

Biological Forum – An International Journal

13(3): 245-248(2021)

ISSN No. (Print): 0975-1130 ISSN No. (Online): 2249-3239

Association and Path Analysis of Morpho-agronomic Traits in Mungbean **Germplasm Under Cold Stress**

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ABSTRACT: Low temperature in the early growing season greatly affects mungbean cultivation and results a significant reduction in relative growth rate and seed yield. Therefore, an experiment comprised of 230 mungbean germplasm lines tested over two locations was aimed to assess inter-relationship of agronomic traits including seed yield in winter season. Seed yield per plant was strongly and positively associated with plant height, pod number per plant, pod length, seed number per pod and 100-seed weight. However, path analysis revealed that pod number per plant is the most desirable contributing trait next to seed number per pod and 100-seed weight towards seed yield. Hence, for genetic improvement in the seed yield, direct selection of genotypes based on component traits exhibiting positive correlation and higher positive direct effect will be more effective and fruitful in mungbean under cold stress in the winter season.

Keywords: Character association, path analysis, seed yield, yield related traits, cold stress, mungbean.

INTRODUCTION

Mungbean [(Vigna radiata (L.) Wilczek] is an important leguminous crop grown in India. The crop is a native of India and Central Asia (Singh and Singh, 2021). It has immense importance for nutritional quality and amenability for multiple cropping systems. Thus, it can be grown as a sole crop and as an intercrop or mixed crop with cereals forming an essential constituent of crop rotation. Being a short duration and photo-thermo insensitive crop, it seems to be an excellent candidate crop for intensification and diversification of crop (Ali and Kumar, 2006). Yield potential of mungbean is reported to be in the range of 2.5-3.0t/ha although, it's average productivity is staggering low at 5.0qt/ha. (Nair et al., 2019; Pratap et. al., 2021) primarily due to low yield potential of the available varieties with indeterminate habit, flower and fruit drop, poor source-sink relationship, poor harvest index and lack of cold and moisture stress (Malla et al., 2014). The main hindrance for breeding in the crop lies with narrow genetic variability and sensitivity to a variety of biotic and abiotic stresses particularly low temperature in the early growing season which greatly affects mungbean cultivation and results a significant reduction in relative growth rate and seed yield (Chen et al., 2017).

Yield is a complex trait and its quantified value depends on various components traits, which have a positive and negative correlation with yield and among Dash et al.,

them. Seed yield being a polygenic trait, it is highly labile to genotype x environment interaction (Allard, 1960), and the direct selection for yield seldom becomes effective. Therefore, the knowledge of the degree of association between yield and its attributing traits is important to assist selection scheme for breeding high yielding genotypes in mungbean. If the variability in the population is basically due to genotype with the least environmental effects, there more possibility of getting desirable genotype(s) in the breeding population.

More often, correlation and regression are carried out to establish inter-relationship among agronomic traits including seed yield. However, path analysis is a unique approach to understand the association of traits. It is in fact the partial regression which helps the breeder in splitting the correlation coefficient of each of the ancillary traits with seed yield (dependent variable) into direct and indirect effects (Dewey and Lu, 1959). Thus, most important specific component trait(s) can be known which would have greater importance for identification of elite genotypes in a set of germplasm as well as exercising selection pressure in the follow-up breeding population. Keeping in view above considerations, an attempt was undertaken to assess association among agronomic traits including seed yield in a set of available mungbean germplasm lines grown under cold stress.

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MATERIALS AND METHODS

A set of 230 genotypes of mungbean comprising standard ruling varieties, important pre-released cultures and popularly adapted local land races were laid out in randomized block design (RBD) in two replications. The trial was sown on 13^{th} December 2018 at Bhubaneswar and 13^{th} January 2020 at Jeypore location in Odisha to expose the crop to low temperature stress at the early growth stage (13-15°C at Bhubaneswar and 11-15°C at Jeypore location respectively). Each genotype was sown in two rows with a spacing of $30 \text{cm} \times 10 \text{cm}$. Fertilizers were applied @ 20:40:20 kg of N: P_2O_5 : K₂O along with 3.0 tons of farm yard manure (FYM) per ha. Other cultural operations or practices were done as per normal package of practices followed in the crop.

A sample size of five random plants of each genotype from each replication were used for the collection of data on 8 quantitative traits including single plant seed yield. The replication mean values of each character was considered for association analysis as per Aljibouri *et al.*, (1958) at both phenotypic and genotypic level.

RESULTS AND DISCUSSION

Association study reflects the magnitude and nature of the inter-relationship of different ancillary traits with seed yield. Grafius (1959) stated that yield may not be governed by any single gene as such, but through its components which are in turn determined by set of genes. So, it is most important for the plant breeders to find out as to which of the traits are correlated with yield and how they are correlated among themselves.

The phenotypic correlation (r_p) among eight agronomic traits ranged from -0.115 between days to 50% flowering and seed number per pod to 0.502 between

pod number per plant and single plant yield (gm) (Table 1). Seed yield revealed significant positive correlation with pod number/plant (0.502), seed number/pod (0.374), hundred seed weight (0.313), plant height (0.239) and pod length (0.232) as also confirmed by Mohan *et al.*, (2019). Further, single plant yield/plant (0.079) recorded positive association with cluster number/plant, but negatively correlated with days to 50% flowering (-0.006). Hundred seed weight maintained negative correlation with number of clusters/plant (-0.139). Again, it positively correlated with days to 50% flowering (0.037) and negatively correlated with cluster number/plant (-0.069), seed number/pod (-0.030), plant height (-0.028) and pod length (-0.001). Number of seeds/pod revealed highly significant negative correlation with number of clusters/plant (0.235) and significant negative correlation with days to 50% flowering (-0.115), pod number/plant (-0.094). Further, it revealed positive correlation with plant height (0.056) and pod length (0.056). Pod length had shown positive significant correlation with plant height (0.267) and pod number/plant (0.238). It was positively correlated with days to 50% flowering (0.089) and number of cluster/plant (0.019). In fact, pod number/plant recorded strong positive correlation with plant height (0.326). It was also positively correlated with cluster number/plant (0.090), days to 50% flowering (0.050). Number of clusters/plant showed highly significant positive correlation with plant height (0.131). Further, it was shown to be negatively correlated with 50% flowering (-0.019). Besides, plant height (cm) revealed strong positive association with days to 50% flowering (0.056).

Characters	Correlation coefficient	Days to 50% flowering	Plant Height (cm)	No of cluster/Pla nt	No. of pods/plant	Pod Length (cm)	Seeds Per Pod	100 Seed Weight (gm)			
Plant Height	rp†	0.056 ^{NS}									
(cm)	rg‡	0.066 ^{NS}									
No of	rp	0.019 ^{NS}	0.131**								
cluster/Plant	rg	0.025 ^{NS}	0.124*								
No. of	rp	0.050 ^{NS}	0.326**	0.090 ^{NS}							
pods/plant	rg	0.057 ^{NS}	0.368**	0.093*							
Pod Length	rp	0.089 ^{NS}	0.267**	0.019 ^{NS}	0.238**						
(cm)	rg	0.094*	0.308**	0.011 ^{NS}	0.286**						
Seeds Per	rp	-0.115*	0.056 ^{NS}	0.235**	-0.094*	0.041 ^{NS}					
Pod	rg	-0.124**	0.067 ^{NS}	0.274**	-0.116*	0.065 ^{NS}					
100 Seed	rp	0.037 ^{NS}	-0.028 ^{NS}	-0.069 ^{NS}	-0.139**	-0.001 ^{NS}	-0.030 ^{NS}				
Weight (gm)	rg	0.042 ^{NS}	-0.034 ^{NS}	-0.087 ^{NS}	-0.159**	0.009 ^{NS}	-0.065 ^{NS}				
Single plant	rp	-0.006 ^{NS}	0.239**	0.079 ^{NS}	0.502**	0.232**	0.374**	0.313**			
Yield(gm)	rg	0.005 ^{NS}	0.0248**	0.075 ^{NS}	0.537**	0.301**	0.415**	0.340**			

 Table 1: Phenotypic correlation matrix of 8 morphological traits pooled over two locations (Bhubaneswar and Jeypore).

† and ‡ enotes correlation co-efficient at phenotypic and genotypic level.

In the current investigation, considering pooled data, the correlation coefficients at genotypic level (r_g) were more or less higher in magnitude than phenotypic values (r_p) indicating that the apparent associations were largely due to genetic reasons. This supports the findings of Jadhav *et al.*, (2019). It is worth to note that 100- seed weight, seed number/pod, pod length, pod number/plant and plant height revealed highly significant positive association with seed yield at both genotypic and phenotypic level. The results were in conformity with the association studies of Marappa *et al.*, (2010); Tabasum *et al.*, (2010); Patel *et al.*, (2012); Patel *et al.*, (2014); Ramakrishnan *et al.*, (2018). Further, yield had feeble positive relationship with days

to 50% flowering indicating scope for recovery of high yielding plant types of medium maturity duration.

The correlation of seed yield with other characters was further partitioned to direct and indirect effects by path analysis to identify nature of contribution of the ancillary traits to the seed yield in the present set of mungbean germmplasm (Table 2). Diagonal figures represent direct effect of respective ancillary traits to seed yield, while indirect effect of each character indicates their role in influencing seed yield via other component characters to reflect correlative response.

Table 2: Path analysis of 7 component characters on yield in mungbean at phenotypic level pooled.

	Path co-efficient	Days to 50% flowering	Plant height (cm)	No. of clusters/pl ant	No. of pods/plant	Pod length (cm)	Seeds per pod	100-seed weight (g)
Days to 50%	Pp†	-0.006	0.001	-0.001	0.029	0.006	-0.052	0.015
flowering	Pg‡	0.013	-0.002	-0.002	0.038	0.007	-0.068	0.020
Plant height (cm)	Рр	0.000	0.025	-0.007	0.189	0.019	0.025	-0.011
	Pg	0.001	-0.034	-0.012	0.248	0.024	0.037	-0.016
No. of	Рр	0.000	0.003	-0.055	0.052	0.001	0.106	-0.028
clusters/Plant	Pg	0.000	-0.004	-0.094	0.063	0.001	0.150	-0.041
No. of pods/plant	Рр	0.000	0.008	-0.005	0.581	0.017	-0.042	-0.056
No. of pous/plant	Pg	0.001	-0.013	-0.009	0.673	0.023	-0.063	-0.075
Pod length (cm)	Рр	0.000	0.007	-0.001	0.138	0.071	0.018	0.000
Fou length (cm)	Pg	0.001	-0.011	-0.001	0.192	0.079	0.035	0.004
Seeds per pod	Рр	0.001	0.001	-0.013	-0.055	0.003	0.449	-0.012
	Pg	-0.002	-0.002	-0.026	-0.078	0.005	0.548	-0.031
100-seed weight	Рр	0.000	-0.001	0.004	-0.080	0.000	-0.014	0.404
(g)	Pg	0.001	0.001	0.008	-0.107	0.001	-0.036	0.472

 \dagger and \ddagger denotes path co-efficient at phenotypic and genotypic level. Residual effect P(R) =0.395.

Residual effect G(R) =0.241. Diagonal values (marked bold) indicate direct effects.

Residual effect of path coefficient analysis was found to be 0.395 at phenotypic level and 0.241 at genotypic level which envisaged that 60.5% and 75.9% of genetic variation have been exploited at phenotypic and genotypic level using eight quantitative traits. Besides, sampling errors and environmental factors are likely to contribute to the above residual effect (Sengupta and Karatia, 1971).

At phenotypic level, the highest direct positive effect (0.581) was revealed by pod number/plant on single plant yield followed by seed number/plant (0.449), hundred seed weight (0.404). In contrast, the highest direct negative effect on seed yield/plant was observed to be in case of number of clusters/plant (-0.055) followed by days to 50% flowering (-0.006). Plant height (0.189) showed highest indirect positive effect on single plant yield followed by pod length (0.138) through pod number/plant. Besides, hundred seed weight revealed highest negative indirect effect (-0.089) on seed yield through pod number per plant. Days to 50% flowering and cluster number/plant are positively correlated with single plant yield but showed direct negative effect on single plant yield due to negative influence of other component traits on the traits.

Conceptually, when the *inter se* trait association is positive and direct effect is negative or negligible, the indirect effect seems to be the cause of association and indirect causal factors simultaneously play significant role in judicial selection. In this study, plant height showed this type of relationship. It was also observed that pod number/plant had the highest direct positive effect on seed yield. This also affirms the finding of Mishra *et al.*, (2014) for pod number/plant, Khajudpam and Tantasawat (2011) for 100-seed weight, Patel *et al.* (2012) for cluster number/plant. Further, pod number/plant, pod length, seed number/pod and 100seed weight showed direct positive effect on seed yield at both level, which have been confirmed earlier by Tabasum et al., (2010); Aijaz et al., (2013); Patel et al., (2014); Pinchhyo et al., (2016); Varma et al., (2018); Mohan et al., (2019). On the other hand, days to 50% flowering, days to maturity, number of branch number/plant and cluster number/plant exhibited direct effects in negative direction on seed yield at either level. This agrees the study of Tabasum et al. (2010) for number, primary branch plant height, pod number/cluster and cluster number/plant. At both phenotypic and genotypic level, pod number/plant exhibited the highest indirect effect on seed yield followed by seed number per pods as also reported earlier by Marappa et al., (2010). Thus, the present findings would be of immense value for identification of valuable germplasm as well as selection of elite segregants in breeding programme of mungbean under cold stress.

FUTURE SCOPE

The present findings would be helpful for formulation of selection strategy for identification of parent materials in a set of germplasm lines as well as selection of elite plant types in mungbean breeding programme under cold stress.

Acknowledgement. The authors highly thanks Centre for Pulses Research, OUAT, Berhampur (Odisha) for providing germplasm stocks for the present study.

Conflict of Interest. The authors declare that there is no conflict of interests.

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How to cite this article: Dash, S., Lenka, D., Tripathy, S.K. and Dash, M. (2021). Association and Path Analysis of Morphoagronomic Traits in Mungbean Germplasm Under Cold Stress. *Biological Forum – An International Journal*, *13*(3): 245-248.