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Research Note

Genetic variability and association studies for yield and pre-harvest sprouting traits in greengram [*Vigna radiata* (L.) Wilczek]

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Abstract
The present study investigates the genetic variability and associations of agronomic traits impacting pre-harvest sprouting (PHS) in 30 greengram genotypes. Significant variability was observed across multiple traits, with seed yield per plant ranging from 2.19 to 7.82 g. Key findings indicate that hard seed percentage and alpha-amylase activity at different germination intervals are having high heritability, demonstrating genetic heritability essential for breeding strategies. High phenotypic variability suggests environmental influence on trait expression, especially in traits such as days to maturity and pod diameter. Correlation analysis revealed robust positive associations between seed yield and days to maturity, while negative correlations were noted with epicuticular wax content and pod wall thickness. The path analysis identified that days to 50 % flowering, along with alpha-amylase activity, directly affects yield, emphasizing the intricacies of trait interrelationships. This research aims to contribute towards developing PHS-resistant mung bean varieties that enhance crop yield and quality.

Keywords: Greengram, genetic variability, pre-harvest sprouting, correlation analysis, path analysis

Greengram, *Vigna radiata*, is an important pulse crop widely cultivated in India. Its cultivation areas extend beyond India to other Asian countries. It is a versatile crop that offers numerous benefits, making it a popular choice among farmers. This short-duration self-pollinating annual legume contributes to the income of marginal farmers and serves as a source of easily digestible protein. Greengram seeds are highly nutritious, rich in proteins, fibre, minerals, and vitamins. The grain of greengram contains 58 per cent carbohydrate and 20-26 per cent protein and it contains aminoacids such as arginine, histidine, lysine, tryptophan, etc (Jayamani *et al.,* 2015). The seeds are also sprouted and consumed as a nutritious snack. Despite its significance, the productivity and quality of mungbean are frequently compromised by various challenges, notably pre-harvest sprouting (PHS). PHS, which involves the premature germination of seeds while still attached to the plant, which drastically reduces both seed yield and quality of the produce.

Understanding and mitigating PHS in mungbean necessitates an in-depth study of genetic variability and the relationship between PHS and other agronomic traits.

Genetic variability is essential for crop improvement, providing the diversity required for the selection of favorable traits. Character association studies further enhance this process by revealing how different traits are interrelated, thus informing breeding strategies aimed at reducing PHS. This study was aimed to quantify genetic variation and to identify traits that influence PHS by examining a diverse collection of mungbean genotypes. The genetic parameters such as phenotypic and genotypic coefficients of variation, heritability, and genetic advance was evaluated for important yield and quality traits. In addition, the correlation and path coefficient analyses were conducted to elucidate the direct and indirect effects of various traits on PHS. The ultimate goal of this study was to aid in the development of PHS-resistant mungbean varieties, thereby improving yield stability and quality across diverse growing conditions.

Table 1. List of thirty genotypes used for the experiment

S.No.	Genotype	Origin
1	OBGG 110	Odisha
2	COGG 912	Tamil Nadu
3	OUM 11-5	Odisha
4	VBN 5	Tamil Nadu
5	VGG 20-234	Tamil Nadu
6	PM 2015	Uttarakhand
7	KM 2401	Uttar Pradesh
8	IGKM 2021-1	Chhattisgarh
9	RVSM 22-13	Madhya Pradesh
10	LGG 685	Andhra Pradesh
11	DGG 214	Karnataka
12	MI 2023-1	Madhya Pradesh
13	IPM 2-14	Uttar Pradesh
14	Pusa 23-71	New Delhi
15	RVSM 22-3	Madhya Pradesh
16	RM 03-79	Chhattisgarh
17	ML 2844	Punjab
18	MGG 514	Telangana
19	RMG 1164	West Bengal
20	OBGG 107	Odisha
21	BCM 20-05	West Bengal
22	MI 13-47	Madhya Pradesh
23	BM 2021-4	Maharashtra
24	RMB 15-14	Jharkhand
25	PM 2031	Uttarakhand
26	VGG 20-157	Tamil Nadu
27	LGG 657	Andhra Pradesh
28	ML 2878	Punjab
29	MH 1890	Haryana
30	JLPM 818-8	Maharashtra

The present investigation was carried out during *Rabi*, 2023- 2024 at Regional Agricultural Research Station, Lam, Guntur with 30 genotypes of greengram in a Randomized Block Design with three replications. Each genotype was grown in paired rows, where each row measured four meters in length with inter-row spacing of 30 cm x 10 cm. Observations for days to 50% flowering and days to maturity were taken on a plot basis from each replication. Observations on plant height (cm), pod length (cm), pod diameter (mm), pod wall thickness, pod beak length (mm), water imbibition by pods (%), seed germination in pods (%) or pre-harvest sprouting (%) and hard seed in pods (%) were recorded from three replications of five pods each. Each set of five pods from each replication was taken from five random plants. The 100-seed weight, water imbibition by seeds (%), fresh seed germination (%), hard seed (%), and seed germination (%) were recorded from three sets of 100 seed samples from the bulk harvest of each genotype. Pod wall thickness and pod diameter were recorded using digital vernier calipers. Epicuticular wax content on the pod wall (mg/g dry weight of pod) was estimated by a colorimetric assay (Ebercon *et al*., 1977). Alpha-amylase activity in the seeds (mg of maltose released per gram of fresh tissue/minute) was estimated at different time intervals after germination, specifically at harvest (0 hrs after germination), 24 hrs after germination, 48 hrs after germination and 72 hrs after germination, according to (Rathi *et al*., 2013). The statistical software used for analysis of the data was Windostat ver. 9.3.

The analyses of variance (ANOVA) among 30 greengram genotypes showed the presence of significant variability for all traits studied **(Table 2)**. A similar result was reported by Sandhiya and Shanmugavel (2018) and Mohammed *et al.* (2020). The mean values for all the traits exhibited a wide range of variations.

The assessment of both heritable and non-heritable components of total variability is essential for the implementation of an appropriate breeding program. In this context, genetic parameters such as variability, heritability and genetic advance are critical for effective selection. In the present study, it was found that for all the traits, the phenotypic coefficient of variation was greater than the genotypic coefficient of variation, indicating that the environment plays a significant role in contributing to variation **(Table 3)**. A similar result was observed by Salman *et al*. (2023). Maximum GCV and PCV were exhibited for the hard seed percentage (66.30 and 66.41) followed by alpha-amylase activity at 24 hrs (46.90 and 47.19), hard seed percentage in pods (46.47 and 46.60) and pre-harvest sprouting percentage in pods (44.76 and 45.15). High genotypic and phenotypic coefficient of variation indicate the complex nature of the traits and the influence of both genetic and environmental factors. This suggests significant genetic diversity within the population, offering the potential for genetic improvement through selective breeding. However, strong environmental

Table 2. Analysis of variance for biometrical traits in greengram

Source	df	DFF	DM	PL	PBL	PWT	PD	WIS%	FSG %	HS%
Replication	2	0.42	14.61	0.38	0.18	0.00	0.01	3.21	35.31	1.20
Treatment	29	14.98 **	15.77 **	0.97 **	2.33 **	0.04 **	0.15 **	1227.16 **	1342.66 **	1346.15 **
Error	58	4.05	7.28	0.22	0.08	0.00	0.06	5.64	16.48	1.50

Source	WIP%	PHS%	HSP%	EWC	AAA at 0 hrs	AAA at 24 hrs	AAA at 48 hrs	AAA at 72 hrs	SYP
Replication	1.20	0.14	3.68	0.06	0.25	3.89	11.77	6.06	0.06
Treatment	186.34 **	1468.11 **	1310.18 **	6.10 **	39.27 **	499.26 **	1062.03 **	1644.84 **	6.44 **
Error	12.48	8.37	2.41	0.03	0.31	2.07	5.31	6.31	0.30

** Significant at 1% level of significance; df- degrees of freedom

CHARACTERS: DFF- Days to 50% flowering, DM-Days to maturity, PL-Pod length (cm), PBL- Pod beak length (mm), PWT-Pod wall thickness (mm), PD- Pod diameter (mm), WIS-Water Imbibition by seeds (%), FSG-Fresh seed germination (%), HS- Hard seed (%), WIP- Water Imbibition by pods (%), PHS- Pre-harvest sprouting (%), HSP- Hard seed (%) in pods, EWC- Epicuticular wax content (mg/g dry weight of pod), AAA - Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) and SYP-Seed yield per plant (g).

Table 3. Genetic variability parameters for biometrical traits in greengram

Trait	Mean	Lowest value	Highest value	GCV	PCV	Heritability (broad sense)	Genetic Advance	GA as percent of Mean
DFF	36.54	32.33	43.33	5.22	7.59	47.40	2.71	7.41
DM	66.39	62.00	69.67	2.53	4.79	28.00	1.83	2.76
PL	7.47	6.32	8.55	6.70	9.14	53.70	0.76	10.12
PBL	4.09	2.90	7.30	21.18	22.23	90.80	1.70	41.59
PD	4.83	4.46	5.35	3.87	6.00	41.50	0.22	5.13
PWT	0.42	0.23	0.70	28.37	28.37	98.30	0.24	57.55
WIS%	47.51	14.13	86.33	42.47	42.77	98.60	41.27	86.86
FSG%	67.71	20.67	100.00	31.05	31.63	96.40	42.52	62.80
HS%	31.93	0.00	79.33	66.30	66.41	99.70	43.55	136.39
WIP%	56.75	29.71	65.83	13.42	14.79	82.30	14.23	25.07
PHS%	49.28	15.74	93.99	44.76	45.15	98.30	45.05	91.42
HSP	44.93	6.01	75.44	46.47	46.60	99.40	42.87	95.42
EWC	3.32	1.53	6.57	42.86	43.14	98.70	2.91	87.71
AAA at harvest	10.71	4.51	20.85	33.63	34.04	97.70	7.34	68.50
AAA at 24 hrs	27.45	11.45	58.56	46.90	47.19	98.80	26.36	96.05
AAA at 48 hrs	47.19	12.95	79.17	39.77	40.07	98.50	38.37	81.31
AAA at 72 hrs	57.87	14.02	113.67	40.38	40.62	98.90	47.89	82.75
SYP	4.55	2.19	7.82	31.47	33.68	87.30	2.76	60.58

GCV- Genotypic coefficient of variation (%), PCV- Phenotypic coefficient of variation (%)

CHARACTERS: DFF- Days to 50% flowering, DM-Days to maturity, PL-Pod length (cm), PBL- Pod beak length (mm), PWT-Pod wall thickness (mm), PD- Pod diameter (mm), WIS-Water Imbibition by seeds (%), FSG-Fresh seed germination (%), HS- Hard seed (%), WIP- Water Imbibition by pods (%), PHS- Pre-harvest sprouting (%), HSP- Hard seed (%) in pods, EWC- Epicuticular wax content (mg/g dry weight of pod), AAA - Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) and SYP-Seed yield per plant (g)

influence implies that environmental conditions also play a crucial role in shaping trait expression. To maximize genetic advance, it is essential to consider both genetic and environmental factors and employ advanced breeding techniques, such as genomic selection. High GCV and PCV for pre-harvest sprouting percentage were reported by Rao *et al*. (2016) and Lamichaney *et al*. (2018). High PCV and moderate GCV for hard seed percentage was reported by Payasi (2015). Lowest GCV and PCV was exhibited for the days to maturity (2.53 and 4.79), pod diameter (3.87 and 6.00), days to 50 percent flowering (5.22 and 7.59) and pod length (6.70 and 9.14). Similar results with days to maturity, days to 50 % flowering and pod length were reported by Thonta (2023) and Salman *et al*. (2023).

Heritability estimates can provide further insight into the relative importance of genetic and environmental factors in determining phenotypic variation. Heritability is the proportion of phenotypic variation that is heritable. High heritability indicates a strong genetic influence on the trait. Heritability measures the genetic influence on a trait's variation, whereas genetic advance is the improvement in mean genotypic value from selection. High heritability indicates a strong genetic basis, which makes selection effective. Genetic advance, influenced by selection intensity, heritability, and phenotypic variation, predicts the magnitude of improvement. Expressing the genetic advance as a percentage of the mean provides a relative measure of the expected change. Considering these factors and employing advanced breeding techniques, breeders can significantly enhance the genetic quality of populations.

Highest heritability (>60%) coupled with high genetic advance as percent of mean (>20%) among all the traits was recorded for hard seed percentage (99.70 and 136.39) followed by hard seed percentage in pods (99.40 and 95.42), alpha-amylase activity at 72 hrs after germination (98.90 and 82.75) and alpha-amylase activity at 24 hrs after germination (98.80 and 96.05). High heritability coupled with high genetic advance is the most favorable condition for selection and it indicates that the trait is controlled by additive genes. It suggests that the trait can be improved through selection in future generations. This favorable genetic architecture allows for the effective use of various breeding methods. Mass selection is suitable for traits with high heritability, whereas pedigree selection can be useful for traits with low heritability or those that are difficult to measure directly. Progeny testing is beneficial for traits with low heritability or late-onset expression. Genomic selection, a modern technique, can accelerate genetic gain by leveraging genomic information. By understanding the genetic basis of the trait and employing appropriate breeding methods, significant improvements in the desired traits can be achieved. These findings were akin to the earlier findings of Lamichaney *et al.* (2018) for high heritability in alpha amylase activity at 72 hrs after germination, alpha amylase activity at 48 hrs after germination, alpha amylase activity at harvest, water imbibition by pods and seeds, fresh seed germination and pre-harvest sprouting, and also with high genetic advance as percent of mean for alpha-amylase activity at 72 hrs after germination, while lowest heritability (>30%) coupled with lowest genetic advance as percent of mean (>10%) among all the traits was observed for days to maturity (28.00 and 2.76). Moderate heritability coupled with low genetic advance as percent of mean was observed for pod diameter (41.50 and 5.13) and days to 50 % flowering (47.40 and 7.41). This suggests that a significant portion of phenotypic variation is due to non-additive genetic effects and environmental factors. In such cases, direct selection may be less effective, as the phenotypic value may not accurately reflect the breeding value. Alternative breeding strategies such as recurrent selection, hybrid breeding and molecular breeding techniques can be more suitable. Similar results were reported earlier for the days to maturity and days to 50 % flowering (Muthuswamy *et al*., 2022 and Yoseph *et al*., 2022). Genetic advance as percent of mean ranged from (2.76-136.39 %) for days to maturity and hard seed percentage respectively.

Seed yield per plant is influenced by many factors as it is a complex trait. Correlation coefficient is a statistical tool that reflects the strength and direction of relationship between seed yield per plant and other traits at both genotypic and phenotypic levels. In the present study, seed yield per plant (g) recorded highly significant and positive association with days to maturity (0.820** and 0.409**) followed by days to 50 % flowering (0.628** and 0.360**), pre-harvest sprouting percentage (0.372** and 0.343**) and fresh seed germination percentage (0.296** and 0.272**) at both genotypic and phenotypic levels. Highly significant and positive correlation between the two traits indicates a strong genetic link. This allows for indirect selection, in which improving one trait indirectly improves the other. Understanding the underlying genetic mechanisms, such as pleiotropy and linkage, can help breeders develop efficient strategies to simultaneously improve multiple traits. A positive correlation between seed yield and maturity traits indicates that late-maturing varieties tend to have higher seed yields. This is likely due to longer vegetative periods for biomass accumulation, avoidance of adverse environmental conditions during the reproductive phase and extended grain-filling periods. However, extremely late-maturing varieties may be susceptible to late-season stresses, which could be a possible cause of pre-harvest sprouting. Therefore, a balance between maturity and yield potential is crucial for achieving optimal crop performance. The unexpected positive correlation between seed yield and pre-harvest sprouting, a detrimental trait, might be due to specific genetic factors or experimental conditions. As laboratory experiments may not fully replicate field conditions, it is crucial to validate these findings in field trials. Understanding the genetic basis of pre-harvest sprouting

can help breeders develop strategies to minimize its occurrence and improve overall crop performance. A positive correlation with seed yield suggests that genotypes with higher germination rates may also have higher yield potential. This could be because of better seed vigor, improved seedling establishment, or increased plant vigor. Significant and positive correlation of seed yield to days to 50 % flowering and days to maturity at both levels were reported by (Jadhav *et al*., 2019); pre-harvest sprouting percentage (Rigatti *et al*., 2019 and Vetch *et al*., 2019). Seed yield per plant (g) also recorded highly significant and negative association with epicuticular wax content (-0.418** and -0.389**) followed by pod wall thickness (-0.397** and -0.356**), hard seed percentage in pods (-0.333** and -0.315**) and hard seed percentage (-0.296** and -0.271**) at both genotypic and phenotypic levels. Lower wax content might be associated with better water uptake, nutrient absorption, and photosynthetic efficiency, ultimately leading to higher seed yield. However, waxes also play a crucial role in protecting plants from biotic and abiotic stresses like pre-harvest sprouting. Therefore, a balance is necessary. Thinner pod walls might facilitate easier seed dispersal and potentially improve seed quality. However, thinner walls could also make pods more susceptible to damage and pathogen attacks. A lower hard seed percentage indicates higher seed viability and germination rate, which can contribute to better seedling establishment and ultimately higher seed yield. Kumar *et al*. (2021) reported positive and non-significant association at phenotypic level and negative and non-significant association at genotypic level with pod wall thickness. Days to maturity recorded highly significant and positive association with days to 50 % flowering (0.754** and 0.301**) at both genotypic and phenotypic levels and association at genotypic level with pre-harvest sprouting percentage (0.501**), alpha amylase activity at 72 hrs after germination (0.494**), pod length (0.446**) and pod beak length (0.288**). The strong positive correlation between days to maturity and days to 50% flowering indicates, as the time taken to reach 50% flowering is a major factor in determining overall maturity. The positive correlation between days to maturity and pre-harvest sprouting suggests that late-maturing varieties may be more susceptible to pre-harvest sprouting. This could be due to extended exposure to environmental factors that favor germination, such as moisture and temperature fluctuations. The positive correlation between days to maturity and alpha-amylase activity at 72 hours after germination suggests that late-maturing varieties may have higher levels of alpha-amylase activity, which can affect seed quality and germination. The positive correlation between days to maturity and pod length and pod beak length indicate that late-maturing varieties may have larger pods and longer beaks. This could be related to the extended vegetative growth and increased resource allocation to reproductive structures. Similar results with days to 50 % flowering at both the levels were reported by Gaikwad *et al*. (2023) and Harsh and Priyal (2023). Pre-harvest sprouting percentage recorded highly significant and positive association with water imbibition by seeds (0.789** and 0.778**), fresh seed germination (0.736** and 0.722**), alpha amylase activity at 48 hrs after germination (0.561** and 0.555**), alpha amylase activity at 72 hrs after germination (0.386** and 0.381**) and water imbibition by pods (0.327** and 0.288**) at both genotypic and phenotypic levels. The significant positive correlation between pre-harvest sprouting and traits such as water imbibition by seeds and pods, fresh seed germination and alpha-amylase activity indicates a close relationship between these factors. High water imbibition capacity increases the susceptibility of seeds to germinate prematurely, especially under humid conditions. Higher germination rates, particularly under unfavourable conditions, can contribute to pre-harvest sprouting. Increased alpha-amylase activity can mobilize stored starch reserves, providing energy for germination. However, high alpha-amylase levels can also lead to premature germination and reduced seed viability. Increased pod water imbibition can create a favourable environment for seed germination, even before pod dehiscence. To mitigate pre-harvest sprouting, breeding programs should focus on developing cultivars with lower water imbibition capacity, reduced seed vigor, and delayed germination. Additionally, appropriate agronomic practices, such as timely harvesting and post-harvest drying, can help minimize pre-harvest sprouting losses. Similar results with water imbibition by seeds, fresh seed germination, alpha amylase activity and water imbibition by pods at both the levels were reported by Verma *et al*. (2024). Fresh seed germination percentage recorded highly significant and positive association with water imbibition by seeds (0.814** and 0.793**), pre-harvest sprouting percentage (0.736** and 0.722**), alpha amylase activity at 48 hrs after germination (0.507** and 0.495**) and alpha amylase activity at 72 hrs after germination (0.334** and 0.329**) at both genotypic and phenotypic levels. Seeds with higher water imbibition capacity, increased germination rates, and elevated alpha-amylase activity are more likely to germinate, which can contribute to pre-harvest sprouting. Lamichaney *et al*. (2018) reported positive and significant association of fresh seed germination with alpha amylase activity at 24, 48 and 72 hrs after germination.

Path analysis is a statistical technique used to examine direct and indirect relationships among multiple variables simultaneously (**Table 5**). Residual effect measures the role of the possible independent variables which were not included in study on the dependent variable. In the present study, residual value of genotypic path effect was 0.075 and residual value of phenotypic path effect was 0.439. Traits *viz.,* days to 50 % flowering (1.083 and 0.292), alpha amylase activity at 72 hrs after germination (0.710 and 0.118) and water imbibition by pods (0.377 and 0.152) had registered a high and positive direct effect on seed yield per plant at both genotypic and phenotypic

Table 4. Genotypic correlation estimates (above diagonal) and phenotypic correlation estimates (below diagonal) of 18 quantitative characters in greengram

Traits	1	2	3	4	5	6	7	8	9
1	**1**	0.754**	0.047	0.068	-0.266*	-0.282**	0.088	-0.013	0.007
2	0.301**	**1**	0.446**	0.288**	-0.083	-0.320**	0.068	0.182	-0.187
3	0.153	0.204	**1**	0.067	0.991**	-0.101	-0.057	0.281**	-0.274**
4	0.028	0.173	0.052	**1**	0.050	0.187	-0.123	0.065	-0.059
5	-0.164	-0.027	0.424**	0.106	**1**	0.113	-0.258*	0.134	-0.156
6	-0.169	-0.153	-0.061	0.184	0.087	**1**	-0.790**	-0.716**	0.705**
7	0.053	0.008	-0.030	-0.117	-0.162	-0.774**	**1**	0.814**	-0.801**
8	0.005	0.104	0.176	0.060	0.112	-0.692**	0.793**	**1**	-0.994**
9	0.001	-0.104	-0.206	-0.057	-0.100	0.693**	-0.796**	-0.987**	**1**
10	-0.219*	-0.078	0.009	-0.077	0.288**	-0.136	0.115	0.186	-0.181
11	0.161	0.246*	0.119	0.03	-0.059	-0.799**	0.778**	0.722**	-0.719**
12	-0.142	-0.210*	-0.074	-0.023	0.087	0.786**	-0.820**	-0.748**	0.748**
13	-0.196	-0.142	0.081	-0.287**	0.104	0.702**	-0.603**	-0.500**	0.493**
14	-0.120	-0.132	-0.236*	-0.104	-0.159	0.012	0.033	-0.101	0.101
15	0.130	0.124	-0.172	-0.185	-0.198	-0.283**	0.373**	0.196	-0.205
16	0.337**	0.113	0.080	0.106	-0.228*	-0.600**	0.660**	0.495**	-0.493**
17	-0.036	0.244*	0.395**	-0.030	0.267*	-0.326**	0.256*	0.329**	-0.329**
18	0.360**	0.409**	0.092	0.183	0.137	-0.356**	0.066	0.272**	-0.271**

Traits	10	11	12	13	14	15	16	17	18
1	-0.331**	0.222*	-0.216*	-0.317**	-0.184	0.178	0.507**	-0.036	0.628**
2	-0.066	0.501**	-0.389**	-0.325**	-0.275**	0.191	0.253*	0.494**	0.820**
3	0.065	0.141	-0.106	0.099	-0.352**	-0.257*	0.112	0.546**	0.175
4	-0.123	0.044	-0.022	-0.307**	-0.122	-0.204	0.117	-0.035	0.208*
5	0.339**	-0.077	0.134	0.157	-0.299**	-0.307**	-0.329**	0.394**	0.084
6	-0.144	-0.820**	0.802**	0.714**	0.009	-0.289**	-0.615**	-0.332**	-0.397**
7	0.117	0.789**	-0.829**	-0.609**	0.035**	0.378**	0.668**	0.259*	0.070
8	0.198	0.736**	-0.763**	-0.514**	-0.106	0.204	0.507**	0.334**	0.296**
9	-0.203	-0.725**	0.752**	0.496**	0.103	-0.205	-0.498**	-0.332**	-0.296**
10	**1**	0.327**	-0.288**	-0.029	0.154	0.166	-0.110	0.160	0.142
11	0.288**	**1**	-0.965**	-0.730**	-0.100	0.273**	0.561**	0.386**	0.372**
12	-0.259*	-0.956**	**1**	0.744**	0.069	-0.294**	-0.593**	-0.300**	-0.333**
13	-0.033	-0.718**	0.735**	**1**	0.208*	-0.291**	-0.605**	-0.217*	-0.418**
14	0.131	-0.098	0.068	0.206	**1**	0.158	-0.070	0.008	-0.101
15	0.149	0.267*	-0.291**	-0.286**	0.156	**1**	0.544**	0.320**	0.081
16	-0.095	0.555**	-0.588**	-0.597**	-0.069	0.535**	**1**	0.323**	0.244*
17	0.163	0.381**	-0.297**	-0.214*	0.004	0.319**	0.317+**	**1**	0.248*
18	0.134	0.343**	-0.315**	-0.389**	-0.096	0.066	0.224*	0.237*	**1**

** Significant at 1% level of significance * Significant at 5% level of significance

CHARACTERS : 1- Days to 50% flowering, 2- Days to maturity, 3- Pod length (cm), 4- Pod beak length (mm), 5- Pod diameter (mm), 6- Pod wall thickness (mm), 7- Water imbibition by seeds (%), 8- Fresh seed germination (%), 9- Hard seed (%), 10-Water imbibition by pods (%), 11- Pre-harvest sprouting (%), 12- Hard seed (%) in pods, 13- Epicuticular wax content (mg/g dry weight of pod), 14- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at harvest, 15- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at 24 hrs after germination, 16- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at 48 hrs after germination, 17- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at 72 hrs after germination and 18- Seed yield per plant (g).

Table 5. Direct and indirect effects of different traits on seed yield in greengram

Traits		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	G	**1.083**	-0.102	-0.027	0.023	-0.006	0.169	-0.065	0.016	-0.013	-0.125	-0.206	0.173	-0.043	0.022	-0.031	-0.213	-0.026	0.628**
	P	**0.292**	0.078	-0.041	-0.003	-0.022	0.027	-0.048	-0.002	-0.001	-0.033	0.000	0.005	0.071	-0.013	-0.024	0.078	-0.004	0.360**
2	G	0.817	**-0.136**	-0.253	0.095	-0.002	0.191	-0.050	-0.230	0.366	-0.025	-0.466	0.312	-0.044	0.033	-0.034	-0.106	0.351	0.820**
	P	0.088	**0.259**	-0.054	-0.020	-0.004	0.024	-0.007	-0.043	0.101	-0.012	0.000	0.007	0.051	-0.014	-0.023	0.026	0.029	0.490**
3	G	0.051	-0.060	**-0.567**	0.022	0.023	0.060	0.042	-0.355	0.538	0.025	-0.131	0.085	0.013	0.042	0.045	-0.047	0.388	0.175
	P	0.045	0.053	**-0.266**	-0.006	0.056	0.010	0.027	-0.073	0.200	0.001	0.000	0.003	-0.029	-0.026	0.032	0.019	0.046	0.092
4	G	0.074	-0.039	-0.038	**0.331**	0.001	-0.112	0.092	-0.082	0.116	-0.047	-0.041	0.017	-0.042	0.015	0.036	-0.049	-0.025	0.208*
	P	0.008	0.045	-0.014	**-0.113**	0.014	-0.029	0.106	-0.025	0.055	-0.012	0.000	0.001	0.103	-0.011	0.034	0.025	-0.003	0.183
5	G	-0.287	0.011	-0.562	0.016	**0.023**	-0.068	0.193	-0.169	0.306	0.128	0.071	-0.108	0.021	0.036	0.054	0.138	0.280	0.084
	P	-0.048	-0.007	-0.113	-0.012	**0.133**	-0.014	0.146	-0.046	0.097	0.044	0.000	-0.003	-0.037	-0.017	0.037	-0.053	0.031	0.137
6	G	-0.305	0.043	0.057	0.062	0.003	**-0.599**	0.590	0.903	-1.384	-0.054	0.762	-0.643	0.096	-0.001	0.051	0.258	-0.236	-0.397**
	P	-0.049	-0.040	0.016	-0.021	0.012	**-0.160**	0.698	0.286	-0.673	-0.021	-0.001	-0.027	-0.253	0.001	0.053	-0.140	-0.038	-0.356**
7	G	0.095	-0.009	0.032	-0.041	-0.006	0.473	**-0.747**	-1.026	1.573	0.044	-0.734	0.665	-0.082	-0.004	-0.067	-0.280	0.184	0.070
	P	0.015	0.002	0.008	0.013	-0.022	0.124	**-0.901**	-0.328	0.772	0.018	0.001	0.028	0.217	0.004	-0.069	0.153	0.030	0.066
8	G	-0.014	-0.025	-0.159	0.022	0.003	0.429	-0.608	**-1.261**	1.975	0.075	-0.684	0.612	-0.069	0.013	-0.036	-0.213	0.237	0.296**
	P	0.001	0.027	-0.047	-0.007	0.015	0.111	-0.714	**-0.413**	0.959	0.028	0.001	0.026	0.180	-0.011	-0.036	0.115	0.039	0.272**
9	G	0.007	0.025	0.155	-0.020	-0.004	-0.422	0.598	1.268	**-1.963**	-0.077	0.674	-0.603	0.067	-0.012	0.036	0.209	-0.236	-0.296**
	P	0.000	-0.027	0.055	0.006	-0.013	-0.111	0.717	0.408	**-0.971**	-0.028	-0.001	-0.026	-0.177	0.011	0.038	-0.115	-0.039	-0.271**
10	G	-0.358	0.009	-0.037	-0.041	0.008	0.086	-0.087	-0.249	0.399	**0.377**	-0.304	0.231	-0.004	-0.018	-0.029	0.046	0.114	0.142
	P	-0.064	-0.020	-0.002	0.009	0.038	0.022	-0.104	-0.077	0.175	**0.152**	0.000	0.009	0.012	0.014	-0.028	-0.022	0.019	0.134
11	G	0.240	-0.068	-0.080	0.015	-0.002	0.491	-0.589	-0.928	1.422	0.123	**-0.930**	0.774	-0.099	0.012	-0.048	-0.235	0.274	0.372**
	P	0.047	0.064	-0.032	-0.004	-0.008	0.128	-0.701	-0.298	0.698	0.044	**0.001**	0.033	0.258	-0.011	-0.050	0.129	0.045	0.343**
12	G	-0.233	0.053	0.060	-0.007	0.003	-0.480	0.619	0.962	-1.475	-0.109	0.897	**-0.802**	0.100	-0.008	0.052	0.249	-0.213	-0.333**
	P	-0.041	-0.054	0.020	0.003	0.012	-0.126	0.739	0.309	-0.726	-0.039	-0.001	**-0.034**	-0.264	0.007	0.054	-0.137	-0.035	-0.315**
13	G	-0.343	0.044	-0.056	-0.102	0.004	-0.427	0.454	0.649	-0.974	-0.011	0.679	-0.596	**0.135**	-0.025	0.051	0.254	-0.154	-0.418**
	P	-0.057	-0.037	-0.021	0.033	0.014	-0.112	0.544	0.207	-0.479	-0.005	-0.001	-0.025	**-0.360**	0.023	0.053	-0.139	-0.025	-0.389**
14	G	-0.200	0.037	0.200	-0.040	-0.007	-0.005	-0.026	0.134	-0.202	0.058	0.091	-0.055	0.028	**-0.120**	-0.028	0.029	0.006	-0.101
	P	-0.035	-0.034	0.063	0.012	-0.021	-0.002	-0.030	0.042	-0.098	0.020	0.000	-0.002	-0.074	**0.109**	-0.029	-0.016	0.000	-0.096
15	G	0.192	-0.026	0.145	-0.067	-0.007	0.173	-0.282	-0.257	0.403	0.063	-0.254	0.236	-0.039	-0.019	**-0.177**	-0.228	0.227	0.081
	P	0.038	0.032	0.046	0.021	-0.026	0.045	-0.336	-0.081	0.199	0.023	0.000	0.010	0.103	0.017	**-0.186**	0.125	0.038	0.066
16	G	0.549	-0.034	-0.063	0.039	-0.008	0.368	-0.499	-0.639	0.978	-0.042	-0.522	0.476	-0.082	0.008	-0.096	**-0.420**	0.229	0.244*
	P	0.099	0.029	-0.021	-0.012	-0.030	0.096	-0.594	-0.204	0.479	-0.014	0.001	0.020	0.215	-0.008	-0.100	**0.233**	0.037	0.224*
17	G	-0.039	-0.067	-0.310	-0.012	0.009	0.199	-0.193	-0.422	0.652	0.061	-0.359	0.240	-0.029	-0.001	-0.057	-0.136	**0.710**	0.248*
	P	-0.010	0.063	-0.105	0.003	0.036	0.052	-0.230	-0.136	0.320	0.025	0.000	0.010	0.077	0.000	-0.059	0.074	**0.118**	0.237*

** Significant at 1% level of significance * Significant at 5% level of significance; P- Phenotypic path values, G- Genotypic path values

CHARACTERS : 1- Days to 50% flowering, 2- Days to maturity, 3- Pod length (cm), 4- Pod beak length (mm), 5- Pod diameter (mm), 6- Pod wall thickness (mm), 7- Water imbibition by seeds (%), 8- Fresh seed germination (%), 9- Hard seed (%), 10-Water imbibition by pods (%), 11- Pre-harvest sprouting (%), 12- Hard seed (%) in pods, 13- Epicuticular wax content (mg/g dry weight of pod), 14- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at harvest, 15- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at 24 hrs after germination, 16- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at 48 hrs after germination, 17- Alpha amylase activity (mg of maltose released per gram of fresh tissue/minute) at 72 hrs after germination and 18- Correlation with seed yield per plant (g).

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levels. A high positive direct effect in path analysis signifies a strong, positive causal relationship between two variables. This implies that as one variable increases, the other also tends to increase. A positive direct effect of the trait days to 50 % flowering on seed yield indicates that delaying flowering can positively impact seed yield. This could be due to extended vegetative growth, increased biomass accumulation, or improved resource allocation to reproductive structures. Alpha amylase activity at 72 hrs after germination on seed yield indicates that crucial role of alpha amylase in starch degradation, providing energy for seed germination and seedling growth can contribute to increased seed yield. Water imbibition by pods on seed yield suggests that increased water uptake by pods can promote seed development and maturation. This could be due to improved nutrient and water supply to the developing seeds. Similar results with days to 50 % flowering were reported by Srivastava *et al*. (2024). Days to maturity exhibited a high indirect positive effect on seed yield per plant through days to 50 % flowering (0.817), hard seed percentage (0.366), alpha amylase activity at 72 hrs after germination (0.351) and hard seed percentage in pods (0.312) at genotypic level. A positive indirect effect in path analysis indicates that an independent variable positively influences a dependent variable through a mediating variable. While days to maturity doesn't directly influence seed yield, it significantly impacts other traits like days to 50% flowering, hard seed percentage, alpha amylase activity at 72 hrs and hard seed percentage in pods. Earlier flowering can lead to a longer reproductive period, potentially increasing seed set and yield. These traits, in turn, directly affect seed yield. This suggests that by focusing on these mediating traits, breeders can indirectly improve seed yield. Similar results with days to 50 % flowering were reported by Dawane *et al*. (2022) and Gajanan and Lal (2022) at genotypic level.

Days to 50 % flowering exhibited a high indirect positive effect on seed yield per plant through hard seed percentage in pods (0.173) and pod wall thickness (0.169) at genotypic level. The study reveals that days to 50% flowering indirectly influences seed yield by affecting hard seed percentage in pods and pod wall thickness. Earlier flowering can lead to changes in seed development and pod maturation, which can ultimately impact seed yield. This suggests that selecting for earlier flowering can indirectly improve seed yield. Similar results with pod wall thickness at genotypic level were reported by Ahmad and Belwal (2020). Pre-harvest sprouting percentage exhibited a high indirect positive effect on seed yield per plant through hard seed percentage (1.422), hard seed percentage in pods (0.774), pod wall thickness (0.491) and days to 50 % flowering (0.240) at genotypic level. Pre-harvest sprouting, while generally detrimental to seed yield, can surprisingly have a positive indirect effect. It can increase hard seed percentage, leading to better seed viability and protection. Additionally, it can promote thicker pod walls and influence flowering time, both of which can contribute to higher seed yield. Fresh seed germination percentage exhibited a high indirect positive effect on seed yield per plant through hard seed percentage (1.975), hard seed percentage in pods (0.612), pod wall thickness (0.429) and alpha amylase activity at 72 hrs after germination (0.237) at genotypic level. Fresh seed germination, while often associated with higher seed yield, can also indirectly influence yield through other factors. In this case, it positively impacts hard seed percentage, a measure of seed dormancy. A higher hard seed percentage can protect seeds from premature germination and improve their viability. Additionally, fresh seed germination can lead to thicker pod walls, providing better protection for developing seeds. Furthermore, it can stimulate alpha-amylase activity, an enzyme crucial for starch breakdown and energy supply during germination. By influencing these factors, fresh seed germination ultimately contributes to higher seed yield per plant.

The study on the complex relationships between pre-harvest sprouting (PHS) traits and seed yield in greengram revealed some important insights. While the pre-harvest sprouting percentage is positively correlated with seed yield, it can also have negative effects by reducing seed quality, which can lead to yield losses. Similarly, other traits, such as fresh seed germination percentage and alpha-amylase activity measured 72 hrs after germination, show complicated relationships. These traits are positively associated with seed yield but are also positively linked to PHS, which is detrimental to overall yield. Conversely, traits like pod wall thickness, hard seed percentage, hard seed percentage in pods, and epicuticular wax content exhibit significant and negative correlations with both seed yield and PHS. Thicker pod walls, a higher percentage of hard seeds, and more epicuticular wax in greengram are associated with lower seed yields but greater resistance to pre-harvest sprouting. Overall, the results suggest that while PHS traits can enhance seed yield, they also increase susceptibility to pre-harvest sprouting. This indicates that breeding programs should aim to achieve a balance between optimizing seed yield and minimizing the impact of PHS.

The results of this study indicate that hard seed percentage and alpha-amylase activity at 24 hrs after germination and alpha-amylase activity 72 hrs after germination significantly influence seed yield per plant, exhibiting strong genetic variability and heritability. Correlation analysis underscore the multifaceted nature of yield determinants in crops. Future research should consider these relationships to develop integrated breeding programs that optimize traits including maturity duration, flowering time and seed quality to enhance overall yield performance in plant populations. On the other hand, the significant negative association with traits such as epicuticular wax content, pod wall thickness and hard seed percentage indicate challenges that may arise in achieving optimal yields. For instance, a high content

of epicuticular wax may impede seed development or retention, while increased pod wall thickness might limit seed filling. Thus, these traits pose potential barriers to yield improvement and warrant careful consideration during the breeding process. The path analysis reveals that traits such as days to 50% flowering, alpha-amylase activity at 72 hrs after germination and water imbibition by pods have significant direct effects on seed yield per plant, while days to maturity and pre-harvest sprouting percentage exhibit substantial indirect positive influences, underscoring the complex interrelationships among these traits in enhancing seed yield.

REFERENCES

Ahmad, S. and Belwal, V. 2020. Study of correlation and path analysis for yield and yield attributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. *International Journal of Conservation Science*, **8** (1): 2140-2143. [Cross Ref]

Dawane, B.K., Patil, D.K., Gite, V.K., Dawane, J.K. and Kale, D.G. 2022. Character association and path analysis studies on seed yield and its yield attributing traits in green gram (*Vigna radiata* (L.) Wilczek). *The Pharma Innovation Journal*, **11** (12): 2476-2481.

Ebercon, A., Blum, A. and Jordan, W. R. 1977. A rapid colorimetric method for epicuticular wax contest of sorghum leaves. *Crop Science*, **17** (1): 179- 180. [Cross Ref]

Gaikwad, S. A., Gite, V. K., Gavhane, N. A., Patil, D. K. and Girnare, V. B. 2023. Assessment of correlation and path analysis in greengram (*Vigna radiata* (L.) Wilczek). *The Pharma Innovation Journal*, **12** (12): 390-396.

Gajanan, P.S. and Lal, G.M. 2022. Component relationship and genetic variability of seed yield and its contributing traits in greengram [*Vigna radiata* (L.) Wilczek]. *The Pharma Innovation Journal,* **11** (5): 620-626.

Harsh, P. and Priyal, P. 2023. Genetic variability and correlation in greengram [*Vigna radiata* (l.) R. Wilczek]. *Plant Archives,* **23** (2): 144-148. [Cross Ref]

Jadhav, R.A., Mehtre, S.P. and Patil, D.K. 2019. Correlation and path analysis studies on yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *International Journal of Current Microbiology and Applied Sciences*, **8** (7): 699-720. [Cross Ref]

Jayamani, P., Muthiah, A.R., Durairaj, C., Pazhanivelan, S., Kamalakanan, A. and Thiyagarajan, K. 2015. Greengram Co 8 A High Yielding, Short Duration Variety with Synchronized Maturity. *Madras Agricultural Journal*, **102** (apr-jun): 1.

Kumar, G.P., Pallavi, M., Swapna, N., Shahana, F., Reddy, G.E. and Rakesh, G. 2021. Genetic variability and correlation studies for pre-harvest sprouting tolerance and associated traits in soybean [*Glycine max* L. Merrill.]. *Current Journal of Applied Science and Technology,* **40** (4): 1-10. [Cross Ref]

Lamichaney, A., Katiyar, P.K., Laxmi, V. and Pratap, A. 2018. Variation in pre-harvest sprouting tolerance and fresh seed germination in mungbean (*Vigna radiata* L.) genotypes. *Plant genetic resources*, **16** (5): 437-445. [Cross Ref]

Mohammed, R.J., Prasanthi, L., Vemireddy, L.R. and Latha, P. 2020. Studies on genetic variability and character association for yield and its attributes in greengram [*Vigna radiata* (L.) Wilczek]. *Electronic Journal of Plant Breeding*, **11**(2): 392-398

Muthuswamy, A., Jayamani, P. and Kumaresan, D. 2022. Genetic variability studies for yield related traits in greengram [*Vigna radiata* (L.) Wilczek]. *The Pharma Innovation Journal,* **11** (5): 1310-1313.

Payasi, D.K. 2015. Genetic variability analysis for seed yield and its components in mungbean (*Vigna radiata* L. Wilczek). *International Journal of Plant Breeding and Genetics*, **9** (3): 177-188. [Cross Ref]

Rao, V.T., Rao, P. J. M. and Reddy, P.R. 2016. Evaluation of genotypes for preharvest sprouting in mungbean (*Vigna radiata* L. Wilczek). *Progressive Research*, **11** (1): 485-486.

Rathi, S., Nathsarma, R. and Singhyadav, R. 2013. Variation in seed dormancy and α-amylase activity in Indian rice (*Oryza sativa*) accessions. *The Indian Journal of Agricultural Sciences,* **83** (1): 56–62.

Rigatti, A., Meira, D., Olivoto, T., Meier, C., Nardino, M., Lunkes, A., Klein, L.A., Fassini, F., Moro, É.D., Marchioro, V.S. and Souza, V.Q.D. 2019. Grain yield and its associations with pre-harvest sprouting in wheat. *Journal of Agricultural Science*, **11** (4): 142-150. [Cross Ref]

Salman, M. A. S., Anuradha, C., Sridhar, V., Babu, E. R. and Pushpavalli, S. N. C. V. L. 2023. Genetic variability for yield and its related traits in green gram [*Vigna radiata* (L.) Wilczek]. *Legume Research-An International Journal*, **46** (6): 700-704.

Sandhiya, V. and Shanmugavel, S. 2018. Genetic variability and correlation studies in greengram (*Vigna radiata* [L.] Wilczek). *Electronic Journal of Plant Breeding*, **9** (3): 1094-1099. [Cross Ref]

Srivastava, M., Manojkumar, H. G. and Singh, A. 2024. Assessment of correlation and path analysis for seed yield and its component characters in greengram [*Vigna radiata* (L.) Wilczek]. *International Journal of Plant and Soil Science*, **36** (5): 402-411. [Cross Ref]

Thonta, R. 2023. Analysis of genetic variability, heritability and genetic advance for growth and yield attributes in green gram (*Vigna radiata* L. Wilczek). *International Journal of Statistics and Applied Mathematics*, **8** (3): 43-47. [Cross Ref]

Verma, J., Gore, P.G., Kumari, J., Wankhede, D.P., Jacob, S.R., Thirumani Venkatesh, A.K., Nair, R.M and Tripathi, K. 2024. Exploring genetic diversity in black gram (*Vigna mungo* (L.) Hepper) for pre-harvest sprouting tolerance. *Agronomy,* **14** (1): 197-213. [Cross Ref]

Vetch, J. M., Stougaard, R. N., Martin, J. M. and Giroux, M. 2019. Allelic impacts of TaPHS1, TaMKK3, and Vp1B3 on preharvest sprouting of northern great plains winter wheats. *Crop Science*, **59** (1): 140-150. [Cross Ref]

Yoseph, T., Mekbib, F., Fenta, B. A. and Tadele, Z. 2022. Genetic variability, heritability, and genetic advance in mungbean [*Vigna radiata* (L.) Wilczek] genotypes. *Ethiopian Journal of Crop Science,* **9** (2): 113-135.