58	3.69	0.94	7.17
3	PH	37.38 \pm 1.48	27.00	51.33	15.66	16.15	0.94	31.28
4	LL	8.69 \pm 0.59	6.03	11.47	15.90	17.31	0.84	30.09
5	PL	7.49 \pm 0.33	4.00	9.47	12.32	13.10	0.88	23.86
6	NPB	2.27 \pm 0.39	0.33	5.00	30.46	34.96	0.76	54.67
7	NCPP	7.73 \pm 0.79	2.67	12.33	18.75	21.35	0.77	33.91
8	NPPC	4.12 \pm 0.44	2.33	5.67	14.10	17.64	0.64	23.21
9	NPPP	25.05 \pm 2.00	12.67	35.33	22.58	23.94	0.89	43.86
10	NSPP	10.45 \pm 0.59	6.33	13.67	11.79	13.07	0.81	21.89
11	SI	4.24 \pm 0.04	2.83	5.66	17.11	17.14	1.00	35.18
12	HI (%)	22.90 \pm 2.68	13.61	37.18	19.66	22.88	0.74	34.80
13	BYPP	38.02 \pm 5.18	16.73	67.67	25.40	28.83	0.78	46.10
14	SYPP	8.27 \pm 0.92	3.89	12.47	23.51	26.02	0.82	43.77

Notations: DF (days to 50% flowering), DM (days to maturity), LL (leaf length), PH (plant height), PL (pod length), NPB (number of primary branch), NCPP (number of clusters per plant), NPPC (number of pods per cluster), NPPP (number of pods per plant), NSPP (number of seeds per pod), SI (seed index), HI (harvest index), BYPP (biological yield per plant), SYPP (seed yield per plant).

sonance with the findings of Kumar *et al.* (2022), for number of pods per plant, harvest index and biological yield per plant, Singh *et al.* (2022) and Salman *et al.* (2021) for seed yield per plant and number of pods per plant; Joshi *et al.* (2021) for number of primary branches, and seed yield per plant. PCV for all the traits were recorded more than GCV and very small difference was present in between GCV and PCV, revealing very little influence of environment for their expression. Days to 50% flowering and days to maturity showed low GCV and PCV (<10%) which was in agreement with the findings of Joshi *et al.* (2021) for days to maturity.

Heritability and genetic advance analysis

High heritability coupled with high genetic advance was recorded for most of the traits under study viz., number of primary branches, biological yield per plant, number of pods per plant, seed yield per plant, seed index, harvest index, number of cluster per plant, plant height and leaf length (Table 1 and Fig. 1). It indicated that direct selection for these traits might be effective since the heritability is most likely due to additive gene effect. This result was in consonance with the finding of Kumar *et al.* (2022) for seed yield

per plant, plant height, number of pods per plant, number of primary branches, biological yield per plant, seed index and harvest index; Singh *et al.* (2022) for seed yield per plant, seed index and number of pods per plant; Joshi *et al.* (2021) for number of primary branches, seed index and seed yield per plant; Salman *et al.* (2021) for number of pods per plant, seed yield per plant, number of cluster per plant, number of primary branches, plant height. High heritability with low genetic advance 5% of mean was observed for days to 50% flowering and days to maturity suggesting non-additive gene effects for the expression of the character and selection for such trait might not be rewarding which was in agreement with the Titumeer *et al.* (2014) for days to 50% flowering.

Correlation coefficient analysis

Correlation analysis reveals the interrelationships between various independent variable and dependent traits such as grain yield/plant. The genotypic correlation coefficients in this study were higher in magnitude than the phenotypic correlation coefficients in the same direction, and magnitude indicated that there is a strong inherent association between each pair of characters, which may be due to the environment's

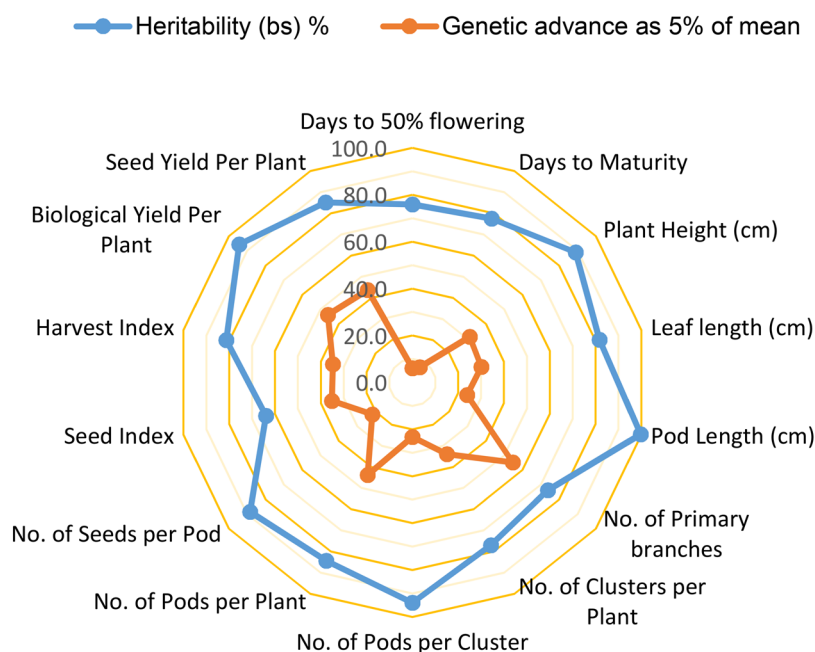


Fig. 1. Graphical representation of heritability and genetic advance as per cent of mean for different traits in *Vigna radiata*.

ability to mask or modify the relationship between the two.

Seed yield per plant exhibited high positive and

significant association with biological yield per plant, number of seed per pod, leaf length, harvest index, number of pods per cluster and number of pods per plant (Table 2 and Fig. 2). These traits should be given

Table 2. Estimates of phenotypic correlation coefficient for yield and yield attributing traits.

Traits	FI	DM	PH	LL	PL	NPB	NCPP	NPPC	NPPP	NSPP	SI	HI	BYPP
FI	1.000	0.398*	0.270	0.129	0.014	-0.041	0.187	0.099	0.142	0.052	0.228	0.093	-0.095
DM		1.000	0.688**	-0.330*	-0.342*	0.272	0.174	-0.248	0.121	-0.525**	-0.112	0.298	-0.562**
PH			1.000	-0.198	0.081	0.009	0.127	0.005	0.160	-0.151	-0.083	0.389*	-0.442**
LL				1.000	0.340*	-0.218	0.045	0.107	0.239	0.457**	-0.005	-0.193	0.492**
PL					1.000	-0.435**	-0.078	-0.016	-0.062	0.418**	0.283	-0.186	0.266
NPB						1.000	0.552**	0.038	0.533**	-0.303	0.013	0.060	-0.124
NCPP							1.000	0.158	0.732**	0.033	-0.090	0.126	0.117
NPPC								1.000	0.497**	0.360*	-0.247	-0.012	0.298
NPPP									1.000	0.112	-0.192	0.125	0.202
NSPP										1.000	0.272	-0.197	0.585**
SI											1.000	-0.156	0.120
HI												1.000	-0.508**
BYPP													1.000
SYPP	-0.030	-0.384*	-0.157	0.420**	0.108	-0.144	0.123	0.316*	0.257	0.494**	-0.037	0.372*	0.577**

Notations: * Significant at 5 % level, ** Significant at 1 % level.

DF (days to 50% flowering), DM (days to maturity), LL (leaf length), PH (plant height), PL (pod length), NPB (number of primary branch), NCPP (number of clusters per plant), NPPC (number of pods per cluster), NPPP (number of pods per plant), NSPP (number of seeds per pod), SI (seed index), HI (harvest index), BYPP (biological yield per plant), SYPP (seed yield per plant).

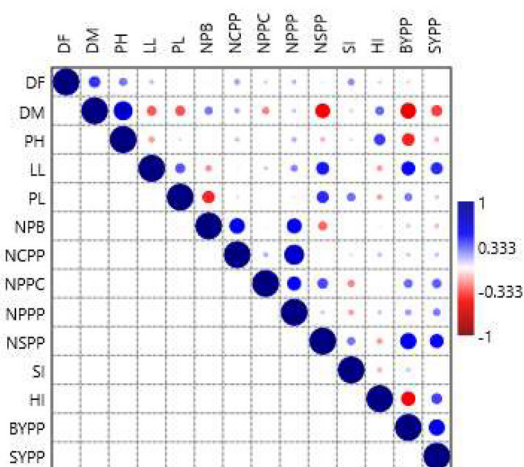


Fig. 2. Graphical representation of association between fourteen yield and yield attributing traits of *Vigna radiata*.

emphasis for further selection since strong association of these traits with seed yield per plant was recorded. This result was in confirmation with Reshmi Raj *et al.* (2022) and Nayak *et al.* (2021) for number of seeds per pod and number of pods per plant; Singh *et al.* (2022) and Goyal *et al.* (2022) for number of pods per cluster and number of pods per plant; Tejaswini *et al.* (2022) for number of pods per plant; Sineka *et al.* (2021) for number of seeds per pod, number of pods per cluster and number of pods per plant. Days

to maturity had negative and significant association with seed yield per plant was confirmed with the findings of Reshmi Raj *et al.* (2022) and Nayak *et al.* (2021). Indirect selection for these characters should be done for yield improvement in mungbean. The undesirable association of some of the component characters may act as deterrent for the formulation of a comprehensive selection programme involving these traits so while formulating a comprehensive selection programme these factors must be considered.

Path coefficient analysis

The direct and indirect effects of different variables on seed yield per plant are presented in Table 3. Path analysis results revealed that the highest positive direct effect on seed yield per plant was observed for number of seeds per pod followed by number of primary branches, number of cluster per plant, harvest index, leaf length and number of pods per cluster. This result was in consonance with findings of Singh *et al.* (2022) for number of seeds per pod and number of clusters per plant; Tejaswini *et al.* (2022), Joshi *et al.* (2021) and Sineka *et al.* (2021) for number of pods per plant; Goyal *et al.* (2021) for number of primary branches per plant and number of pods per cluster; Nayak *et al.* (2021) for number of seeds per pod; Pod length and seed index showed negative direct effect with seed yield per plant was in agreement with the result of Reshmi Raj *et al.* (2022) for pod length.

Table 3. Direct and indirect effect of various yield and yield related traits on seed yield per plant.

Traits	DF	DM	PH	LL	PL	NPB	NCPP	NPPC	NPPP	NSPP	SI	HI	BYPP
DF	-0.1172	-0.0194	-0.0238	-0.0067	0.0136	-0.0535	-0.0048	-0.0132	-0.0287	0.0002	-0.0361	0.0038	-0.0219
DM	-0.0170	-0.1030	-0.0052	-0.0586	-0.0655	0.0378	-0.0391	-0.0158	0.0009	-0.0567	0.0213	0.0297	-0.0288
PH	-0.0250	-0.0063	-0.1232	-0.0053	-0.0176	-0.0258	0.0090	-0.0340	0.0129	-0.0150	-0.0165	-0.0928	-0.1079
LL	0.0185	0.1835	0.0139	0.3225	0.2384	-0.1954	0.1539	0.1632	0.0984	0.1921	-0.0540	-0.1416	0.0341
PL	0.1577	-0.8662	-0.1940	-1.0067	-1.3618	0.9083	-0.4316	-0.6770	-0.1899	-0.8380	0.7101	0.2183	-0.3194
NPB	0.3346	-0.2689	0.1534	-0.4443	-0.4891	0.7333	-0.2688	-0.2217	-0.0829	-0.3376	0.5329	0.2452	0.0935
NCPP	0.0223	0.2073	-0.0396	0.2603	0.1729	-0.2000	0.5455	-0.0127	0.1670	0.0662	0.0421	-0.3071	-0.0431
NPPC	0.0253	0.0345	0.0622	0.1140	0.1120	-0.0681	-0.0053	0.2253	-0.0717	0.0927	0.0004	0.0181	0.1474
NPPP	-0.0342	0.0012	0.0146	-0.0426	-0.0195	0.0158	-0.0427	0.0444	-0.1396	0.0058	0.0120	-0.0028	0.0287
NSPP	-0.0027	0.7364	0.1631	0.7963	0.8227	-0.6155	0.1622	0.5501	-0.0553	1.3369	-0.2433	-0.2569	0.4192
SI	-0.1445	0.0970	-0.0629	0.0786	0.2447	-0.3411	-0.0362	-0.0009	0.0403	0.0854	-0.4694	-0.0114	-0.0829
HI	-0.0171	-0.1541	0.4027	-0.2347	-0.0857	0.1788	-0.3010	0.0430	0.0108	-0.1027	0.0130	0.5346	0.3182
BYPP	-0.0479	-0.0717	-0.2242	-0.0271	-0.0601	-0.0327	0.0202	-0.1675	0.0527	-0.0803	-0.0452	-0.1525	-0.2562
SYPP	0.1528	-0.2296	0.1368	-0.2544	-0.4950	0.3421	-0.2389	-0.1168	-0.1849	0.3488	0.4673	0.0846	0.1809

R square = 0.9469
Residual effect = 0.2305

Notations: DF (days to 50% flowering), DM (days to maturity), LL (leaf length), PH (plant height), PL (pod length), NPB (number of primary branch), NCPP (number of clusters per plant), NPPC (number of pods per cluster), NPPP (number of pods per plant), NSPP (number of seeds per pod), SI (seed index), HI (harvest index), BYPP (biological yield per plant), SYPP (seed yield per plant).

The value of residual effect (0.2305) indicates that 87% of variations in the genotypes are due to the 14 variables studied. Thus low residual value suggested the appropriateness of the traits for defining diversity in the present study.

CONCLUSION

The mean sum of squares due to genotypes for all the characters were highly significant for all the traits under study and indicated that the genotypes possessed inherent genetic differences. All traits had PCV values that were higher than GCV values, and there was very little difference between GCV and PCV values, indicating that the environment had little impact on how those traits were expressed. High heritability accompanied with high genetic advance was observed for the traits number of primary branches, biological yield per plant, number of pods per plant, seed yield per plant, seed index, harvest index, number of cluster per plant, plant height and leaf length. It suggests that the additive gene effect is most likely responsible for the heritability, and that direct selection for these qualities may be successful. Selection for this trait may not be worthwhile due to the high heritability and limited genetic advance as a percentage of the mean for the trait days to 50% flowering. Based on the results from correlation and path coefficient analysis, it is concluded that number of seeds per plant, harvest index, leaf length and number of pods per cluster showed positive correlation with seed yield per plant and at same time exhibited high positive direct effect towards seed yield. Therefore, they seem to be primary yield contributing character and thus can be used as direct selection to improve genetic yield potential of *Vigna radiata*.

ACKNOWLEDGMENT

The authors declare no known conflict of interests that could have appeared to influence the work reported in this paper.

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