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Correlation Studies for Quantitative Traits in Greengram [*Vigna radiata* (L.) Wilczek] Genotypes

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Greengram, an important grain legume of the arid and semi-arid regions has enough genetic diversity both for quantitative and qualitative characters. Genotypic correlation studies enable breeders to assess the inherent pattern relationship between various traits since it is based on heritable traits. The genotypic correlation for 40 greengram germplasm for 10 quantitative traits *viz.,* days to 50 per cent flowering, number of branches/plant, plant height (cm), number of clusters/plant, number of pods/plant, number of pods/cluster, number of seed/pod, pod length (cm), single plant yield (g) and hundred seed weight (g) were evaluated at two different centers *viz.,* Agricultural College and Research Institute, TNAU, Madurai (*kharif* 2012 and *rabi* 2012), and Agricultural Research Station, TNAU, Vaigai Dam (*kharif* 2012*)*. The correlation of yield and yield contributing characters indicated that seed yield/plant was positive and significantly associated with days to maturity, plant height, number of pods/plant, number of seeds/pod and hundred seed weight. Hence, characters such as plant height, numbers of pods/plant, number of branches/plant, number of clusters/plant and number of seeds/pod has to be given importance during the selection programme to improve the yield potential of the crop.

Key Words: Correlation, Germplasm, Mungbean, Quantitative characters

Introduction

Pulses are major source of dietary protein in the vegetarian diet in our country. Among the cultivated Asian *Vigna*, mungbean [*V. radiata* (L.)Wilczek] is the most important one (Rahman *et al.,* 2003). Besides being a rich source of protein, it maintains soil fertility through biological nitrogen fixation in soil and thus, plays a vital role in furthering sustainable agriculture. Mungbean is a short duration grain legume crops with wide adaptability and deep root system, low input requirements, and suitable for crop rotations, intercropping, relay cropping and as catch crop (Payasi *et al*., 2010). Genetic diversity in mungbean is an important factor and also a pre-requisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable recombinations (Gokulakrishnan *et al.,* 2012). Genotypic correlation enables the breeder to assess the inherent pattern relationship between various traits, since it is based on the heritable part. Hence, the present investigation was carried out with the aim to study the genotypic correlation for the yield contributing characters over different environments in mungbean germplasm.

Materials and Methods

The present investigation was carried out in 40 mungbean genotypes during *kharif* 2012 and *rabi* 2012. The trials were laid out in randomized block design with three replications at three different environments *viz.*, Agricultural College and Research Institute (ACRI), TNAU, Madurai (E1) *kharif* 2012, Agricultural Research Station, TNAU, Vaigai Dam (E2) *kharif* 2012 and ACRI, TNAU, Madurai (E3) *rabi* 2012. In this study, genotypic correlation for 10 quantitative traits *viz.*, days to 50 per cent flowering, number of branches/plant, plant height, number of clusters/plant, number of pods/plant, number of pods/cluster, number of seed/pod, pod length, single plant yield and hundred seed weight were analyzed. Phenotypic and genotypic correlation coefficients were calculated as outlined by Kwon and Torrie (1964). Genotypic correlation was tested for its statistical significance using the method of Reeve (1955). The genotypic correlation between yield and its component traits and among themselves was worked out as per the method suggested by Johnson *et al.* (1955) for three different locations.

Results and Discussion

Genetic diversity analyses can be performed on both qualitative and quantitative data or on a combination of both. To formulate any breeding programme with an objective of improving the yield and quality through selection, the inter-relationship among different characters is of paramount importance. It has been generally accepted

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that correlation between different characters represents a coordination of physiological processes, which is often achieved through well regulated gene expression (Mather and Jinks, 1971). Correlation coefficients at genotypic level were generally of higher magnitude than the corresponding phenotypic level indicating the strong association between the characters. The genotypic correlation for the 10 quantitative traits are presented location wise in Table 1 (E1 location), Table 2 (E2 location) and Table 3 (E3 location).

Seed yield was significant and positively correlated to number of pods/plant, hundred seed weight at genotypic level in E1 and E2 locations. Seed yield was significant and positively correlated to number of pods/cluster, at genotypic level in E2 and E3 locations. The correlation of yield and yield contributing characters indicated that seed yield/plant was positive and significantly associated with days to maturity, plant height, number of pods/plant, number of seeds/pod and hundred seed weight. Parameswarappa and Salimath (2007) reported similar findings in greengram.

It is obvious that improvement of one trait results in the simultaneous improvement of all positively associated component characters (Kalloo, 1998). Number of branches/plant exhibited positive and significant association with days to 50 percent flowering at E1 and E3 locations. Similar results were reported by Suresh *et al.* (2010) in greengram. Plant height had significant positive correlation with days to 50 percent flowering, number of branches/plant at all the locations. Number of pods/plant exhibited positive and significant association with number of clusters/plant at all the three locations. This was in confirmation with the findings of Muhammad Zubair *et al*. (2007) for number of pods/plant, number of clusters/plant and 100-seed weight, Rahim *et al.* (2010) for number of pods/plant and pod length in mungbean.

Table 1. Genotypic correlation coefficient of yield and yield attributing characters in AC & RI, Madurai, Kharif 2012 (E1)

Trait	Days to 50% flowering	Number of branches/ plant	Plant height	Number of clusters/ plant	Number of pods/ plant	Number of pods/ cluster	Number of seeds/ pod	Pod length	Hundred seed weight	Seed yield/ plant
Days to 50% flowering	1.000	0.747*	0.657*	-0.158	0.036	0.169	0.180	-0.179	-0.121	-0.193
Branches/ plant		1.000	0.813*	0.139	0.110	0.034	0.383*	-0.217	0.192	0.061
Plant height			1.000	0.069	0.204	0.053	0.395*	-0.228	0.228	0.122
Clusters/plant				1.000	0.445*	0.247*	0.596*	0.661*	0.283*	1.031*
Pods/plant					1.000	0.147	-0.012	-0.072	0.496*	0.522*
Pods/cluster						1.000	0.282*	0.223	0.026	0.153
Seeds/pod							1.000	0.923*	0.280*	0.539*
Pod length								1.000	0.194	0.574*
100-seed weight									1.000	0.456*
Seed yield/plant										1.000

*Significance at 5% level

Table 2. Genotypic correlation coefficient of yield and yield attributing characters in ARS, Vaigai Dam, Kharif 2012 (E2)

Trait	Days to 50% flowering	Branches/ plant	Plant height	Clusters/ plant	Pods/ plant	Pods/ cluster	Seeds/ pod	Pod length	100-seed weight	Seed yield/ plant
Days to 50% flowering	1.000	0.235	0.389*	0.084	0.307*	0.014	0.083	-0.325*	0.266*	0.198
Branches/plant		1.000	0.712*	-0.087	0.160	0.029	0.159	-0.353*	0.010	-0.005
Plant height			1.000	-0.070	0.014	-0.093	0.217	-0.274*	-0.118	-0.072
Clusters/plant				1.000	0.438*	0.063	0.406*	0.205	0.435*	0.300*
Pods/plant					1.000	0.604*	0.299*	-0.137	0.676*	0.765*
Pods/cluster						1.000	0.273*	-0.251*	0.186	0.445*
Seeds/pod							1.000	0.340*	0.015	-0.088
Pod length								1.000	0.040	-0.113
100-seed weight									1.000	0.487*
Seed yield/plant										1.000

*Significance at 5% level

Table 3. Genotypic correlation coefficient of yield and yield attributing characters in AC &RI, Madurai, Rabi 2012 (E3)

Trait	Days to 50% flowering	Branches/ plant	Plant height	Clusters/ plant	Pods/ plant	Pods/ cluster	Seeds/ pod	Pod length	100-seed weight	Seed yield/ plant
Days to 50% flowering	1.000	0.409*	0.624*	0.023	-0.218	0.019	0.120	0.016	-0.026	-0.052
Branches/ plant		1.000	0.654*	-0.174	-0.134	0.068	0.355*	0.104	0.040	0.096
Plant height			1.000	0.118	-0.022	0.031	0.249*	-0.004	0.008	0.256*
Clusters/plant				1.000	0.297*	0.161	0.668*	-0.073	-0.178	0.420*
Pods/plant					1.000	0.243	0.270*	-0.226*	0.360*	0.217
Pods/cluster						1.000	0.299*	-0.056	0.190	0.311*
Seeds/pod							1.000	0.009	0.302*	0.131
Pod length								1.000	-0.224	-0.124
100-seed weight									1.000	0.243
Seed yield/plant										1.000

*Significance at 5% level

The positive association between number of pods/ plant and plant height was observed by Suresh *et al.* (2010) in greengram. The positive association between number of pods/plant with number seeds/plant was observed by Konda *et al*. (2008). Number of seeds/pod had positive significant correlation with number of clusters/plant, number of pods/plant, number of pods/cluster at E1 and E3 locations. Mallikarjuna Rao *et al*. (2006) found significant positive correlation for number of branches/ plant in greengram. Hundred seed weight exhibited positive and significant association with number of pods/ plant, number of seeds/pod at E1 and E2 locations. In this study, the estimated correlation coefficients showed that not all the characters were interrelated with seed yield or among themselves.

Conclusions

It is concluded from the present study that seed yield/ plant was positive and significantly associated with days to maturity, plant height, number of pods/plant, number of seeds/pod and hundred seed weight. All the yield component traits *viz.*, days to 50 % flowering, plant height, number of branches/plant, number of clusters/ plant, number of pods/plant, pod length, number of seeds/pod and hundred seed weight were inter correlated among themselves. Therefore, these traits are to be given priority during selection programme to increase the single plant yield in greengram.

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