Determination of Association for yield and yield related traits in an RIL population of Green gram (*Vigna radiata* (L.) Wilezek)

Abstract

Background: Green gram (*Vignaradiata* (L.) Wilczek), a significant annual legume, is a member of the family Fabaceae, subfamily Papilionoideae, and genus Vigna. Despite its importance, large-scale cultivation of green gram faces limitations due to various biotic and abiotic constraints. To address this challenge, our research is focused on the development of green gram genotypes with broader adaptability, enhanced genetic variability, and high-yielding potential. This involves a comprehensive study of the nature and magnitude of associations among yield and related traits to facilitate more effective and sustainable production practices.

Methods: The present investigation was carried out at the experimental plots of Institute of Biotechnology (IBT), College farm, College of Agriculture, Hyderabad (TS). The present experiment was conducted to determine correlation and path analysis among morphological traits and their contribution towards yield among the F_6 Recombinant inbred lines (RILs) in green gram.The RILs differed significantly for all the characters studied.

Result:~~The estimates of correlation revealed that seed yield per plant had positive and non-significant association with number of branches per plant, number of pods per cluster, number of cluster per plant, number of pods per plant, of seeds per plant, plant height(cm), seed weight (g), Pod length (cm) had maximum direct contribution on seed yield at both phenotypic and genotypic level.~~Correlation estimates revealed that seed yield per plant was positively associated but not significant with the number of branches per plant. Furthermore, the number of pods per cluster, the number of clusters per plant, the number of pods per plant, seed yield per plant, plant height (cm), seed weight (g), and pod length (cm) showed a maximum direct contribution to seed yield both phenotypically and genotypically.Path analysis

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revealed that days to 50% flowering, Plant height(cm), number of branches per plant, number of cluster per plant exerted a high magnitude of positive direct effect.

Conclusion:Selection strategy based on these characters having high direct effect coupled with positive correlation with seed yield will be profitable in Green gram improvement programme.

Keywords: Greengram, Correlation, Genotypes, Path analysis, Traits

INTRODUCTION

Green gram (*Vigna radiata* (L.) R. Wilczek var. *radiata*), commonly known as Mung bean or moong, is a crucial legume crop cultivated in Asia, Africa, and Latin America. Belonging to the papilionoid subfamily of the genus *Vigna*, subgenus Ceratotrophis, and family Fabaceae, it finds widespread cultivation in tropical and subtropical regions worldwide (references). Countries such as India, Pakistan, Bangladesh, Sri Lanka, Myanmar, Thailand, Philippines, Laos, Cambodia, Vietnam, Indonesia, Malaysia, South China, and Taiwan extensively cultivate this crop, with major production in Indian states like Orissa, Andhra Pradesh, and Maharashtra~~. Notably, green gram has a historical cultivation presence in India, being considered a native crop~~Green gram (mung bean) is a historically significant crop in India and is considered an indigenous crop. (Vavilov, 1926).

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Green gram is valued for its easily digestible protein, particularly rich in lysine, an amino acid typically deficient in cereal grains. In contrast to cereals, which are rich in methionine, cystine, and cysteine (Sulfur-bearing amino acids), green gram stands out for its nutritional composition. A hundred grams of green gram seeds contain energy (234 cal), protein (24.6%), fat (1.0%), fiber (2.2 g), carbohydrates (57.5%), calcium (0.08 g), phosphorus (0.045 g), iron (5.7 mg), vitamin B (300 mg), and thiamin (0.525 mg) (Srivastava and Ali, 2004).

Green gram is a self-pollinated diploid grain legume (2n=2x=22) with a small genome size of 579 Mb/1C (Arumuganathan et al., 1991). It exhibits sensitivity to both light and temperature, thriving best at temperatures of 30-35°C with optimal atmospheric humidity. The crop plays a vital role in crop rotation due to its ability to fix atmospheric nitrogen, enhancing soil fertility and benefiting subsequent crops. Its adaptability to a short growing season, low water supply, and poor soil fertility underscores its agricultural significance.

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In the context of effective plant breeding programs, understanding the correlation and path coefficient between yield and yield criteria is crucial. While correlation coefficients indicate the extent and nature of associations between yield and its components, path analysis delves into the direct and indirect effects of different yield attributes on overall yield. Recognizing the importance of these statistical approaches, an experiment was conducted to assess the association, direct, and indirect effects of yield and its attributing characters.

Materials and Methods

The Experimental material comprised of 128 F_6 RIL (Recombinant inbred line) population derived from a cross of MGG-295 and WGG-42. The experiment was laid out in a Randomised Completely Block Design (RBD) consisting of 128 RILs of Green gram in two replications. The study of correlation and path analysis in Green gram for yield and yield attributing traits was carried out at college farm, Professor Jayashankar Telangana State Agricultural University. Each RIL line was grown in 2 rows of 4m length with row to row spacing of 30 cm and plant to plant spacing of 10 cm.Observations for all the yield and yield contributing traits were recorded on five plants in each RIL. Observations were recorded from five randomly selected plant for twelve morphological characters

The data was recorded for twelve yield related traits viz., days to initial flowering, days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per clusters, number of pods per plant, number of seeds per pod, plant height (cm), pod length (cm), Seed yield per plant (g) and hundred seed weight (g). The 100 seed-weight and seed yield per plot were recorded after threshing of the harvested crop. The data recorded on the above characters were subjected to Biometrical analysis such as correlation coefficient analysis and path coefficient analysis. Seed yield was considered as dependent variable as factors assumed to be influenced by the other characters called independent variables as causes.

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Correlation coefficient: Genotypic and Phenotypiccorrelation coefficients among different quantitative and chemical characters were calculated using INDOSTAT software.

Path coefficient analysis: Seed yield per plot was taken as dependent character, its coefficient of correlation with other independent characters was partitioned in to direct and indirect effects by path coefficient analysis. Coefficient of determination (R2) and residual effect were also calculated using formula given by Dewey and Lu (1959).

Results and Discussion

Correlation coefficient analysis

The correlation coefficients for all of the twelve characters measured are presented in Table 1.The correlation coefficient becomes more meaningful when correlation coefficient ~~are~~is partitioned into components of direct and indirect effects through path analysis, because correlation coefficients indicate only the inter relationship of the characters irrespective of cause and effect (Dewey and Lu, 1959).

The genotypic and phenotypic correlation among yield and yield contributing traits revealed that Seed Yield showed non-significant positive correlations with the number of branches per plant, number of pods per cluster, number of cluster per plant, number of pods per plant, number of seeds per plant, plant height~~(cm)~~, seed weight ~~(g)~~ and Pod length ~~(cm)~~.In contrast, it showed non-significant negative correlations with days to initial flowering, days to 50% flowering, days to maturity at both genotypic and phenotypic level. This result indicates that seed yield had relationships with various traits, but these relationships were not statistically significant. Positive correlations suggest that when one of the traits increases, seed yield tends to increase as well, while negative correlations suggest that when one of the traits increases, seed yield tends to decrease.

.Similar findings were reported by Thonta*et al.* (2023) for Number of cluster per plant and days to 50% flowering. Similar findings were reported by Parihar*et al*. (2018) for number of branches per plant, number of seeds per pod, seed weight and Asari*et al.* (2019) for plant height~~(cm)~~, number of branches per plant, number of seeds per pod. Shalini*et al.* (2019) for days to 50% flowering, days to maturity and 100 seed weight in black gram.Srivastava*et al.* (2024) reported similar results for number of pods per plant and number of seeds per pod. Alam*et al*. (2014) reported similar results for days to 50% flowering and 100 seed weight at both phenotypic and genotypic level. Hence,these characters shouldbe given due consideration while selecting for increased yield.

Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into direct and indirect effects. In order to achieve a clear picture of the interrelationship of various component traits with yield, direct and indirect effects were calculated using path analysis at both Phenotypic and genotypic level.For path analysis, seed yield was taken as the dependent variable and all other eleven characters used for correlation studies were taken as independent variables. The results are presented in table 2. Path analysis revealed that Days to 50% flowering, plant height(cm), exerted a high magnitude of positive direct effect on seed yield.This results were collaborating with the findings of Asari*et al.* (2019), Ghimire*et al*. (2018) and Parihar*et al.* (2018) which indicated that high positive direct effects of days to 50% flowering. Moderate direct effect showed by number of branches per plant, number of cluster per plant, while days to maturity and seed weight exerted low magnitude of direct effect.

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Among the characters studiedpositive direct effect was obtained for Days to 50% flowering (1.58), plant height (0.31), number of branches per plant (0.24), number of cluster per plant (0.20) , days to maturity (0.17) and seed weight (0.10) while high negative indirect effect obtained via number of seeds per pod (-0.003), number of pods per cluster (-0.01) pod length (-0.03), number of pods per plant (-0.11), days to initial flowering (-1.58), 100 seed weight (-3.411) at Genotypic level.Manivelan*et al.* (2019) reported similar results for number of cluster per plant, number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight at phenotypic level. Similar results for days to 50% flowering, pod length (positive direct effect) and number of pods per plant (negative direct effect) at genotypic level was reported by Ghimire *et al.* (2018).Eswaran*et al.* (2015) reported similar results for days to initial flowering, plant height, number of branches per plant and number of pods per cluster. Alom *et al*. (2014) reported similar results for days to 50% flowering at phenotypic level, plant height and 100 seed weight at both phenotypic and genotypic level. Therefore, selection strategy based on these characters for seed yield improvement will be rewarding in Green gram.

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Conclusion

~~Based on the above investigation, it can be concluded thatgenotypes were having wide diversity and variability for mostof the traits.~~In general, correlation coefficients were high atgenotypic level than phenotypic level. Results also indicatedthat number of branches per plant, number of pods per cluster, number of cluster per plant, number of pods per plant, of seeds per plant, plant height(cm), seed weight (g) and Pod length (cm) were positively correlated with seed yield per plant. Hence, these traits should be given consideration while selecting for increasing yield. Path analysis for seed yield revealed that Days to 50% flowering, plant height(cm), number of branches per plant, number of cluster per plant, days to maturity and seed weight had positive direct effect. Hence direct selection for yield improvement through these traits would be rewarding.From the combinedresults of correlation coefficient and pathanalysis, it may be concluded thatplant height(cm), number of branches per plant, number of cluster per plant and 100 seed weight should be considered as indicesfor selecting high yielding green gram variety.These traits may be given more emphasis for directselection of RILs in future Green gram breeding programmes. Hence, there is ample scope ofselection for these traits.

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References

Alam, A.M., Somta, P. and Srinives, P. 2014. Generation mean and path analyses of reaction to mungbean yellow mosaic virus (MYMV) and yield-related traits in mungbean (*Vignaradiata* (L.) Wilczek). *SABRAO Journal of Breeding & Genetics*, 46(1).

Alom, Muzibul. K. M., Rashid, M. H.and Biswas. M. 2014. Genetic Variability, Correlation and Path Analysis in Mungbean(*Vignaradiata* L). *J. Environ. Sci. & Natural Resources*, 7(1): 131–138.

Arumuganathan, K and Earle, E.D. 1991. Nuclear DNA content of some important plant species. *Plant molecular biology reporter*, *9*(3), pp.208-218.

Asari, T., Patel, B.N., Patel, R., Patil, G.B. and Solanki, C. 2019. Genetic variability, correlation and path coefficient analysis of yield and yield contributingcharacters in mung bean [*Vigna radiata* (L.) Wilczek]. IJCS, 7(4), pp.383- 387.

Dewey, D.R. and Lu, K.1959. A Correlation and Path□Coefficient Analysis of Components of Crested Wheatgrass Seed Production. *Agronomy journal*, 51(9), pp.515-518.

Eswaran, R. and Senthilkumar, N. 2015. Correlation and path analysis in greengram [*Vigna radiata* (L.) Wilczek] for drought stress. *Plant Archives*, 15(1), pp.247-249.

Ghimire, S., Khanal, A., Kohar, G., Acharya, B., Basnet, A. and Kandel, P. 2018. Variability and path coefficient analysis for yield attributing traits of mungbean [*Vignaradiata* (L.) Wilczek]. *Azarian Journal of Agriculture*. 5(1):7-11.

Manivelan, K., Karthikeyan, M., Blessy, V., Priyanka, A.R., Palaniyappan, S. and Thangavel, P. 2019. Studies on correlation and path analysis for yield and yield related traits in greengram [*Vignaradiata* (L.) Wilczek].*The Pharma Innovation Journal*. 8(9): 165-167.

Package, I.C. 1994. Indostat service. Hyderabad, India.

Parihar, R., Agrawal, A.P., Sharma, D.J. and Minz, M.G.2018. Character association and path analysis studies on seed yield and its yield attributing traits in mungbean (*Vignaradiata* (L.) Wilczek). *Journal of Pharmacognosy and Phytochemistry*, 7(1), pp.2148-2150.

Shalini, Ch. and Lal, G. M. 2019. Correlation and path coefficient analysis for yield andyield components in blackgram (*Vigna mungo* (L.)Hepper). *The Pharma Innovation Journal*, 8(6): 65-68.

Srivastava, R.P. and Ali, M. 2004. Nutritional quality of common pulses. *Indian Institute of Pulses Research*.

Thonta, R. 2023. Studies on correlation and path coefficient for growth and yield attributes in green gram (*Vigna radiata* L. Wilczek). MH, 934, p.20.

Vavilov, N.I. 1926. Centers of origin of cultivated plants. *Bull. Appl. Bot.*, 26:1-248.

Table 1. Genotypic and Phenotypic correlation for the traits studied in field experiment

Traits	r	DFF (Days)	DF50 (Days)	DM (Days)	NBP (nos.)	NPC (nos.)	NCP (nos.)	NPP (nos.)	NSP (nos.)	PH (cm)	PL (cm)	SW (g)	PDI(%)
DFF	**G**	**1.00**	0.99	-0.12	-0.53	-0.29	-0.36	-0.19	0.02	-0.47	0.43	-0.14	-0.21
	P	**1.00**	0.99***	0.62***	-0.04	-0.05	-0.2***	-0.1***	-0.2***	-0.02	-0.28***	-0.06	-0.09
DF50	**G**		**1.00**	-0.23	-0.57	-0.30	-0.37	-0.17	0.04	-0.51	0.49	-0.16	-0.22
	P		**1.00**	0.62***	-0.03	-0.04	-0.1***	-0.14*	-0.2***	-0.01	-0.29***	-0.06	-0.08
DM	**G**			**1.00**	-0.55	-0.36	-0.20	-0.05	0.31	-0.38	0.64	-0.05	-0.16
	P			**1.00**	0.07	-0.03	-0.07	-0.07	-0.13*	0.1258*	-0.32**	-0.01	-0.02
NBP	**G**				**1.00**	0.30	0.52	0.51	0.47	0.33	0.23	-0.04	0.06
	P				**1.00**	0.33***	0.48***	0.45***	0.29***	0.41***	-0.07	-0.02	0.08
NPC	**G**					**1.00**	0.50	0.41	-0.10	0.02	-0.25	-0.19	0.12
	P					**1.00**	0.49***	0.39***	-0.152*	0.08	-0.29***	-0.12*	0.12*
NCP	**G**						**1.00**	0.52	0.30	0.40	-0.13	-0.15	0.02
	P						**1.00**	0.50***	0.27***	0.37***	-0.11***	-0.10	0.02
NPP	**G**							**1.00**	0.40	0.37	-0.22	-0.38	0.19
	P							**1.00**	0.39***	0.32***	-0.12*	-0.26***	0.18**
NSP	**G**								**1.00**	0.46	0.15	0.04	-0.05
	P								**1.00**	0.29***	0.31***	0.02	-0.06
PH	**G**									**1.00**	0.41	0.07	-0.07
	P									**1.00**	0.07	0.05	-0.04
PL	**G**										**1.00**	0.41	0.02
	P										**1.00**	0.20***	-0.02
SW	**G**											**1.00**	-0.21

	P											**1.00**	-0.1*
PDI	**G**												**1.00**
	P												**1.00**
SYP	**G**	-0.43	-0.46	-0.35	0.22	0.06	0.33	0.27	0.34	0.28	0.40	0.02	0.17
	P	-0.16	-0.15	-0.04	0.26	0.08	0.32	0.25	0.27	0.31	0.20	0.02	0.17

DFF: Days to initial flowering, DF50: Days to 50% flowering, DM: Days to maturity, NBP: number of branches per plant, NPC: Number of Pods per cluster, NCP: Number of cluster per plant, NPP: Number of pods per plant, NSP: Number of seeds per pod, PH: plant height, PL: pod length, SYP: Seed yield per plant, SW: 100 Seed weight, PDI: Percent disease infection, G-genotypic level, P- phenotypic level, r- correlation, ***: Significance at 0.01 probability levels; ** & * :Significance at 0.05 and 0.1 probability levels.

Table 2. Phenotypic and genotypic path coefficients of yield and its component traits in Green gram.

Traits	r	DFF (Days)	DF50 (Days)	DM (Days)	NBP (nos.)	NPC (nos.)	NCP (nos.)	NPP (nos.)	NSP (nos.)	PH (cm)	PL (cm)	SW (g)	PDI(%)
DFF	**G**	**-1.5775**	-1.5669	0.1841	0.8325	0.4540	0.5669	0.3069	-0.0266	0.7474	-0.6805	0.2214	0.3317
	P	**-0.2665**	-0.2654	-0.1667	0.0094	0.0137	0.0553	0.0442	0.0616	0.0060	0.0754	0.0150	0.0231
DF50	**G**	1.5687	**1.5793**	-0.3630	-0.9060	-0.4790	-0.5900	-0.2750	0.0591	-0.8105	0.7750	-0.2526	-0.3489
	P	0.2143	**0.2152**	0.1347	-0.0057	-0.0090	-0.0429	-0.0317	-0.0498	-0.0028	-0.0631	-0.0128	-0.0175
DM	**G**	-0.0198	-0.0390	**0.1694**	-0.0934	-0.0617	-0.0333	-0.0091	0.0522	-0.0636	0.1082	-0.0090	-0.0265
	P	0.0430	0.0430	**0.0687**	0.0047	-0.0019	-0.0048	-0.0050	-0.0091	0.0086	-0.0221	-0.0004	-0.0014
NBP	**G**	-0.1233	-0.1341	-0.1280	**0.2377**	0.0705	0.1220	0.1190	0.1101	0.0766	0.0543	-0.0099	0.0134
	P	-0.0016	-0.0012	0.0030	**0.0441**	0.0149	0.0215	0.0200	0.0132	0.0181	-0.0032	-0.0008	0.0033
NPC	**G**	0.0024	0.0025	0.0030	-0.0025	**-0.0083**	-0.0042	-0.0034	0.0009	-0.0001	0.0020	0.0016	-0.0010
	P	0.0011	0.0009	0.0006	-0.0069	**-0.0205**	-0.0101	-0.0080	0.0031	-0.0015	0.0061	0.0026	-0.0026
NCP	**G**	-0.0740	-0.0770	-0.0405	0.1075	0.1036	**0.2059**	0.1064	0.0624	0.0814	-0.0269	-0.0315	0.0048
	P	-0.0467	-0.0449	-0.0158	0.1096	0.1107	**0.2251**	0.1140	0.0618	0.0841	-0.0257	-0.0224	0.0055
NPP	**G**	0.0206	0.0185	0.0057	-0.0540	-0.0431	-0.0548	**-0.1059**	-0.0423	-0.0389	0.0228	0.0403	-0.0199
	P	-0.0068	-0.0061	-0.0030	0.0187	0.0161	0.0209	**0.0412**	0.0163	0.0134	-0.0052	-0.0108	0.0076
NSP	**G**	-0.0001	-0.0001	-0.0011	-0.0017	0.0004	-0.0011	-0.0014	**-0.0030**	-0.0017	-0.0005	-0.0002	0.0002
	P	-0.0171	-0.0172	-0.0098	0.0221	-0.0113	0.0203	0.0292	**0.0741**	0.0219	0.0234	0.0016	-0.0048
PH	**G**	-0.1459	-0.1580	-0.1156	0.1009	0.0050	0.1218	0.1132	0.1417	**0.3079**	0.1269	0.0216	-0.0210
	P	-0.0035	-0.0020	0.0193	0.0632	0.0116	0.0574	0.0499	0.0455	**0.1537**	0.0100	0.0075	-0.0065
PL	**G**	-0.0112	-0.0127	-0.0165	-0.0060	0.0064	0.0034	0.0056	-0.0039	-0.0107	**-0.0259**	-0.0107	-0.0006
	P	-0.0586	-0.0608	-0.0666	-0.0149	-0.0613	-0.0237	-0.0263	0.0655	0.0135	**0.2072**	0.0424	-0.0047
SW	**G**	-0.0139	-0.0159	-0.0053	-0.0042	-0.0189	-0.0152	-0.0378	0.0042	0.0070	0.0411	**0.0993**	-0.0212
	P	-0.0011	-0.0012	-0.0001	-0.0004	-0.0025	-0.0020	-0.0053	0.0004	0.0010	0.0041	**0.0202**	-0.0031
PDI	**G**	-0.0536	-0.0563	-0.0398	0.0146	0.0309	0.0060	0.0480	-0.0122	-0.0174	0.0060	-0.0543	**0.2549**
	P	-0.0151	-0.0142	-0.0036	0.0132	0.0225	0.0042	0.0320	-0.0113	-0.0074	-0.0039	-0.0271	**0.1741**
SYP	**G**	-0.4276	-0.4598	-0.3489	0.2214	0.0592	0.3268	0.2661	0.3421	0.2776	0.4025	0.0160	0.1660
	P	-0.1587	-0.1537	-0.0394	0.2571	0.0830	0.3212	0.2542	0.2714	0.3087	0.2030	0.0150	0.1728

Bold values are direct effect; G- Genotypic correlation coefficient; P- Phenotypic correlation coefficient; Residual effect (P)- 0.87
Residual effect (G)- 0.95