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Correlation and path analysis for yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]

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Abstract
The present experiment was conducted at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch Campus during *Kharif* 2021. The Experimental materials consist of 19 genotypes of Mungbean representing different geographical origins. The experiment was laid out in Randomized Block Design (RBD) with three replications for various traits to assess the correlation and path analysis in Mungbean. Seed yield per plant was found to be highly significant and positively correlated with pods per cluster, pods per plant and seeds per pod at both genotypic and phenotypic levels indicating that these attributes were mainly influencing the seed yield in Mungbean. A high positive direct effect on seed yield per plant was recorded for pod length followed by branches per plant, pods per plant, seeds per pod, days to maturity and days to 50% flowering. Negative direct effects on seed yield per plant were unveiled by 100 seed weight, plant height, protein content and pods per cluster.

Keywords: Mungbean, genotypic & phenotypic correlation coefficient, path analysis

Introduction
One of the most valuable pulse crops is the Mungbean [*Vigna radiata* (L.) Wilczek], also known as green gram or moong in India. 2n = 2x = 22 is the diploid chromosomal number (Karpechenko, 1925) [14]. *Vigna radiata* is divided into three subgroups: one domesticated (*Vigna radiata* subsp. *radiata*) and two wild (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*). It is a wonderful source of easily digested and high-quality protein for India's mostly vegetarian population. It has a dry weight of 59 to 65% carbohydrates, 22 to 28% total protein, 21 to 25% amino acids, 1.5 to 2.63% lipids, 1.0 to 1.5% fat, 3.5 to 4.5% fiber and 4-5% ash and it has 334 to 344 kcal of energy per serving (Srivastava and Ali, 2004). It fulfills the country's vegetarian population's protein needs. Mungbean seeds are a good source of dietary protein and contain higher levels of folate and iron than most other legumes (Keatinge *et al*., 2011) [15]. It contains a lot of important amino acids, including phenylalanine, isoleucine, Leucine, and lysine (Lambrides and Godwin, 2007) [17].
India is the world's greatest Mungbean producer, accounting for 65% area and 54% of production. In India, Mungbean occupies an area of 4.34 million hectares with a production of 2.12 million tones and 489 kg per hectares productivity (Anon., 2020) [3]. The area under Mungbean cultivation in Gujarat is about 154690 hectares with the production of 110140 tones and 711 kg per hectares productivity (Anon., 2021) [4]. In India, Orissa, Maharashtra, Andhra Pradesh, Telangana, Rajasthan, Gujarat, Madhya Pradesh, Bihar, Karnataka, and Uttar Pradesh are among the states where Mungbean is commercially harvested.
The analysis of correlation coefficients between characters that contribute directly or indirectly to seed yield is crucial when carrying out a selection program. A correlation analysis alone is insufficient to provide an accurate picture of the relative relevance of direct and indirect influences of each component trait on seed yield. Path analysis is a standardized partial regression analysis that also enables the division of the correlation coefficient into aspects of the direct and indirect effects of the independent variable on the dependent variable. As a result, the findings of this study will help determine the yield contributing characteristics that may be used to improve seed yield in Mungbean.
Yield is a complex trait that is influenced by different factors. These components are typically less subject to environmental changes than yield, making them more adaptable to modification. If the type and size of inter-relationships among component traits and seed yield are recognized, selection efficiency will be improved.

Materials and Methods

The present research work was conducted at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch Campus during *Kharif* 2021. The Experimental materials consist of 19 (18 + 1 check) genotypes of Mungbean representing different geographical origins. The pure seeds of these genotypes were provided by Pulse Research Station, Navsari Agricultural University, Navsari. The details of the genotypes are GP – 6, GP – 7, GP – 16, GP – 17, GP – 19, GP – 20, GP – 24, GP – 25, GP – 26, GP – 27, GP – 28, GP – 30, GP – 38, GP – 39, GP – 45, GP – 48, GP – 63, GP – 70 and GM – 7 (check). The experiment is laid out in Randomized Block Design (RBD) with three replications. Each entry was accommodated in a single row of 2 m with a spacing of 45 x 15 cm. A line of 12 plants was grown as a gross plot and from both sides, 1 plant each was excluded to consider 10 plants as a net plot. Observations were taken on 5 random plants in the plot. All cultural practices were followed and timely plant protection measures were taken to avoid damage through pests and diseases.

The following characters like days to 50% flowering, days to maturity, plant height (cm), branches per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, seed yield per plant (g), 100 seed weight (g), protein content (%) and Mungbean yellow mosaic virus (MYMV) incidence %. The observations were recorded on five randomly selected plants from each line in each replication except for days to 50% flowering and days to maturity where all 10 plants of the net plot are considered. All the weights were recorded in grams with the help of Precisa Analytical Weight balance. In this experiment, MYMV incidence was not observed, so it was not calculated. A representative sample of seeds was taken at maturity from each entry per replication and dried in an oven at 60 °C for 24 hrs. and then was ground in a grinder-cum-mixer. The nitrogen content in seeds was determined with the micro-Kjeldahl procedure (Jackson, 1967) [12] and the percentage of protein was calculated using the factor 6.25. Genotypic (r_g) and phenotypic (r_p) correlation coefficients were calculated by adopting the method explained by Miller *et al.* (1958) [20]. Path analysis suggested by Wright (1921) and Dewey and Lu (1959) [8] was adopted for portioning the genotypic correlation between variables with seed yield into direct and indirect effects of those variables on yield.

Results and Discussion

Table 1 shows the calculated genotypic (r_g) and phenotypic (r_p) correlation coefficients. The results of this research are discussed below. At the genotypic and phenotypic levels, there was a positive, highly significant correlation between seed yield per plant and pods per cluster (r_g = 0.706, r_p = 0.460), pods per plant (r_g = 0.999, r_p = 0.586), and seeds per pod (r_g = 0.654, r_p = 0.415). At the genotypic level, there was a positive highly significant correlation between seed yield per plant and 100 seed weight (r_g = 0.375), as well as a positive significant correlation at the phenotypic level (r_p = 0.316). At the genotypic level, there was a positive significant correlation between seed yield per plant and days to 50% flowering, days to maturity, and protein content (r_g = 0.281, r_g = 0.313, and r_g = 0.312, respectively). and phenotypic level, there was a positive non-significant correlation between seed yield per plant and days to 50% flowering, days to maturity and protein content (r_p = 0.214, r_p = 0.212, r_p = 0.229). Plant height and pod length at the genotypic level reported positive highly significant correlations with seed yield per plant (r_g = 0.353, r_g = 0.410) and positive non-significant correlations with seed yield per plant (r_p = 0.240, r_p = 0.189) respectively. At both the genotypic and phenotypic levels, there was a positive, non-significant connection between seed yield per plant and the branches per plant (r_g =0.143, r_p = 0.104).

Table 1: Genotypic (r_g) and phenotypic (r_p) correlation coefficients among eleven characters in Mungbean

Characters		Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100 seed weight	Protein content
Seed yield per plant	r_g	0.281*	0.313*	0.353**	0.143^{NS}	0.706**	0.999**	0.410**	0.654**	0.375**	0.312*
	r_p	0.214^{NS}	0.212^{NS}	0.240^{NS}	0.104^{NS}	0.460**	0.586**	0.189^{NS}	0.415**	0.316*	0.229^{NS}
Days to 50% flowering	r_g	1.00	0.152^{NS}	-0.011^{NS}	-0.311*	0.090^{NS}	0.266*	0.054^{NS}	-0.096^{NS}	-0.123^{NS}	-0.059^{NS}
	r_p	1.00	-0.003^{NS}	0.014^{NS}	-0.233^{NS}	0.040^{NS}	0.180^{NS}	0.053^{NS}	-0.046^{NS}	-0.179^{NS}	0.023^{NS}
Days to maturity	r_g		1.00	0.882**	0.128^{NS}	0.205^{NS}	0.516**	0.293*	0.447**	0.208^{NS}	0.231^{NS}
	r_p		1.00	0.410**	-0.026^{NS}	0.067^{NS}	0.312*	0.082^{NS}	0.074^{NS}	0.169^{NS}	0.085^{NS}
Plant height	r_g			1.00	-0.046^{NS}	0.366**	0.437**	0.386**	0.741**	0.189^{NS}	0.383**
	r_p			1.00	-0.017^{NS}	0.235^{NS}	0.321*	0.354**	0.351**	-0.002^{NS}	0.222^{NS}
Branches per plant	r_g				1.00	0.525**	0.295*	-0.226^{NS}	0.116^{NS}	0.178^{NS}	0.177^{NS}
	r_p				1.00	0.420**	0.189^{NS}	-0.171^{NS}	0.093^{NS}	0.134^{NS}	0.143^{NS}
Pods per cluster	r_g					1.00	0.558**	0.282*	0.321*	0.293*	0.562**
	r_p					1.00	0.279*	0.159^{NS}	0.202^{NS}	0.173^{NS}	0.333*
Pods per plant	r_g						1.00	0.309*	0.644**	0.224^{NS}	0.227^{NS}
	r_p						1.00	0.192^{NS}	0.372**	0.058^{NS}	0.197^{NS}
Pod length	r_g							1.00	0.700**	0.899**	0.411**
	r_p							1.00	0.399**	0.544**	0.345**
Seeds per pod	r_g								1.00	0.597**	0.494**
	r_p								1.00	0.333*	0.248^{NS}
100 seed weight	r_g									1.00	0.376**
	r_p									1.00	0.308*
Protein content	r_g										1.00
	r_p										1.00

The data revealed a consistent pattern in the association between genotypic and phenotypic levels. In most situations, the values of the genotypic correlation coefficients were higher than the values of the corresponding phenotypic correlation coefficients, indicating that there was a strong and innate ability association between the two traits. However, there were other circumstances where the phenotypic correlation was just a little bit higher than its genotypic counterpart, suggesting that the non-genetic factors overestimated the genotypic correlation due to the influence of environmental factors. Singh *et al*. (2009) [7], Tabasum *et al*. (2010) [26], Thippani *et al*. (2013) [27], Azam *et al*. (2018) [6], Asari *et al*. (2019) [5], Manivelan *et al*. (2019) [18], and Dhunde *et al*. (2021) [9] all found evidence of a similar type. Pods per cluster, pods per plant, and seeds per pod were shown to be highly significant and positively correlated with seed yield per plant at both the genotypic and phenotypic levels, showing that these traits were primarily impacting the seed yield in Mungbean. Hemavathy *et al*. (2015) [11] for pods per cluster, Bhanu *et al*. (2016) [7] for pods per plant and seeds per pod, Kurandale *et al*. (2020) [16] for pods per plant, Marawar *et al*. (2020) [19] for seeds per pod, Dhunde *et al*. (2021) [9] for pods per cluster and pods per plant and Singh *et al*. (2022) [4] for pods per plant all reported results that were similar These characters should be carefully chosen when looking to increase yield.

Table 2: Direct and indirect effects of eleven characters on seed yield per plant in nineteen genotypes of Mungbean

Characters	Days to 50% flowering	Days to maturity	Plant height	Branches per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100 seed weight	Protein content	Seed yield per plant
Days to 50% flowering	0.00675	0.00102	-0.00007	-0.00210	0.00061	0.00179	0.00036	-0.00065	-0.00083	-0.00040	0.281*
Days to maturity	0.03348	0.22054	0.19446	0.02813	0.04515	0.11387	0.06453	0.09862	0.04583	0.05099	0.313*
Plant height	0.00881	-0.71428	-0.81007	0.03736	-0.29628	-0.35425	-0.31233	-0.60053	-0.15333	-0.31017	0.353**
Branches per plant	-0.41650	0.17060	-0.06168	1.33728	0.70182	0.39446	-0.30164	0.15548	0.23751	0.23661	0.143NS
Pods per cluster	-0.00318	-0.00725	-0.01295	-0.01858	-0.03540	-0.01974	-0.01000	-0.01136	-0.01036	-0.01991	0.706**
Pods per plant	0.09403	0.18261	0.15466	0.10432	0.19717	0.35366	0.10921	0.22790	0.07932	0.08018	0.999**
Pods length	0.19107	1.03525	1.36406	-0.79800	0.99890	1.09249	3.53790	2.47597	3.18204	1.45528	0.410**
Seeds per pod	-0.02047	0.09487	0.15728	0.02467	0.06806	0.13671	0.14847	0.21215	0.12660	0.10487	0.654**
100 seed weight	0.37965	-0.64091	-0.58375	-0.54776	-0.90217	-0.69173	-2.77389	-1.84043	-3.08410	-1.15852	0.375**
Protein content	0.00754	-0.02934	-0.04858	-0.02245	-0.07137	-0.02877	-0.05219	-0.06272	-0.04766	-0.12689	0.312*

Table 2 shown the direct and indirect effects of eleven characters on the seed yield per plant over 19 Mungbean genotypes. Pod length showed a significant positive direct effect on seed yield per plant, followed by branches per plant, pods per plant, seeds per pod, days to maturity, and days to 50% flowering. This result is consistent with the findings of Pandey *et al*. (2007) [21] for pod length, Ahmed *et al*. (2013) [2] for seeds per pod, Sarkar *et al*. (2014) [23] for seeds per pod, Govardhan *et al*. (2015) [10] for pods per plant and days to 50% flowering, Bhanu *et al*. (2016) [7] for seeds per pod, Marawar *et al*. (2020) [19] for branches per plant and pods per plant, Kurandale *et al*. (2020) [16] for branches per plant and days to 50% flowering; Agbeleye *et al*. (2021) [1] for pod length and pods per plant; Joshi *et al*. (2021) [13] for pods per plant.

100 seed weight, plant height, protein content, and pods per cluster showed negative direct effects on seed yield per plant. Comparable outcomes were revealed by Tabasum *et al*. (2010) [26] for pods per cluster; Sarkar *et al*. (2014) [23] for plant height; Govardhan *et al*. (2015) [10] for 100 seed weight; Parihar *et al*. (2018) [22] for plant height; Manivelan *et al*. (2019) [18] for 100 seed weight; Dhunde *et al*. (2021) [9] for 100 seed weight; Joshi *et al*. (2021) [13] for plant height and protein content.

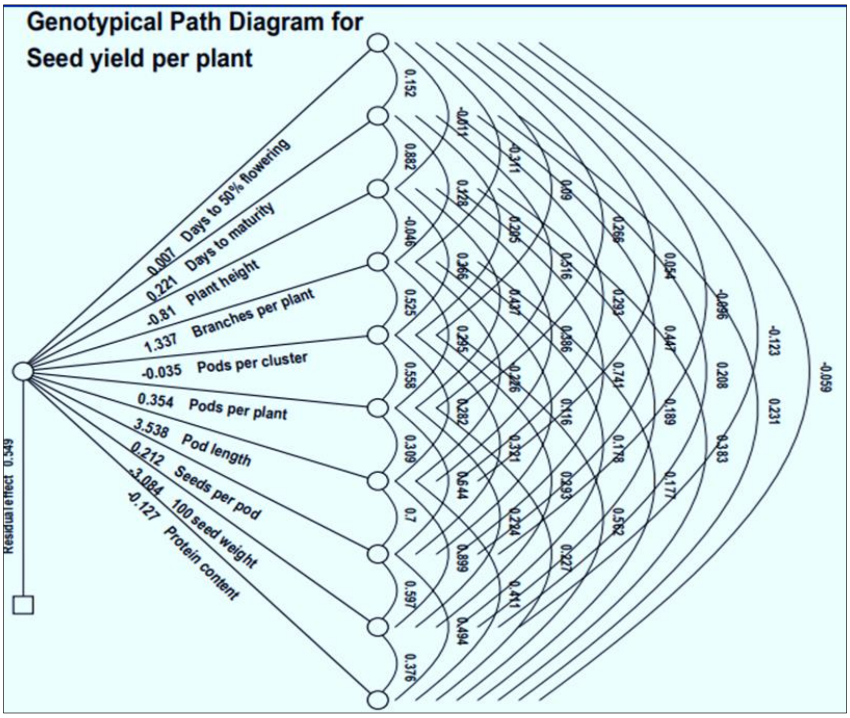

Fig 1: Genotypic path diagram for seed yield per plant

An important consideration for formulating the path diagram (Figure 1) is that all the important causal factors affecting the seed yield per plant are included. The residual effect at the genotypic level was 0.5490 which suggested that there might be a few more component traits responsible to influence the seed yield per plant than those studied. The traits pod length followed by pods per plant had the highest positive direct effect as well as a high correlation with seed yield per plant. Further, it is interesting to note that a highly significant correlation between pod length and pods per plant came from their own high positive direct effect. Hence, direct selection for this trait may be useful for further improvement of seed yield in mungbean.

Conclusion

In the majority of cases, genotypic correlation coefficient values were higher than phenotypic correlation coefficient values for the related traits. Seed yield per plant was found to be highly significant and positively correlated with pods per cluster, pods per plant and seeds per pod at both genotypic and phenotypic levels indicating that these attributes were mainly influencing the seed yield in mungbean. A high positive direct effect on seed yield per plant was recorded for pod length followed by branches per plant, pods per plant, seeds per pod, days to maturity and days to 50% flowering.

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