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STUDIES ON GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR YIELD AND ITS ATTRIBUTES IN MUNG BEAN (*VIGNA RADIATA* L. WILCZEK)

Amrish Verma*, Shiva Nath, Baudh Bharti, Javed, Alok Pal, Arvind Patel and Parsa Ram
Department of Plant Breeding and Genetics, Acharya Narendra Deva University of Agriculture and Technology,
Narendra Nagar (Kumarganj) Ayodhya-224229, India.
*Corresponding author e-mail: amrishverma224122@gmail.com

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ABSTRACT

An experiment was carried out to estimate the genetic parameters such as variability, heritability, genetic advance, character association and path analysis for thirteen quantitative characters in 35 genotypes of green gram [*Vigna radiata* (L.) Wilczek]. Generally, the phenotypic correlation coefficients were higher than the corresponding genotypic coefficients of variation for all traits. The high heritability in broad sense was recorded for plant height, pods per plant, seed yield per plant, secondary branches per plant, 100-seed weight and primary branches per plant. The highest genetic advance as percent of mean was recorded for seed yield per plant, biological yield per plant and the high for the characters viz., pods per plant, secondary branches per plant, and primary branches per plant. Character association studies revealed that the number of plant height, primary branches per plant, secondary branches per plant, clusters per plant, pods per clusters, pods per plant, seeds per pod, 100 seed weight, biological yield per plant and harvest index showed a positive and highly significant correlation with seed yield per plant. Path analysis revealed that the pods per plant had a high positive and direct effect on seed yield.

Keywords: Genetic variability, heritability, genetic advance, character association, path analysis.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is self-pollinated diploid (2n=2x=22) with a smallest genome size of 579 MB/1C (Arumuganathan and Earle E. D. 1991). Mungbean probably originated in India (De Candole, 1886) or the Indo-Burma region (Vavilov, 1951). The mung bean (*Vigna radiata* (L.) R. Wilczek) are divided in 3 subgroups: it is cultivated edibile mung bean (*Vigna radiata* subsp. *radiata*), and that are two wild subgroups (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*). The seed colours and presence or absence of a rough layer are used to distinguish different types of golden gram (Lambrides *et al*., 2006; Mogotsi, 2006). Cultivated types of mung bean, green or golden and can be light or dull depending on the presence of a texture layer (Lambrides *et al.,* 2006). Pulses are pretty naturalistic gifts. These are novel in their capability to fix biological nitrogen (30-40 kg N/ha), have a deep root system, mobilized to insoluble soil nutrients, improvement in soil physical attributes and restoring soil fertility. For example, green gram can be increasing the productivity of consequential rice crops by up to 8% because its fixes soil nitrogen via symbiosis and helps to cleave pest and disease cycles (Weinberger, 2003). The first draft genome sequence of green gram constructed to facilitate genomic research Kang *et al*., (2014). In addition, the World Vegetable Center (WorldVeg) has created a mung bean mini–core germplasm collection representing genetic resources from more than 6,700 accessions based on genotypic and phenotypic traits (Schafleitner *et al.*, 2015). This mini-core collection has enabled the identification of valuable lines and candidate genes for various traits, including hypocotyl pigmentation and maturation characteristics under extreme heat conditions and varying photoperiods (Sokolkova *et al.,* 2020), seed coat lustre (Breria *et al.,* 2020), Salinity tolerance during the germination stage is also a trait that has been studied and identified within this mini-core collection (Breria *et al.,* 2020), seed size (Akhtar *et al.,* 2021), additionally, advantageous root traits linked to resistance against heat and drought stress have been pinpointed within this mini-core collection (Aski *et al.,* 2021). Through this technique, yield attributing characters can be ranked and the specific traits, producing a given correlation can be headed (Rao *et al.,* 2006). In highly self-pollinated crops like green gram, natural variability for yield and related traits is often limited. The intricate floral structure and specific micro conditions required for pollen dehiscence and fertilization make ahead selection for improvement impractical. Nonetheless, assessing the extent of genetic variation for yield components, their heritability values, and genetic advances can greatly assist breeders in identifying superior genotypes for enhancement. Estimates of genetic parameters offer insights into the relative importance of different types of gene effects influencing plant traits. Genotypic and phenotypic coefficients of variation, along with heritability and genetic advance, are crucial parameters for improving traits. It's paramount to select and evaluate varieties for their quantitative and yield traits in any breeding program before introducing them to specific local environments (Jonson, Robinson, & Comstock 1955). For efficient plant breeding programs, understanding the relationships among yield and its contributing traits is vital. Correlation coefficients between traits aid in constructing selection indices, but they can be misleading due to complex interrelations. To provide a more accurate interpretation, it's essential to split correlations into direct and indirect effects. Therefore, correlation analysis in conjunction with path coefficient analysis is necessary to quantitatively assess the direct and indirect influences of yield related traits. Additionally, studying genetic parameters such as genotypic and phenotypic coefficients of variation for the most influential traits is crucial for improving seed yield. When multiple traits influence a given characteristic, splitting the total correlation into direct effects is devised to gain deeper insights (Rahman *et al.,* 1982). Indeed, path coefficient analysis offers a more meaningful explanation for the causes of association between traits. By quantifying the direct and indirect influences of one character on another, this method helps elucidate the underlying factors driving correlations among traits. It provides a systematic approach to understanding the complex interrelations within a breeding program, ultimately facilitating more informed decision-making for trait selection and crop improvement (Dewey and Lu, 1959). The objective of the present study was to determine the variability parameters along with the correlation and path analysis is to understand the mode of inheritance and degree and direction of association of different yield component traits with the seed yield.

Material and Methods

The present investigation was carried out during *kharif*, 2022 at the Field Experimentation Centre, Genetics and Plant Breeding research farm, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya, India. The experimental material comprised of 35 green gram genotypes, which were raised in Randomized Block Design with three replications. Sowing was done by dibbling the seeds at a distance of 10 cm in the rows of 2 m length with row to row spacing of 30 cm. Non-experimental rows were planted around the layout to eliminate border effects. A basal dose of 20 kg N and 40 kg P_2O_5 ha-1 was applied at sowing time. All recommended cultural practices and plant protection measures were adopted to raise a good crop. The data on five randomly selected competitive plants in 35 treatments per replication were recorded for 13 quantitative traits viz., Days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pods per plant, seeds per pod, 100 seed weight, biological yield per plant, harvest index and seed yield per plant. The statistical analysis for variance was worked out according to Panse and Sukhatme (1961). Phenotypic and genotypic coefficients of variation were calculated based on the method advocated by (Searle, 1961). Computation of heritability in broad sense (Hanson *et al.,* 1963) and genetic advance in per cent of mean (Johnson *et al.,* 1955). The path coefficient analysis was worked as suggested by Dewey and Lu (1959).

Results and Discussion

The analysis of variance (Table 1.) reveled highly significant differences for all thirteen characters among the genotypes in mung bean. Which gives the evidence of sufficient variability among the genotypes. The estimates of the phenotypic coefficients of variation were higher than the genotypic coefficient of variation indicating the influence of the environment in governing the characters. Signifying the presence of ample variation in the studied material (Supreetha *et al.,* 2023, Kamble *et al.,* 2023).

Table 2. The high estimates (>20%) of phenotypic (PCV) and genotypic (GCV) coefficient of variation were recorded for seed yield per plant (PCV = 26.76%, GCV = 24.31%), biological yield per plant (PCV= 23.99%, GCV=19.15%). The moderate estimates (10-20%) of PCV and GCV were recorded for pods per plant (PCV = 16.19%, GCV =14.84%) and pods per cluster (PCV=14.99%, GCV=7.77%), secondary branches per plant (PCV=14.85%, GCV=13.06%) and primary branches per plant (PCV=14.72%, GCV=12.91%), 100- seed weight, clusters per plants, harvest index, seeds per pod had moderate PCV with low GCV. The remaining characters days to 50% flowering, maturity, plant height exhibited low estimates (<10%) of PCV or GCV. This finding aligns with similar results reported by Srivastava *et al.* (2024), Jain *et al.* (2024), Mishra *et al.* (2023), Pinchhyo *et al.* (2016), Garg *et al.* (2017) and Kumar *et al.* (2020).

The estimates of heritability in broad sense (h2 b) and genetic advance in % of mean estimated for thirteen characters have been presented in Table 2. Quantitative characters are influenced more by the environment, obstructing the transmission of the phenotype observed to the next generation. Therefore, the study on the heritable portion of the variability is necessary. Heritability is a good index of characters from parents to off springs and helps as a tool for the selection of elite genotypes. Heritability estimates are categorized by Johnson et al. (1955). The estimates of broad sense heritability ranged from 26% (pods per cluster) to 84% (plant height and pods per plant). The high heritability in broad sense (>75%) was recorded for plant height (84%), pods per plant (84%), seed yield per plant, secondary branches per plant, 100-seed weight and primary branches per plant. Biological yield per plant, days to 50% flowering, harvest index showed moderate broad sense heritability (>50% to <75%) while low heritability (<50%) was found for clusters per plant, seeds per pod, pods per cluster only. Similar findings were obtained by Srivastava *et al.* (2024), Jain *et al.* (2024), Choudhry *et al.* (2017), Ghimire *et al.* (2017), Payasi (2015) and Kumar *et al.* (2013).

The highest genetic advance as a percentage of the mean was observed for seed yield per plant (45.51%) and biological yield per plant (31.51%). Additionally, significant genetic advances (>20%) were noted for traits such as pods per plant (28.03%), secondary branches per plant (23.67%) and primary branches per plant (23.31%). Moderate estimates of genetic advance (ranging from >10% to 20% of the mean) were seen for 100-seed weight (19.56%), plant height (16.06%), harvest index (11.51%), maturity (10.07%), clusters per plant (8.55%) and pods per cluster (8.30%). Conversely, traits such as days to 50% flowering exhibited genetic advances of less than 10%. These findings closely align with the results reported by Aparna *et al.* (2015) and Azam *et al.* (2018) high estimates of heritability were found for pods per plant, plant height, seed yield per plant, days to maturity and 100-seed weight.

Table 3. Genotypic correlations were higher than the phenotypic correlations (Table 3) for most of the characters, which can be explained due to the masking or modifying effects of the environment on the genetic association between characters. Seed yield per plant exhibited highly significant and positive correlations with various traits: biological yield per plant (r_p = 0.91** and r_g = 0.98**), pods per plant (r_p = 0.78** and r_g = 0.86**), seeds per pod (r_p = 0.60** and r_g = 0.74**), 100-seed weight (r_p = 0.53** and r_g = 0.64**), secondary branches per plant (r_p = 0.52** and r_g = 0.66**), harvest index (r_p = 0.48** and r_g = 0.76**) and plant height (r_p = 0.40** and r_g = 0.46**). Additionally, primary branches per plant (r_p = 0.36** and r_g = 0.48**) and pods per cluster (r_p = 0.39** and r_g = 0.75**) displayed moderate positive correlations, highly negatively correlated with days to maturity (r_p = -0.56** and r_g = -0.66**) and days to 50% flowering (r_p = -0.45** and r_g = -0.64**). These findings are consistent with earlier research by Srivastava *et al.* (2024), Mishra *et al.* (2023), Navya *et al.* (2023).

Table 4. Path coefficient analysis revealed that the number of pods per plant had a phenotypic positive and direct effect on seed yield per plant (0.48) followed by seeds per pod (0.34), 100 seed weight (0.31), biological yield per plant (026), plant height (0.013), days to maturity (0.010), harvest index (0.09), days to 50% flowering (0.02), and primary branches per plant (0.007) and the pods per cluster had a genotypic positive and direct effect on seed yield per plant (0.53) followed by pods per plant (0.49), seeds per pod (0.48), 100 seed weight (0.44), primary branches per plant (0.29) and clusters per plant (0.03). These findings are consistent with earlier research by Patel *et al.* (2024), Aravinth *et al.* (2023), Kumar *et al.* (2018), Parihar *et al.* (2018), Ahmad and Belwal, (2020), Agbeleye *et al.* (2020) and Ghimire *et al.* (2017).

Table 1 : Analysis of variance for randomized block design for 13 characters in mung bean

Source of variation	Mean Squares		
	Replications	Treatments	Error
d.f.	2	36**	72
Days to 50% flowering	0.17	15.10**	3.07
Days to maturity	1.54	43.93**	3.01
Plant height (cm)	0.68	115.71**	6.57
Primary branches per plant	0.16	0.35**	0.03
Secondary branches per plant	0.50	0.56**	0.04
Clusters per plant	0.72	1.59**	0.67
Pods per cluster	0.75	1.45**	0.69
Number of pods per plant	9.81	159.42**	9.48
Number of seeds per pod	0.27	1.15**	0.57
100 seed weight (g)	0.01	0.93**	0.07
Biological yield per plant (g)	58.65	303.71**	48.36
Harvest index (%)	2.90	30.50**	7.35
Seed yield per plant (g)	5.003	56.33**	3.70

Table 2 : Estimate of range, coefficient of variation (PCV, GCV), heritability, genetic advance and genetic advance in percent of mean for 13 characters in mung bean

Traits	General Mean	Range				Coefficient of variation (%)		Heritability (%)	Genetic Advance	Gen. Adv % of Mean 1%
		Crosses		Parents						
		Min	Max	Min	Max	PCV	GCV			
Days to 50% flowering	43.09	38	44.33	40.33	47.67	6.17	4.64	56	3.10	7.19
Days to maturity	68.36	61.67	75.67	65.33	78.33	5.96	5.40	81	6.88	10.07
Plant height (cm)	71.18	65	80.33	57.67	74.33	9.20	8.47	84	11.43	16.06
Primary branches per plant	2.54	2.20	3.50	1.73	2.53	14.72	12.91	76	0.59	23.31
Secondary branches per plant	3.16	3.10	4.03	2.30	2.93	14.85	13.06	77	0.74	23.67
Clusters per plant	7.43	6.33	9.00	6.00	8.00	13.31	7.43	31	0.63	8.55
Pods per cluster	6.48	5.33	7.66	5.33	7.00	14.99	7.77	26	0.53	8.30
Number of pods per plant	47.62	40	62.33	35.33	48.33	16.19	14.84	84	13.35	28.03
Number of seeds per pod	7.14	6.33	8.66	6.00	7.00	12.28	6.16	25	0.45	6.38
100 seed weight (g)	5.02	4.3	5.93	3.80	6.00	11.92	10.64	79	0.98	19.56
Biological yield per plant (g)	48.15	38.42	71.32	33.64	50.02	23.99	19.15	63	15.17	31.51
Harvest index (%)	35.55	33.02	38.97	27.21	38.57	10.91	7.81	51	4.09	11.51
Seed yield per plant (g)	17.22	14.58	27.54	10.16	16.10	26.76	24.31	82	7.84	45.51

Table 3 : Phenotypic and genotypic correlation coefficients between different characters in Mung bean

Traits	Phenotypic (r_p), Genotypic (r_g)	Maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Clusters per plants	Pods per cluster	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Days to 50% flowering	r_p	0.10	-0.43**	-0.18	-0.39**	-0.33**	-0.15	-0.43**	-0.29**	-0.16	-0.41**	-0.29**	-0.45**
	r_g	0.009	-0.70**	-0.19*	-0.64**	-0.69**	-0.46**	-0.58**	-0.71**	-0.30**	-0.49**	-0.90**	-0.64**
Maturity	r_p		0.008	-0.40**	-0.24*	-0.23*	-0.27	-0.46**	-0.23*	-0.39**	-0.57**	-0.17	-0.56**
	r_g		0.02	-0.47**	-0.33**	-0.46**	-0.62**	-0.57**	-0.43**	-0.47**	-0.72**	-0.37**	-0.66**
Plant height (cm)	r_p			0.09	0.40**	0.25**	0.20	0.40**	0.24**	0.11	0.26**	0.45**	0.40**
	r_g			0.10	0.49**	0.51**	0.38**	0.48**	0.51**	0.08**	0.37**	0.57**	0.46**
Primary branches per plant	r_p				0.53**	0.12	0.21	0.23*	0.14	0.37**	0.31**	0.23*	0.36**
	rg				0.71**	0.26**	0.52**	0.32**	0.45**	0.43**	0.47**	0.39**	0.48**
Secondary branches per plant	r_p					0.31**	0.30	0.49**	0.29**	0.25**	0.38**	0.46**	0.52**
	r_g					0.56**	0.77**	0.64**	0.67**	0.28**	0.57**	0.69**	0.66**
Clusters per	r_p						-0.34	0.49**	0.19*	0.21*	0.39**	0.32**	0.46**

plant	r_g						0.86**	0.98**	0.59**	0.33**	0.81**	0.83**	0.86**
Pods per cluster	r_p							0.58**	0.04	0.03	0.36**	0.19*	0.39**
	r_g							0.88**	0.50**	0.22*	0.73**	0.65**	0.75**
Number of pods per plant	r_p								0.21*	0.17	0.69**	0.42**	0.78**
	r_g								0.60**	0.25**	0.84**	0.72**	0.86**
Number of seeds per pod	r_p									-0.002	0.55**	0.29**	0.60**
	r_g									0.25**	0.65**	0.78**	0.74**
100 seed weight (g)	r_p										0.50**	0.26**	0.53**
	r_g										0.67**	0.39**	0.64**
Biological yield per plant (g)	r_p											0.11	0.91**
	r_g											0.65**	0.98**
Harvest index (%)	r_p												0.48**
	r_g												0.76**

Table 4 : Phenotypic and Genotypic direct and indirect effects of different characters on seed yield per plant in Mung bean

Traits		**Days to 50% flowering**	**Maturity**	**Plant height (cm)**	**Primary branches per plant**	**Secondary branches per plant**	**Clusters per plant**	**Pods per clusters**	**Number of pods per plant**	**Number of seeds per pod**	**100 seed weight (g)**	**Biological yield per plant (g)**	**Harvest index (%)**	**Seed yield per plant (g)**
Days to 50% flowering	**P**	**0.02**	0.001	-0.006	-0.001	0.007	0.01	0.007	-0.21	-0.10	-0.05	-0.11	-0.02	-0.45**
	G	**-1.26**	-0.003	0.04	-0.05	0.39	-0.02	-0.24	-0.29	-0.34	-0.13	0.12	1.16	-0.64**
Days to maturity	**P**	0.003	**0.010**	0.000	-0.003	0.004	0.01	0.01	-0.22	-0.07	-0.12	-0.15	-0.01	-0.56**
	G	-0.01	**-0.33**	-0.00	-0.13	0.20	-0.01	-0.33	-0.28	-0.20	-0.21	0.18	0.48	-0.66**
Plant height (cm)	**P**	-0.01	0.000	**0.013**	0.001	-0.007	-0.01	-0.009	0.19	0.08	0.03	0.07	0.04	0.40**
	G	0.89	-0.007	**-0.05**	0.02	-0.30	0.01	0.20	0.24	0.25	0.03	-0.09	-0.74	0.46**
Primary branches per plant	**P**	-0.004	-0.004	0.001	**0.007**	-0.009	-0.006	-0.009	0.11	0.04	0.11	0.08	0.02	0.36**
	G	0.25	0.15	-0.006	**0.29**	-0.43	0.009	0.28	0.16	0.22	0.19	-0.12	-0.51	0.48**
Secondary branches per plant	**P**	-0.009	-0.002	0.005	0.004	**-0.018**	-0.01	-0.01	0.24	0.10	0.08	0.10	0.04	0.52**
	G	0.81	0.11	-0.02	0.20	**-0.61**	0.02	0.41	0.31	0.32	0.12	-0.14	-0.89	0.66**
Clusters per plant	**P**	-0.008	-0.002	0.003	0.001	-0.005	**-0.04**	0.01	0.24	0.06	0.06	0.10	0.03	0.46**
	G	0.87	0.15	-0.03	0.07	-0.34	**0.03**	0.46	0.48	0.28	0.14	-0.20	-1.06	0.86**
Pods per cluster	**P**	-0.004	-0.003	0.003	0.002	-0.005	0.01	**-0.04**	0.28	0.01	0.01	0.09	0.01	0.39**
	G	0.58	0.20	-0.02	0.15	-0.47	0.03	**0.53**	0.43	0.24	0.10	-0.18	-0.84	0.75**
Number of pods per plant	**P**	-0.01	-0.005	0.005	0.002	-0.009	-0.02	-0.02	**0.48**	0.07	0.05	0.18	0.04	0.78**
	G	0.74	0.19	-0.02	0.09	-0.39	0.03	0.47	**0.49**	0.29	0.11	-0.21	-0.93	0.86**
Number of seeds per pod	**P**	-0.007	-0.002	0.003	0.001	-0.005	-0.009	-0.002	0.10	**0.34**	-0.001	0.14	0.02	0.60**
	G	0.90	0.14	-0.03	0.13	-0.41	0.02	0.27	0.29	**0.48**	0.11	-0.16	-1.003	0.74**
100 seed weight (g)	**P**	-0.004	-0.004	0.002	0.003	-0.005	-0.01	-0.002	0.08	-0.001	**0.31**	0.13	0.02	0.53**
	G	0.38	0.15	-0.005	0.12	-0.17	0.01	0.12	0.12	0.12	**0.44**	-0.17	-0.50	0.64**
Biological yield per plant (g)	**P**	-0.01	-0.006	0.003	0.002	-0.007	-0.01	-0.01	0.34	0.18	0.15	**0.26**	0.01	0.91**
	G	0.63	0.24	-0.02	0.13	-0.35	0.02	0.39	0.41	0.31	0.30	**-0.25**	-0.84	0.98**
Harvest index (%)	**P**	-0.007	-0.002	0.006	0.002	-0.008	-0.01	-0.008	0.20	0.10	0.08	0.03	**0.09**	0.48**
	G	1.14	0.12	-0.03	0.11	-0.42	0.02	0.35	0.35	0.37	0.17	-0.16	**-1.28**	0.76**

*,** Significant at 5% and 1% level , respectively. P= Phenotypic & G= Genotypic, R SQUARE = 0.9888 RESIDUAL EFFECT = 0.1060 & R SQUARE = 1.0205 RESIDUAL EFFECT =SQRT (1-1.0205)

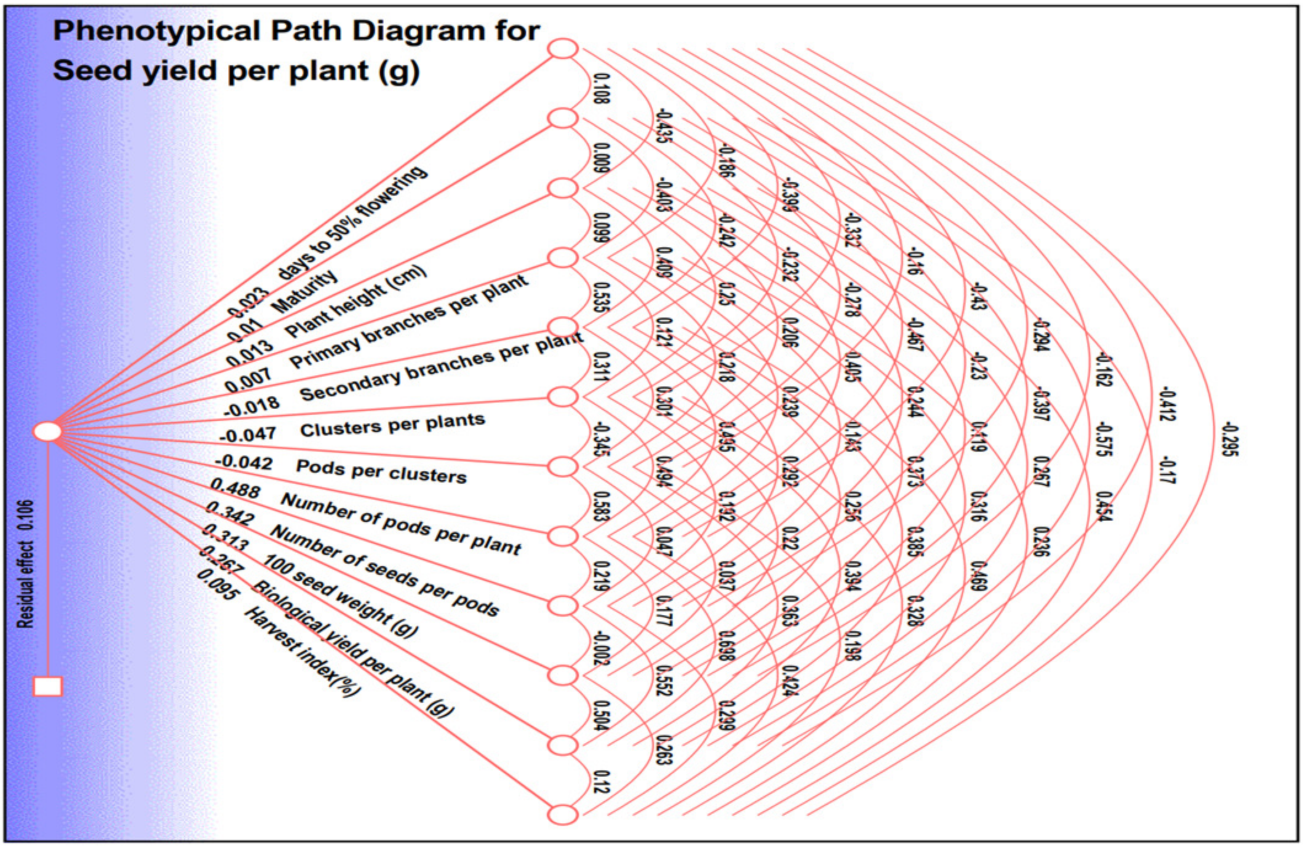

Fig. 1 : Phenotypical path diagram for seed yield and yield components in mung bean

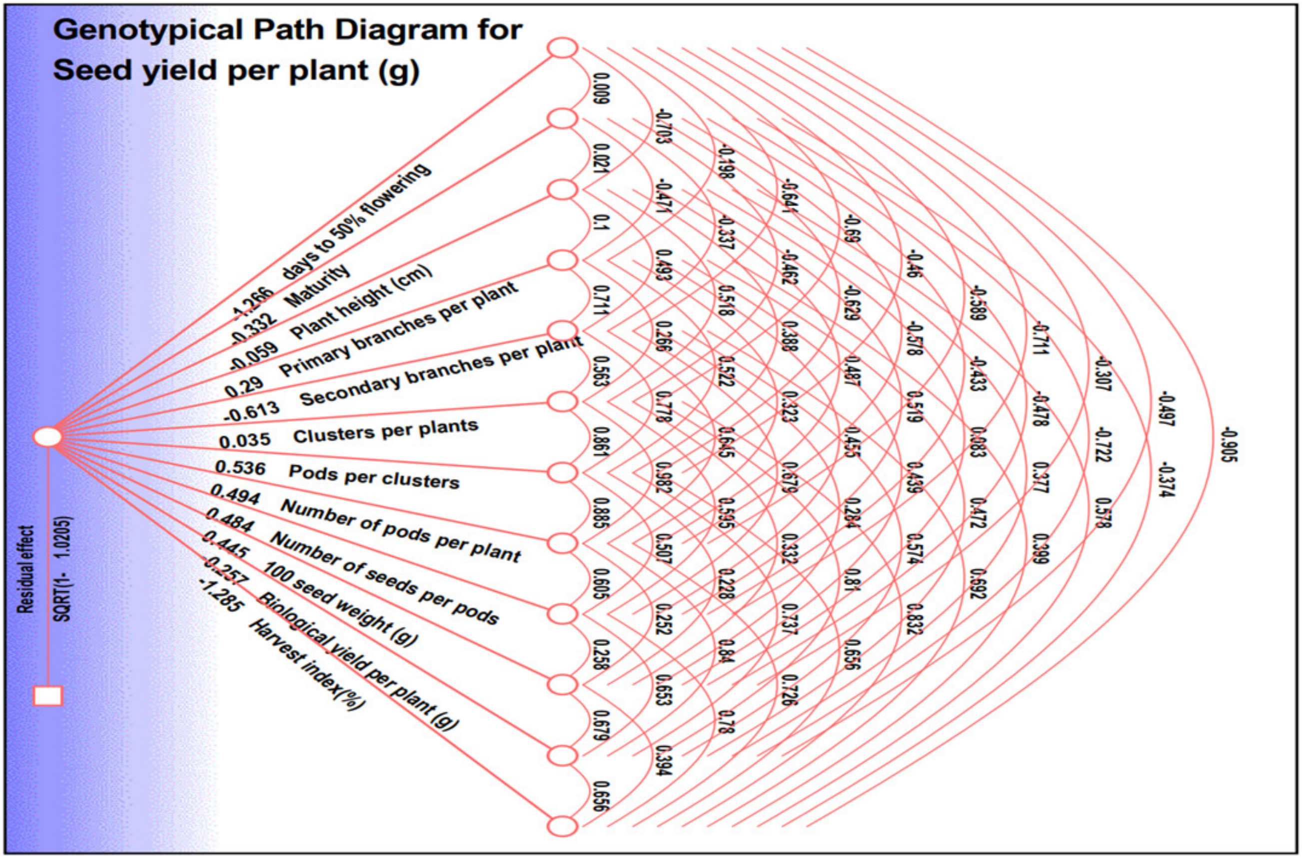

Fig. 2 : Genotypical path diagram for seed yield and yield components in mung bean

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