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Estimation of variability, correlation and path coefficient in mungbean [*Vigna radiata* (L.) Wilczek] genotypes for seed yield and its attributing characters

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Abstract

The research was conducted at S.D.A.U. during *kharif*-2019 to study variability, heritability, genetic advance, correlation and path coefficient in a set of thirty genotypes of mungbean [*Vigna radiata* (L.) Wilczek]. Randomized block design was used with four replications. Ten traits showed significance differences in analysis of variance. Majority traits showed higher genotypic variance than their relevant environmental variance. PCV values were closer to GCV for most of the characters. Seed yield per plant and number of branches per plant had highest GCV. Number of branches per plant, seed yield per plant and 100-seed weight expressed high genetic advance and high heritability. Seed yield per plant gave highly significant and positive correlations with number of pods per plant, pod length, 100-seed weight, while highly significant and negative with days to flowering. Highest positive direct effect on seed yield was noticed by 100-seed weight followed by number of pods per plant and days to flowering. Negative direct effect on seed yield was found with plant height followed by protein content. In conclusion, 100-seed weight, number of pods per plant, number of seeds per pod, pod length and number of branches per plant were found key contributors for seed yield.

Keywords: Variability, correlation, path analysis, mungbean

Introduction

In Indian vegetarian diet, pulses occupy second place next to cereal. High protein of pulses makes it rich man's vegetable and poor man's meat. Although, obtainability of pulses *per capita* is mere 42 g/person/day while World Health Organization's recommendation is 80 g/person/day. Mungbean is also known as greengram, greenbean, greensoy, goldengram, moong and mashbean. Scientific classification of mungbean is Kingdom: Plantae; Clade: Rosids in Eudicots of Angiosperms; Order: Fabales; Family: Fabaceae; Sub-family: Faboideae; Tribe: Phaseoleae; Sub-tribe: Phaseolinae; Genus: *Vigna* and Species: *radiata* (Source: USDA ARS, 2018) [36]. Hindustan and Central Asiatic region might be the origin of it. In India moong is extensively grown under rainfed (*kharif*) and irrigated (summer) condition of semi-arid and arid regions. Rabi season cultivation is restricted to the southern and eastern parts.

To raise the production and productivity of pulses, better management practices and selection of better genotypes or lines and varieties are required. Study of variability present in the crop species is a precondition for effective selection of genotypes. Yield is a complex character which relies on many yield contributing characters which inherited quantitatively and affected by environment extremely. Genotypic and phenotypic variance, genetic gain, heritability and genetic advance are useful to decide nature of variability. Genetic advance indicates whether the traits are governed by non-additive genes or additive genes. Correlation studies provide estimates of the level of association of yield with its components and between the components. Path coefficient analysis is used when a correlation study includes number of variables. Independent variables have direct and indirect effects on the dependent variables. Correlation due to direct effect reflects true relationship and selection is practiced for such a trait for improving the yield. If the indirect effect through another component character is noticed, then select the latter character through which indirect effect is applied.

Materials and Methods

Research details

The research conducted during *kharif*-2019 at Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar (Gujarat).

Climate was sub-tropical characterized by semi-arid and arid condition. Thirty genotypes of mungbean were selected from the enormous genetic resources maintained at the Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The sets of 30 entries were planted in Randomized Block Design (RBD) with four replications. Each entry was allotted in a single row plot of 3 m length with 45 cm × 10 cm spacing.

Study of traits

Ten traits *viz.*, days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g), protein content (%) and seed yield per plant (g) were studied by taking measurements on individual plants (five randomly selected competitive plants per genotype in each replication) and visual assessment.

Statistical analysis

Data were analysed at the Department of Agricultural Statistics. Statistical methods used for the statistical analysis were: Analysis of variance - linear additive model (Panse and Sukhatme, 1978) [26]; coefficient of genotypic variation

(GCV) and phenotypic variation (PCV) [Burton, 1952] [8]; broad sense heritability (H^2_b) [Allard, 1960] [3]; genetic advance (GA) and genetic advances expressed as percentage of mean [Johnson *et al.*, 1955] [14]; phenotypic, genotypic and environmental correlation coefficients (Al-Jibouri *et al.*, 1958) [2]; path coefficient (Dewey and Lu, 1959) [10]. Range, mean, genotypic variance, phenotypic variance and error variance were also calculated.

Results and Discussion

Analysis of variance (ANOVA)

The ANOVA revealed highly significant differences among the genotypes for all the traits (Table 1). It had proved the existence of high amount of genetic variability in the studied traits with an ample chance to identify desirable genotypes to improve various traits. Similar results were reported for days to flowering, days to maturity and protein content (Makeen *et al.*, 2007) [20]; plant height, number of pods per plant, seed yield per plant, number of seed per pod, pod length and 100-seed weight (Makeen *et al.*, 2007 and Tabasum *et al.*, 2010) [20, 35] and number of branches per plant (Asari *et al.*, 2019 and Sneha *et al.*, 2019) [5, 32].

Table 1: ANOVA for different quantitative characters in mungbean

Source of variation	d.f.	Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant
Replications	3	16.989	32.097	180.620	0.015	0.300
Genotypes	29	69.723**	162.564**	463.262**	0.252**	23.664**
Error	87	8.035	12.034	70.983	0.006	3.957
Source of variation	d.f.	Number of seeds per pod	Pod length (cm)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
Replications	3	0.716	0.159	0.072	1.358	0.681
Genotypes	29	1.122**	0.970**	0.710**	2.186**	2.350**
Error	87	0.478	0.064	0.031	0.504	0.264
**		Significant at 1 per cent level of significance.				

Variability

The computed data of phenotypic variance (σ^2_p), genotypic variance (σ^2_g), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (H^2_b) and genetic advance as per cent of mean are presented in Table 2. Graph showing comparison of GCV, PCV, heritability (H^2_b) and genetic advance as percentage of mean is given in Fig. 1.

Genotypic variance was higher than environmental variance for days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, 100-seed weight and seed yield per plant, which indicates the reliability on phenotypic variability to measure genotypic variability and for selection of these traits.

The results were in accordance for days to flowering (Rahim *et al.*, 2010; Anand *et al.*, 2016 and Asari *et al.*, 2019) [28, 4, 5], for days to maturity (Asari *et al.*, 2019) [5], for plant height, number of pods per plant and seed yield per plant (Malik *et al.*, 1983; Rahim *et al.*, 2010; Kumar *et al.*, 2013; Anand *et al.*, 2016; Susmitha and Jayamani, 2018 and Asari *et al.*, 2019) [5], [21, 28, 16, 4, 34], for number of branches per plant (Malik *et al.*, 1983) [21], for pod length and 100-seed weight (Malik *et al.*, 1983; Kumar *et al.*, 2013; Susmitha and Jayamani, 2018 and Asari *et al.*, 2019) [21, 16, 34, 5].

GCV is used for measuring the range of variability available in a trait and to compares it among traits. Close PCV values to GCV values for majority traits showed possibility of improvement by phenotypic selection. Value of GCV was

higher for number of branches per plant (45.07%) and seed yield per plant (20.61%) and selection for such characters will be effective.

GCV and PCV were moderate for plant height (13.14%), number of pods per plant (14.69%) and 100-seed weight (13.18%). Low GCV and moderate PCV were observed for days flowering, while GCV and PCV were lower for days to maturity, number of seeds per pod, pod length and protein content which suggests more influence of environment on these traits and one should not use them in selection. Although, they can be used in hybridization programme. Similar results were found by Kumar *et al.* (2013) [16] for number of pods per plant, 100-seed weight and pod length; Pandiyan *et al.* (2006) [24] for protein content; Das and Barua (2015) [9] for seed yield per plant, plant height, number of pods per plant and 100-seed weight; Hemavathy *et al.* (2015) [13] for seed yield per plant, plant height, 100-seed weight, days to maturity and number of seeds per pod; Payasi (2015) [27] for seed yield per plant, plant height, 100-seed weight, days to maturity and pod length; Baisakh *et al.* (2016) [7] for 100-seed weight and pod length; Shiv *et al.* (2017) [31] for days to flowering and Susmitha and Jayamani (2018) [34] for number of branches per plant, seed yield per plant, plant height, 100-seed weight, days to maturity, number of seeds per pod and pod length.

Heritability and genetic advance

Heritability point towards effectiveness with which selection

of genotypes could be based on phenotypic performance. Traits showed high heritability were number of branches per plant (91.20%), 100-seed weight (84.56%), pod length (78.03%), days to maturity (75.77%), seed yield per plant (66.40%) and days to flowering (65.75%). The characters are reliable for selection of genotype.

The results were in accordance with Malik *et al.* (1983) [21] for number of branches per plant, pod length and 100-seed weight; Ahmad *et al.* (2006) [1] for days to flowering, days to maturity, pod length and 100-seed weight; Reddy *et al.* (2011) [30] for days to flowering, days to maturity and

Table 2: Range, Mean, Genotypic, Phenotypic and Environmental variances, GCV, PCV, H² (broad sense), GA and GA as per cent of Mean for different quantitative characters in mungbean

Characters	Range	Mean	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Environmental variance (σ^2_e)	GCV (%)	PCV (%)	H ² b (%)	GA	GA as % of Mean
Days to flowering	37.75-55.75	44.98	15.42	23.46	8.03	8.73	10.77	65.75	6.56	14.58
Days to maturity	54.75-84.75	71.36	37.63	49.67	12.03	8.60	9.88	75.77	11.00	15.42
Plant height (cm)	51.30-98.90	75.35	98.07	169.05	70.98	13.14	17.26	58.01	15.54	20.62
Number of branches per plant	0.00-1.00	0.55	0.06	0.07	0.01	45.07	47.20	91.20	0.49	88.67
Number of pods per plant	10.35-20.36	15.11	4.93	8.88	3.96	14.69	19.72	55.46	3.41	22.53
Number of seeds per pod	9.64-12.08	10.55	0.16	0.64	0.48	3.80	7.57	25.21	0.42	3.93
Pod length (cm)	6.28-8.43	6.98	0.23	0.29	0.06	6.82	7.72	78.03	0.87	12.41
100-seed weight (g)	2.56-4.39	3.13	0.17	0.20	0.03	13.18	14.34	84.56	0.78	24.97
Protein content (%)	19.94-23.18	21.42	0.42	0.92	0.50	3.03	4.49	45.46	0.90	4.20
Seed yield per plant (g)	2.10-5.88	3.50	0.52	0.79	0.26	20.61	25.29	66.42	1.21	34.60

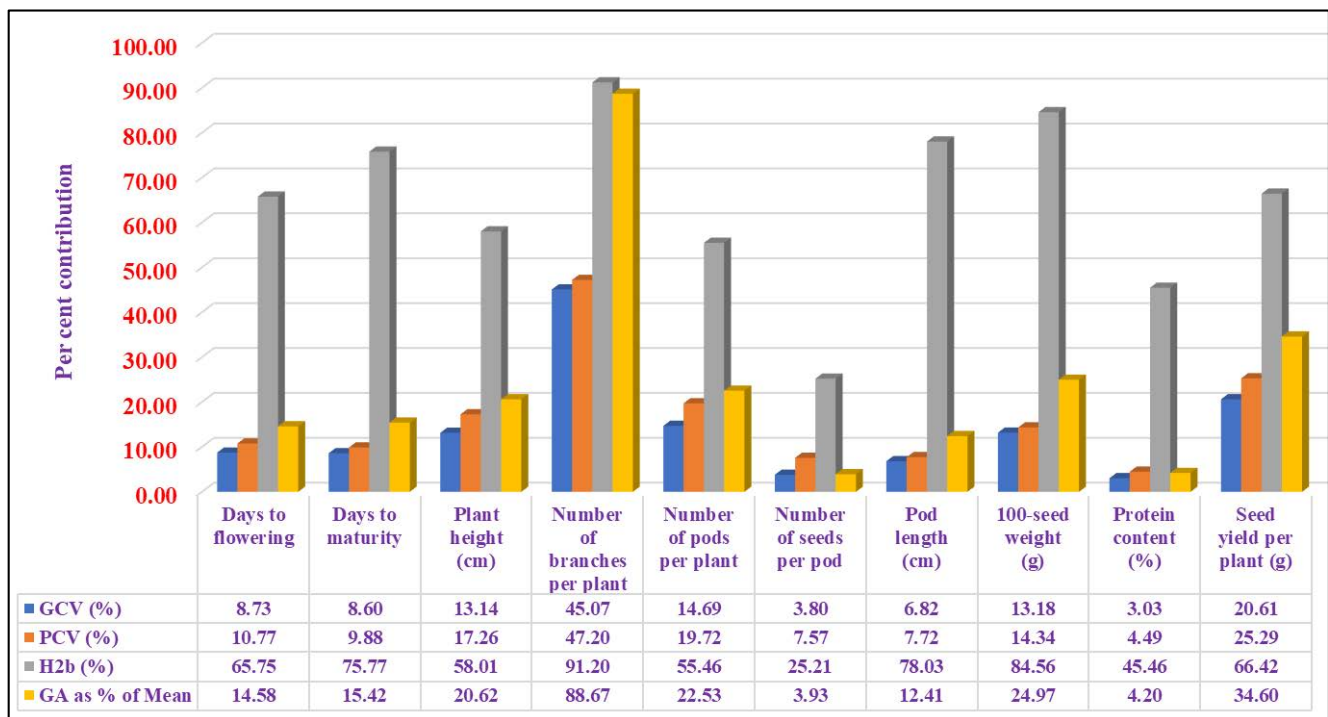


Fig 1: Graphical comparison of GCV, PCV, heritability (H²b) and genetic advance as per cent of mean for ten quantitative characters in mungbean

100-seed weight; Babu *et al.* (2012) [6] for number of branches per plant; Ramakrishnan *et al.* (2018) [29] for number of branches per plant and pod length and Pandiyan *et al.* (2006) [24] and Mariyammal *et al.* (2019) [22] for seed yield per plant. Under the pressure of selection gene frequency shift towards superior side is called as genetic advance, which is expressed as percentage of mean (genetic gain). The limitation of heritability (broad sense) is that, it possesses both epistasis and additive gene effect. Therefore, use heritability estimates with genetic advance to predict the outcome from choosing the better individuals (Johnson *et al.*, 1955) [14]. We noticed high heritability with high genetic gain for number of branches per plant, 100-seed weight and seed yield per plant; which points toward additive gene action (Panse, 1957) [25]. These characters are important in selection

programme and their direct selection would be fruitful. Similar results were obtained for number of branches per plant (Malik *et al.*, 1983; Payasi, 2015 and Asari *et al.*, 2019) [21, 27, 5], for 100-seed weight (Malik *et al.*, 1983; Ahmad *et al.*, 2006; Reddy *et al.*, 2011 and Baisakh *et al.*, 2016) [21, 1, 30, 7] and for seed yield per plant (Pandiyan *et al.*, 2006; Makeen *et al.*, 2007; Rahim *et al.*, 2010; Sunil *et al.*, 2011; Hemavathy *et al.*, 2015; Anand *et al.*, 2016 and Mariyammal *et al.*, 2019) [24, 20, 28, 33, 13, 4, 22]. High heritability and moderate genetic advance indicate that additive and non-additive gene actions have equal importance. These were recorded for days to maturity, days to flowering and pod length. Three cycles of recurrent selection should follow by pedigree or single seed descent methods improves the traits. Similar results were obtained for days to flowering

(Ahmad *et al.*, 2006; Das and Barua, 2015 and Payasi, 2015) [1, 9, 27], for days to maturity (Ahmad *et al.*, 2006; Reddy *et al.*, 2011 and Payasi, 2015) [1, 30, 27] and for pod length (Ahmad *et al.*, 2006; Kumar *et al.*, 2013 and Asari *et al.*, 2019) [1, 16, 5].

Moderate heritability and high genetic advance observed for plant height and number of pods per plant. Results proved the presence of additive gene effects coupled with high environmental impact for these traits. The results were in accordance with Kumar *et al.* (2005) [17], Babu *et al.* (2012) [6] and Susmitha and Jayamani (2018) [34] for number of pods per plant.

Moderate heritability but low genetic advance was obtained for protein content, which showed effect of environment on trait expression due to non-additive gene action. Here recombination breeding is useful over selection.

Moderate to high GCV with high genetic advance was obtained for number of branches per plant, 100-seed weight and seed yield per plant, which favours directional selection for improvement in seed yield.

The overall discussion on variability parameters proved that the traits *viz.*, plant height, number of branches per plant, number of pods per plant, 100-seed weight and seed yield per plant possessed considerable to high genetic variability due to more differences in the genetic makeup of genotypes and was controlled by additive gene effects. Selection practiced on these traits for these genotypes would lead to an improvement.

Correlation coefficient analysis

For genetic improvement in seed yield, it is required to study relationship of seed yield and its components and among the components because seed yield is a polygenic and complex trait which relies on different yield attributing traits.

The phenotypic correlation deals with directly observed characters. It is the result of environment and genotypic interaction therefore; it is not enough to evaluate the association. The genotypic correlation predicts the correlated response and evaluate the relative influence of one character on another, which helps in the construction of selection indices. Hence, the correlation coefficients at genotypic and phenotypic levels were estimated between seed yield and its component traits and among the component traits (Table 3).

Seed yield per plant showed positive and highly significant correlation with number of pods per plant ($r_g = 0.6103^{**}$ and $r_p = 0.4870^{**}$), pod length ($r_g = 0.6408^{**}$ and $r_p = 0.4656^{**}$) and 100-seed weight ($r_g = 0.7779^{**}$ and $r_p = 0.6278^{**}$) at both genotypic and phenotypic levels. Number of branches per plant showed negative non-significant correlation at genotypic level ($r_g = -0.0056$) and positive non-significant correlation at phenotypic level ($r_p = 0.0300$) with seed yield per plant. Days to flowering ($r_g = -0.2430^{**}$ and $r_p = -0.1643$) had negative correlation with seed yield per plant and significant result at genotypic level only. Seed yield per plant was positively correlated with plant height, number of seeds per pod, protein

content and negatively correlated with days to maturity, but did not reach the level of significance.

This findings were close in agreement with Kumar *et al.* (2005) [17] for days to flowering and number of seeds per pod; Sunil *et al.* (2011) [33] for days to flowering, plant height, number of branches per plant and number of seeds per pod; Nand and Anuradha (2013) [23] for number of branches per plant and number of seeds per pod; Lal and Singh (2014) [18] for days to maturity, number of pods per plant and 100-seed weight; Baisakh *et al.* (2016) [7] for days to flowering, number of seeds per pod and pod length; Asari *et al.* (2019) [5] for plant height, number of pods per plant, number of seeds per pod and protein content and Sneha *et al.* (2019) [32] for number of pods per plant, pod length and 100-seed weight.

The level of correlation observes between attributes relies on the relationship among them and on segregating genes which contribute to the variation. Some genes may increase both the traits resulting the positive correlation, while other decrease one and increase other causing negative correlation. Negative correlations arise because of competition among traits for common precursors which are having restricted supply. On the other hand, positive correlations occur because of the changes of genes supplying precursors (Madhur and Jinks, 1994) [19].

The genetic correlation is mainly due to pleiotropy. Also, population which is obtained from crosses among diverse strains show transient correlation due to linkage. Mostly, the value of phenotypic correlations was lower than the genotypic correlations which indicated strong inherent association between traits at genotypic level. However, sometime reverse ratio found because of non-genetic causes (environment) on the genotypic correlation.

High genetic correlation indicates that the two characters could be substantially same and will produce little difference regards to environment in which selection is carried out (Falconer, 1960) [11]. After analysing present interrelationship, it can be said that an ideal plant type to improve seed yield in mungbean for increasing grain yield is early flowering, a greater number of pods per plant, with a medium to long pods and high 100-seed weight.

Path coefficient analysis

Correlation study alone cannot be used in the selection programme, when a larger number of variables are considered. To resolve this issue, path analysis (Wright, 1921 and Dewey and Lu, 1959) [37, 10] is used. It divides the correlation into indirect and direct effects, establish the relative merits of each character and reduce their number.

Path coefficient analysis was done by considering seed yield per plant as dependent character (effect) while nine characters as independent characters (causes). Genotypic correlation coefficient of different characters with seed yield were divided into direct and indirect effects, to know the role of various characters towards seed yield (Table 4 and Fig. 2).

Table 3: Genotypic and phenotypic correlation coefficients among ten quantitative characters in mungbean

Characters	(r)	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
Days to flowering	r_g	0.9165**	0.7623**	0.3718**	-0.1651	0.6972**	-0.2344**	-0.3878**	-0.3077**	-0.2430**
	r_p	0.7474**	0.3457**	0.2390**	-0.2715**	0.3519**	-0.1992*	-0.3068**	-0.2793**	-0.1643
Days to maturity	r_g		0.7758**	0.3745**	0.1056	0.6210**	-0.0260	-0.2788**	-0.2098*	-0.0376
	r_p		0.4919**	0.2810**	-0.0112	0.2829**	-0.0570	-0.2719**	-0.2200*	-0.0336
Plant	r_g			0.4075**	0.0326	-0.0087	0.1647	0.1056	-0.1714	0.1065

height (cm)	r _p			0.3242**	0.2141*	0.0174	0.1839*	0.0840	0.0980	0.1149	
Number of branches per plant	r _g				0.2431**	0.0864	-0.0363	-0.1707	0.1813*	-0.0056	
	r _p				0.2279*	-0.0264	-0.0442	-0.1402	0.1655	0.0300	
Number of pods per plant	r _g					-0.1701	0.1398	0.1911*	0.3216**	0.6103**	
	r _p					-0.1651	0.0787	0.1015	0.3497**	0.4870**	
Number of seeds per pod	r _g						0.1016	-0.0907	-0.3793**	0.1524	
	r _p						0.2552**	-0.0794	-0.3604**	0.0583	
Pod length (cm)	r _g							0.8085**	0.0736	0.6408**	
	r _p							0.6976**	0.0382	0.4656**	
100-seed weight (g)	r _g								0.0374	0.7779**	
	r _p								0.0606	0.6278**	
Protein content (%)	r _g									0.0959	
	r _p									0.0972	
*, **		Significant at 5 and 1 per cent level of significance, respectively.									

Table 4: Direct and indirect effects of different quantitative characters on seed yield in mungbean

Characters	Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	100-seed weight (g)	Protein content (%)	Genotypic Correlation with seed yield per plant (g)	
Days to flowering	0.3420	0.0864	-0.2622	0.0011	-0.0844	0.0037	-0.0007	-0.3394	0.0105	-0.2430**	
Days to maturity	0.3135	0.0943	-0.2668	0.0011	0.0540	0.0033	-0.0001	-0.2440	0.0071	-0.0376	
Plant height (cm)	0.2608	0.0733	-0.3441	0.0012	0.0167	-0.0001	0.0005	0.0924	0.0058	0.1065	
Number of branches per plant	0.1272	0.0353	-0.1402	0.0030	0.1243	0.0005	-0.0001	-0.1494	-0.0062	-0.0056	
Number of pods per plant	-0.0565	0.0100	-0.0112	0.0007	0.5114	-0.0009	0.0004	0.1673	-0.0109	0.6103**	
Number of seeds per pod	0.2385	0.0585	0.0030	0.0003	-0.0870	0.0053	0.0003	-0.0794	0.0129	0.1524	
Pod length (cm)	-0.0802	-0.0025	-0.0566	-0.0001	0.0715	0.0005	0.0030	0.7077	-0.0025	0.6408**	
100-seed weight (g)	-0.1326	-0.0263	-0.0363	-0.0005	0.0977	-0.0005	0.0024	0.8753	-0.0013	0.7779**	
Protein content (%)	-0.1052	-0.0198	0.0590	0.0005	0.1645	-0.0020	0.0002	0.0327	-0.0340	0.0959	
*, **		Significant at 5 and 1 per cent level of significance, respectively. Residual effect = 0.1308									

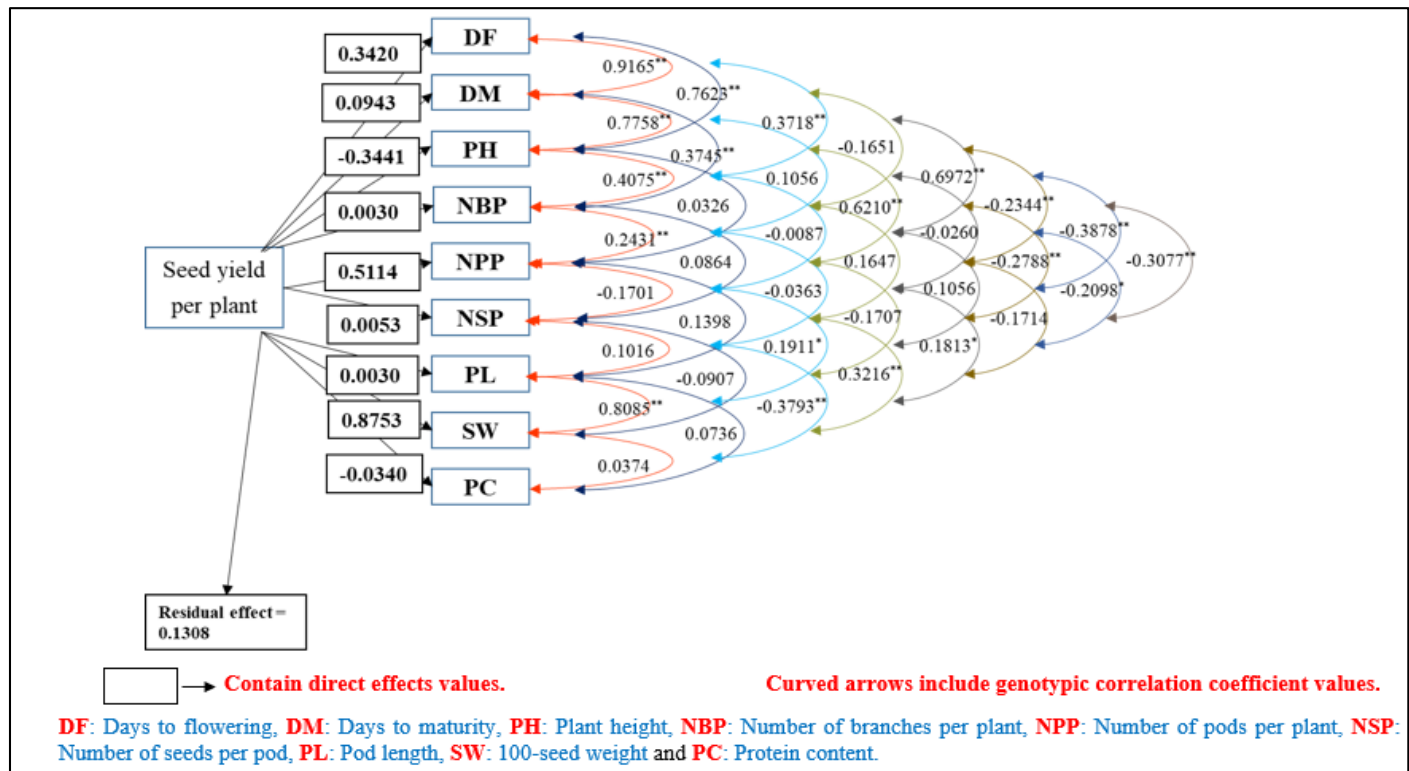


Fig 2: Genotypic path diagram in mungbean

By knowing the direct effect of character on seed yield, one can estimate reliability on indirect selection for yield increment through that character. In the present study, highest positive direct effect on seed yield was noticed by 100-seed weight (0.8753) followed by number of pods per plant (0.5114), days to flowering (0.3420), days to maturity (0.0943), number of seeds per pod (0.0053), number of

branches per plant (0.0030) and pod length (0.0030). The results were in conformity with Makeen *et al.* (2007) [20] and Hemavathy *et al.* (2015) [13] for 100-seed weight, number of pods per plant and number of seeds per pod; Garg *et al.* (2017) [12] for 100-seed weight, number of pods per plant, days to flowering, days to maturity, number of branches per plant and pod length; Asari *et al.* (2019) [5] for 100-seed

weight, number of pods per plant, days to flowering, number of seeds per pod, number of branches per plant and pod length; Lal and Singh (2014) [18] for 100-seed weight, number of pods per plant, days to maturity and number of seeds per pod; Keerthiga *et al.* (2018) [15] for 100-seed weight, days to flowering, number of seeds per pod and number of branches per plant and Das and Barua (2015) [9] for 100-seed weight, number of pods per plant, days to flowering and number of seeds per pod.

Negative direct effect on seed yield was found with plant height (-0.3441) followed by protein content (-0.0340). This indicated that, if these characters are selected directly then, it will result in poor selection so indirect causal factors must be considered especially the characters contributing positively. The results were in conformity with the results of Tabasum *et al.* (2010) [35], Reddy *et al.* (2011) [30], Lal and Singh (2014) [18], Hemavathy *et al.* (2015) [13], Anand *et al.* (2016) [4], Garg *et al.* (2017) [12], Asari *et al.* (2019) [5] and Sneha *et al.* (2019) [32] for plant height.

To make the path diagram, all the important causal factors affecting the seed yield should be included. Being a complex trait, seed yield gets affected by many factors. So, it wasn't feasible to include all the traits. The residual effect helps to know the capability of causal factors to study the variability in seed yield. In the present study, the residual effect was found low and positive 0.1308 which indicated that the traits studied contributed 86.92% of yield. The rest 13.08% was contribution of other factors.

Overall results of path analysis suggested to put weightage on 100-seed weight, number of pods per plant, days to flowering, days to maturity, number of seeds per pod, number of branches per plant and pod length during selection to improve seed yield.

In conclusion, ANOVA for ten traits showed significance differences and enough amount of variability among the genotypes. GCV was high for number of branches per plant and seed yield per plant which indicates that noticeable amount of genetic variability presents for these characters and their selection will be fruitful. The high heritability estimates coupled with high genetic advance were noticed for number of branches per plant, 100-seed weight and seed yield per plant. These may be a sign of additive gene action and therefore; these characters are important in selection programme and direct selection of these characters would be fruitful.

Seed yield per plant exhibited highly significant and positive correlations with number of pods per plant, pod length, 100-seed weight at both the levels, while highly significant and negative correlations with days to flowering at genotypic level.

Path coefficient analysis showed that highest positive direct effect on seed yield was noticed by 100-seed weight followed by number of pods per plant, days to flowering, days to maturity, number of seeds per pod, number of branches per plant and pod length. Negative direct effect on seed yield was found with plant height followed by protein content.

Combined results of path analysis and correlation coefficient revealed that selection of 100-seed weight, number of pods per plant, number of seed per pod and pod length are effective due to their positive correlation coefficient and positive direct effect (true relationship of correlation). While days to flowering, days to maturity and number of branches per plant showed negative correlation coefficient, but the direct effect was positive so direct selection should be practiced for this

trait to reduce the undesirable indirect effects.

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