Genetic Variability, Correlation Studies and Path Analysis for Yield Related Traits in Mungbean [(*Vigna radiata* (L.) Wilczek] RIL Population Derived from a Cross of Chinamung × LM-1668

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ABSTRACT

The study was initiated to determine the genetic variability, correlation coefficients and path coefficient analysis for yield and yield related traits among the 64 recombinant inbred lines (RILs) derived from a cross of Chinamung and LM-1668. The RILs significantly differed for all the traits studied. Analysis of variance revealed significant differences among the RILs, indicating the presence of genetic variability for almost all the traits studied except for days to 50 per cent flowering. Presence of minimum difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters indicated that the phenotypes were true to the genotypes and the expression of these traits had low environmental influence. Heritability estimates in broad sense and genetic advance were high for all the characters except for test weight indicating that estimates revealed the presence of additive gene action in the expression of all the traits of interest except test weight. Correlation studies indicated that, seed yield per plant showed significant positive correlation with pod yield per plant followed by number of pods per plant, number of clusters per plant and threshing percentage. Among the characters studied, pod yield per plant exerted very high positive direct effect followed by the number of pods per plant, threshing percentage and number of clusters per plant towards seed yield per plant.

Keywords: Mungbean, Correlation coefficient, Genetic variability, RILs

MUNGBEAN (*Vigna radiate* (L.) Wilczek) also known as greengram is an important nutritive grain legume grown in many tropical and subtropical countries. It is grown on more than 6 million ha worldwide (about 8.5 per cent of the global pulse area). Mungbean production trend in India has been increasing for the past few years and this is attributed to its short maturity period, tolerance to drought and adaptability to a wide range of soils (Anon., 2018). It is an excellent source of easily digestible good quality protein hence playing an important role in alleviating protein malnutrition in developing countries like India (Tang *et al.*, 2014). The average yield of mungbean is 341 kg/ha in India, despite its yield potential of 800 kg/ha attained in country like Thailand, Taiwan, Indonesia etc. (Bainade *et al.*, 2014). Although the number of varieties have been developed and recommended for cultivation, the total mungbean productivity in India is still low and there is a need for yield improvement (Narasimhulu *et al.,* 2013). Therefore the development of high yielding and disease resistant mungbean cultivars remains the main objective of any mungbean breeding programs in the world. Yield is a polygenic trait which is determined by several component traits, thus, affecting the final seed yield (Das and Barua, 2015). According to Srivastava and Singh (2012), yield correlates with various inter-related traits and are associated to each other either positively or negatively.

Studying genetic variability using parameters such as Genetic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) heritability and genetic advance are of paramount importance, since every crop improvement objective is to increase the seed yield coupled with disease resistance (Divya Ramakrishnan *et al.*, 2018). The estimates of heritable and non- heritable variance gives an idea on the possible characters under study to be considered for improvement while correlation and path analysis help

to understand the contribution of different characters to seed yield.

This experiment was therefore geared towards studying the genetic variability, heritability, genetic advance as percent and to understand the association between yield and yield related attributes using correlation and path analysis in 64 mungbean recombinant inbred lines.

MATERIAL AND METHODS

Sixty four F_8 recombinant inbred lines (RIL) derived from a cross of Chinamung × LM-1668 were used to identify the important yield attributing traits by correlation and path analysis. These RILs were planted in a 2 m × 2 m plots with a spacing of 60 cm × 30 cm experimental plot laid out in an augmented design (Federer, 1956) during *rabi*, 2018-2019 at the University of Agricultural Sciences, Bangalore. All the recommended agronomic practices were carried out during the crop growth period. The observations were recorded in 5 randomly selected plants for 11 different traits *viz.,* days to fifty per cent flowering, plant height at maturity number of clusters per plant, number of pods per plant, hundred seed weight and grain yield. The mean values were used for estimating correlation and path analysis according to Dewey and Lu (1959). Correlation and path analysis were performed using window stat version 8.0.

Mean values were calculated and subjected to standard statistical procedures for the analysis of variance for augmented designs (Federer, 1956). The genotypic and phenotypic coefficients of variation (Burton and Devane, 1952), heritability in broad sense (Hanson *et al.*, 1956) and genetic advance as per cent of mean (Johnson *et al.,* 1955) for both yield and its attributing characters were also computed. The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and covariance. The path coefficient analysis was done according to the method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance: In this study, Analysis of variance (Table 1) was statistically significant for most of the traits studied suggesting the presence of high genetic variability for all traits of interest except Days to 50 per cent flowering. Similar findings were obtained by Divya Ramakrishnan *et al.*, 2018.

Estimation of PCV, GCV and heritability

The extent of variability was also assessed by computing the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The results demonstrating PCV and GCV, heritability and genetic advance estimates in the study are presented in Table 2.

The magnitude of PCV was higher than the corresponding GCV for all the characters studied except for seed yield and test weight though the differences were minor. In the present study, the highest PCV was observed in pod yield (57.26) with the highest GCV too (48.25).

The presence of a narrow gap between PCV and GCV for all the characters under study revealed that the expression of these traits had low environmental influence (Geeta *et al.*, 2014). Similar findings were earlier reported by Divya Ramakrishnan *et al.* (2018). Low PCV and GCV in traits such as 50 per cent flowering indicated less scope for selection since it is environmentally influenced. In addition, these results also suggested that improvement by phenotypic selection would be possible.

Broad sense heritability for different characters showed that heritability was highest for pods per plant (71.22), seed yield (70.50) and branches per plant (70.43) with low heritability being recorded for seeds per pod (Table 2). Heritability which is an index of transmissibility is primarily of interest to a plant breeder. Higher the heritability value of a character, less will be the environmental influence for expression of that character, thereby indicating better opportunity for selecting a genetically good individual. In the present experiment, very high to high heritability was observed suggesting that these characters might be highly heritable and less influenced by environment and selecting genotypes on the basis of such characters would be rewarding worthwhile.

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TABLE 1

Analysis of variance of different characters

Source of Variation	DF	DFF	PH	B/P	C/P	P/P	PL	S/P	PY/P	SY	T%	TW
Blocks	4	0.57	155.99	15.72	11.58	51.64	0.71	5.64	7.98	5.17	803.03	0.052
Entries (RILs + Checks)	67	3.48	10.48 ***	2.44 **	3.84 *	29.85 *	0.64 ***	3.86 **	5.91 **	2.14 *	349.72	1690.34 ***
Checks	3	2.32	19.27 **	5.62 **	1.27 *	5.063	0.34	9.71	1.70	0.79	754.13	0.04
RILs	63	3.59	10.84 **	2.26 ***	4.00 *	31.11 *	0.62 **	3.64 **	6.20 **	2.23 *	335.34 *	1790.591 **
Checks *vs.* RILs	1	0.00	18.35 ***	8.40	1.31 *	24.57	3.52 ***	14.68 **	0.09 **	0.82 **	42.05 *	445.07 ***
ERROR	12	3.10	75.66	4.37	1.48	9.19	1.57	3.08	1.52	0.90	29.74	0.18
CD@ 5%		2.42	11.98	2.88	1.67	4.80	1.73	2.42	1.70	1.31	9.74	0.58

*Significant @ P =0.05 **   Significant @ P = 0.01 ***   Significant @ P = 0.001

DF: Degrees of freedom   DFF: Days to fifty per cent flowering   S/P: Seeds per pod.   PY/P: Pod yield per plant (g)

PH: Plant height (cm)   SY: Seed yield per plant   B/P: Branches per plant.   T%: Threshing per cent

TW: Test weight   P/P : Pods per plant   PL: Pod length (cm)   C/P: Clusters per plant

TABLE 2

Estimation of variability, heritability, genetic advance and genetic advance as per cent of mean for
11 characters in 64 F_8 RILs of the cross Chinamung × LM-1668

Charcter	Mean ± SE	Range		Coeffficient of variability		Broad sense h² (%)	GAM (%)
		Min	Max	PCV	GCV		
Days to 50% flowering	41 ± 0.25	36	47	9.5	8.5	41.2	12.33
Plant Height	28.8 ± 1.20	3.6	50	34.27	15.94	38.67	19.57
Branches/plant	7.54 ± 0.36	2.4	16.4	44.59	37.36	70.43	42.72
Clusters/plant	4.88 ± 0.24	1.4	13.2	38.16	28.98	50.20	58.10
Pods/plant	11.23 ± 0.71	1.6	31.4	46.44	37.60	71.22	80.39
Pod length	5.90 ± 0.17	1.2	8.6	23.54	15.95	50.87	11.10
Seeds/pods	7.54 ± 0.24	1.44	10.8	25.29	18.04	37.43	8.54
Pod yield	4.02 ± 0.31	3.5	14.87	57.26	48.25	40.00	83.75
Seed yield	2.51 ± 0.18	0.356	9.524	55.90	41.08	70.50	79.70
Threshing %	62.86 ± 2.34	24	99.3	47.37	30.52	62.32	33.20
Test weight	4.53 ± 0.08	2.2	4.77	49.58	42.61	58.79	34.04

Genetic advance as percentage of mean was high for all the traits studied with seed yield having the highest and pod length being had the least.

Correlation studies

Correlation coefficient analysis depicts the degree and extent of relationship among important plant traits and it is a main basis for crop selection. Therefore, it is usually important to select plants with consistent desirable characteristics. The results of the study revealed that days to 50 per cent flowering were positively and significant correlated with days taken to maturity and test weight (Divya Ramakrishnan *et al.*, 2018). Days taken to 50 per cent flowering were positively and significantly correlated with all the other traits.

Days taken to maturity were positively correlated and significant with number of pod length, seeds per pod and test weight (Bhattacharya and Vijayalaxmi, 2005). Plant height was associated positively and significantly with number of branches, number of pods per plant,

pod length, number of seeds per pod, and hundred seed weight. Among them seed yield per plant had the highest positive correlation value. Number of branches was positively correlated and significant with number of pods per plant, pod length, number of seed per pod, 100 seed weight seed yield per plant. Among these number of seeds per pod, 100 seed weight were positively correlated with all the characters. Seed yield per plant showed significant positive correlation with pod yield per plant followed by number of pods per plant, number of clusters per plant and threshing percentage. Simlar results have been reported in various studies (Rajan *et al.* (2000), Ahmad *et al.* (2013) and Narasimhulu *et al.* (2013) Makeen *et al.* (2007), Kumar *et al.* (2010), Srivastava and Singh (2012), Haritha and Reddy Shekar (2002), Motiar and Hussain (2003), Anuradha and Suryakumari (2005) and Mallikarjuna Rao *et al.* (2006).

The number of clusters per plant and number of pods per plant exhibited highly significant and positive

association with grain yield (Table 3). The significant association of number of clusters per plant with grain yield has also been reported by Reddy *et al.* (2011), Hemavathy *et al.* (2015), Pinchhyo *et al.* (2016) and Keerthiga *et al.* (2018). The significant correlation between numbers of pods per plant with grain yield has been reported by Reddy *et al.* (2011), Hemavathy *et al.* (2015), Pinchhyo *et al.* (2016), Dhoot *et al.* (2017) and Keerthiga *et al.* (2018). The yield improvement in mungbean can be accomplished by the selection of parents with these traits. Correlation among the component characters revealed that the plant height showed significant positive correlation with hundred seed weight. The association of plant height to hundred seed weight was similar to the findings of Keerthiga *et al.* (2018). On the contrary, the negative correlation of plant height with hundred seed eight was reported by Narasimhulu *et al.* (2013). The number of clusters per plant exhibited highly significant association with number of pods per plant. Similar findings were displayed by Narasimhulu *et al.* (2013), Dhoot *et al.* (2017), Keerthiga *et al.* (2018). Since the pods are produced in clusters, the increase in number of clusters automatically increases the number of pods per plant.

Path coefficient analysis

Correlation coefficients measure the mean relationships among the traits. The association between traits is an important aspect to deal with in breeding programs, because genetic change in a given trait may change positively or negatively with other traits. In addition, in most breeding programs the strategy is based on selection for several traits simultaneously and therefore, knowledge on the genetic association between traits is inevitably useful for the establishment of selection criteria.

Among the studied characters plant height, number primary branches, number of pods/plant, pod length and number of seeds/pod showed the positive direct effect on the seed yield per plant. Pod length recorded the highest direct effect on the seed yield per plant followed by the number of pods per plant and plant height. Number of seeds per pod recorded the positive direct effect on seed yield per plant as the values were low. Days taken to 50 per cent flowering, days taken to maturity and 100 seed weight was showed negative direct effects on the seed yield per plan, but 100 seed weight was significant with seed yield. This was due to indirect effect of 100 seed weight through number of pods per plant and pod length on seed yield which was bit high. This result is in agreement with the results obtained by Venkateshwarlu (2001), Haritha and Reddy Shekar (2002), Anuradha and Suryakumari (2005) and Mallikarjuna Rao *et al.* (2006).

Days taken to 50 per cent flowering showed negative indirect effects and the values were low to all the characters except to the number of pods per plant with positive indirect effects. It is found that all the characters except days taken to maturity recorded the positive indirect effect on the seed yield per plant but days to maturity recorded negative indirect effect on the seed yield per plant and also found negative indirect effect of days to maturity which was larger than the positive indirect effect because of negative and non-significant association with seed yield per plant. Higher positive indirect effect was recorded by plant height and number of branches on seed yield per plant through pod length followed by number of branches. It was found that pattern of contributing characters for indirect effect of plant height and number branches per plant to the seed yield was same. The highest effect of these two characters was through pod length followed by number pods per plant, because these two characters are highly significant to the seed yield per plant. The highest indirect effect was recorded for the pod length through the number of pods per plant followed by the number of branches per plant. 100 seeds weight had significant association to seeds per plant but showed negative indirect effects through all the characters. Number of pods per plant and pod length showed similar indirect effect. This result was in correspondence with the finding reported by Tabasum *et al.* (2010) and Das & Barua (2015).

The results obtained in the study revealed that there is a wide range of genetic variability in the RILs which allows for simultaneous improvement in seed yield through selection. High heritability estimates with

TABLE 3

Phenotypic correlation coefficients yield attributing characters

Characters	DFF	DM	PH	B/P	C/P	P/P	PL	S/P	TW%	SY	TH
Days to 50% Flowering	1.000	0.895 **	0.101	0.50	0.017	-0.034	0.086	0.147 *	0.354 **	0.012	0.064
Days taken to Maturity		1.000	0.046	0.036	0.487	-0.047	0.039 **	0.160 *	0.345 **	-0.023	0.008
Plant Height (cm)			1.000	0.855 **	0.358 **	0.874 **	0.885 **	0.719 **	0.179 *	0.915 **	0.075
No.of Branches				1.000	0.047	0.941 **	0.946 **	0.727 **	0.215 **	0.953 **	0.464 **
No. of Clusters					1.000	0.267 **	0.032	0.145	0.157 *	0.130 **	0.485 **
No.of pods/Plant						1.000	0.925 **	0.687 **	0.196 **	0.961 **	0.209 *
Pod Length(cm)							1.000	0.729 **	0.221 **	0.965 **	0.034
No.of seeds/Pod								1.000	0.234 **	0.731 **	0.031
100 Seed Weight									1.000	0.191 **	0.099
Seed Yield/Plant.										1.000	0.959 **
Threshing Percentage											1.000

TABLE 4

Path coefficient analysis showing direct and indirect effects of yield contributing characters in mungbean

Characters	DFF	DM	PH	B/P	C/P	P/P	PL	S/P	TW	PY	TH %
Days to50% Flowering	-0.006	-0.027	0.018	0.006	0.065	-0.010	0.031	0.003	-0.002	0.079	-0.104
Days to Maturity	-0.005	-0.031	0.008	0.004	0.027	-0.015	0.014	0.003	-0.002	0.034	-0.090
Plant Height (cm)	-0.000	-0.001	0.183	0.118	0.126	0.279	0.320	0.016	-0.001	0.058	0.086
No.of Branches	-0.000	-0.001	0.158	0.138	0.018	0.301	0.342	0.016	-0.001	0.211	-0.034
No of Clusters	0.002	0.035	-0.134	-0.198	0.415	0.030	0.016	0.034	0.013	0.212	0.450
No.of Pods/Plant	0.000	0.001	0.161	0.130	-0.199	0.320	0.335	0.015	-0.001	0.291	0.288
Pod Length(cm)	-0.000	-0.001	0.162	0.130	0.015	0.296	0.362	0.016	-0.001	0.171	0.234
No.of Seeds/Pod	-0.000	-0.004	0.132	0.100	0.014	0.220	0.264	0.022	-0.001	0.037	0.034
100 Seed Weight	-0.002	-0.010	0.033	0.029	-0.110	0.062	0.080	0.005	-0.007	0.065	-0.051
Pod Yield/Plant	-0.185	-0.155	-0.179	0.083	0.102	0.050	-0.185	0.061	-0.195	1.345	0.345
Threshing percentage	-0.031	-0.057	0.042	-0.055	0.025	0.029	-0.055	0.037	0.066	0.143	0.333

DFF : Days to fifty per cent flowering.   S/P: Seeds per pod   PY/P: Pod yield per plant (g).   PH: Plant height (cm).   B/P: Branches per plant
TH (%): Threshing per cent   C/P: Clusters per plant   TW: Test weight.   P/P: Pods per plant   PL: Pod length (cm)

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moderate to high genetic advance were observed for seed yield per plant, number of pods per plant and number of seeds per pod suggesting genotypic variation in the present material for these traits which was due to high additive gene effects. Directs selection for these traits may be rewarding. Significant positive association and high direct effect was noticed with number of pods per plant followed by number of clusters per plant, pod yield and threshing percentage on seed yield per plant. Strong association of these traits revealed that the selection based on these traits would ultimately improve the pod yield. Hence, the above mentioned characters should be given top most priority while formulating a selection strategy for improvement of yield in greengram.

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