Association Analysis Studies in Mung bean (*Vigna radiata* (L.) Wilczek) Genotypes for Yield and its Contributing Traits

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ABSTRACT: Green gram (*Vigna radiata* L. Wilczek) is a vital pulse crop in India, providing a significant source of protein for the predominantly vegetarian population. However, the productivity of green gram is currently low, and there is a need to develop high-yielding varieties that are resistant to diseases and pests while maintaining nutritional value. In this study, a total of 94 green gram genotypes were evaluated to assess the relationships between yield and various contributing traits. Correlation and path coefficient analyses were performed to determine the associations between traits and yield. The results revealed significant positive correlations between yield and its contributing traits such as plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight, and harvest index. These findings were consistent with previous studies, further supporting the importance of these traits in determining yield potential of green gram. Path coefficient analysis identified harvest index as the trait with the highest positive direct effect on yield, followed by days to fifty per cent flowering. However, indirect effects were observed between early flowering and traits such as the number of pods per plant and protein content. Similarly, the number of primary branches per plant and number of clusters per plant exhibited negative direct effects on yield, indicating potential limitations in maximizing yield. Overall, this study provides valuable insights into the relationships between yield and its contributing traits in green gram. The findings can guide plant breeding programs in selecting and prioritizing traits to develop improved varieties with enhanced yield potential. Additionally, these identified trait associations contribute to a deeper understanding of the genetic and physiological mechanisms governing yield determination, facilitating more targeted and efficient crop improvement efforts. Association analysis studies in mung bean genotypes face various challenges when assessing yield and its contributing traits. One of the primary obstacles is the extensive phenotypic variation observed in mung bean, which makes it difficult to accurately measure and characterize these traits across different genotypes. Factors such as growth habit, flowering time, pod setting, and seed size contribute to this complexity, further complicating the phenotypic evaluation. Another challenge lies in the genetic complexity of mung bean genomes, which are influenced by both additive and non-additive genetic effects. Yield and its contributing traits are controlled by multiple genes, and their expression can be influenced by environmental interactions. Understanding the intricate genetic architecture and deciphering the effects of individual genes amidst complex genetic interactions pose significant challenges for researchers. To ensure reliable results, association analysis requires a substantial sample size of genotypes that adequately represents the genetic diversity within mung bean. Obtaining a diverse and representative set of genotypes is crucial for accurate analysis.

Keywords: Association studies, green gram, correlation, path coefficient, crop improvement.

INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek] is the third important pulse crop grown in India after chickpea and pigeon pea. Green gram is a self-pollinating diploid grain legume (2n = 22), a significant source of nutritional protein for India's largely vegetarian population. Green gram is an upright or sub erect annual with branches that twine in the higher branches. It grows to a height of 40 to 120 cm. India's total area

of production of green gram is 5.13 million hectares but productivity is less (601 kg/ha) (Bindu *et al.,* 2023). Therefore, there is a lot of potential to boost productivity by creating high-yielding varieties that are resistant to disease and pest and have a good nutritional value in them.

Green gram is an essential pulse crop because of its ability to adapt to short growing low water requirements, soil fertility, easy digestion, and low

flatulence production. They have such high levels of protein, ranging from 20 to 30%, as well as lysine, an essential amino acid. Aside from these characteristics, pulse crops have a deep penetrating root structure that allows them to better utilize available moisture than other crops. Pulses like green gram are important components in India's cropping system because they can fix atmospheric nitrogen into soil *via* rhizobium nodules, can take water from deeper layers of soil *via* their taproot system, and provide organic matter to soil by dropping leaves. Farmers grow them as extra crops, intercropping with other crops and without manuring them. Green gram yields are low for a variety of causes, including cultivation in unfertile land, inadequate fertilizer application, and a lack of improved varieties or hybrids. To address the rising demand for green gram, yield constraints must be overcome by producing high yielding and biotic/abiotic resistant genotypes. Yield is a variable trait that is influenced by several other variables. Selecting yield component qualities that have a strong relationship with yield will help increase yield. To meet the demand for pulses, production and productivity must be raised by better management methods, better variety selection, genotypes/lines and crop improvement. Green gramhas several morphological characters like days of fifty per cent flowering, Plant height (cm), Number of primary branches per plant, Number of pods per plant, Number of seeds per pod, Hundred seed weight (g), Protein content (%), Harvest index and Single plant yield (g) which can be identified as selection criteria to produce a high yielding elite green gram genotypes. Correlation analysis is a valuable tool for breeders as it enables them to effectively select and prioritize traits that contribute to yield. By examining the associations between various traits and yield, breeders can determine whether the relationship is a direct one or if it occurs indirectly through the influence of other component traits.

The major research problem in association analysis of mung is to understand the genetic factors influencing yield and its associated traits in mung bean cultivars. This involves identifying the specific genes with desirable traits, such as high yield, early flowering, pod setting, and seed size. The goal is to provide valuable insights into the genetic variability underlying these traits and aid in the development of improved mung bean varieties through various breeding strategies.

Major drawbacks of previous study is that the previous study might have had a limited number of genotypes, resulting in an incomplete representation of the genetic diversity present in mung beanand the previous study might have lacked validation of the identified associations between the mung bean population.

This proposed study aims to overcome the limitations of the previous study by incorporating a diverse set of genotypes and validating associations andthis study aimed to assess the association between seed yield and its contributing traits in a set of 94 green gram genotypes, providing valuable insights into the factors influencing yield in this crop.

MATERIALS AND METHODS

For the field experiment, a total of 94 green gram genotypes were gathered from diverse sources in India. These genotypes were raised at Karunya Institute of Technology and Sciences, Coimbatore, during October 2022. The research farm is situated approximately at 11° 56′N latitude and 76° 44′E longitude, with an elevation of 467 meters above Mean Sea Level. This experiment followed a Randomized Block Design with three replications. Each row measured 2.5 meters in length, with a spacing of 30 × 10 cm between and within rows. The recommended agronomic practices were implemented to ensure the healthy growth of the genotypes. To assess the quantitative traits, such as days to fifty per cent flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, and single plant yield, five plants were randomly selected from each genotype. Association analysis like correlation and path coefficient analysis were carried out.

RESULTS AND DISCUSSION

A. Correlation analysis

The correlation analysis, considering both genotypic and phenotypic coefficients of correlation, revealed valuable insights into the relationships between yield and its contributing traits. The results highlight the significant correlations among various traits and their potential influence on yield per plant (Table 1 and 2).

The genotypic coefficient of correlation indicated a highly positive and significant correlation between single plant yield and several traits like plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight, and harvest index exhibited strong positive correlations with yield. These findings suggest that these traits play crucial roles in determining yield potential. Current results are on par with Sandhiya and Saravanan (2018); Majhi *et al.* (2020); Anand *et al.* (2016) who observed that the number of pods per plant was positively correlated with the trait single plant yield. Hemavathy *et al.* (2015); Kandel *et al.* (2017) studies also revealed comparable results for the trait number of clusters per plant. Nalajala *et al.* (2022); Saikumar *et al.* (2022) observed positive correlation of plant height with single plant yield. Mahla *et al.* (2022); Jyothsna *et al.* (2016) also studies also revealed similar results. Furthermore, the genotypic correlation analysis revealed interesting associations among the traits themselves. For instance, plant height showed positive correlations with the number of primary branches per plant, hundred seed weight, and harvest index. Similar results were found by Garg *et al.* (2017); Reddy *et al.* (2022); Kumar *et al.* (2022). On the other hand, it displayed negative correlations with protein content, indicating a trade-off between plant height and protein content. Similarly, the number of primary branches per plant positively correlated with the number of clusters per plant, hundred seed weight, and harvest index, suggesting

their combined contribution to yield enhancement. These results were in accordance with the studies conducted by Nikhil *et al.* (2022) for number of clusters per plant, hundred seed weight and harvest index whereas findings of Muralidhara *et al.* (2015); Ramakrishnan *et al.* (2018); Mahalingam *et al.* (2020); Desai *et al.* (2020); Reddy *et al.* (2022); Saini *et al.* (2022) were in accordance for number of clusters per plant

The phenotypic coefficient of correlation supported the findings of the genotypic correlation analysis. It demonstrated highly positive and significant correlations between single plant yield and traits such as plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight, and harvest index. This suggests that these traits not only exhibit strong genetic relationships with yield but also demonstrate significant phenotypic associations. The phenotypic correlation analysis also highlighted associations between the contributing traits. Plant height exhibited positive correlations with the number of primary branches per plant, number of clusters per plant, hundred seed weight, and harvest index, aligning with the genotypic correlation findings. Similarly, the number of primary branches per plant positively correlated with the number of clusters per plant, hundred seed weight, and harvest index, emphasizing their collective impact on yield. The observed correlations between traits such as days to fifty per cent flowering, number of pods per plant, and protein content are also significant. Days to fifty per cent flowering displayed negative correlations with the number of pods per plant and protein content, indicating potential trade-offs between early flowering and these traits. This suggests that early-flowering varieties may have fewer pods per plant and lower protein content. Such insights can guide breeders in developing cultivars with specific trait combinations to meet diverse market and consumer preferences.

B. Path coefficient analysis
Analysis of the genotypic coefficient of correlation and phenotypic coefficient of correlation, as well as path analysis, was conducted to determine the relationships between various traits and yield per plant (Table 3 and 4).

Combining the findings from both genotypic and phenotypic coefficient of correlation analyses with the results of genotypic and phenotypic path analyses provides a comprehensive understanding of the relationships between yield and its contributing traits.

The genotypic coefficient of correlation identified several traits that displayed strong positive correlations with yield per plant, including plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight, and harvest index. Kate *et al.* (2017); Azam *et al.* (2018); Ramakrishnan *et al.* (2018); Mohammed *et al.* (2020); Rahangdale *et al.* (2023); Desai *et al.* (2020); Gaur *et al.* (2021).

These findings were consistent with the phenotypic coefficient of correlation, further reinforcing the importance of these traits in determining yield potential. The genotypic path analysis provided insights into the direct effects of each trait on yield per plant. Harvest index emerged as the trait with the highest positive direct effect on yield, indicating its strong contribution to overall yield performance. This finding was supported by the phenotypic path analysis, which also identified harvest index as the trait with the highest positive direct effect on yield per plant. These results highlight the significance of harvest index as a key trait for maximizing yield in plant breeding programs. Days to fifty per cent flowering showed a positive direct effect on yield per plant in both genotypic and phenotypic path analyses. This indicates that early flowering varieties have the potential to achieve higher yields. However, it is important to note that other traits may indirectly influence the relationship between flowering time and yield, as indicated by the negative indirect effects observed in both analyses. For example, the number of pods per plant and number of seeds per pod exhibited negative indirect effects, suggesting a potential trade-off between early flowering and these yield-contributing traits. Plant height demonstrated a positive direct effect on yield per plant in both analyses. This finding suggests that taller plants may have a greater capacity for photosynthesis and resource allocation, leading to increased yield. However, traits like days to fifty per cent flowering and plant height have also exhibited negative indirect effects through other traits, such as the number of pods per plant and protein content. These indirect effects highlight the complex relationships among traits and the need for a comprehensive understanding of their interactions.

The number of primary branches per plant, number of clusters per plant, and pod length exhibited negative direct effects on yield per plant in the genotypic path analysis, indicating their potential limitations in terms of maximizing yield. These findings were consistent with the negative indirect effects observed in both genotypic and phenotypic path analyses. These results suggest that increasing the number of primary branches and clusters per plant may divert resources away from yield components, leading to reduced yield potential. Hundred seed weight demonstrated both positive and negative direct effects on yield per plant in the genotypic path analysis. This suggests a complex relationship between seed weight and yield, influenced by other traits. Phenotypic path analysis also revealed a positive direct effect of hundred seed weight on yield per plant, highlighting its potential importance. Similar results were found by Dash *et al.* (2021). However, both genotypic and phenotypic analyses indicated negative indirect effects of hundred seed weight through other traits, emphasizing the need to consider the broader trait associations when evaluating its impact on yield. Protein content showed a positive direct effect on yield per plant in the genotypic path analysis, indicating its potential contribution to yield. However, this effect was mediated through hundred seed weight, and both genotypic and phenotypic path analyses

revealed negative indirect effects of protein content on yield per plant. These results suggest that while protein content may have a direct positive association with yield, it may also indirectly affect yield through its interaction with other traits. Overall, the combined results of the genotypic and phenotypic coefficient of correlation, as well as the genotypic and phenotypic path analyses, provide valuable insights into the relationships between yield and its contributing traits. These findings can guide plant breeding programs by identifying key traits with strong direct effects on yield, such as harvest index, and highlighting potential trade-offs and indirect effects among traits. By considering these relationships, breeders can prioritize and select traits to develop improved varieties with enhanced yield potential. Additionally, the identified trait associations can contribute to a deeper understanding of the underlying genetic and physiological mechanisms governing yield determination, enabling more targeted and effective crop improvement efforts.

Table 1: Genotypic correlation of yield and its contributing traits of green gram.

	DFF	PH	NBP	NCP	NPP	PL	NSP	HSW	PC	HI	SYD
DFF	1.0000**										
PH	0.1555	1.0000**									
NPB	0.1159	0.475**	1.0000**								
NCP	0.1479	0.1877	0.5979**	1.0000**							
NPP	-0.5827**	-0.2015	0.0865	0.4577	1.0000**						
PL	-0.0457	-0.0115	-0.0414	-0.1269	-0.1246	1.0000**					
NSP	-0.1371	0.0684	-0.0388	-0.0038	0.0469	0.1694	1.0000**				
HSW	0.4876**	0.3501**	0.2658**	0.248*	-0.2693**	-0.0876	-0.1108	1.0000**			
PC	-0.3131**	-0.2692**	0.0095	0.1841	0.339**	0.0225	0.1078	-0.3352**	1.0000**		
HI	-0.0237	0.2189*	0.3363**	0.5319**	0.4288**	-0.0479	0.4108**	0.6656**	-0.0384	1.0000**	
SYP	-0.0521	0.2355*	0.3517**	0.5097**	0.4626**	-0.0445	0.4845**	0.7097**	-0.0623	1.0353**	1.0000**

*Significant at 5% level ** Significant at 1% level
DFF: Days to fifty per cent flowering, **PH**: Plant height, **NPB**: Number of primary branches per plant, **NCP**: Number of clusters per plant, **NPP**: Number of pods per plant, **PL**: Pod length, **NSP**: Number of seeds per pod, **HSW**: Hundred seed weight, **PC**: Protein content, **HI**: Harvest index, **SYD**: Single plant yield.

Table 2: Phenotypic correlation of yield and its contributing traits of green gram.

	DFF	PH	NBP	NCP	NPP	PL	NSP	HSW	PC	HI	SYD
DFF	1.0000**										
PH	0.1032	1.0000**									
NPB	0.063	0.2935**	1.0000**								
NCP	0.0997	0.1565**	0.3399**	1.0000**							
NPP	-0.48**	-0.1857**	0.0542	0.3997**	1.0000**						
PL	-0.0418	-0.006	-0.0119	-0.1125	-0.1261*	1.0000**					
NSP	-0.1589**	0.0634	-0.0539	-0.0185	0.0275	0.1193*	1.0000**				
HSW	0.3626**	0.3061**	0.185**	0.2143**	-0.2293**	-0.0679	-0.0492	1.0000**			
PC	-0.2652**	-0.2466**	0.0067	0.1535**	0.3317**	0.0211	0.0606	-0.3034**	1.0000**		
HI	-0.0216	0.1992**	0.2403**	0.4387**	0.4181**	-0.0433	0.2273**	0.5998**	-0.0384	1.0000**	
SYP	-0.0382	0.1998**	0.2062**	0.3693**	0.3582**	-0.01	0.2413**	0.5112**	-0.0543	0.8946**	1.0000**

* Significant at 5% level ** Significant at 1% level

Table 3: Genotypic direct and indirect effects of yield and its contributing traits.

	DFF	PH	NPB	NCP	NPP	PL	NSP	HSW	PC	HI
DFF	0.06564	0.00459	-0.0005	-0.02229	0.21826	0.00107	0.04287	-0.31578	-0.0026	-0.04338
PH	0.01021	0.02948	-0.00204	-0.02829	0.07548	0.00027	-0.02139	-0.22677	-0.00223	0.40082
NPB	0.00761	0.014	-0.00429	-0.09012	-0.0324	0.00097	0.01212	-0.17218	0.00008	0.61592
NCP	0.00971	0.00553	-0.00256	-0.15072	-0.17144	0.00297	0.0012	-0.16059	0.00153	0.97413
NPP	-0.03825	-0.00594	-0.00037	-0.06899	-0.37455	0.00292	-0.01467	0.17441	0.00281	0.78521
PL	-0.003	-0.00034	0.00018	0.01913	0.04667	-0.02342	-0.05295	0.05676	0.00019	-0.08774
NSP	-0.009	0.00202	0.00017	0.00058	-0.01758	-0.00397	-0.3126	0.07176	0.00089	0.75225
HSW	0.032	0.01032	-0.00114	-0.03737	0.10086	0.00205	0.03464	-0.6477	-0.00278	1.21885
PC	-0.02055	-0.00794	-0.00004	-0.02774	-0.12699	-0.00053	-0.0337	0.2171	0.0083	-0.07025
HI	-0.00155	0.00645	-0.00144	-0.08017	-0.1606	0.00112	-0.12841	-0.43108	-0.00032	1.83131

Residual: 0.19

Table 4: Phenotypic direct and indirect effects of yield and its contributing traits.

	DFF	PH	NPB	NCP	NPP	PL	NSP	HSW	PC	HI
DFF	**-0.01888**	0.00221	-0.00057	-0.00066	0.02695	-0.00066	-0.00224	-0.02967	0.00617	-0.02083
PH	-0.00195	**0.02143**	-0.00268	-0.00104	0.01047	-0.0001	0.00089	-0.02506	0.00573	0.19211
NPB	-0.00119	0.00629	**-0.00912**	-0.00226	-0.00306	-0.0002	-0.00076	-0.01509	-0.00015	0.23165
NCP	-0.00188	0.00335	-0.0031	**-0.00664**	-0.02252	-0.00178	-0.00027	-0.01747	-0.00357	0.42308
NPP	0.00903	-0.00398	-0.0005	-0.00265	**-0.05636**	-0.00201	0.00039	0.01878	-0.00771	0.40321
PL	0.00078	-0.00013	0.00011	0.00074	0.00711	**0.01591**	0.0017	0.00552	-0.00048	-0.04176
NSP	0.003	0.00136	0.0005	0.00013	-0.00154	0.00192	**0.01409**	0.00406	-0.00141	0.21921
HSW	-0.00684	0.00656	-0.00168	-0.00142	0.01292	-0.00107	-0.0007	**-0.08197**	0.00705	0.57825
PC	0.00501	-0.00528	-0.00006	-0.00102	-0.01869	0.00033	0.00086	0.02484	**-0.02324**	-0.03703
HI	0.00041	0.00427	-0.00219	-0.00291	-0.02356	-0.00069	0.0032	-0.04911	0.00089	**0.9643**

Residual: - 0.03

CONCLUSIONS

In conclusion, the correlation analysis, considering both genotypic and phenotypic coefficients, has provided valuable insights into the relationships between yield and its contributing traits. The findings highlight the significance of traits such as plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight, and harvest index in determining yield potential. These results are consistent with previous studies, confirming the importance of these traits in maximizing yield. Additionally, the correlation analysis revealed interesting associations among the traits themselves, shedding light on their combined contribution to yield enhancement.

The path coefficient analysis further elucidated the direct effects of each trait on yield per plant. Harvest index emerged as the trait with the highest positive direct effect on yield, indicating its crucial role in overall yield performance. Days to fifty per cent flowering also showed a positive direct effect on yield, suggesting that early-flowering varieties have the potential to achieve higher yields. However, trade-offs and indirect effects among traits were observed, emphasizing the need for a holistic approach in trait selection.

The comprehensive understanding provided by these analyses has practical implications for plant breeding programs. Breeders can prioritize and select traits based on their positive correlations and direct effects on yield, such as harvest index and early flowering. By targeting these key traits, improved varieties with enhanced yield potential can be developed. Furthermore, the identified trait associations can guide future research on the underlying genetic mechanisms governing these relationships, facilitating more targeted and efficient crop improvement efforts.

Overall, the correlation and path coefficient analyses offer valuable insights into the complex relationships between yield and its contributing traits. These findings contribute to our understanding of crop yield determination and can inform breeders and researchers in their efforts to develop high-yielding and resilient crop varieties to meet the increasing demands for food security and sustainability.

FUTURE SCOPE

The findings from the correlation analysis and path coefficient analysis provide a foundation for future research and breeding programs aimed at improving crop yield. These identified trait associations and their relationships with yield can be further explored to unravel the underlying genetic mechanisms and physiological processes involved. This could involve investigating specific genes or molecular pathways that influence these traits and yield. Additionally, conducting field trials and genetic studies on diverse germplasm can help validate the observed correlations and explore new trait combinations for yield enhancement. Furthermore, integrating advanced genomic techniques, such as marker-assisted selection or genomic selection, can expedite the breeding process by targeting favourable trait combinations more efficiently. Overall, future research should focus on leveraging the insights gained from these analyses to develop novel breeding strategies and genetic resources that contribute to sustainable and high-yielding crop varieties.

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