



## **Correlation and Path Coefficient Analysis in Rainfed Mung Bean Genotypes [*Vigna radiata* (L.) Wilczek]**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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### **ABSTRACT**

Correlation and path analysis was carried out using sixteen genotypes of mung bean for eight component characters including seed yield. Field experimental was laid out under a randomized block design with three replications; observation was recorded on ten plants were selected at random from each plot for plant height, pod length, number of seeds per pod, test weight, seed yield per plot and seed yield per hectars whereas for days to 50% flowering and days to maturity data were recorded on whole plot basis among the genotypes of mung bean. The plant height, pod length and test weight had positive correlation with seed yield both at genotypic and phenotypic levels. Days to flowering, days to maturity and no. of seeds per pod had negative correlation with seed yield both at genotypic and phenotypic levels. Path analysis showed positive and high direct effect of days to maturity, pod length, seed yield per hectars and negative & high direct effect of days to flowering, plant height, test weight, whereas indirect effects of other component characters through these characters towards seed yield per plot. Hence, these traits should be given more emphasis while selecting genotypes for yield improvement in mung bean.

**Keywords:** *Mung bean; vigna radiate; correlation; path analysis; seed yield.*

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## 1. INTRODUCTION

“Mung bean (*Vigna radiata* (L.) Wilczek) is one of the important pulse crops in arid region because of its short growth duration, adaptation to low water requirement and low soil fertility. It is favored for consumption due to its easy digestibility and low production of flatulence” [1]. “Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet. Average protein content in the seed is around 24 per cent. The protein is comparatively rich in the amino acid lysine but predominantly deficient in cereal grains” [2]. “Presently, the yield of mung bean is well below the optimum level compare to other pulses. The average yield of mung bean is very low not only in India (425 kg/ha) but in entire tropical and sub-tropical Asia. India is the largest producer of mung bean in the world and accounts for 65 per cent acreage and 54 per cent production” [3].

“Seed yield is a dependent character, which is influenced by many independent characters. Studies on the correlation of characters and their relative direct and indirect effects on Seed yield are important, as it is helpful in selection of desirable characters” [4]. Hence, an attempt was made to study eight characters, their correlations and effects on genotypes of Mung bean. Correlation and path analysis showed that due importance should be given for plant height, pod length and test weight had positive correlation with seed yield both at genotypic and phenotypic levels. Path analysis showed positive and high direct effect of days to maturity, pod length, seed yield per hectars because of its correlation and high direct effects. This indicates that there is always scope for enhancement of seed yield by selection of these characters.

Therefore, organized and concerted efforts are required to enhance its productivity. Yield a complex polygenic character, direct selection would not be a reliable approach on account of being highly influenced by environmental factors. Correlation provides information on the nature and magnitude of association of different component characters with seed yield under rainfed conduction. Path analysis permits a critical examination of specific forces acting to produce a given correlation and measure the relative importance of each factor. Thus, characters highly contributing to yield can be selected, since genotypes serves as the most valuable reservoir in providing needed attributes

for developing successful varieties of mung bean.

## 2. MATERIALS AND METHODS

Sixteen genotypes of mung bean were raised in randomized block design with three replications during *Kharif*, 2019 at research farm of Agricultural Research Station, Fatehpur-Shekhawati, Sikar (Rajasthan) under rainfed conduction. These genotypes of mung bean were obtained from All India Coordinated Research Project on MULLaRP, RARI, Durgapur (Jaipur). Each genotype was given in a four row plot of 4 m length with a spacing of 30 cm between rows and 10 cm between plants. Ten plants were selected at random from each plot and data were recorded on 8 characters viz., plant height, pod length, number of seeds per pod, Test weight, seed yield per plot and seed yield per hectars whereas for days to 50% flowering and days to maturity data were recorded on whole plot basis. Genotypic and phenotypic correlations were determined according to Fisher [5] and Al-Jibouri et al. [6]. The path analysis was done according to the method Dewey and Lu [7].

## 3. RESULTS AND DISCUSSION

“In the present investigation, the correlation coefficients were estimated among different characters is presented in Table 1 and Fig. 1. The values of genotypic correlation coefficients (rg) were higher than the corresponding phenotypic correlation coefficients (rp) for all the characters. Seed yield per plot was positively associated with plant height, pod length and test weight indicating that selection based on these characters may result in high seed yield, which was in close agreement with early findings of” Dadepeer et al. [8]; Rahim et al. [9] and Prasanna et al. [10] “for number of primary branches per plant, number of cluster per plant, number of pods per cluster and number of pods per plant. Highly significant and positive association of seed yield per plant was observed with plant height and number of pods per plant by” Kumar et al. [11]; Srivastava and Singh [12] and Mahalingam et al. [13] “in green gram. Interestingly, there were significant correlation exist among the above characters as well as seed yield which, suggested that these characters may be considered for improvement of seed yield. Further, based on these relationships, presumed that for improving seed yield in mungbean, a model plant type would be

**Table 1. Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients between yield and its component characters in mungbean**

S.No	Characters	r	Days to flowering	Days to maturity	Plant height	Pod length	No. of seeds per pod	Test weight	Seed yield per ha.
1.	Days to flowering	$r_g$	1.0000	0.5228	-0.7348	-0.0577	0.7171	0.0337	-0.5291
		$r_p$	1.0000	0.3642 *	-0.6598 **	-0.0889	0.2839	0.0173	-0.4533 **
2.	Days to maturity	$r_g$		1.0000	0.0633	-0.2287	0.3713	0.2627	-0.2294
		$r_p$		1.0000	0.0686	0.0244	0.1752	0.2147	-0.1362
3.	Plant height	$r_g$			1.0000	0.0953	-0.6350	0.1407	0.4700
		$r_p$			1.0000	0.0731	-0.3273 *	0.1147	0.4234 **
4.	Pod length	$r_g$				1.0000	-0.3922	0.4998	0.3494
		$r_p$				1.0000	-0.0109	0.2479	0.1862
5.	No. of seeds per pod	$r_g$					1.0000	-0.1682	-0.3166
		$r_p$					1.0000	-0.0451	-0.2798
6.	Test weight	$r_g$						1.0000	0.2444
		$r_p$						1.0000	0.2150
7.	Seed yield per ha.	$r_g$							1.0000
		$r_p$							1.0000

\*, \*\* significant at 5% level and 1% level, respectively

**Table 2. Direct (diagonal) and indirect effect of different characters towards seed yield per plot in mungbean**

S.No	Characters	Days to flowering	Days to maturity	Plant height	Pod length	No. of seeds per pod	Test weight	Seed yield per ha.	r
1.	Days to flowering	-0.0313	-0.0164	0.0230	0.0018	-0.0224	-0.0011	0.0166	0.0165
2.	Days to maturity	0.0051	0.0097	0.0006	-0.0022	0.0036	0.0026	-0.0022	-0.0023
3.	Plant height	0.0006	-0.0001	-0.0008	-0.0001	0.0005	-0.0001	-0.0004	-0.0004
4.	Pod length	-0.0026	-0.0104	0.0043	0.0453	-0.0178	0.0226	0.0158	0.0168
5.	No. of seeds per pod	0.0221	0.0114	-0.0195	-0.0121	0.0308	-0.0052	-0.0097	-0.0097
6.	Test weight	-0.0004	-0.0031	-0.0017	-0.0059	0.0020	-0.0118	-0.0029	-0.0029
7.	Seed yield per ha.	-0.5214	-0.2261	0.4631	0.3443	-0.3120	0.2409	0.9855	0.9881

Residual Effect: SQRT (1-1.0062)

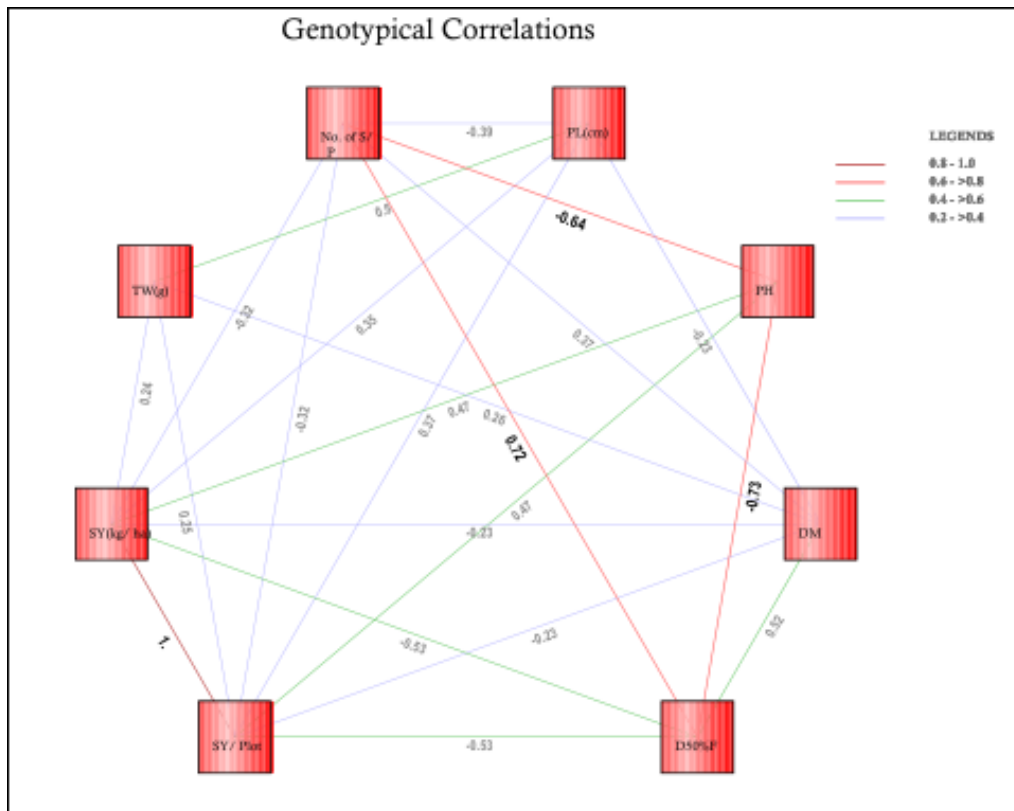


Fig. 1. Genotypic correlation

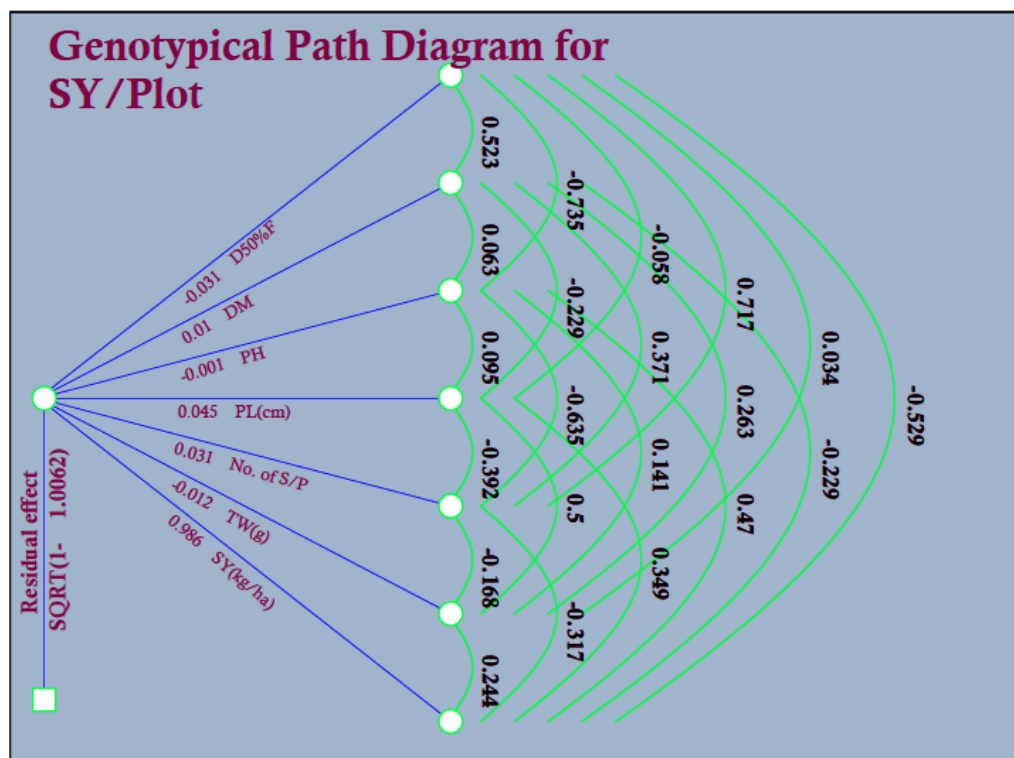


Fig. 2. Genotypic path diagram for seed yield per plot

that increased plant height, pod length and test weight". "Seed yield per plot was negatively associated with days to flowering, days to maturity and no. of seeds per pod indicating that could be ineffective for increasing seed yield, which was in close agreement with findings of" Muthuswamy et al. [4]; Rahim et al. [9] and Prasanna et al. [10]. Hence, it may be concluded that simultaneous selection for these characters would help for improvement of yield.

"Path analysis partitions the total correlation coefficient into direct and indirect effects and measures the relative importance of the causal factor individually" [7]. In the present study, seed yield was considered as dependent character and other characters were taken as independent characters. The results of path analysis are presented in Table 2 and the same depicted in Fig. 2 (Path Diagram). The days to maturity, pod length, seed yield per hectars had positive direct effects on seed yield per plot indicating that there is always scope for enhancement of seed yield by selecting these characters. The present results are in agreement with findings of Prasanna et al. [10], Narasimhulu et al. [14] and Muthuswamy et al. [4]. The characters, days to flowering, plant height, test weight had a negative influence on seed yield per plot [15]. Therefore, selection of these characters could be ineffective for increasing seed yield.

"The days to flowering and pod length exhibited positive and high indirect effects through seed yield per hectars on seed yield per plot. The days to maturity, plant height, no. of seeds per pod and test weight exhibited negative and high indirect effects through seed yield per hectars on seed yield per plot These results were accordance with the findings of" [15-17]. The test weight had exhibited negative contribution to the seed yield per plot with the characters days to flowering, plant height and no. of seeds per pod. The no. of seeds per pod had exhibited positive high indirect effects on seed yield per plot through days to maturity, plant height and test weight. Selection based on the pod length would increase the seed yield per plot indirectly through the days to flowering and seed yield per hectars. Plant height had exhibited negative contribution to the seed yield per plot with the characters no. of seeds per pod, test weight and seed yield per hectars. The days to maturity and flowering had exhibited negative high indirect effects on seed yield per plot through pod length, test weight and seed yield per hectars. The residual effect of SQRT (1-1.0062) suggested that there are some

characters which contribute to the seed yield which need to be studied. Correlation and path analysis showed that due importance should be given for plant height, pod length and test weight, days to maturity, seed yield per hectars because of its positive correlation and high direct effects. This indicates that there is always scope for enhancement of seed yield by selection of these characters. Hence, selection should be practiced for these characters in order to isolate superior genotype having higher seed yield for mung bean improvement programme.

#### 4. CONCLUSION

The plant height, pod length and test weight of seeds had positive correlation with seed yield both at genotypic and phenotypic levels. Days to flowering, days to maturity and number of seeds per pod had negative correlation with seed yield both at genotypic and phenotypic levels. Path analysis showed positive and high direct effect of days to maturity, pod length, seed yield per hectars and negative & high direct effect of days to flowering, plant height, test weight, whereas indirect effects of other component characters through these characters towards seed yield per plot. Hence, these traits should be given more emphasis while selecting genotypes for yield improvement in mung bean.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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