



Character Association Studies on Yield and Attributing Traits of Fifty-two Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes

Ghosh Sanhita^{1*}, Roy Anindita², Kundagrami Sabyasachi³

¹Ph.D. Research Fellow, Department of Genetics and Plant Breeding, Institute of Agricultural Science, University of Calcutta 51/2, Hazra Road, Kolkata-700019, West Bengal, India; ²Associate Professor, Department of Genetics and Plant Breeding, Institute of Agricultural Science, University of Calcutta 51/2, Hazra Road, Kolkata-700019, West Bengal, India.

ABSTRACT

Aim: Mungbean is one of the most important pulse crops due to the high content of protein as well as the ability to nitrogen fixation in soil. Seed yield is the most complex trait which highly influenced by other traits and also the environment. In this view, the study was aimed to evaluate the relationship between yield and yield attributing traits.

Methodology: In the present study, fifty-two mungbean genotypes were evaluated at the experimental farm of the University of Calcutta, Baruipur, South 24 Parganas, West Bengal in the three different years of 2015-2017. The data of eight yield and yield attributing traits (pooled over years) were calculated through the SPAR software, version 2.0.

Results: The association study revealed that branches plant⁻¹, pods plant⁻¹ and pod length were exhibited as the most yield contributing traits.

Conclusion: Selection based on traits namely branches plant⁻¹, pods plant⁻¹ and pod length would be helpful for future mungbean yield improvement program.

Key Words: Mungbean, Yield, Association, Correlation, Path

INTRODUCTION

Mung bean [*Vigna radiata* (L.) Wilczek] is the one of short duration important legume crop which grown under the tropical and sub-tropical region of Asia, America. It is the third most important pulse crop to the Indian subcontinent. The plant roots of mungbean can fix atmospheric nitrogen through symbiosis with nitrogen-fixing rhizobia. That is why this crop valuable for both economically and nutritionally because it can improve soil quality and reduce the amount of nitrogen fertilizer required in the soil when grown in rotation with cereals, thereby increasing cereal grain and straw yields due to its residual effects (Perera *et al.* 2017). It is playing an important role to increase the quantity of food and constitutes a noteworthy part of human diet for all segments of individuals where it providing the vast majority of the proteins or in adjust-

ing the deficiencies of the cereal proteins in vegetarian population (Rehman *et al.* 2009). But the productivity of mungbean is less increased compare to other pulse crop where it is grown up to four times into the kharif, pre-kharif and rabi seasons. Yield is a complex trait dependent on various constituent traits (Tabasum *et al.* 2010). Knowledge of the relationship between yield and yield contributing traits is necessary for any selection program which provides information regarding on the nature and magnitude of the association between any two pairs of these metric agro-morphological traits (Ofga and Petros 2017). The correlation analysis showed the relationship between two or more series of variables where direct and indirect effects of path coefficient analysis split correlation variables and visualized the relationship in a more meaningful way (Rahim *et al.* 2010).

Corresponding Author:

Ghosh Sanhita, Ph.D. Research Fellow, Department of Genetics and Plant Breeding, Institute of Agricultural Science, University of Calcutta, Kolkata; Phone: +91-9433566757; Email: skundagrami@gmail.com

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Keeping in view of these facts, the present study was conducted to evaluate the association between seed yield and its attributing traits.

MATERIALS AND METHOD

In the present study, fifty-two mungbean genotypes were evaluated at Experimental Farm of University of Calcutta, Baruipur, South 24 Parganas West Bengal during the period of mid-March to end May in the year of 2015, 2016 and 2017. The experiment was laid out in a Random Block Design (RBD) using three replications with experimental plot and cultural practices were performed according to Park(1978). Data were collected on five randomly selected healthy harvested plants from each replication and each genotype. The pre and post harvesting observations were recorded from five randomly selected plants from each replication on different parameters such as plant height (PH), branches plant⁻¹ (BPP), pods plant⁻¹ (PPP), pod length(PL), seeds pod⁻¹ (SPP), 100 seed weight(HSW), harvest index(HI) and seed yield plant⁻¹ (SYPP) and these traits were determined according to Moussa *et al.* (2000). Pods of each plant were kept separately in envelop and dried. Path coefficient analysis was done according to Dewey and Lu (1959).

Statistical Analysis

The correlation and path coefficient analysis (pooled over years) of yield and yield-related traits were calculated using the software SPAR version 2.0.

RESULTS

Association Studies

Correlation Analysis (Genotypic and Phenotypic):

Perusal data have been shown genotypic correlation greater than phenotypic correlation in Table 1. Seed yield per plant was possessed that genotypic and phenotypic correlation exhibited significantly positive with number of pods plant⁻¹ (0.665, 0.578 respectively) at P>0.01 where number of seeds pod⁻¹ (0.261) showed significant positive correlation only in genotypic level at P>0.05. The branches plant⁻¹ and pod length were showed significant positive correlation in genotypic level (0.387, 0.346 respectively) at P>0.01 and in phenotypic level (0.256, 0.245 respectively) at P>0.05. In the genotypic and phenotypic correlation, higher significant positive interrelationship was observed between the number of seeds pod⁻¹ with 100 seed weight (0.693, 0.616 respectively), branches plant⁻¹ with pods plant⁻¹ (0.417, 0.301 respectively), pods plant⁻¹ with harvest index (0.406, 0.392 respectively).

Path Coefficient Analysis

The path coefficient analysis (pooled over years) is shown in Table 2. The path coefficient analysis exhibited that pods plant⁻¹ (0.717) have been exerted maximum positive direct effect on seed yield plant⁻¹ followed by pod length (0.405) and the number of seeds pod⁻¹ (0.241), number of branches plant⁻¹ (0.188) where plant height (0.048) showed minimum positive direct effect on seed yield through 100 seed weight (0.071), harvest index (0.85). Here, branches plant⁻¹ have been exhibited a positive direct effect on seed yield plant⁻¹ through the highest positive pods plant⁻¹ (0.299) among the other traits. Pods plant⁻¹ have been showed the maximum negative indirect effect on seeds pod⁻¹ (- 0.211) through pod length (- 0.177).

DISCUSSIONS

Correlation Analysis (Genotypic and Phenotypic)

In the present study, assessment of genotypic correlation between different characters has been exhibited close parallelism with their corresponding phenotypic correlation. The genotypic correlation was higher in magnitude than the analogous correlation at the phenotypic level. Singh and Bains (2014), Ofga and Petros (2017), Narasimhulu *et al.* (2013), Srivastava *et al.* (2012) agreed with the present findings. It is demonstrated that vigorous intrinsic relationship could be remotely marked at a phenotypic level due to environmental influences to alter the degree of association among all the traits (Singh and Bains, 2014). Pods plant⁻¹ is exhibited as a most important yield attributing traits due to the higher significant positive correlation at both levels. Branches plant⁻¹ also showed a significant positive correlation with seed yield plant⁻¹ and suggested that it could be increased the seed yield plant⁻¹ through increased the pods plant⁻¹. The traits with significant positive associated have been demonstrated a constituent collaboration in a gene modeling where one trait will give impact on another trait through conditional consistency (Ofga and Petros, 2017). The present results have collaborated with previous results reported by Alom *et al.* (2014), Khajudpar *et al.* (2011), Singh and Kumar(2014). In the higher interrelationship between pods, plant⁻¹ and harvest index have been suggested a healthy plant provided maximum seed yield. On the other hand, the interrelationship between branches plant⁻¹ and pods plant⁻¹ have been clearly indicated that more branches would deliver more pods plant⁻¹ which could finally enhance the seed yield plant⁻¹. From this present study, it has been conceivable to realize that the genetic up gradation in one trait depended on the other pair.

Path Coefficient Analysis

Every component has two sections of activity (i) the straight impact (direct effect) and (ii) roundabout impacts (indirect

effect) along with the constituent traits which are not exhibited from the correlation studies. In the present study, yield and yield attributing traits have been exhibited as genotypic path due to the genotype correlation higher than phenotypic correlation. Correlation and path coefficient analysis were varied according to both genetic differences (genotypes) and environmental factors (Khajudpar *et al.* 2011). The direct effect of any character on seed yield per plant has been giving an idea regarding the successful traits determination while the indirect effect demonstrates the interrelationship between constituent traits towards yield contribution (Kumar *et al.* 2013). In this study, genotypic path analysis has been representing cause and effect relationships among quantitative traits and seed yield per plant. Since pods, plant⁻¹ and pod length have been indicated high direct impacts could be considered for direct selection for high seed yield in contrast with the rest of the other traits which are valuable in indirect selection towards yield. The present results have been agreed with the previous result reported by Khajudpar *et al.* (2011), Srivastava and Singh (2012) for pods plant⁻¹ and seeds pod⁻¹, 100 seed weight, Ambachew *et al.* (2015) for 100 seed weight and Singh *et al.* (2009) for plant height. Residual effects measure the role of other possible independent variables. The result of residual effect (0.18) revealed that the variables studied in the present investigation explained 82% of the variability in the yield and the other attributes besides the traits have been studied to contribute for seed yield per plant (Srivastava and Singh, 2012). It suggested that maximal emphasis should be given on pods plant⁻¹, branches plant⁻¹ and pod length was the most important yield contributing traits. Thus, the selection based on these traits would give better response for the improvement of yield in mungbean genotypes.

CONCLUSION

The present study has been suggested that maximal emphasis should be given on pods plant⁻¹, branches plant⁻¹ and pod length because they are the most important yield contributing traits. Finally, it concluded that the selection of genotypes based on these traits could be exploited for a future breeding program to improve the mungbean yield.

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Table 1: Genotypic and Phenotypic Correlation Matrix (Pooled over years) of Different Agro Morphological Traits in Mungbean

Traits		Plant Height (cm)	No. of Branch Plant ⁻¹	No. of Pods Plant ⁻¹	Pod Length (cm)	No. of Seeds Pod ⁻¹	100 Seeds weight (g)	Harvest index	Seed yield plant ⁻¹ (g)
Plant Height	G	1.000	-0.049	0.131	0.084	0.097	0.044	0.036	0.051
	P	1.000	-0.107	0.121	0.056	0.054	0.035	0.050	0.041
No. of Branch Plant ⁻¹	G		1.000	0.417**	0.252*	0.371**	0.201	0.139	0.387**
	P		1.000	0.301*	0.155	0.201	0.140	0.080	0.256*
No. of Pods Plant ⁻¹	G			1.000	0.342**	0.321*	0.185	0.406**	0.665**
	P			1.000	0.261*	0.282*	0.127	0.392**	0.578**
Pod Length	G				1.000	0.372**	0.693**	0.289*	0.346**
	P				1.000	0.310*	0.616**	0.251*	0.245*
No. of Seeds Pod ⁻¹	G					1.000	0.276*	0.122	0.261*
	P					1.000	0.202	0.064	0.179
100 seeds Weight	G						1.000	0.107	0.201
	P						1.000	0.097	0.157
Harvest Index	G							1.000	0.142
	P							1.000	0.084
Seed yield plant ⁻¹ (gm)	G								1.000
	P								1.000

Note**= significant at $P > 0.01$ level, *= significant at $P > 0.05$. G=Genotypic correlation, P= Phenotypic correlation

Table 2: Pooled Path Coefficient Analysis for Different Agro Morphological Traits

Traits	Plant Height(cm)	No. of Branch Plant ⁻¹	No. of Pods Plant ⁻¹	Pod Length(cm)	No. of Seeds Pod ⁻¹	100 Seeds weight(g)	Harvest index
Plant height (cm)	0.048	0.009	0.073	-0.141	-0.036	0.071	0.027
No. of Branch Plant ⁻¹	0.055	0.188	0.299	-0.121	0.059	-0.158	0.065
No. of Pods Plant ⁻¹	0.034	0.078	0.717	-0.177	-0.211	0.039	0.165
Pod length (cm)	0.004	0.047	-0.025	0.405	-0.059	-0.111	0.085
No. of Seeds Pod ⁻¹	-0.192	0.033	-0.032	0.083	0.241	0.044	0.084
100 Seed weight(g)	-0.042	0.037	0.030	0.053	0.024	0.071	0.028
Harvest Index	0.001	0.005	0.026	0.012	0.010	0.003	0.085

Residual effect: 0.18

Note: The bold values were represented the direct effect on seed yield.