

Correlation and Path Coefficient Analyses of Mung Bean [*Vigna radiata* (L.) Wilczek] Genotypes, in South Ethiopia

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Abstract

Understanding the nature and extent of association between seed yield and yield-related traits is important for sustainable genetic improvement. However, there is a lack of sufficient information on seed yield and yield-related trait correlation and path coefficient analysis of mung bean in Ethiopia. Therefore, there is a need to conduct correlation analysis among traits, and path coefficient analysis which splits the correlation variables into direct and indirect effects and which visualizes the relationship in a more meaningful way. To address these knowledge gaps, the present study was conducted to determine the nature and extent of phenotypic and genotypic correlation and path coefficient analysis among 17 quantitative traits. A total of 60 mung bean genotypes were tested using a 6×10 alpha lattice design at Jinka Agricultural Research Center during the 2018 cropping season. Seed yield was positively and significantly correlated with most of the traits at phenotypic and genotypic levels, indicating the presence of a strong inherent association between seed yield and other traits. Seed yield in mung bean can be improved through indirect selection for traits like plant height, the number of primary branches per plant, seeds per pod, and pod length. The information obtained from this study can be used for the genetic enhancement of mung bean thereby developing high-yielding varieties.

Key words: Direct Effect, Genotypic Association, Indirect Effect, Phenotypic Association, Seed Yield

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INTRODUCTION

Mung bean [*Vigna radiata* (L.) Wilczek] is one of the most important food legumes grown worldwide, and the most common crops in most tropical and sub-tropical regions (Allahmoradi et al., 2011). The importance of mung beans is related to desirable characteristics such as high protein content, broad adaptation, low need for agricultural inputs, and high ability to increase soil fertility. It is a valuable source of

carbohydrates 51%, protein 24-26%, minerals 4%, and vitamins 3% (Karthikeyan et al., 2011; Nair et al., 2013). Mung bean improves soil fertility by fixing atmospheric nitrogen (Yaqub et al., 2010), making it an economically and nutritionally valuable crop since it reduces the amount of nitrogen fertilizer required in the soil when grown in rotation with cereals. Perera et al. (2017) reported that mung bean improves grain and straw yields of the component crops due to its residual effects.

The existing morphological diversity of mung beans provides a great scope for genetic improvement as well as for increasing their productivity through varietal improvement. However, seed yield is a complex trait and is affected by agronomic, morphological, and physiological traits. Therefore, the genetic control of seed yield can be achieved by studying agronomic, morphological, and physiological traits (Tabasum et al., 2010). As suggested by Cruz et al. (2012), studies on correlations between characters enable one to perform an indirect selection for a quantitative trait, usually hard to be selected visually; besides, it is also able to access how a trait can interfere with another. Benti and Yohannis (2017) suggested that understanding the relationship between yield and yield contributing traits is necessary for any selection program which provides information regarding the nature and magnitude of the association between any two pairs of agromorphological traits. Similar to other crops, seed yield in mung bean is a complex character determined by various components and depends upon numerous genetic factors interacting with the environment. Thus, the knowledge of correlations between traits is useful especially for mung bean seed yield since it allows the breeder to use that additional information to discard or promote genotypes of interest. Studies on correlations between characters are indeed important to breeding programs as it enables to perform an indirect selection for a quantitative trait, usually hard to be selected, by another directly correlated trait of higher genetic gain or easy visual selection; as well, it is also able to access how a trait can interfere with another (Cruz et al., 2012). It is known that the selection for a certain trait can eventually bring effects on others with or without the interest in the intended breeding programs. Accordingly, the knowledge of correlations between traits is to use that additional information to discard or promote genotypes of interest. The correlation analysis showed the relationship between two or more series of variables (Bhanu et al., 2016). Correlation analysis between characters may be sometimes misleading due to complex interactions consequently not providing the exact impression of one character over another.

Therefore, there is a need to go further for path coefficient analysis which splits the correlation variables into direct and indirect effects and which visualizes the relationship in a more meaningful way. As suggested by (Jogdhande et al., 2017; Manisha et al., 2018), path analysis avoids the complication by measuring the direct influence of one trait on the other as well as permits the partitioning of correlation coefficients into its components of direct and indirect effects.

But information on the correlation and path coefficient analysis of seed yield and yield-related traits on mung bean genotypes in Ethiopia is limited. Therefore, the objectives of the present study were to determine the nature and extent of phenotypic and genotypic correlations among the studied quantitative traits and to identify the most important traits for indirect selection in the future mung bean breeding programs.

MATERIALS AND METHODS

Description of the Study Area

The field experiment was conducted during the main cropping season, therefore from March to June 2018 at Jinka Agricultural Research Center (JARC). Jinka Agricultural Research Center is located 729 km southwest of Addis Ababa at 36° 33' 02.7" E, 05° 46' 52.0" N, and at an altitude of 1420 m above sea level. The maximum, minimum, and average temperatures of the center for ten years (2009-2019) are 27.68°C, 16.61°C, and 22.14°C, respectively while the mean annual rainfall is 1381 mm. The soil type of the center is Cambisols (Mesfin et al., 2017).

Experimental Materials

A total of 60 mung bean genotypes were used. Out of these, 44 genotypes were obtained from Melkassa Agricultural Research Center (MARC) and 16 genotypes were collected from Southern Nations, Nationalities, and People's (SNNP) region.

Experimental Design and Procedures

The experiment was conducted using a 6×10 alpha lattice design. The plot size was 3 m long, 0.3 m between rows, and 0.05 m between plants. Each plot consisted of five rows, accommodating 80 plants per row. The distance between plots,

blocks, and replications was 1 m, 1.5 m, and 2 m, respectively.

Data Collection

The quantitative data were collected according to the descriptor of the mung bean developed by the International Board for Plant Genetic Resources (IBPGR, 1980). The data collected on a plot basis were; days to flowering (days), days to maturity (days), hundred seed weight (g), seed yield per plot (g), biomass (g), and harvest index (%). The data collected on a plant basis were; plant height (cm), number of primary branches per plant, number of seeds per pod, pod length (cm), peduncle length (cm), number of pods per cluster,

terminal leaflet length (cm), and terminal leaflet width (cm).

Data Analyses

The collected data were subjected to analysis of variance (ANOVA) to test for the presence of variation among the genotypes for the studied traits and then based on the ANOVA result; all significant traits were promoted for correlation and path coefficient analyses. Phenotypic and genotypic correlations between seed yield and yield-related traits were estimated using the method described by Miller *et al.* (1958) as:

$$\text{The phenotypic correlation coefficient } (r_{p_{xy}}) = \frac{Cov_{pxy}}{\sqrt{(\sigma^2_{px})(\sigma^2_{py})}}$$

$$\text{The genotypic correlation coefficient } (r_{g_{xy}}) = \frac{Cov_{gxy}}{\sqrt{(\sigma^2_{gx})(\sigma^2_{gy})}}$$

Where, r_{pxy} is phenotypic correlation coefficient and Genotypic correlation coefficient ($r_{g_{xy}}$) between character x and y; Cov_{pxy} and Cov_{gxy} are phenotypic covariances and genotypic covariance between character x and y; σ^2_{gx} and σ^2_{gy} are genotypic variances traits x and y; σ^2_{px} and σ^2_{py} are phenotypic variances of traits x and y, respectively. The coefficient of correlation was tested using tabulated value at n-2 degree of freedom, at 5% and 1% probability level, where n is the number of treatments (genotypes) as described by Robertson (1959). META-R Version 6. 01 (Alvarado *et al.*, 2017) was employed for phenotypic and genotypic correlation coefficient analysis. Microsoft Excel computer program was employed for phenotypic and genotypic path coefficient analysis as well as estimation of residual effect. Path coefficient analysis was conducted as suggested by Dewey and Lu (1959) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield and other traits based on the following relationship.

$R_{ij} = P_{ij} + \sum_{rik} \dot{a}_{rik} P_{kj}$; Where, r_{ij} is the mutual association between the independent character (i) and dependent traits (j) as measured by correlation coefficients, p_{ij} is components of direct effects of the independent traits (i) on the dependent traits (j), $\sum_{rik} \dot{a}_{rik} P_{kj}$ = summation of components of the indirect effect of a given independent character (i) on the dependent traits (j) via all other independent traits (k).

The residual effect (R) was estimated using the formula shown below (Dewey and Lu, 1959).

$$R = \sqrt{1-R^2} \quad \text{Where, } R^2 = \sum_{ij} r_{ij} p_{ij}$$

RESULTS AND DISCUSSION

Genotypic and Phenotypic Correlations Coefficient Analysis

The analysis of variance results for correlation coefficients among seed yield and its contributing traits were computed and the values for phenotypic and genotypic correlation coefficients between each pair of traits are presented in Table 1. The present study revealed that the magnitudes of genotypic correlation coefficients (r_g) were

higher than their corresponding phenotypic correlation coefficients (r_{ph}) except in few cases, indicating the presence of strong inherent association among these traits due to the genetic factors and the dominance of genetic variance in the expression of traits. This finding is in agreement with the report of Ghosh *et al.* (2019) on 52 mung bean genotypes, who reported that the genotypic correlation was higher in magnitude than the phenotypic correlation, which coincides with the previous works (Begum *et al.*, 2012; Srivastava and Singh, 2012; Narasimhulu *et al.*, 2013; Singh and Bains, 2014; Benti and Yohannis, 2017; Abbas *et al.*, 2018; Ghosh *et al.*, 2019) on mung bean and (Bharti *et al.*, 2013; Reni *et al.*, 2013; Sarkar, 2014; Kumar *et al.*, 2015; Arya *et al.*, 2017; Partap *et al.*, 2019) on black gram genotypes. These authors reported that the magnitudes of genotypic correlation were higher as compared to their corresponding phenotypic correlation for most of the traits indicating the preponderance of genetic variance in the expression of characters. On the contrary, Tabasumet *al.* (2010) and Patel *et al.* (2014) reported that the magnitude of phenotypic correlation was higher than the genotypic correlation. Similarly; Sandhiya and Saravanan (2018) reported that the magnitude of the phenotypic coefficient of variation for 10 traits on 36 mung bean genotypes was higher than the genotypic coefficient of variation indicating the involvement of both genotype and environment for the variation. In this study, almost all the studied traits showed a significantly positive correlation with seed yield at the genotypic level.

Correlations of Seed Yield with other Traits

In this study, seed yield exhibited significant and positive correlations with hundred seed weight, biomass, and harvest index at the genotypic and phenotypic levels (Table 1). Genetic relationships between seed yield and yield-related characters are prerequisites in selecting desirable types for the target environment. Some of the yield components are highly interrelated while, seed yield is governed by many genetic as well as environmental factors that are interdependent and influenced by various components towards yield, which is associated with low heritability. Therefore, the present study suggested that the

presence of strong inherent association among the studied traits lead to direct phenotypic selection might be worthwhile for the improvement of mung bean and which implies that there is an enormous chance of exploiting the potential of these traits for effective selection in the mung bean improvement program.

This indicated that these traits are considered important for the improvement of mung bean yield through a direct selection of these traits. This finding is in agreement with the work of Al-Ballat and Al-Araby (2019) on common bean, who reported that the selection for those traits having strong and positively significant correlations with seed yield is expected to improve seed yield in common bean, suggesting that the true relationship of these traits with seed yield since these traits are seed yield predictors. Similarly, Gonçalves *et al.* (2017) indicated that the traits which have moderate to strong correlations with the desired trait are important for successful indirect selection.

Traits such as seeds per pod, seed yield per plant, and pods per cluster had a significant positive correlation with seed yield at genotypic and phenotypic levels. This finding is in agreement with the report of Partap *et al.* (2019) on the black gram genotypes, who indicated that the strong and positive association of yield-related traits might be due to the linkage of genes determining these traits which leads to the simultaneous improvement in seed yield through these traits could be achieved within a short period by simple selection procedures. Therefore; these results give some clues that simultaneous improvement in any of these traits will lead to an increase through direct selection for seed yield in mung bean. Based on these results, the genotypic and phenotypic correlations indicate that the extent to which the corresponding traits are under the control of the same set of genes having a physiological basis for their expression. Likewise, Ghosh *et al.* (2019) on mung bean genotypes, reported that seed yield exhibited a significantly ($P \leq 0.01$) positive correlation with the number of pods per plant at the genotypic (0.665) and phenotypic (0.578) levels, respectively while it had exerted significantly

($P \leq 0.05$) positive correlation with the number of seeds per pod only at the genotypic (0.261) level. Similarly, seed yield per plant showed a significantly ($P \leq 0.01$) positive correlation with the number of branches per plant at the genotypic level while it had a significantly ($P \leq 0.05$) positive correlation with the number of branches per plant at the phenotypic level. On the other hand, seed yield showed a negative and highly significant genotypic and phenotypic correlation with days to flowering (Table 1)

Path Coefficient Analysis

Whether the correlation between two characters is of phenotypic, genotypic, or environmental nature, it is the genotypic one that determines higher interest for genetic breeding as it involves an association of heritable nature (Nogueira et al., 2012). By considering this view, path analysis was made to understand the nature of correlations among yield and yield components to improve production and mitigate future demand (Kate et al., 2017). Regarding the values for direct and indirect effects, Lenka and Mishra (1973) suggested that a scale for the importance of direct and indirect effects and classified as negligible for values from (0.00 to 0.09), low, for values from (0.10 to 0.19), moderate, for values from (0.20 to 0.29), high, for values from (0.30 to 0.99), while values greater than 0.99, were considered as very high. In this study, seed yield was considered as a dependent trait while the rest of the traits that were positively correlated with seed yield were used as causal traits (Tables 2 and 3).

Phenotypic Path Coefficient Analysis of Seed Yield with other Traits

The phenotypic path coefficient analysis results of seed yield with the other 16 traits were presented (Table 2). The path coefficient analysis result revealed that days to maturity, petiole length, peduncle length, plant height, pod length, pods per cluster, pods per plant, seeds per pod, seed yield per plant, hundred seed weight, and harvest index had a positive direct effect on seed yield at the phenotypic level. Peduncle length possessed a positive direct effect (0.13) on seed yield but its negative indirect effects through petiole length (-0.26), terminal leaf length (-0.14),

terminal leaf width (-0.07), and biomass yield (-0.04), as well as its significant negative genotypic (-0.49) and phenotypic (-0.35) coefficients, contributed to a negative association with seed yield. The results showed that pods per cluster had a maximum direct positive effect on seed yield (0.41) followed by pods per plant (0.33), suggesting that the simultaneous selection of the two traits may improve genetic gain in mung bean breeding. These results showed that the selection based on these traits except the peduncle length would be highly effective for improving seed yield since the positive direct effect of the peduncle length on seed yield is diluted due to its negative indirect effects. In this study, those traits with positive direct effects should be considered as the selection criteria for yield improvement in mung bean, and it is important to reveal the effectiveness of direct selection through these traits. Direct negative effects on seed yield were attributed by days to flowering, terminal leaf length, terminal leaf width, the number of primary branches per plant, and biomass yield at the phenotypic level, indicating that improvement of these traits is essential before selecting them for high seed yield. Therefore, the results indicated that these traits are not directly associated with yield hence, selection directly through these characters results in poor selection, so indirect causal factors must be considered especially the traits contributing positively.

Days to flowering had a negative direct effect (-0.16) on seed yield because of its negative indirect effect through terminal leaf length, terminal leaf width, plant height, number of primary branches per plant, pods per cluster, pods per plant, seeds per pod, seed yield per plant, biomass yield and harvest index at the phenotypic level. This finding complies with the results of Bhanu *et al.* (2016) who reported that days to flowering showed a negative direct effect on seed yield at the phenotypic level. Terminal leaf length had exerted a negative direct effect (-0.15) on seed yield due to its negative indirect effects through days to flowering, days to maturity, terminal leaf width, seed yield per plant, hundred seed weight, and biomass yield. Terminal leaf width had exerted a negative direct effect (-0.02) on seed yield due to its negative indirect effects

through days to flowering, days to maturity, terminal leaf length, the number of primary branches per plant, pods per plant, seeds per pod, and seed yield per plant. The number of primary branches per plant exerted a negative direct effect (-0.23) on seed yield due to its negative indirect effects through days to flowering, days to maturity, terminal leaf width, plant height, pods per plant, hundred seed weight, and biomass yield. The negative direct influence (-0.27) of biomass yield on seed yield was nullified by its positive indirect effects via petiole length, terminal leaf length, terminal leaf width, plant height, pod length, pods per plant, seeds per pod, and seed yield per plant.

Days to maturity had affected seed yield positively and indirectly through days to flowering, petiole length, peduncle length, the number of primary branches per plant, pod length, and 100-seed weight at the phenotypic level. Whereas, the negative indirect effect of plant height on seed yield was observed through days to flowering, days to maturity, petiole length, the number of primary branches per plant, and pods per cluster at the phenotypic level. Similarly, a negative indirect effect of harvest index on seed yield was noted through days to flowering, days to maturity, and biomass yield at the phenotypic level. The considerable indirect effect of pods per cluster through petiole length (-0.28) and hundred seed weight (-0.19) were counter-balanced by the positive direct effect of pods per cluster (0.41) on seed yield and reduced the correlation coefficient to 0.25. Pods per plant are affected positively and indirectly via petiole length, terminal leaf length, peduncle length, plant height, pod length, pods per cluster, biomass yield, and harvest index at the phenotypic level. Hundred seed weight had influenced positively and indirectly seed yield via days to flowering, days to maturity, and terminal leaf width, peduncle length, and plant height, seeds per plant, and harvest index at the phenotypic level. Likewise, a positive indirect effect of biomass yield on seed yield was noted through terminal leaf width, pods per cluster, and pods per plant at the phenotypic level. Harvest index affected seed yield negatively and indirectly through days to flowering and days to

maturity at the phenotypic level. The result of phenotypic path analysis showed that due importance should be given for plant height, pods per plant, pods per cluster, hundred seed weight, and harvest index because of their significant correlation and high direct effects. This indicates that there is always scope for enhancement of grain yield by the selection of these traits at the phenotypic level.

The residual effect at the phenotypic level ($h = 0.2047$) was relatively low indicating that the traits considered in this study are enough to adequately explain the variation in seed yield. About 79.53% of the total variation on seed yield was contributed by 16 independent traits that were included in this study. The remaining 20.47% is explained by other traits not considered in the study. This further clarified that seed yield attributing traits included in this study were good enough. It is also suggested that further study should be made with more characters to find out other traits that contribute to the rest of the proportion of the yield. Generally, the present investigation suggested that maximum emphasis should be given to the phenotypic traits studied in selecting mung bean with higher seed yields. The contribution of residual effects that influenced seed yield was low at the phenotypic levels, reflected that the traits in the study were sufficient enough to account for the variability in the dependent character. This finding was supported by the previous reports on black gram genotypes (Mohammad *et al.*, 2016; Arya *et al.*, 2017; Partap *et al.*, 2019). Similarly, Khan *et al.* (2016), observed the phenotypic residual effect ($h = 0.0925$), indicating that about 91% of the phenotypic total variation was explained by the included traits and how best the causal factors account for the variability of the dependent factor on snake gourd genotypes.

Therefore, path analysis indicated that petiole length, plant height, pods per plant, pods per cluster, hundred seed weight, and harvest index were the main determinants of seed yield. Thus, more emphasis should be given during the selection of these traits for yield improvement in mung beans. Generally, the seed yield is an important parameter among all the morphological

as well as yield traits. Improvement in seed yield in mung bean could be brought through the selection of component characters like pods per plant, pod length, 100 seed weight, and harvest index which are directly related to final yield in mung bean and exhibited positive direct effects at the phenotypic level.

Genotypic Path Coefficient Analysis of Seed Yield with other Traits

The genotypic path coefficient analysis results of seed yield with the other 16 traits were presented (Table 3). Days to maturity, terminal leaf width, peduncle length, plant height, number of primary branches per plant, pod length, pods per cluster, pods per plant, seeds per pod, seed yield per plant, hundred seed weight, biomass yield, and harvest index had a positive direct effect on seed yield. Plant height possessed a high positive direct effect (0.54) on seed yield but its negative indirect effects were also detected through days to maturity (-0.17), petiole length (-0.01), pods per plant (-0.11), seeds per pod (-0.08), and biomass yield (-0.76). Biomass yield had exerted a positive direct effect (0.21) on seed yield but its negative indirect effects through days to maturity (-0.07), terminal leaf length (-0.33), peduncle length (-0.05), pods per cluster (-0.05), seeds per pod (-0.16), seed yield per plant (-0.12) and harvest index (-0.10). The results showed that plant height had a maximum direct positive effect on seed yield (0.54) followed by the number of primary branches per plant and seeds per pod (0.36), days to maturity (0.34), and biomass yield (0.21), respectively suggesting that the simultaneous selection of these traits may improve genetic gain in mung bean breeding. The strong indirect effect of plant height through biomass yield (-0.76), days to maturity (-0.17), the number of pods per cluster (-0.11), petiole length (-0.01), and the number of seeds per pod (-0.08) were counterbalanced by the positive direct effect of plant height (0.54) on seed yield and reduced the correlation coefficient to -0.01. Similarly, the indirect effect of biomass yield through terminal leaf length (-0.33), days to maturity (-0.07), peduncle length (-0.05), pods per cluster (-0.05), the number of seeds per pod (-0.16), seed yield per plant (-0.12), and harvest index (-0.1) were counter-balanced by the direct

effect of biomass yield (0.21) on seed yield and reduced the correlation coefficient to (-0.1). The positive direct effects of plant height and biomass yield on seed yield were diluted due to their negative indirect effects. The selection of these traits except plant height and biomass yield would be highly effective for improving seed yield. Direct negative effects on seed yield were attributed to days to flowering, petiole length, terminal leaf length, pod length, and pods per cluster, indicating that improvement of these traits is essential before selecting them for high seed yield. The negative direct effect of days to flowering on seed yield was nullified by its positive indirect effects via petiole length, terminal leaf length, terminal leaf width, peduncle length, the number of primary branches per plant, plant height, seeds per pod, seed yield per plant, hundred seed weight, biomass yield, and harvest index. Petiole length had exerted a negative direct effect (-0.17) on seed yield due to its negative indirect effects through days to flowering, days to maturity, pods per plant, seed yield per plant, and hundred seed weight. The negative direct influence of terminal leaf length on seed yield was nullified by its positive indirect effects via days to flowering, days to maturity, petiole length, peduncle length, plant height, number of primary branches per plant, pods per plant, seeds per pod, seed yield per plant and harvest index. Terminal leaf width had exerted a positive direct effect (0.09) on seed yield due to its positive indirect effects through days to maturity, terminal leaf length, the number of primary branches per plant, plant height, pod length, pods per cluster, seeds per pod, hundred seed weight and harvest index. Pod length had exerted a negative direct effect (-0.11) on seed yield due to its negative indirect effects through days to maturity, terminal leaf length, peduncle length, seeds per pod, seed yield per plant, and hundred seed weight. Pods per cluster exerted a negative direct effect (-0.17) on seed yield because of its negative indirect effects through terminal leaf width, seed yield per plant, hundred seed weight, and harvest index.

Days to maturity had exerted positive and indirect effects on seed yield through terminal leaf length, terminal leaf width, peduncle length, number of primary branches per plant, pods per cluster, and

Pods per plant at the genotypic level. The number of pods per cluster exhibited positive and indirect effects on seed yield through days to maturity, petiole length, terminal leaf width, peduncle length, plant height, pod length, seeds per pod, seed yield per plant, hundred seed weight, and harvest index at the genotypic level. This result is in agreement with other reports (Gadakh *et al.*, 2013; Itafa *et al.*, 2014; Muthuswamy *et al.*, 2019). Selection based on the number of pods per cluster would increase the seed yield indirectly via the number of pods per plant. Path coefficient analysis also revealed that the number of pods per plant had a positive direct effect on seed yield. This trait also recorded a strong positive genotypic correlation with seed yield per plant. This indicated that the selection of the genotypes having more pods per plant along with optimum seed weight would be rewarding for isolating high-yielding genotypes in this crop. This is in agreement with Ghosh *et al.* (2019) on mung bean, who reported that pods per plant have been exerted maximum positive direct effect (0.717) on seed yield per plant, which coincides with the similar works (Katiyar *et al.*, 2012; Manggoel *et al.*, 2012) who reported that positive direct effect of pods per plant on seed yield of mung bean. Pods per cluster had exerted a negative direct effect on seed yield. This result is controversial with the previous reports (Anand *et al.*, 2016) who described that pods per cluster had exerted a positive direct effect on seed yield of mung bean.

There were positive indirect effects of pods per plant through terminal leaf length, terminal leaf width, peduncle length, pod length, pods per cluster, seed yield per plant, and biomass yield at the genotypic level. Likewise, a positive indirect effect of pods per plant on seed yield was observed through terminal leaf length, terminal leaf width, peduncle length, pod length, pods per cluster, seed yield per plant, and biomass yield at the genotypic level. Positive indirect effects of 100-seed weight on seed yield were observed through days to flowering, terminal leaf width, plant height, seeds per pod, seed yield per plant, and biomass yield at the genotypic level. Biomass yield affected seed yield indirectly and negatively through the traits like days to maturity, terminal leaf length, terminal leaf width, plant height, the

number of primary branches per plant, seeds per pod, pods per plant, seed yield per plant, and hundred seed weight at genotypic level; while it affected positively and indirectly seed yield through days to flowering, petiole length, peduncle length, pod length, pods per cluster and harvest index at the genotypic level. Harvest index affected seed yield negatively and indirectly through days to maturity, pods per cluster, seeds per pod, and biomass yield at the genotypic level. This result confirmed the previous findings (Lalinia and Khameneh, 2014; Abbas *et al.*, 2018). The result of genotypic path analysis showed that due importance should be given for days to maturity, the number of primary branches per plant height, and seed yield per plant because of their significant correlation and high direct effects. This indicates that there is always scope for enhancement of grain yield by the selection of these traits at the genotypic level. Days to maturity, the number of primary branches per plant, seed yield per plant, and plant height are the most important yield contributing components as they recorded high direct effects towards seed yield in mung bean.

The residual effect at the genotypic level ($h = 0.0943$) was low, signifying that the traits considered in this study are enough to adequately explain the variation in seed yield. The estimation of direct and indirect effects was more pronounced in the genotypic path than the phenotypic path. About 90.57% of the total variation on seed yield was contributed by 16 independent traits that were included in this study, while other factors not included in the study might explain 9.43%. Therefore, the traits included in this study were good enough to explain the variability in seed yield. Generally, the low residual effect indicated the independent traits explained the dependent trait (seed yield) more than two-thirds ($2/3$); "therefore, selection based on genotypic path coefficient analysis for mung bean improvement is very appropriate." This finding is supported by the report of Asari *et al.* (2019) who observed a low genotypic residual effect ($h = 0.0324$). Likewise, Anand *et al.* (2014) observed a low residual effect and stated that the appropriateness of the traits chosen to explain the variability. Similar results were also supported on

black gram genotypes (Mohammad *et al.*, 2016; Arya *et al.*, 2017; Partap *et al.*, 2019). Similarly, Khan *et al.* (2016), observed the genotypic residual effect ($h^2 = 0.024$), indicating that about 98% of the genotypic total variation was explained by the included traits and how best the causal factors account for the variability of the dependent factor on snake gourd genotypes.

This result is contradictory with the reports of Kumar (2014) and; Bhanu *et al.* (2016) who reported that the high residual effect observed at the genotypic level is due to the warm and dry weather condition indicating that some of the characters influencing the seed yield of mung bean have not been included in this study.

Table 1. Genotypic (Above Diagonal) and Phenotypic (Below Diagonal) Correlation Coefficients among 17 Traits on Mung Bean.

	DTF	DTM	PTL	TLL	TLW	PDCL	PHT	BRN	PODL	PPC	PPP	SPP	SYPP	HSW	SYLD	BM	HI
DTF		0.08*	-0.39ns	-0.38*	0.26*	0.06ns	0.03**	0.02*	0.23**	0.06*	-0.26**	-0.01*	0.07**	0.17**	-0.22**	0.16*	0.01*
DTM	0.06*		0.92ns	-0.06*	0.18*	0.06*	-0.31**	0.03*	0.08ns	0.26ns	0.29*	0.21*	0.24*	0.15**	0.43**	0.33**	0.15*
PTL	0.31ns	0.03ns		-0.18*	0.17*	0.16ns	-0.25**	0.11ns	0.19**	0.16ns	-0.31**	0.23ns	-0.29**	-0.13**	-0.45**	0.41**	-0.01*
TLL	0.04*	-0.11*	0.12ns		-0.06ns	-0.13*	0.04**	0.05*	-0.24**	-0.13*	0.51ns	0.19ns	0.06*	-0.48*	0.23**	-0.43ns	-0.01*
TLW	0.17*	0.14*	0.06**	0.04*		0.09*	0.15**	0.19ns	0.11*	0.09ns	0.12*	0.21*	-0.43*	0.20*	0.11*	0.11*	-0.01ns
PDCL	-0.08*	0.03*	0.10**	0.02*	0.05*		0.17**	0.08*	-0.08ns	0.04*	0.03ns	0.09ns	0.48**	0.02*	-0.49**	-0.07*	-0.19*
PHT	0.18*	0.05*	0.06*	-0.03*	0.09*	0.10*		0.12*	0.03*	0.17*	-0.23*	-0.08*	-0.11**	0.09*	0.24**	0.20**	-0.01*
BRN	0.04ns	-0.11*	0.12*	-0.29*	0.04*	0.02*	-0.03**		0.05*	0.08*	-0.07*	0.02*	0.04**	0.10**	0.14**	0.03**	-0.09*
PODL	-0.12*	-0.25*	0.06*	0.13*	-0.16*	-0.15*	0.19**	0.13*		-0.08*	-0.03ns	-0.10*	0.03ns	0.25ns	0.11ns	0.28ns	0.16ns
PPC	-0.03*	0.02*	0.07*	0.18*	-0.05*	0.01*	-0.04**	0.18*	0.10*		0.02**	-0.11*	0.08**	-0.40*	0.05*	0.55**	-0.01*
PPP	-0.08*	0.09*	-0.10*	0.46*	0.08*	0.02*	0.03*	0.46*	-0.16*	-0.15*		-0.04*	-0.20*	-0.14*	0.17*	0.24*	0.12*
SPP	-0.04*	-0.19*	0.26*	-0.02*	0.08*	0.18*	0.14*	-0.02*	0.13*	-0.12*	0.11*		0.05*	0.07**	0.65**	0.15*	0.03**
SYPP	0.08*	0.12*	0.03*	0.02*	0.15*	0.17*	0.21*	0.02*	-0.43*	-0.09*	0.26*	0.13*		0.68**	0.93**	-0.03*	-0.01*
HSW	0.12*	-0.06*	-0.16*	-0.35*	-0.10*	-0.09*	0.23*	-0.35*	-0.02*	-0.08*	-0.29*	-0.24*	0.02*		0.43**	0.33*	0.21**
SYLD	-0.20*	0.06*	0.25*	0.10*	0.13*	-0.35*	0.16*	0.10*	0.31*	0.17*	0.22*	0.56*	0.48*	-0.15*		0.70*	0.01*
BM	-0.23*	-0.02*	0.27*	0.21*	0.15*	0.45*	0.07*	0.21*	-0.02*	0.21*	0.29*	0.51*	0.43*	0.45*	0.55*		0.67*
HI	-0.23*	-0.23*	-0.02*	0.27*	0.21*	0.15*	0.35*	0.07*	0.21*	-0.02*	0.21*	0.29*	0.51*	0.43*	0.44*	0.65*	

DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield (kg ha⁻¹), BM= biomass yield (kg ha⁻¹), HI=harvest index.

Table 2. Phenotypic Path Coefficients, Direct and Indirect Effects.

	DTF	DTM	PTL	TLL	TLW	PDCL	PHT	BRN	PODL	PPC	PPP	SPP	SYPP	HSW	BM	HI	r _{ph}
DTF	<u>-0.16</u>	0.07	0.02	-0.14	-0.11	0.02	-0.01	-0.04	0.06	-0.07	-0.01	-0.06	-0.01	0.05	-0.03	-0.03	-0.45
DTM	0.07	<u>0.07</u>	0.02	-0.14	-0.07	0.02	-0.02	0.2	0.02	-0.04	-0.02	-0.02	-0.02	0.04	-0.03	-0.03	0.05
PTL	0.02	0.02	<u>0.21</u>	-0.02	0.2	0.02	-0.01	0.03	-0.03	-0.17	0.1	0.05	0.12	-0.07	-0.03	0.01	0.45
TLL	-0.14	-0.14	0.01	<u>-0.15</u>	-0.23	0.08	0.12	0.02	0.08	0.01	0.04	0.06	-0.07	-0.01	-0.02	0.03	-0.31
TLW	-0.11	-0.07	0.05	-0.05	<u>-0.02</u>	0	0.01	-0.02	0	0.08	-0.11	-0.12	-0.01	0.01	0.09	0.03	-0.24
PDCL	0.02	0.02	-0.26	-0.14	-0.07	<u>0.13</u>	0.02	0.02	0.02	0.1	0.01	0.04	0.01	0.02	-0.04	0.02	-0.08
PHT	-0.01	-0.02	0	0.01	0.1	0.01	<u>0.2</u>	0.06	-0.01	0.04	0.01	0	0.04	0.1	-0.01	0.05	0.57
BRN	-0.04	-0.04	0.01	0.01	-0.01	0.01	-0.02	<u>-0.23</u>	0.01	0.09	-0.01	0.02	0.08	-0.12	-0.06	0.01	-0.29
PODL	0.06	0.04	0.02	-0.03	-0.23	0.01	0.02	-0.03	<u>0.11</u>	0.02	0.06	0.31	0.01	0.01	-0.16	0.03	0.25
PPC	-0.07	-0.07	-0.28	0.07	0.14	0.04	-0.09	0.12	0.08	<u>0.41</u>	0.03	-0.11	-0.04	-0.19	0.2	0.01	0.25
PPP	-0.01	-0.01	0	0.05	0.11	-0.06	0.2	-0.01	0.06	0.03	<u>0.33</u>	-0.1	-0.06	-0.01	0.02	0.03	0.57
SPP	-0.06	-0.06	0.03	-0.03	0.15	0.05	0.01	0.02	0.31	-0.11	-0.1	<u>0.07</u>	0.01	0.09	-0.13	0.04	0.29
SYPP	-0.01	-0.01	-0.13	0.17	-0.01	0.02	0.04	0.03	0	0.03	-0.03	0.03	<u>0.23</u>	-0.08	-0.03	0.07	0.32
HSW	0.05	0.04	0.03	0.01	0	0.1	0.1	0.12	0.01	-0.25	-0.05	0.15	0.08	<u>0.19</u>	-0.02	0.06	0.62
BM	-0.03	-0.03	0.04	0.1	0.21	-0.06	0.03	-0.06	0.09	0	0.02	0.08	0.06	-0.02	<u>-0.27</u>	-0.06	0.1
HI	-0.03	-0.03	-0.01	0.12	0.09	-0.04	0.05	0.01	0.03	0.01	0.03	0.04	0.07	0.06	-0.04	<u>0.13</u>	0.49

Residual = 0.2047

DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield (kg ha⁻¹), BM= biomass yield (kg ha⁻¹), HI=harvest index, r_{ph}=phenotypic correlation

Table 3. Genotypic Path Coefficients, Direct and Indirect Effects.

	DTF	DTM	PTL	TLL	TLW	PDCL	PHT	BRN	PODL	PPC	PPP	SPP	SYPP	HSW	BM	HI	rg
DTF	<u>-0.81</u>	-0.12	0.2	0.03	0.02	0	0.2	0.08	-0.03	-0.01	-0.12	0.01	0.07	0.09	0.19	0.21	0.01
DTM	0.26	<u>0.34</u>	-0.07	-0.01	0.01	0.03	-0.11	0	-0.01	0.03	-0.11	0.11	-0.03	-0.11	-0.02	-0.04	0.27
PTL	-0.17	-0.02	<u>-0.17</u>	0	0.09	0.02	0.03	0	0.04	0.02	-0.31	0.02	-0.2	-0.04	0.13	0	-0.56
TLL	0.82	0.11	0.18	<u>-0.08</u>	-0.02	0.01	0	0.02	-0.01	-0.13	0.01	0.19	0.08	-0.37	-0.04	0.2	0.97
TLW	-0.01	0.02	-0.01	0	<u>0.09</u>	-0.02	0.07	0.03	0	0.07	0.06	0.01	-0.03	0.05	-0.13	0.21	0.41
PDCL	0.01	0.12	0.01	-0.01	0.01	<u>0.06</u>	0.06	0.08	-0.06	0.01	0.04	0.03	0.08	-0.05	0.02	0.15	0.56
PHT	0.02	-0.17	-0.01	0	0.01	0.01	<u>0.54</u>	0.1	0.02	0.22	-0.11	-0.08	0.04	0.16	-0.76	0	-0.01
BRN	0.12	0.01	0	0.03	0.05	0.04	0.07	<u>0.36</u>	0.07	-0.01	-0.03	-0.06	0.08	-0.23	-0.01	0	0.49
PODL	0.08	-0.01	0.03	-0.01	0	-0.03	0	0.02	<u>-0.11</u>	0.01	0.09	-0.19	-0.06	-0.02	0.02	0.02	-0.16
PPC	0.03	0.05	0.04	0	-0.01	0	0.03	0.01	0	<u>-0.17</u>	0.01	0.25	-0.01	-0.04	0.01	-0.3	-0.1
PPP	0	0.05	0	-0.01	0.1	-0.02	0.2	0.03	0.02	-0.02	<u>0.07</u>	0.01	-0.02	-0.01	-0.11	0.09	0.38
SPP	0.03	-0.01	-0.04	0.03	-0.02	0.22	-0.01	0.02	0.01	0.22	-0.05	<u>0.36</u>	0.12	0.14	-0.06	-0.02	0.94
SYPP	0.28	-0.05	-0.01	-0.17	0.07	0.01	0.03	0.4	0.09	0.1	0.03	-0.07	<u>0.06</u>	0.4	-0.41	0	0.76
HSW	0.04	-0.01	0.06	-0.02	0.05	0.01	0.53	0.11	0.17	0.01	-0.4	-0.14	0.17	<u>0.18</u>	-0.05	0.15	0.86
BM	0.02	-0.07	0	-0.33	0.09	-0.05	0	0.03	0.21	-0.05	0.06	-0.16	-0.12	0.16	<u>0.21</u>	-0.1	-0.1
HI	0.07	-0.06	-0.26	-0.01	0.16	0.21	0.09	0.01	0.05	0.21	-0.21	0.03	0.33	-0.06	0.12	<u>0.09</u>	0.77

Residual = 0.0943

DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield (kg ha⁻¹), BM= biomass yield (kg ha).

CONCLUSIONS

Assessment of genotypic correlation between different traits exhibited close parallelism with their corresponding phenotypic correlation. The result depicted that for most of the trait pairs, the genotypic and phenotypic associations were in the same direction and the genotypic estimates were higher than the phenotypic ones, demonstrating that these traits had an inherited association between the studied characters. All the studied parameters showed a significant correlation with days to flowering except petiole and the number of primary branches per plant at the phenotypic level.

In this study, all traits had significantly correlated with the seed yield both at the genotypic and phenotypic levels.

The present investigation showed that days to maturity, plant height, seeds per plant, and pods per plant had exerted a positive direct effect on seed yield of mung bean both at the genotypic and phenotypic levels. Additionally, a hundred seed weight and harvest index had exerted a positive direct effect on seed yield both at the genotypic and phenotypic levels. Therefore, direct selection for these traits may prove effective for the improvement of seed yield in the germplasm under study. The residual effect ($h = 0.2047$), shows traits that are included in the phenotypic path coefficient analysis explained by 79.53% of the total variation in seed yield. The genotypic residual effect was low ($h = 0.0943$), indicating that the traits which were included in the genotypic path analysis explained 90.57% of the total variation by seed yield showing that the independent traits were explained the dependent trait more than two-third, therefore, the genotypic path coefficient analysis based selection for mung bean improvement is very appropriate. This analysis confirmed that day to maturity, plant height, the number of primary branches per plant, and seeds per pod produced a high positive direct effect on seed yield, which appeared to be the prominent traits when selecting for seed yield in mung bean genotypes. Therefore, the present study put forward that days to maturity, plant height, number of primary branches per plant, and seeds per pod exerted the highest direct effect on seed yield and it should be given maximum consideration for total yield improvement as the appropriate selection indices. The selection procedure should be formulated so that the advance in one component is not risked by the deterioration effect of the other. Therefore, the results of the path coefficient analysis

indicated that days to maturity, plant height, number of primary branches per plant, and seeds per pod were the main determinants of seed yield in mung bean.

CONFLICTS of INTEREST

The authors declare that there is no conflict of interest.

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