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Association for Yield and Yield Related Traits in an RIL Population of Green Gram (*Vigna radiata* (L.) Wilezek)

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Background: Green gram (*Vigna radiata* (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.

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Results: Correlation estimate revealed that number of pods cluster^{-1}, the Number of clusters plant^{-1}, the Number of pods plant^{-1}, Seed yield plant^{-1}, plant height (cm), seed weight (g), and pod length (cm) showed a maximum direct contribution to seed yield both phenotypically and genotypically. Path analysis revealed that the parameters demonstrating a significant positive direct impact include days to 50% flowering, plant height (cm), number of branches plant^{-1} and number of clusters plant^{-1}. The RILs for each character examined showed considerable variability.

Conclusion: The green gram improvement program will benefit from a selection strategy that focuses on traits with a significant direct impact and a positive correlation with seed yield.

Keywords: Green gram; correlation; genotypes; path analysis; traits.

1. 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. 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. Green gram (mung bean) is a historically significant crop in India and is considered an indigenous crop" [1].

"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. In 100 grams of green gram seeds, there are 234 calories, 24.6% protein, 1.0% fat, 2.2 grams of fiber, 57.5% carbohydrates, 0.08 grams of calcium, 0.045 grams of phosphorus, 5.7 milligrams of iron, 300 milligrams of vitamin B, and 0.525 milligrams of thiamine" [2].

Green gram is a self-pollinated diploid grain legume (2n=2x=22) with a genome size of 543 Mb [3]. 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.

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. By breaking down the correlations into direct and indirect effects, path analysis helps breeders understand the causal relationships between traits. This knowledge can inform more effective selection strategies. Understanding the path coefficients can help in prioritizing traits that have significant direct effects on yield

2. MATERIALS AND METHODS

A total of 128 F6 Recombinant Inbred Lines (RILs) resulting from the cross between MGG-295 and WGG-42 were utilized as the experimental material. The study employed a Randomized Completely Block Design (RBD) to carry out the experiment, with the 128 RILs of Green gram arranged over two replications. Research focused on path analysis and correlation concerning yield and yield-attributing traits was conducted at the college farm of Professor Jayashankar at Telangana State Agricultural University. Each RIL was grown in two rows, each 4 meters long, with a spacing of 30 cm between rows and 10 cm between plants. Observations were made on five randomly selected plants from each RIL for twelve traits related to yield.

Once the harvested crop was threshed, the hundred seed weight and seed yield plant^{-1} were recorded. The data collected on these characteristics were analyzed using biometrical methods, specifically correlation coefficient analysis and path coefficient analysis.

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

Table 1. Morphological yield contributing parameters considered in the present study with their codes

S. No	Morphological parameters	Code
1.	Days to initial flowering	DFF
2.	Days to 50% flowering	DF50
3.	Days to maturity	DM
4.	Number of branches plant^{-1}	NBP
5.	Number of clusters plant^{-1}	NPC
6.	Number of pods clusters^{-1}	NCP
7.	Number of pods plant^{-1}	NPP
8.	Number of seeds pod^{-1}	NSP
9.	Plant height (cm)	PH
10.	Pod length (cm)	PL
11.	Seed yield plant^{-1} (g)	SYP
12.	Hundred seed weight (g)	SW

Path coefficient analysis: A normalized partial regression coefficient, also known as path coefficient analysis, decomposes the correlation coefficient into its direct and indirect effects. Path analysis was employed at both the genotypic and phenotypic levels to calculate these direct and indirect effects, providing a holistic view of the relationships among various component traits and their contributions to yield. In this study, eleven yield-related traits were treated as independent variables, while seed yield served as the dependent variable for the path analysis. Additionally, the formula established by Dewey and Lu [4] was utilized to calculate the residual effect and the coefficient of determination (R^2).

3. RESULTS AND DISCUSSION

3.1 Correlation Coefficient Analysis

"Table 1 presents the correlation coefficients for each of the twelve measured characters. Since correlation coefficients only indicate the interrelationship between the characters without implying causation, their significance increases when analyzed through components of direct and indirect effects using path analysis" [4].

Seed yield exhibited non-significant positive correlations with the number of branches per plant, number of pods per cluster, number of clusters per plant, number of pods per plant, number of seeds per plant, plant height, seed weight, and pod length, as determined by the genotypic and phenotypic correlations among yield and yield-contributing traits. Conversely, both genotypically and phenotypically, it showed non-significant negative correlations with the days to initial flowering, days to 50% flowering, and days to maturity.

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.

Thonta et al. [5] "found similar results for days to 50% flowering and number of clusters plant^{-1} in his experiments in green gram". Comparable results were observed by Parihar et al. [6] in Character association and path analysis studies for Number of branches plant^{-1}, Number of seeds pod^{-1} and seed weight. Genetic variability studies done by Asari et al. [7] found similar results for plant height (cm), Number of branches plant^{-1} and Number of seeds pod^{-1}. Similarly Correlation studies done in Black gram by Shalini et al. [8] for days to 50% flowering, days to maturity and 100 seed weight. Similar findings were observed by Srivastava et al. [9] in correlation tests for the number of seeds pod-1 and the number of pods plant^{-1}. Alam et al. [10] observed comparable results in correlation tests for days to 50% flowering and 100 seed weight at both phenotypic and genotypic level. Hence, these traits should be given appropriate consideration while selecting for improved production.

3.2 Path Coefficient Analysis

Path analysis revealed that Days to 50% flowering, plant height (cm) had a substantial positive effect on seed production. This results were collaborating with the findings from Correlation and path analysis studies done by Asari et al. [7], Ghimire et al. [11] and Parihar et al. [6] indicating that high positive direct effects

Table 2. 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 3. 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 on days to 50% flowering. Moderate direct effect showed by Number of branches plant^{-1}, Number of clusters plant^{-1}, while days to maturity and seed weight exerted low magnitude of direct effect.

Among the characters studied positive direct effect was obtained for Days to 50% flowering (1.58), plant height (0.31), Number of branches plant^{-1} (0.24), Number of clusters plant^{-1} (0.20), days to maturity (0.17) and seed weight (0.10) while high negative indirect effect obtained via Number of seeds pod^{-1} (-0.003), number of pods cluster^{-1} (-0.01) pod length (-0.03), Number of pods plant^{-1} (0.11), days to initial flowering (1.58), 100 seed weight (-3.411) at Genotypic level. Studies done on correlation and path by Manivelan et al. [12] reported similar results for Number of clusters plant^{-1}, Number of branches plant^{-1}, Number of pods plant^{-1}, Number of seeds pod^{-1}, 100 seed weight at phenotypic level. Similar results for days to 50% flowering, pod length (positive direct effect) and Number of pods plant^{-1} (negative direct effect) at genotypic level were reported by Ghimire et al. [11] on genetic variability and path analysis studies. Eswaran et al. [13] reported similar results for days to initial flowering, plant height, Number of branches plant^{-1} and number of pods cluster^{-1}. Genetic variability and correlation studies done by Alom et al. [14] reported similar results for days to 50% flowering at phenotypic level, plant height and 100 seed weight at both phenotypic and genotypic level. Therefore, utilizing these traits as the foundation for a selection strategy to enhance seed production in greengram will be beneficial [15,16].

4. CONCLUSION

Correlation coefficients tended to be higher at the genotypic level compared to the phenotypic level. Results also indicated that Number of branches plant^{-1}, number of pods cluster^{-1}, Number of clusters plant^{-1}, Number of pods plant^{-1}, Number of seeds plant^{-1}, plant height (cm), seed weight (g) and Pod length (cm) were positively correlated with Seed yield plant^{-1}. 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 plant^{-1}, Number of clusters plant^{-1}, days to maturity and seed weight had positive direct effect. Hence direct selection for yield improvement through these traits would be rewarding. From the combined results of correlation coefficient and path analysis, it may be concluded that plant height (cm), Number of branches plant^{-1}, Number of clusters plant^{-1} and 100 seed weight should be considered as indices for selecting high yielding green gram variety. Future Green gram breeding programs may focus on enhancing these traits to facilitate the direct selection of RILs. As a result, there is significant potential for selecting specific characteristics.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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