CORRELATION AND PATH ANALYSIS IN F_2 GENERATION OF MUNGBEAN (*Vigna radiata* (L.) R. Wilczek)

A.YUSUFZAI SANA [1], M. S. PITHIA[2], D. R. MEHTA [1] AND LATA RAVAL[1]*
[1]Department of Genetics and Plant Breeding, College of Agriculture,
[2]Pulses Research Station
Junagadh Agricultural University, Junagadh-362001, Gujarat
e-mail:lataraval@jau.in

ABSTRACT
Twenty six F_2 populations of green gram (*Vigna radiata* (L.) R. Wilczek) were evaluated in Randomized Block Design with three replications during *kharif* season to study character association for 10 yield and its component characters. There was positive, significant and strong association of seed yield per plant with plant height ($r_p = 0.254$ and $r_g = 0.299$) and number of pods per plant ($r_p = 0.607$ and $r_g = 0.654$). Days to maturity had positive, high and significant association with number of branches per plant ($r_p = 0.236$), 100- seed weight had positive significant and high correlation with number of seeds per pod ($r_p = 0.303$) and number of leaves per plant ($r_p = 0.254$), while days to flowering had positive and significant association with number of seeds per pod and negative and significant association with plant height ($r_p = -0.261$) at phenotypic level. Path coefficient analysis at genotypic as well as at phenotypic levels showed that days to maturity (-0.178) negative and plant height (0.226) and 100-seed weight (0.132) made positive high to moderate direct contribution towards seed yield per plant, indicating importance of these characters and can be strategically used to improve the seed yield per plant of green gram.

INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek) also known as greengram, mash bean, munggo, green bean and golden gram is one of the most important legume crop of India.Mungbean (*Vigna radiata* (L.) Wilczek) is one of the major pulse crops of India, which is cultivated from humid tropic to arid and semi-arid regions. Mungbean is cultivated in Bangladesh, China, India, Pakistan, Srilanka, Thailand, Philippines, Myanmar, Indonesia, East Africa, Nepal and Bhutan. Mungbean was originated in India from where it spread to Java, Eastern and Central Africa, West Indies, Warmer parts of China and U.S. The genus *vigna* belongs to Fabaceae family, species *Vigna radiata* with diploid chromosome number 2n = 22. It is an annual plant with erect to semi erect plant type. India is the largest producer and consumer of pulses in the world contributing around 25-28% of the total global production.The daily per capita availability of pulses in India has decreased from 69 g in 1961 to a meagre 35 g against FAO recommended dose of 80 g/day (Praharaj and Singh, 2015). During 2013-14 the import was to the tune of 3049.29 thousand tonnes. The import bill can be minimized by increasing production on one hand reducing post-harvest losses on the other (Anonymous, 2015). The country grows a variety of pulse crops, such as chickpea, pigeon pea, greengram, black gram, dry peas and lentils under a wide range of agro-climate conditions.Farmers grow this crop not as a principal crop but as a bonus crop, mixed with other crops on marginal lands and that too without manuring

(Patel *et al.*, 2014).Mungbean occupies an area of about 3.02 million hectares with a total production of 1.50 million tonnes

and a productivity of 498 kg per hectares in India (Anonymous, 2016 a). In Gujarat, the area under mungbean has been 0.117 million hectares with a total production of 0.073 million tonnes and a productivity of 625 kg per hectares (Anonymous, 2016 b). The productivity of mungbean is also very low as in case of other pulse crops. So there is an urgent need to raise the productivity and thereby total pulse production in order to meet protein requirement of our vegetarian people and to save the foreign exchange. Seed yield in mungbean like another crop is highly variable and complex character which has cumulative effect may contributed traits which are interrelated. Therefore, direct selection for yield may not be very effective. Owing to the complexity of the traits the significance of component approach in formulating successful breeding programme aimed at yield improvement has been emphasized. It has also been suggested that there may not be specific genes, for yield as such, but its various components that is available. A major cause of concern to a plant breeder is the constant improvement of the best available genotypes for further enhancement in their yield potential either directly or through improvement of various factors which contribute indirectly to high yield. The major consideration for a superior genotypes are high economic yield, desirable maturity duration and quality traits (Rathore *et al.*, 2015). Selection procedure is more difficult in a trait, where heritability is low or is not precisely measurable. Indirect selection in such a situation is more effective and study of correlation among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits (Searle,1965) and sequence of variation will also be influenced

(Waddington and Robertson,1966). Hence, the knowledge of genotypic and phenotypic correlation between yield and its contributing characters is very essential. Correlation studies measure only mutual association between two traits and it does not imply the cause and effect of relationship. Path coefficient analysis has been found useful direct and indirect causes of association and allows a detailed examination of specific forces acting to produce a given correlation and measures the relative importance of each causal factor (Kumar *et al.*, 2013). Therefore, keeping above said facts in mind, the present investigation was planned with 26 F_2 populations of mungbean.

MATERIALS AND METHODS

The present field experiment was conducted at Pulses Research Station, Junagadh Agricultural University, Junagadh during *kharif* season of year 2015-16. The experimental material for the present study consisted of 26 F_2 populations of mungbean, which were received from Research Scientist (Chickpea), Pulses Research Station, Junagadh Agricultural University, Junagadh. Experiment was laid in Randomized Block Design with three replications. Each row consisted of 4 m. inter and intra row spacing was kept 45 cm and 10 cm, respectively. The recommended package of practices was adopted to raisea good crop. The phonological characters were recorded on 20 randomly selected plans in each cross in each replication. The replication wise mean values were used for statistical analysis.Correlation coefficients were computed by the method suggested by Al- Jibouri *et al.* (1958). The data were subjected to covariance analysis from which different components of mean sum of products were estimated. Path coefficient analysis was carried out as outlined by Dewey and Lu (1959). Genotypic correlation coefficients of 9 variables with seed yield per plant were used to estimate the path coefficients for their direct effects of various independent characters on yield.

RESULTS AND DISCUSSION

In the present investigation, most of the character pairs recorded higher values of genotypic correlations than their corresponding phenotypic correlations. Such high amount of genotypic correlations could result due to masking or modifying effect of environment on the association of characters. This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environmental factors. Estimation of correlation coefficients at genotypic and phenotypic levels is presented in Table 1. The values of genotypic correlation were higher than the phenotypic correlation coefficients. The character plant height ($r_p = 0.254$ and $r_g = 0.299$) and number of pods per plant ($r_p = 0.607$ and $r_g = 0.654$) had positive, significant and strong correlation with seed yield per plant at phenotypic and genotypic level. These results were in accordance with Kumar *et al.* (2013), Patel *et al.* (2014), Hemavathy *et al.* (2015) and Indu (2015).While, it was observed negative by Rahim *et al* (2010).

Day to flowering was significantly and positively associated with number of seeds per pod ($r_p = 0.571$) at phenotypic level. Similar findings were obtained by Ahmad *et al.* (2015). While contrary to this Patel *et al.* (2014) observed negative and significant relation. Days to flowering had negative, but significant correlation with pod length ($r_p = -0.261$). Srivastava and Singh, (2012) and Patel *et al.* (2014) also found same relationship, but Makeen *et al.* (2007) observed positive and significant association between days to flowering and pod length. The difference might be due to different climate conditions, type and nature of genetic material used in the study.

Days to maturity had positive and significant association with pod length ($r_p = 0.346$) and number of branches per plant

Table 4.5: Genotypic (r_g) and phenotypic (r_p) correlation coefficients among ten characters of 26 F_2 populations of mungbean

Characters		Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Number of leaves per plant	100-seed weight (g)	Seed yield per plant (cm)
Days to flowering	r_g	-0.237	-0.037	-0.196	-0.157	-0.38	0.832	0.047	0.154	0.096
	r_p	-0.155	-0.07	-0.136	-0.11	-0.261*	0.571**	0.067	0.106	0.029
Days to maturity	r_g		0.335	0.293	0.189	0.473	0.039	0.199	0.305	-0.047
	r_p		0.144	0.236*	0.181	0.346**	0.008	0.034	0.143	-0.061
Plant height (cm)	r_g			0.235	0.208	0.238	-0.25	-0.002	-0.322	0.299
	r_p			0.164	0.189	0.13	-0.16	0.104	-0.205	0.254*
Number of branches per plant	r_g				0.088	0.371	-0.124	-0.11	0.157	0.001
	r_p				0.041	0.154	-0.165	0.051	0.013	-0.018
Number of pods per plant	r_g					0.335	-0.141	-0.051	0.447	0.654
	r_p					0.208	-0.115	0.083	0.215	0.607**
Pod length (cm)	r_g						0.128	0.016	0.489	0.117
	r_p						0.035	-0.083	0.303**	0.028
Number of seeds per pod	r_g							0.074	0.5	-0.002
	r_p							0.103	0.254*	-0.023
Number of leaves per plant	r_g								-0.583	-0.156
	r_p								-0.192	-0.023
100-seed weight (g)	r_g									0.297
	r_p									0.188

*, ** Significant at 5 and 1 % levels, respectively

Table 4.7: Phenotypic (P) and Genotypic (G) path coefficient analysis showing direct and indirect effects of different characters on seed yield in 26 F$_2$ populations in mungbean

Characters		Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Number of leaves per plant	100-seed weight	Genotypic and Pheno typic corre lation with seed yield per plant
Days to flowering	G	0.346	0.018	-0.003	0.01	-0.113	-0.057	-0.066	-0.011	-0.028	0.096
	P	0.017	0.027	-0.015	0.001	-0.067	0.028	0.029	-0.005	0.014	0.029
Days to maturity	G	-0.082	-0.079	0.028	-0.015	0.136	0.071	-0.003	-0.046	-0.056	-0.047
	P	-0.002	-0.178	0.032	-0.002	0.11	-0.037	0.001	-0.002	0.018	-0.061
Plant height (cm)	G	-0.012	-0.026	0.085	-0.012	0.15	0.035	0.02	0.001	0.059	0.299
	P	-0.001	-0.025	0.226	-0.001	0.114	-0.014	-0.008	-0.008	-0.027	0.254*
Number of branches per plant	G	-0.068	-0.023	0.02	-0.054	0.063	0.055	0.009	0.025	-0.029	0.001
	P	-0.002	-0.042	0.037	-0.008	0.025	-0.016	-0.008	-0.004	0.001	-0.018
Number of pods per plant	G	-0.054	-0.015	0.017	-0.004	0.72	0.05	0.011	0.011	-0.083	0.654
	P	-0.002	-0.032	0.042	-0.001	0.606	-0.022	-0.005	-0.006	0.028	0.607**
Pod length (cm)	G	-0.132	-0.037	0.02	-0.02	0.241	0.15	-0.01	-0.003	-0.091	0.117
	P	-0.004	-0.061	0.029	-0.001	0.126	-0.108	0.001	0.006	0.04	0.028
Number of seeds per pod	G	0.288	-0.003	-0.021	0.006	-0.102	0.019	-0.079	-0.017	-0.093	-0.002
	P	0.01	-0.001	-0.036	0.001	-0.069	-0.003	0.051	-0.008	0.033	-0.023
Number of leaves per plant	G	0.016	-0.015	-0.001	0.006	-0.036	0.002	-0.006	-0.231	0.108	-0.156
	P	0.001	-0.006	0.023	-0.001	0.05	0.009	0.005	-0.081	-0.025	-0.023
100-seed weight (g)	G	0.053	-0.024	-0.027	-0.008	0.322	0.073	-0.039	0.134	-0.185	0.297
	P	0.001	-0.025	-0.046	-0.001	0.13	-0.033	0.013	0.015	0.132	0.188

*, ** Significant at 5 and 1 % levels, respectively;Residual effect: R= 0.683 (Genotypic) R=0.734(Phenotypic);Bold letters indicates direct effect of respective characters

(r_p = 0.236, r_g = 0.293) at phenotypic level. In addition to above, comparatively strong association was reported between days to maturity and plant height (r_g = 0.335) at genotypic level. Makeen *et al.* (2007) and Patel *et al.* (2014) confirmed the results by reporting same relationship of days to maturity with pod length. There was strong association between days to maturity with pod length (r_g = 0.473), number of branches per plant (r_g = 0.293) at genotypic level. While, it was observed negative for number of branches per plant by Patel *et al.* (2014). Plant height (r_p = 0.254) and number of pods per plant (r_p = 0.607) had positive and significant association with seed yield per plant at phenotypic level. This finding is in conformity with of Kumar *et al.* (2013), Patel *et al.* (2014), Hemavathy *et al.* (2015) and Indu (2015). Plant height also had positive and strong genotypic association with number of branches per plant (r_g = 0.235) and pod length (r_g = 0.238). Number of pods per plant (r_g = 0.654) had very strong relation with seed yield per plant at genotypic level. Pod length showed positive and significant association with 100-seed weight (r_p = 0.303). These findings are in accordance with Rathore *et al.* (2015). Number of seeds per pod had positive and significant interrelationship with 100-ssed weight (r_p = 0.254) at phenotypic level. Rathore *et al.* (2015) recorded same results.

From all above discussed phenotypic correlations most of them were supported with strong genotypic correlation of high magnitude and in the same direction. So, in all these cases the role of environment was found to be limited and hence, the selection practiced on the basis of phenotypic correlation would be fruitful for those characters.

Considering the seed yield as the effect and nine quantitative characters as causes, the path coefficient analysis was done to find out the direct and indirect contribution of yield contributing characters towards seed yield in mungbean. The phenotypic (0.734) and genotypic (0.638) residual effects were high. This indicated that high contribution of those characters which were not included in the present investigation.

Number of pods per plant (r_p = 0.606) showed maximum direct contribution towards seed yield per plant. The similar results were obtained by Raturi *et al.* (2015), Rathore *et al.* (2015), Murlidhara *et al.* (2015) and Katiyar *et al.* (2015). Hundred seed weight (0.132) had positive and moderate direct effect towards seed yield per plant which was supported by Hemavathy *et al.* (2015) and Rathore *et al.* (2015).While, there was positive and low direct effect of days to maturity (-0.061), plant height (0.226) and number of seeds per pod (0.051) on seed yield per plant. The similar results were obtained by Srivastava and Singh (2012) for days to maturity and plant height; Suresh *et al.* (2013) and Ahmad *et al.* (2015) for number of seeds per pod. Day to maturity (-0.178) and pod length (-0.108) exerted negative and moderate direct effect on seed yield per plant which was supported by Rahim *et al.* (2010). Katiyar *et al.* (2015) and Rathore *et al.* (2015). While, number of branches per plant (-0.008) and number of leaves per plant (-0.081) had negative and low direct effect on seed yield per plant. The above said characters which had positive and high to moderate direct effect are of immense importance for mungbean improvement programme. Breeder can consider the above characters on the basis of their phenotypic performance because some of these characters also possessed good genotypic association.While days to flowering (-0.067), plant height (0.114), pod length (0.126) and 100-seed weight (0.130) exerted appreciable indirect influence towards seed yield per plant through number of pods per plant both at genotypic and phenotypic level. These findings were in accordance with Kumar *et al.* (2013) and Hemavathy *et al.* (2015).

To conclude, it indicated that the number of pods per plant was the most important yield contributing character while, 100-seed weight and plant height were of secondary important yield component. Breeder can consider the above characters on the basis of their phenotypic performance because some of these characters also possessed good genotypic association.

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