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Genetic Parameters of Variation and Character Association for Seed Yield and its Attributes in Mungbean (*Vigna radiata* L. Wilczek)

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ABSTRACT

Background: The yield levels in mung bean reached a plateau, which emphasizes breeding for varieties with improved productivity. The basic requirements of any breeding include the understanding of different genetic parameters of various yield related traits along with the knowledge with regards to interrelationships and cause and effect of those relations among the quantitative traits.

Methods: In the present investigation, sixty germplasm lines were evaluated using Augmented Randomized Complete Block Design in respect of eleven quantitative traits for three years *i.e.,* during kharif seasons of 2017-18, 2018-19 and 2019-20 to understand the genetic architecture of different genetic parameters along with associations and their cause and effects of different traits on grain yield.

Result: The pooled analysis revealed significant variability for majority of traits. High heritability coupled with high genetic advance was observed in case of pods per plant, clusters per plant, plant height, test weight, seeds per pod, pods per cluster and grain yield indicating probable operation of additive gene action in inheritance of these traits. Clusters per plant and pods per plant which registered high GCV, high heritability and high genetic advance as percent of mean. The association studies revealed significant associations of pods per plant, clusters per plant, pods per cluster, branches per plant, days to maturity, pod length with grain yield per plant at both phenotypic and genotypic levels in desirable direction. Further, it was found that all these six traits which had significant association with yield also established significant magnitude of direct effects in desirable direction which contributed to the significant associations hence, can be considered simultaneously during selection.

Key words: Genetic parameters of variation, Trait associations, Yield and Yield attributes, *Vigna radiata.*

INTRODUCTION

Mungbean is considered as a major pulse crop in Asia since ancient times which originated in Indian sub-continent (De Candolle, 1886). It is an easily digestible pulse crop and. occupies an important position in the diets of vast majority of population in the Indian sub-continent. It contains 51% carbohydrate, 24-26% protein, 4% mineral and 3% vitamins. Being rich in nutritional profile, it is an inseparable component of human diet. This crop is cultivated in 4.75 million hectares in India with the production and productivity of 2.45 million tonnes and 516 kg/ha, respectively. In Andhra Pradesh it is cultivated in 0.12 million hectares with a production 84.71 thousand tonnes and productivity of 700 kg/ha. (Indiastat.com, 2018-19). Though the productivity of Andhra Pradesh is higher than that of India, there is still lot of potential to increase the productivity which can be attributed to the low management practices and cultivation of varieties with low productivity. Further, the average consumption of mungbean in India is about 24g per day, which is lower than the Recommended Dietary Allowances (RDA) of 35g per consumption unit per day as per National Institute of Nutrition. Hence, there is a great need for increased production of greengram through better understanding of constraints in its production.

The success of any breeding programme for increased productivity depends upon the quantum of genetic variability present in the population. In addition to the genetic variability, knowledge on heritability and expected genetic advance helps the breeder to employ the suitable breeding strategy. The change in one character brings about a series of changes in the other characters, since they are interrelated. Therefore, the correlation studies are of considerable importance in any selection programme as they provide degree and direction of relationship between two or more component traits. Path coefficient analysis provides a thorough understanding of contribution of various characters by partitioning the correlation coefficient into components of direct and indirect effects (Wright, 1921), which helps the

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breeder in determining the yield components. Hence, the present investigation was conducted for three years with sixty germplasm lines with respect to eleven quantitative traits for estimation of variability, heritability and genetic advance, correlations and their direct and indirect effects.

MATERIALS AND METHODS

Plant Material

Sixty germplasm line of mungbean., LGG 629, LGG 639, PM 110, SMP 17-16, LGG 595, LGG 644, LGG 600, LGG 555, LGG 602, OBGG 56, LGG 632, OBGG 58, LGG 636, RM 16-9, LGG 631, LGG 605, LGG 625, LGG 509, RM 16-2, SMP 17-14, LGG 407, WGG 42, TLM 24, LGG 576, LGG 626, RM 16-3, LGG 634, AGG 35, LGG 630, LGG 604, LGG 609, LGG 578, Pusa Vishal, PM 5, LGG 607, PM 115, LGG 616, LGG 627, LGG 610, LGG 615, LGG 617, LGG 650, LGG 647, OBGG 57, PM 112, LGG 603, GGG 1, Pusa 0972, TARM 1, VBN (G8)-2, VGG 15-30, MGG 385, CO 6, MGG 387, VGG 036, NVL 722, CoGG 13-39, VGG 16-027, VGG 16-057, LGG 586 were used for present investigation. Along with the above sixty lines four genotypes *viz.,* LGG 460, TM 96-2, LGG 450, IPM 2-14were employed as checks.

Experimental technique

Present investigation was taken up at Advanced P.G. Center, Lam, Guntur Andhra Pradesh, India which is located at 16.36° N latitude, 80.42° E longitude and 31.5 m altitude. The experiment was carried out in three consecutive years *i.e*., during *kharif* seasons of 2017-18, 2018-19 and 2019-20. Sixty germplasm lines along with the mentioned four checks were grown in Augmented Randomized Completely Block Design (ARCBD) with five blocks. In each block 12 test genotypes were grown at random along with four checks. In all the blocks the four checks were randomly grown. Each entry was grown in two rows of four meter length. The seed was sown with a spacing of 30 cm between rows and 10 cm with in rows. The required crop protection practices were followed as per the requirement. Basal application of 20kg N and 50kg P was given in the last ploughing.

The data collected on eleven traits *viz.,* days to 50% flowering, plant height, branches per plant, days to maturity, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, test weight and grain yield per plant on the sixty germplasm lines along with four checks over three years was subjected to Bartlett's test for confirming homogeneity between the seasons before pooling the data (Gomez and Gomez, 1984). The pooled data was subjected to analysis of variance (ANOVA) characters wise as per standard statistical procedure for Augmented Randomized Complete Block Design (Augmented Design II) as given by Federer (1956). The significance of mean sum of squares was tested by referring to "F" table value given by Fisher and Yates (1963)**.** Phenotypic and genotypic variances were estimated using the formula given by Federer and Searle (1976). The genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated using the formula given by Burton (1952). Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage. Genetic advance for each trait was calculated based on formula given by Johnson *et al.* (1955).

The phenotypic and genotypic correlation coefficients were worked out to as per Falconer (1964). Path coefficient analysis was carried out by using the both phenotypic and genotypic correlation coefficients to know the direct and indirect effects of the component characters on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Further coefficient of determination (R^2) and residual effects were also calculated using the formula given by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance, PCV and GCV

The pooled analysis of variance for three years of Augmented Randomized Complete Block Design (Table 1) revealed significant differences in the set of genotypes under study for all the traits except for branches per plant and days to maturity. The checks vs Genotypes component of source of variation had significant differences in terms of days to 50% flowering, clusters per plant, pods per cluster, pod length and seeds per pod. None of the traits are significant at block level.

The MSS (Table 1) of different traits at genotypic level is further confirmed by the respective PCV and GCV values. Highest estimate of GCV magnitude (reliable portion of variation) among the traits which had significant MSS over years, was recorded for pods per plant (43.73%) followed by clusters per plant (36.13%), seeds per pod (17.69%), plant height (16.66%), test weight (16.28%), pods per cluster (15.33%), grain yield per plant (14.97%), branches per plant (14.63%) and pod length (10.11%). Similar PCV and GCV magnitudes were earlier indicated for various traits in mungbean by different scientists [Muralidhara *et al.* (2015), Raturi *et al.* (2015), Anand *et al.* (2016), Garg *et al.* (2017), Ghimire *et al.* (2017), Kate *et al.* (2017), Shiv *et al.* (2017) Azam *et al.* (2018)]. In general, the values of PCV were higher than GCV indicating the role of environment on the visible variation. These results of variance, PCV and GCV indicate ample amount of variation in the material under investigation for different traits, giving scope for utilization of the material in crop improvement programmes.

Heritability and Expected Genetic advance

The information on magnitude of GCV alone may not be trusted and these GCV values are to be viewed along with the heritability of that trait in question. Burton way back in 1952 itself emphasized the consideration of genetic variability along with heritability estimates to get an idea on expected genetic gain under selection. Highest magnitude of heritability over years was recorded in case of pods per plant followed by test weight, clusters per plant, plant height, pod length and seeds per pod. While least magnitude of heritability was recorded in case of days to maturity followed by days to 50% flowering. Low heritability was observed in case of days to maturity. While, days to 50% flowering and branches per plant registered moderate magnitude of heritability. Higher magnitudes of GCV coupled with high heritability were observed in case of pods per plant (43.73% GCV, 93.50 h^2_{bs}) and clusters per plant (36.13% GCV, 87.76% h^2_{bs}). The existence of higher amount of genotypic variation with high heritability will be fruitful in selection. Similarly, moderate GCV (10% to 20%) and high heritability (>60%) were recorded in case of test weight, plant height, pod length, seeds per pod, grain yield per plant and pods per cluster (Table 2).

These traits with moderate GCV and high heritability may also result in considerable gain during selection. However, it is not necessary that a trait showing higher heritability should always exhibit higher genetic advance (Johnson *et al*., 1955). Therefore, estimation of expected genetic advance is important before actually planting the material for taking up selection. High expected genetic advance as per cent of mean (> 20%) was found in seven out of eleven traits, moderate (10% to 20%) in one trait (pods per plant) and low (< 10%) in two traits (days to maturity and days to 50% flowering). The characters with highest heritability [pods per plant (93.50%), test weight (89.19%), clusters per plant (87.76%) and plant height (87.56%),] have recorded highest genetic advances as per cent of means [pods per plant (87.11%), test weight (31.67%), clusters per plant (69.72%) and plant height (32.12%)]. However, the traits varied in ranking with respect to heritability and genetic advance as per cent of mean. Further, pod length which had high heritability (78.28%) recorded only moderate (18.42%) genetic advance as per cent of mean (Table 2) indicating that one can not completely rely on broad sense heritability estimates. Further, it can be inferred that considering genetic parameters separately will be always misleading hence all the genetic parameters need to be studies simultaneously for proper understanding of the trait. Higher estimates of PCV, GCV, h^2_{bs} and genetic advance as per cent of mean were recorded for pods per plant and clusters per plant. Similar higher estimates of all the genetic parameters for these two traits were also observed by Ahamed *et al*. (2015) and Muralidhara *et al*. (2015).

The estimates of heritability and genetic advance as per cent of mean were high for the characters *viz.,* plant height, clusters per plant, pods per cluster, pods per plant, seeds per pod, test weight and grain yield per plant indicating the probable operation of additive gene action in inheritance of these traits. Similar results for the above seven traits were earlier reported by Ahmad *et al.* (2015), Muralidhara *et al.* (2015), Anand *et al.* (2016), Garg *et al.* (2017), Shiv *et al.* (2017), Mehandi *et al.* (2018), Ramakrishnan *et al.* (2018) and Sharma *et al.* (2018).High heritability coupled with

Table 1: Analysis of variance for grain yield and other characters in mung bean [*Vignaradiata* (L.) Wilczek].

Sources of variations	d.f	DFF	PH	BPP	DTM	CPP	PPC	PPP	PL	SPP	TW	GYP
		Mean sum of squares										
Block	4	1.89	59.26	2.13	28.03	30.95	0.31	180.01	0.08	1.87	0.29	1.67
Entries	63	8.91*	82.83**	0.86	21.37	8.58**	0.47*	76.74**	0.66**	6.41**	0.48**	1.58**
Checks	3	61.67**	134.45**	1.25	160.98*	47.13**	0.20	444.33**	1.66**	5.52	1.41**	10.05**
Genotypes	59	5.52	85.32**	0.90*	14.79	6.53**	0.41*	68.61**	0.60**	4.41*	0.45**	1.16*
Checks vs. Genotypes	1	50.79**	0.99	1.87	0.29	13.94**	5.41**	20.77	1.18*	127.03**	0.59	1.16
Error	12	2.75	10.62	0.37	12.40	0.80	0.16	4.46	0.13	1.64	0.05	0.45

* Significant at 5% level

** Significant at 1% level

DFF=Days to 50% flowering, PH=Plant height, BPP=Branches per plant, DTM=Days to maturity, CPP=Clusters per plant, PPP=Pods per plant, PL=pod length, SPP=Seeds per pod, TW=Test weight and GYP=Grain yield per plant.

moderate genetic advance as per cent of mean was observed for pod length. Moderate heritability coupled with low genetic advance as per cent of mean was observed for days to 50% flowering. While days to maturity had low heritability and low genetic advance as per cent of mean.

Trait associations

The character associations at both phenotypic and genotypic levels over three years of evaluation with respect to eleven characters for the sixty mungbean genotypes were presented in the Table 3. From the phenotypic and genotypic correlations, it was observed that genotypic correlations are higher than phenotypic correlations. This indicates that apparent associations are largely due to genetic reasons. The traits *viz.,* pods per plant (0.7872**, 0.8521**), clusters per plant (0.6946**, 0.7628**), pods per cluster (0.6452**, 0.7631**), branches per plant (0.2713**, 0.3800**), days to maturity (-0.1780*, -0.2293**) and pod length (0.1781*, 0.2060**) were found to possess significant positive association with grain yield per plant in desirable direction at both phenotypic and genotypic levels. This infers that mungbean lines with higher pod number, more clusters per plant, more pods per cluster, more branches per plant and lengthier pods with less duration to maturity are productive in terms of grain yield. Further, plant height (-0.2559*) and seeds per pod (0.1494*) had negative and positive significant associations respectively, at genotypic level with grain yield per plant. Hence, selection for these two characters in the specified direction will also help in selecting genotypes with high grain yield per plant. Positive correlations are due to control of the traits which are under control of genes responsible for direct production of precursors. While, negative correlations occur due to the restricted supply of precursor for which traits compete against each other (Madhur and Jinks, 1994). The pictorial representation of phenotypic and genotypic correlations are also indicated in Fig 1 and 2, respectively. Darker the shade stronger is the association between the traits (Fig 1 and 2).

The dependent variable also had non significant associations with days to 50% flowering (-0.0344, -0.0697) and test weight (0.0010, 0.0055), at both phenotypic and genotypic levels. This demonstrates that early flowering need not strongly associate with higher yields in mungbean despite having significant positive association between days to 50% flowering and days to maturity at both levels. The traits which are not having any significant association with yield might have assorted independently with respect to yield controlling genes. However, these traits may contribute through indirect effects of other traits.

Many researchers established associations of various quantitative characters with grain yield per plant indicating the scope of indirect selection for yield improvement in mungbean. Ahamed *et al.* (2015) and Anand *et al*. (2016) reported significant positive associations of pods per plant and clusters per plant with grain yield per plant at both phenotypic and genotypic levels. Thippani *et al.* (2013) confirmed the significant positive association of pods per cluster with grain yield at both levels, indicating the importance of these traits during selection. The significant association of branches per plant and days to maturity with grain yield per plant in the desirable direction was reinforced by the observations of Eswaran and Senthilkumar (2015) at genotypic level for branches per plant and Kumar *et al*. (2018) for days to maturity at phenotypic level. While, Das and Barua (2015) found significant positive association of pod length with grain yield per plant at both phenotypic and genotypic levels which is in accordance with current results. Among various traits (independent variables), maximum association at both phenotypic and genotypic level was observed between; clusters per plant and pods per plant; pod length and seeds per pod;pods per cluster and pods per plant; days to 50% flowering and days to maturity and;

Table 2: Estimates of variability, heritability and genetic advance as per cent of mean for grain yield and other traits in mung bean [*Vigna radiata* (L.) Wilczek].

Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as % of mean
		Minimum	Maximum	PCV (%)	GCV (%)		
Days to 50% of flowering	34.11	28.66	39.00	6.89	4.88	50.18	7.12
Plant height (cm)	51.87	35.32	76.40	17.81	16.66	87.56	32.12
Branches per plant	4.97	3.00	7.20	19.13	14.63	58.47	23.04
Days to maturity	69.31	61.00	78.66	5.55	2.23	16.16	1.85
Clusters per plant	6.63	2.00	13.20	38.57	36.13	87.76	69.72
Pods per cluster	3.27	2.00	4.80	19.57	15.33	61.32	24.73
Pods per plant	18.32	5.20	36.60	45.23	43.73	93.50	87.11
Pod length (cm)	6.79	5.46	9.31	11.42	10.11	78.28	18.42
Seeds per pod	9.41	4.80	13.60	22.32	17.69	62.81	28.88
Test weight (g)	3.90	2.80	5.90	17.24	16.28	89.19	31.67
Grain yield per plant (g)	5.63	3.54	7.26	19.10	14.97	61.43	24.17

PCV = Phenotypic coefficient of variation
GCV = Genotypic coefficient of variation

Table 3: Phenotypic and genotypic correlations among grain yield and component characters in mung bean (*Vigna radiata* L. Wilczek).

		Plant height	Branches per plant	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	Test weight	Grain yield per plant
Days to 50% flowering	P	0.1418	-0.0799	0.5062**	0.0676	-0.0846	0.0393	-0.0691	-0.0634	-0.1573*	-0.0344
	G	0.2351**	-0.1796*	0.7297**	0.0656	-0.0741	0.0405	-0.1880*	-0.0444	-0.2478**	-0.0697
Plant height	P		-0.1181	0.1814*	-0.0034	-0.0093	0.0457	-0.2890**	-0.1172	-0.2985**	-0.1155
	G		-0.1738*	0.2765**	-0.0251	-0.0475	0.0599	-0.3640**	-0.1352	-0.3579**	-0.1539*
Branches per plant	P			-0.1944**	0.2728**	0.1426	0.2850**	0.2780**	0.4559**	0.1363	0.2713**
	G			-0.3468**	0.3435**	0.1530*	0.3637**	0.4323**	0.5386**	0.1931**	0.3800**
Days to maturity	P				-0.1446	-0.1005*	-0.0815	-0.1110	-0.0797	-0.1868*	-0.1780*
	G				0.1676*	-0.1827*	-0.1296	-0.2789**	-0.1014	-0.2940**	-0.2293**
Clusters per plant	P					0.3890**	0.8443**	0.0490	0.0081	0.1068	0.6946**
	G					0.4351**	0.8812**	0.0666	-0.0024	-0.1108	0.7628**
Pods per cluster	P						0.5934**	-0.0088	0.1628*	-0.1312	0.7631**
	G						0.6577**	0.1715*	0.0330	-0.1751*	0.6452**
Pods per plant	P							0.1057	0.0610	-0.1448	0.7872**
	G							0.1135	0.0660	-0.1604**	0.8521**
Pod length	P								0.6532**	0.4843**	0.1781*
	G								0.7653**	0.5989**	0.2060**
Seeds per pod	P									0.2860**	0.1243
	G									0.3277**	0.1494*
Test weight	P										0.0010
	G										0.0055

* Significant at 5% level ** Significant at 1% level

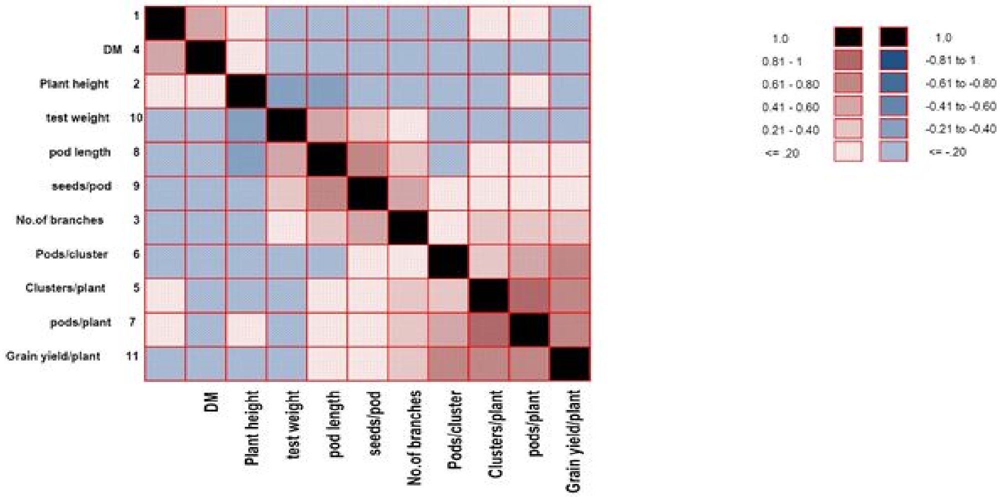

Fig 1: Shaded phenotypic correlation matrix for all the characters under study in mungbean (*Vigna radiata* L. Wilczek).

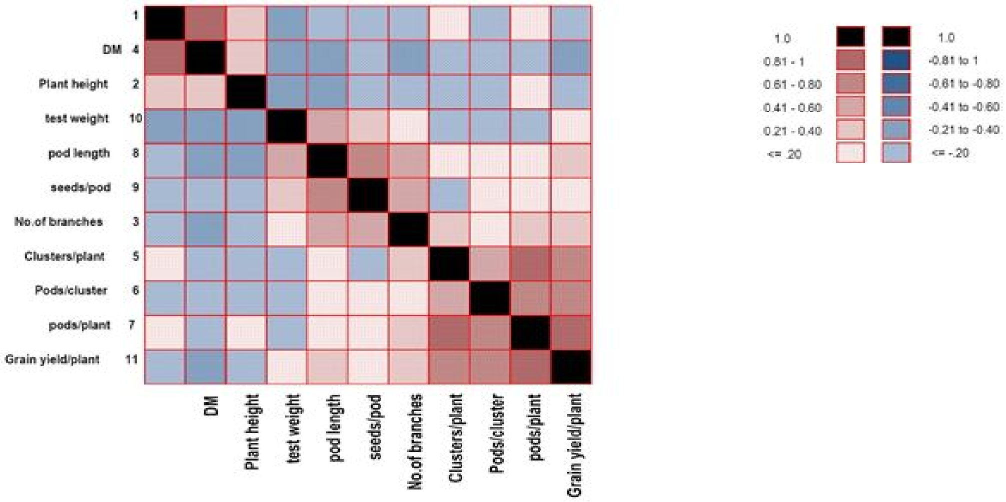

Fig 2: Shaded genotypic correlation matrix for all the characters under study in mungbean (*Vigna radiata* L. Wilczek).

pod length and test weight. Similar associations were earlier observed in mungbean by; Anand *et al*. (2016) between clusters per plant and pods per plant; Marak (2017) between pod length and seeds per pod, betweenpod length and test weight; Makeen *et al*. (2007) between pods per cluster and pods per plant and; Ahmad *et al*. (2015) and Ramachandra and Lavanya (2017) between days to 50% flowering and days to maturity.These pairs of associations indicate that selection for one character of a pair will enable improvement in another character in that pair. This information would be helpful in improvement through indirect selection.

Direct and indirect effects of correlations

The traits, pods per plant (0.4043 and 0.3236), pods per cluster (0.3359 and 0.4579), clusters per plant (0.2071 and 0.1972), pod length (0.1130 and 0.1007) and branches per plant (0.0268 and 0.0804) had positive direct effects at phenotypic and genotypic levels and also established significant positive association at both levels with grain yield per plant (Table 4). This indicate true relationship between the above traits and grain yield per plant. Similar true relations with grain yield per plant were observed in mungbean by; Kumar *et al*. (2018) for pods per plant at both phenotypic and genotypic level; Sinha *et al*. (2018) for pods per cluster at genotypic level; Anand *et al*. (2016) for clusters per plant at phenotypic level; Kumar *et al.* (2018) for pod length at both levels; Garg *et al*. (2017) at phenotypic level and Marak (2017) at genotypic level for branches per plant. Further, days to maturity was also observed to have direct effects at phenotypic (-0.0528) and genotypic (-0.2307) levels as well as significant correlation with grain yield in negative direction. Since, early genotypes are preferred, days to maturity is to be considered to have true relation with the dependent variable and should be taken care of during selection. The true relation of these six traits is also evident from the respective R^2 values of these six traits *viz.,* pods per cluster (0.2168 and 0.3491), pods per plant (0.3183 and 0.2757), clusters per plant (0.1438 and 0.1529), days

Table 4: Phenotypic and genotypic direct and indirect effects of different traits on grain yield in mung bean (*Vigna radiata* L. Wilczek).

	P/G	Days to 50% flowering	Plant height	Branches per plant	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	Test weight	Grain yield per plant	Partial R^2Values
Days to 50% flowering	P	**0.0161**	-0.0112	-0.0021	-0.0267	0.0140	-0.0284	0.0159	-0.0078	0.0045	-0.0086	-0.0344	-0.0006
	G	**0.2432**	-0.0174	-0.0144	-0.2375	0.0129	-0.0339	0.0131	-0.0189	0.0054	-0.0222	-0.0697	-0.0170
Plant height	P	0.0023	**-0.0790**	-0.0032	-0.0096	-0.0007	-0.0031	0.0185	-0.0326	0.0083	-0.0163	-0.1155	0.0091
	G	0.0572	**-0.0738**	-0.0140	-0.0638	-0.0050	-0.0217	0.0194	-0.0367	0.0165	-0.0321	-0.1539*	0.0114
Branches per plant	P	-0.0013	0.0093	**0.0268**	0.0103	0.0565	0.0479	0.1152	0.0314	-0.0323	0.0075	0.2713**	0.0073
	G	-0.0437	0.0128	**0.0804**	0.0800	0.0678	0.0700	0.1177	0.0435	-0.0659	0.0173	0.3800**	0.0306
Days to maturity	P	0.0082	-0.0143	-0.0052	**-0.0528**	-0.0299	-0.0338	-0.0330	-0.0125	0.0056	-0.0102	-0.1780*	0.0094
	G	0.2505	-0.0204	-0.0279	**-0.2307**	-0.0331	-0.0837	-0.0419	-0.0281	0.0124	-0.0264	-0.2293**	0.0526
Clusters per plant	P	0.0011	0.0003	0.0073	0.0076	**0.2071**	0.1307	0.3414	0.0055	-0.0006	-0.0058	0.6946**	0.1438
	G	0.0160	0.0019	0.0276	0.0387	**0.1972**	0.1992	0.2852	0.0067	0.0003	-0.0099	0.7628**	0.1529
Pods per cluster	P	-0.0014	0.0007	0.0038	0.0053	0.0806	**0.3359**	0.2399	-0.0010	-0.0115	-0.0072	0.6452**	0.2168
	G	-0.0180	0.0035	0.0123	0.0422	0.0858	**0.4579**	0.2128	0.0033	-0.0210	-0.0157	0.7631**	0.3494
Pods per plant	P	0.0006	-0.0036	0.0076	0.0043	0.1748	0.1993	**0.4043**	0.0119	-0.0043	-0.0079	0.7872**	0.8183
	G	0.0098	-0.0044	0.0292	0.0299	0.1738	0.3011	**0.3236**	0.0114	-0.0081	-0.0144	0.8521**	0.2757
Pod length	P	-0.0011	0.0228	0.0074	0.0059	0.0101	-0.0030	0.0427	**0.1130**	-0.0463	0.0265	0.1781*	0.0201
	G	-0.0457	0.0269	0.0348	0.0643	0.0131	0.0151	0.0367	**0.1007**	-0.0936	0.0537	0.2060**	0.0207
Seeds per pod	P	-0.0010	0.0093	0.0122	0.0042	0.0017	0.0547	0.0246	0.0738	**-0.0708**	0.0156	0.1243	-0.0088
	G	-0.0108	0.0100	0.0433	0.0234	-0.0005	0.0785	0.0213	0.0771	**-0.1223**	0.0294	0.1494*	-0.0183
Test weight	P	-0.0025	0.0236	0.0037	0.0099	-0.0221	-0.0441	-0.0586	0.0547	-0.0202	**0.0547**	-0.0010	0.0001
	G	-0.0603	0.0264	0.0155	0.0678	-0.0219	-0.0802	-0.0519	0.0603	-0.0401	**0.0897**	0.0055	0.0005

* Significant at 5% level

** Significant at 1% level

Diagonal values are direct effects

Residual Effect at phenotypic level = 0.53

Residual Effect at genotypic level = 0.38

to maturity (0.0094 and 0.0526), branches per plant (0.0073 and 0.0306) and pod length (0.0201 and 0.0207) at phenotypic and genotypic levels respectively.

Apart from the direct positive effects, indirect positive effects through different traits are also important which actually adds up to direct effect in resulting total correlation. Such indirect positive effects were found for pods per plant (*via* pods per cluster, clusters per plant, pod length, branches per plant, days to maturity and days to 50% flowering), pods per cluster (*via* pods per plant, clusters per plant, days to maturity, branches per plant and plant height), clusters per plant (*via* pods per plant, pods per cluster, days to maturity, branches per plant, pod length, days to 50% flowering and plant height), pod length (*via* pods per plant, test weight, plant height, clusters per plant, branches per plant and days to maturity)and branches per plant(*via* pods per plant, clusters per plant, pods per cluster, pod length, days to maturity, plant height and test weight) at both phenotypic and genotypic levels (Table 4). The direct effects of pods per plant, pods per cluster, clusters per plant, pod length and branches per plant on yield accounted for major portion in the total correlation. This indicate that direct selection for this trait will be effective for improvement of grain yield per plant. Further, other indirect positive casual factors of the above five traits may also be considered simultaneously along with pods per plant during selection for grain yield.

The validity of the conclusions drawn in present investigation conducted over three years is evident from the residual effect at genotypic level is 0.38 (Table 4), indicating that the characters included in present investigation had contributed around 62 percent to the dependent variable *i.e.,* grain yield per plant and only about 38 per cent is due to the other factors that were not considered in the present investigation.

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