

Assessment of Genetic Variability for Yield and Component Traits in Early Segregating Generation of Mung Bean (*Vigna radiata* L. wilczek)

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ABSTRACT

Indirect selection for yield contributing traits in segregating generation is practiced to realize the potential of yields which depends on nature and magnitude of genetic variability. The present study aims to estimate genetic variability and relation between yield and its related attributes of segregating population of mung bean. A high yielding mung bean variety China mung was crossed with LM-1668. The F_2 segregating population was generated. The population comprised of 150 F_2 plants along with parents were evaluated during *summer 2022*. The observations on pod and seed traits were recorded and data was subjected to statistical analyses to estimate genetic variability, heritability and correlation among the traits and path coefficients. Wide range of variation was observed in the F_2 segregating generation for pod and seed traits. The skewness of all the traits except seed yield and test weight was less than 1.0 which suggested that the traits followed normal distribution. Around 12 transgressive segregants were observed for seed yield in this cross which can be further selected for breeding higher seed yield varieties in mung bean. High heritability coupled with high genetic advance was found for plant height, primary branches, seeds per pod, and test weight suggesting that these traits are under the control of the additive gene action and can be improved by simple phenotypic selection. A Significant positive association and high direct effect was noticed with number of seeds per plant on seed yield revealed that the selection based on these traits would ultimately improve the pod yield. Hence, the above mentioned characteristics should be given top most priority while formulating a selection strategy for improvement of yield in mung bean.

Keywords : Mung bean, Genetic variability, Heritability, Correlation, Yield traits

MUNGBEAN (*Vigna radiata* (L.) Wilczek var. *radiata*) is a diploid ($2n = 2x = 22$) annual legume belonging to the family Leguminosae with the estimated genome size of 509Mb (Arumuganathan and Earle, 1991). In India, it is grown across a 4.6 Mha area with a mean production of 2.44Mt and an average yield of 531 Kg/ha (Directorate of Economics and Statistics, Department of Agriculture and Cooperation, 2022). While in Karnataka, area covered by mung bean is of 0.41 Mha with an average production of 0.143 Mt and 346 kg/ha of yield (Directorate of Economics and Statistics, Department of Agriculture

and Cooperation, 2022). Although a number of varieties have been developed and recommended for cultivation, the total mung bean productivity in India is still low and there is a need for yield improvement (Narasimhulu *et al.*, 2013). Therefore, the main objective of any mung bean breeding programs in the world is to develop high yielding mung bean cultivars. Yield is a polygenic trait which is determined by several component traits, thus, affecting the final seed yield (Das and Barua, 2015). According to Srivastava and Singh (2012), yield correlates with various inter-related traits and are associated to each other either positively or negatively.

Genetic variability is a requirement for any breeding program and allows a plant breeder the opportunity to choose high-yielding genotypes. Nonetheless, knowledge on the yield relationship with its different parameters provides the basis for selection of improved varieties (Saleem *et al.*, 2005). A thorough knowledge of the existing genotypic variation for yield and its components and their association is required for the development of high yielding cultivars. The variability in genotypes indicates sufficient possibilities to select superior and desirable genotypes to significantly improve mung bean. The phenotypic and genotypic coefficient of variations show the degree of variability that exists with various characteristics. The phenotypic variability observed is a combined estimate of genetic and environmental variability of which only the genetic component is heritable (Al-Tabbal *et al.*, 2011). Estimating the heritability explains whether the differences observed among the individuals are a result of genotypic differences or due to environmental causes. Heritability acts as a predictive tool in determining the reliability of phenotypic traits for selection purpose. Thus, high heritability accompanied by estimates of genetic advance can assist in selection of characteristics efficiently and formulate future breeding strategy to improve mung bean. Information on skewness and kurtosis provides the nature of gene action and gene numbers controlling the trait. Skewness in the positive direction reveals the presence of complementary gene action, while the gene action is duplicate (additive \times additive) when skewness has a negative sign. Positive sign of kurtosis value on the characteristics indicates the presence of gene interactions, whereas a negative sign or a value near zero for kurtosis indicates the absence of gene interactions.

Correlation explores the inter-relationship amongst diverse plant traits and decides the direct indirect partitioning of contributing traits on which selection can be done to ameliorate yield improvement. The path coefficient analysis helps to know whether the association of different traits with seed yield is because of their direct effect or due to their indirect effects *via* other independent components of seed yield. The selection process is more difficult for traits where

heritability is low or not exactly determined as seed yield. Knowledge on the correlation and path analysis becomes important for the successful selection program and breeding lines with increased yield potential for plant breeders. Keeping this in view, the objective of the present study is to understand genetic variation, correlation and path analysis for pod and seed traits in F_2 segregating population of mung bean.

MATERIAL AND METHODS

The basic materials consisted of two elite parents, namely Chinamung and LM-1668 which contrasts for pod and seed traits (Table 1). While Chinamung is high yielding, LM-1668 is a low yielding variety. Chinamung and LM-1668 were crossed during 2021 *rainy* season to obtain F_1 s (Chinamung \times LM-1668). The plants of the F_1 s were grown and selfed during 2022 *summer*. F_2 population derived from the F_1 s along with their parents were grown in 2022-23 *rabi* season at the experimental plot of Department of Genetics and Plant Breeding (GPB), University of Agricultural Sciences, Bangalore, India which is located at an altitude of 930 m above mean sea level 12^o58' North and 77^o35' East latitude and longitude, respectively. Twenty seeds of each of the parents were sown in each row of 2m length and 150 F_2 seeds were sown with 30cm spacing between rows and 10 cm distancing between the plants in a row. The recommended production package was practiced to raise two parents, and F_2 generations.

TABLE 1

Important features of parents, Chinamung (P_1) and LM-1668 (P_2) used in this study

Features	Chinamung	LM-1668
Days to Flowering	33.33	34.33
Plant Height (cm)	35.93	40.80
No. of Branches per Plant	2.80	2.73
No. of Pods per Plant	34.73	30.87
No. of Seeds per Pod	11.00	10.00
Test Weight (g)	3.68	3.52
Pod yield (g)	16.80	13.39
Seed Yield (g)	11.88	8.30

Sampling of Plants and Data recording

Data were recorded on 10 randomly selected plants from two parents and from each of the 150 F_2 progenies for eleven traits, namely, days to flowering, plant height, number of primary branches, number of secondary branches, number of clusters, pod length, and weights of sun-dried pods and grains. The average of these traits across ten sample plants was computed and expressed as days to flowering, plant height (cm), primary branches plant^{-1} , secondary branches plant^{-1} , clusters plant^{-1} , pods plant^{-1} , pod length (cm), seeds pod^{-1} , seeds plant^{-1} , Test weight (g), and seed yield plant^{-1} (g).

Statistical analysis

The data was subjected to statistical analyses. Mean, range, variance, coefficient of variance, and standard deviation of the traits in F_2 generations was estimated using 'psych' package in R software version 3.3.2.

Variability Parameters

Broad sense heritability (h^2) was estimated using the following formula given by Allard (1960).

$$h_b^2 = \sigma^2g / \sigma^2p \times 100$$

Where,

σ^2g = genotypic variance,

σ^2p = phenotypic variance

Phenotypic and genotypic coefficient of variation (PCV and GCV) for all the studied characters were calculated by the formula reported by Burton and DeVane (1953).

$$\text{PCV} = (\sqrt{\sigma^2p}/\mu) \times 100$$

$$\text{GCV} = (\sqrt{\sigma^2g}/\mu) \times 100$$

Where,

μ = Grand mean

Expected Genetic advance (GA) was figured by the following formula given by Allard (1960).

$$GA = k \times h_b^2 \times \sqrt{\sigma_b^2}$$

Where, k = selection differential (2.06) at 5% selection intensity

$\sqrt{\sigma_b^2}$ = phenotypic standard deviation

The genetic advance as a percentage of the mean was estimated as:

$$GAM = (GA/\mu) \times 100$$

Skewness and kurtosis statistics were estimated for understanding the nature of distribution of the F_2 population for yield its related traits to identify a superior segregant in the F_2 generation under study. Skewness and kurtosis values were computed using the 'psych' package in R software version 3.3.2.

Correlation Coefficient Analysis

The correlation coefficients were estimated to understand the degree of relationship of characters with yield and component traits. The variance and covariance components were used to assess correlation coefficients between two characters at genotypic and phenotypic levels.

$$r_g(xy) = \frac{\text{Cov}_g(xy)}{\sqrt{\sigma_g^2(x) \cdot \sigma_g^2(y)}}$$

$$r_p(xy) = \frac{\text{Cov}_p(xy)}{\sqrt{\sigma_p^2(x) \cdot \sigma_p^2(y)}}$$

Where,

$r_g(xy)$ - genotypic correlation coefficient

$r_p(xy)$ - phenotypic correlation coefficient

$\text{Cov}_g(xy)$ - genotypic covariance of xy

$\text{Cov}_p(xy)$ - phenotypic covariance of xy

The calculated value of 'r' was compared with table value with $n-2$ degrees of freedom at 5 per cent and 1 per cent level of significance where, n is the number of pairs of observation.

Path Coefficient Analysis

Phenotypic path coefficient analysis was carried out to estimate the direct and indirect effects of

independent variables on the dependent variable seed yield. This method gives the direct and indirect effects of individual characters on yield. The unexplained variation of residual factors was obtained from the following equations:

$$Residual\ factor = \sqrt{1 - R^2}$$

Where,

$$R^2 = P_1 Y_{r_1 Y} + P_2 Y_{r_2 Y} + \dots + P_n Y_{r_n Y}$$

R² - Squared multiple correlation coefficient and is the amount of variation in yield that can be accounted by the yield component character

P₁Y - Path coefficient between the 1st component character and yield

r₁Y - Correlation coefficient between 1st component character and yield

Correlation and path coefficients were computed using the ‘metan’ package in R software version 3.3.2.

RESULTS AND DISCUSSION

Phenotypic Variation of F₂ Genotypes

As selection based on the mean value of the early segregating generations does not provide the range

and distribution pattern within each population, decision on early segregating population cannot be based on only mean values of the traits (Welsh, 1981). In populations rejected on their mean value, low frequency of high yielding individuals may be lost. Therefore, range of variation and coefficient of variation are the two parameters, which needs to be considered in assessing the early segregating generations. The results pertaining to these aspects are presented in Table 2.

Days to flowering of F₂ individuals ranged from 34 - 49 DAS with mean value of 41.4 suggests that F₂ plants are late flowering when compared to its parents (Table 2). F₂ genotypes were found to be dwarf (33.6 cm) in comparison to its parents. The shorter plant height of F₂ individuals leads to lower lodging, may be beneficial feature under situations amenable to luxurious vegetative development, where the yields of severely lodged plants could be reduced significantly compared to those of lesser lodged plants. Number of seeds per plant showed wide range of variation which ranged from 21 to 310 with an average of 120.0. The F₂ genotypes exhibited high variations among themselves for number of seeds per pod varied from 2 to 11 with an average of 6.04. Some of the F₂ individuals outyielded its parents with mean yield of

TABLE 2

Descriptive statistics of quantitative traits of F₂ genotypes derived from Chinamung × LM-1668

Characters	Mean	Standard error	Standard deviation	Range	Skewness	Kurtosis
Days to flowering	41.38	0.27	3.35	34.0 - 49.0	0.31	0.25
Plant height (cm)	33.58	0.63	7.77	9.0 - 49.50	-0.66	0.69
No. of primary branches per plant	1.97	0.05	0.59	1.0 - 3.10	0.13	-1.13
No. of secondary branches per plant	8.21	0.18	2.19	3.0 - 15.0	0.86	0.80
No. of clusters per plant	6.67	0.13	1.53	2.0 - 11.0	0.05	0.15
No. of pods per plant	19.71	0.49	6.05	7.0 - 33.0	-0.03	-0.73
Pod length (cm)	4.93	0.12	1.51	1.50 - 7.90	-0.36	-0.73
No. of seeds per pod	6.04	0.15	1.85	2.0 - 11.0	-0.05	-0.28
No. of seeds per plant	119.99	4.59	56.19	21.0 - 310.0	0.78	0.64
Test weight	5.86	0.09	1.08	3.72 - 10.71	1.43	3.74
Pod yield per plant (g)	12.11	0.29	3.50	5.0 - 20.0	0.08	-0.80
Seed yield per plant (g)	6.78	0.24	2.98	1.50 - 18.93	1.03	1.65

6.78 g. Around 12 transgressive segregants were observed for seed yield in this cross. Around 14 transgressive segregants were found for pod yield of F_2 individuals with an average of 12.11g. In the present study, greater number of transgressive segregants were noticed for all the characteristics that can be further selected for breeding higher seed yield varieties. This cross-combination may also be a great resource for the selection of suitable F_2 recombinants.

Skewness is a measure of symmetry, or more precisely, the lack of symmetry of the normal distribution. Kurtosis is a measure of the peakedness of a distribution. The original kurtosis value is sometimes called kurtosis (proper). Most of the statistical packages such as SPSS provide 'excess' kurtosis (also called kurtosis [excess]) obtained by subtracting 3 from the kurtosis (proper). A distribution is called approximate normal if skewness or kurtosis (excess) of the data are between -1 and +1. In our study, all the yield attributes found to be normally distributed except seed yield and test weight. Frequency distribution of various quantitative traits are presented in Fig. 1. Seed yield and test weight are positively skewed and leptokurtic in nature suggesting the presence of complementary gene action and are controlled by few genes (Table 2).

Estimates of Genetic Parameters

The utility of agronomic traits as selection criteria in any breeding programme depends upon the magnitude of genetic variability that exists for these traits in the genetic material. The PCV, GCV, h^2 , GA and GAM for seed yield and agronomic traits are tabulated in Table 2. The estimated PCV and GCV were of similar magnitude for days to flowering, primary branches, and test weight suggesting that these traits are relatively stable over locations or the minimum influence of environment on the expression of these traits, and whatever the variation observed was mostly due to the genotype. However, the magnitude of PCV was greater than that of GCV for plant height, secondary branches, clusters, seeds per pod, pod length, pods per plant, pod yield per plant, seeds per plant and seed yield per plant indicating that apparent variation is not only due to genetic variation but also due to influence of environment in the expression of these traits in mung bean. The estimated GCV was high (> 20.0%) for plant height, primary branches, seeds per pod, pod length, pods per plant, pod yield, seeds per plant and seed yield suggesting the higher proportion of genetic variation and little influence of environment on the expression of these traits in mungbean. Selection for the improvement of such

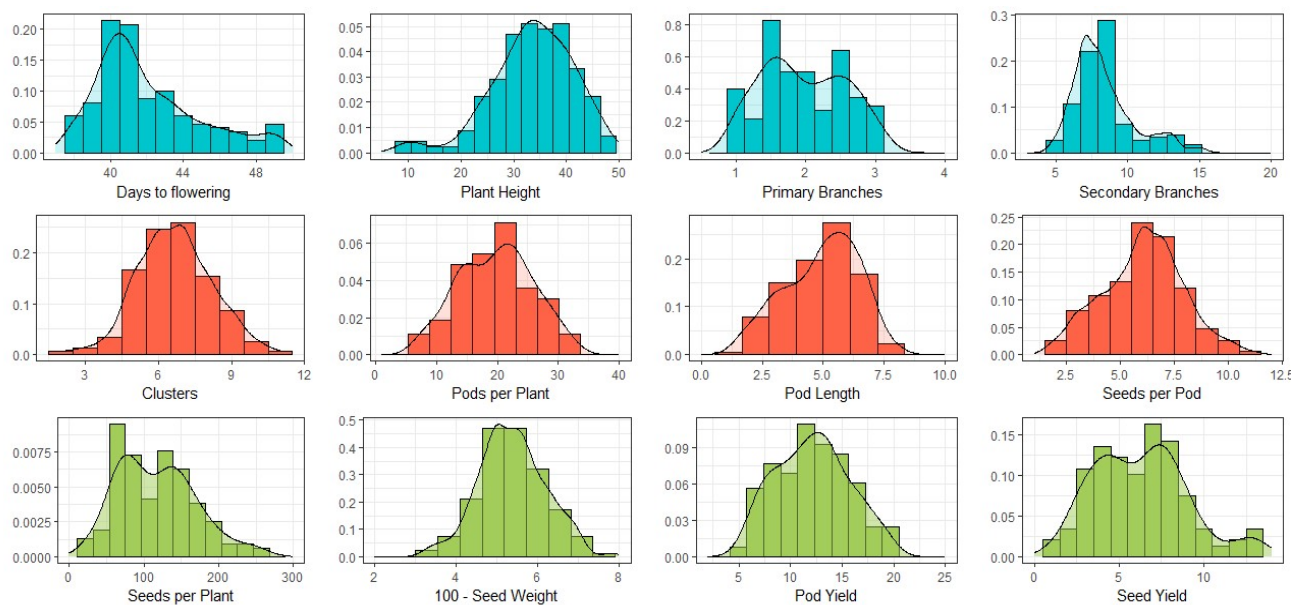


Fig. 1: Frequency distribution of various quantitative traits in F_2 generation derived from Chinamung \times LM-1668

TABLE 3
Estimates of genetic parameters of various quantitative traits of F₂ population

Characters	Mean	PV	GV	PCV	GCV	h ² (%)	GA	GAM
Days to flowering	41.38	11.19	10.69	8.06	7.90	95.53	6.56	15.86
Plant height (cm)	33.58	60.45	48.59	23.08	20.76	80.38	12.83	38.21
No. of primary branches per plant	1.97	0.35	0.35	30.13	30.13	99.31	1.21	61.64
No. of secondary branches per plant	8.21	4.81	1.06	26.62	12.53	22.01	0.99	12.07
No. of clusters per plant	6.67	2.34	0.69	22.89	12.44	29.36	0.92	13.84
No. of pods per plant	19.71	36.57	29.12	30.58	27.38	79.63	9.89	50.17
Pod length (cm)	4.93	2.28	1.43	30.48	24.25	62.88	1.95	39.48
No. of seeds per pod	6.04	3.43	2.93	30.58	28.36	85.44	3.25	53.83
No. of seeds per plant	119.99	3136.69	1856.51	46.68	35.91	59.19	68.29	56.91
Test weight	5.86	1.18	1.16	18.45	18.41	98.91	2.20	37.58
Pod yield per plant (g)	12.51	12.23	6.42	28.69	20.85	52.48	3.77	31.01
Seed yield per plant (g)	6.78	8.88	2.47	43.81	23.20	27.85	1.70	25.14

(PV - Phenotypic variance, GV - Genotypic variance, PCV - Phenotypic coefficient of variation, GCV - Genotypic Coefficient of variation, h² - Broad sense heritability, GA - Genetic advance, GAM - Genetic advance as a percentage of the mean)

traits will be rewarding. Mariyappan *et al.* (2022) also recorded high GCV for these traits in mung bean in different genetic material and environment.

The magnitude of PCV and GCV is a mere indication of the extent of variation and not the heritable portion of the total variation present in the genetic material for different traits. In addition to PCV and GCV, the estimates of heritability and genetic advance for different traits would provide better information on the reliability of using them as selection criteria in a breeding programme. High heritability indicates the reliability with which a genotype can be identified based on the phenotypic expression (Lush, 1949). The broad sense heritability (h² bs) estimates were high for days to flowering, plant height, primary branches, seeds per pod, and test weight. The genetic advance over per cent of the mean (GAM) was high for plant height, primary branches, pods per plant, pod length, seeds per pod, seeds per plant, pod yield, test weight, and seed yield. Joseph *et al.* (2020) and Mariyappan *et al.* (2022) based on the evaluation of mung bean germplasm and RIL population, respectively have also recorded high GAM for these traits.

Heritability in combination with GAM provides a good indication of the nature of inheritance of a trait and effectiveness of its selection in breeding (Johnson *et al.*, 1955). The plant height, primary branches, seeds per pod and test weight recorded high heritability coupled with high genetic advance suggesting that these traits are under the control of the additive gene action and can be improved by simple phenotypic selection. Similar findings have also been reported by Joseph *et al.* (2020), Dhunde *et al.* (2021) and Mariyappan *et al.* (2022).

Correlation coefficients among seed yield and component characters

Seed yield in mung bean is a complex polygenic trait dependent on several other independent component traits. Knowledge of association existing among various characteristics and the magnitude of their contribution towards grain yield is necessary and required to plan the most effective selection criteria for improving seed yield. In the present study, the data recorded on each F₂ individuals was utilized for the correlation and path coefficient analysis. The

phenotypic correlation coefficients thus estimated for seed yield and other agronomic traits based on the F₂ individuals are depicted in Fig. 2. Seed yield per plant has shown highly significant positive association with seeds per plant (0.96), pods per plant (0.71), seeds per pod (0.68), pod yield per plant (0.68), secondary branches per plant (0.22), and clusters per plant (0.22) suggesting that positive selection for these traits is expected to result in increased seed yield in mung bean. A strong association of seed yield with seeds per plant, pods per plant, seeds per pod, pod yield, secondary branches, and clusters per plant in mung bean has also been reported by many workers in diverse environments (Joseph *et al.*, 2020; Dhunde *et al.*, 2021; Dhoot *et al.*, 2017). Therefore, the strategy

of selection for component traits in mung bean should aim at the improvement of seed yield. However, efficiency of selection for component traits in increasing grain yield in mung bean depends not only on the strong association of component traits with grain yield, also the absence of any undesirable correlations among the components.

In the present investigation, seeds per plants has shown highly significant positive association with pods per plant (0.73), seeds per pod (0.72), pod yield per plant (0.70), pod length (0.66), secondary branches per plant (0.22) and clusters per plant (0.22). A highly significant positive association was observed between pods per plant and pod yield per plant (0.98). These

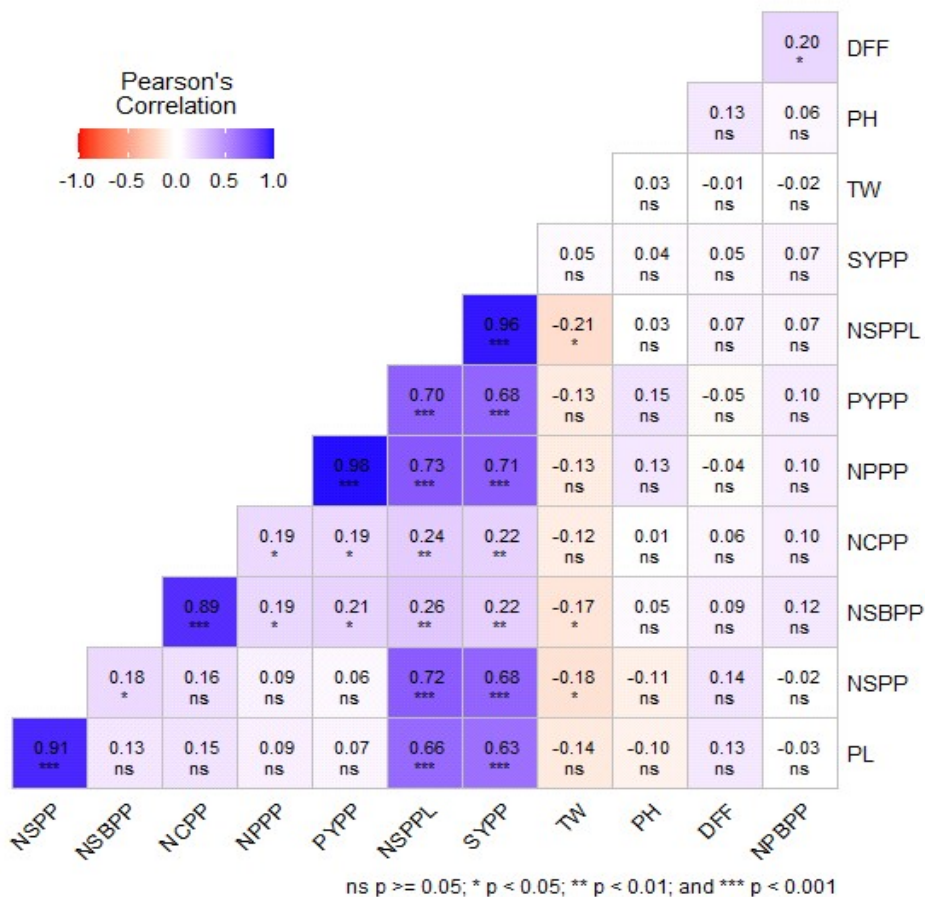


Fig. 2 : Heat map of Phenotypic correlation coefficients for seed yield and agronomic traits in F₂ genotypes

(DFP - Days to flowering, PH - Plant height, NPBPP – No. of primary branches per plant, NSBPP – No. of secondary branches per plant, NCPP - No. of clusters per plant, NPPP – No. of pods per plant, PL – Pod length, NSPP - No. of seeds per plant, NSPPL - No. of seeds per plant, TW – Test weight, PYPP – Pod yield per plant, SYPP – Seed yield per plant)

are in close agreement with the results reported by Prasanna *et al.* (2013); Khajudparn and Tantasawat (2011). Similarly, there was a highly positive correlation of no. of secondary branches with no. of clusters per plant (0.89). Similar studies were reported by Gadakh *et al.* (2013); Prasanna *et al.* (2013). In this study, test weight was found to be significantly negative correlated with seeds per plant (-0.21), seeds per pod (-0.18), secondary branches (-0.17), and clusters (-0.12). Thus, the selection for plant types with more no. of seeds per plants, pods per plant, seeds per pod, pod yield per plant, secondary branches, and clusters per plant is expected to ultimately increase seed yield in mung bean.

Path Coefficients - Direct and Indirect Effects

The path coefficient analysis provides an effective measurement of direct and indirect contributions of independent variables on the dependent variables

(Dewey and Lu, 1959). It helps in understanding whether the correlation of independent component traits with seed yield is due to their direct effect or a result of their indirect effects through other independent component traits. Therefore, in the present study, the path coefficient analysis considering grain yield as dependent variable was also carried out to understand the relative importance of each of the component traits in determining seed yield in mung bean. The direct and indirect contributions of various component traits to grain yield are represented in Fig. 3. The value of the residual effect (R) was low (0.281) suggesting that the component traits included in the study contributed adequately towards total variation in seed yield. The seeds per plant showed the highest positive direct effect (0.909) on seed yield suggesting the true relationship between seed yield and seeds per plant and hence direct selection for higher values of seeds per plant will be very effective

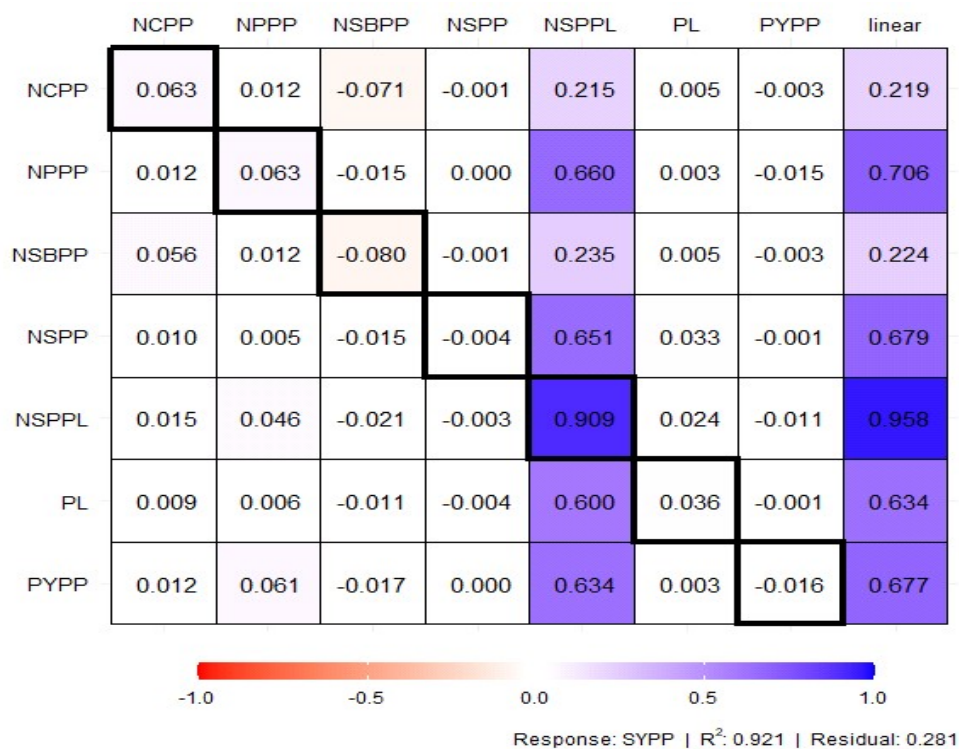


Fig. 3: Path coefficients for seed yield and agronomic traits in F₂ genotypes

(DFF - Days to flowering, PH - Plant height, NPBPP – No. of primary branches per plant, NSBPP – No. of secondary branches per plant, NCPP - No. of clusters per plant, NPPP – No. of pods per plant, PL – Pod length, NSPP - No. of seeds per plant, NSPPL - No. of seeds per plant, TW – Test weight, PYPP – Pod yield per plant, SYPP – Seed yield per plant)

in increasing seed yield of mung bean. This result is in agreement with the results obtained by Anuradha and Suryakumari (2005), Mallikarjuna Rao *et al.* (2006) and Joseph *et al.* (2020). The pods per plant (0.660), seeds per pod (0.651), pod yield per plant (0.634) and pod length (0.60) had high positive indirect effect on seed yield per plant via seeds per plant indicating that selection of long pod types with more number of pods per plant, seeds per pod and greater pod yield will be effective in the simultaneous improvement of seeds per plant and grain yield in mung bean. The component traits identified in the study are easily observable and can be effectively utilized for indirect selection to increase total biomass and seed yield in mung bean. This result was in correspondence with the finding reported by Joseph *et al.* (2020).

This study illustrated the presence of large genetic variation in F_2 individuals for yield and yield contributing traits. Large number of transgressive segregants were found for all the traits which can be selected further for breeding varieties with higher seed yield. Therefore, this cross combination can be a good source for selection of desirable recombinants. High heritability coupled with high genetic advance as a percentage of mean were observed plant height, primary branches, seeds per pod and test weight suggesting genotypic variation for these traits was due to high additive gene effects. Directs selection for these traits may be rewarding. A significant positive association and high direct effect was noticed with number of seeds per plant on seed yield and revealed that the selection based on these traits would ultimately improve the pod yield. Hence, the above mentioned characteristics should be given top most priority while formulating a selection strategy for improvement of yield in mung bean.

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