International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

Crossref

IJBSM May 2025, 16(5): 01-08

Article AR6054

Research Article

Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2025.6054

Genetic Variability and Association Analysis Between Yield and Yield-related Traits in Greengram (*Vigna radiata* (L.) Wilczek)

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0009-0007-3522-1726

ABSTRACT

The experiment was conducted during *rabi* season (November, 2023–February, 2024) at the Regional Agricultural Research Station (RARS), Lam, Guntur, Andhra Pradesh, India to study the genetic variability, heritability, genetic advance, and correlations between plant yield and quantitative traits by evaluating eighty-three greengram genotypes following an augmented complete randomized block design. All studied traits showed significant variability through the analysis of variance (ANOVA) and most of the traits showed a near-normal distribution in their mean phenotypic distribution. The study found that the pods plant^{-1} exhibited the highest variability, while test weight and seeds pod^{-1} showed the least variability. Pods plant^{-1} displayed a high range of values for genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). In contrast, low GCV and PCV values were observed for the trait's days to 50% flowering and days to maturity. Heritability ranged from 74.23% for seeds pod^{-1} to 99.72% for pods plant^{-1}. Broad sense heritability estimates and GAM were high for all the characteristics, except for the trait days to maturity. This suggested the predominant influence of additive gene action on these traits, making them suitable for selection-based improvements. Through correlation studies, the traits clusters plant^{-1}, pods plant^{-1}, and seeds pod^{-1} obtained a strong significant positive association with seed yield plant^{-1}. These traits are effective for direct selection in crop improvement. Overall, yield and yield-attributing traits exhibited significant variations and high heritability, indicating their potential for enhancing greengram.

KEYWORDS: Greengram, augmented RCBD, PCV, GCV, and heritability

Citation* (VANCOUVER)*: Mokshith et al., Genetic Variability and Association Analysis Between Yield and Yield-Related Traits in Greengram (*Vigna radiata* (L.) Wilczek). *International Journal of Bio-resource and Stress Management,* 2025; 16(4), 01-08. HTTPS://DOI.ORG/10.23910/1.2025.6054.

RECEIVED on 01st January 2025 RECEIVED in revised form on 17th April 2025 ACCEPTED in final form on 02nd May 2025 PUBLISHED on 06th May 2025

1. INTRODUCTION

Vigna radiata (L.) Wilczek commonly known as greengram or mungbean, leguminous crop of subgenus *Ceratotropis* (2n=2x=22). It is a short-duration, cleistogamous, self-pollinating, diploid grain legume and belongs to the family *Leguminaceae* (Kanavi et al., 2023). In India, greengram is considered as 3rd most important pulse crop after chickpea and pigeon pea (Sridhar et al., 2022). The word "Pulse" originated from the Latin word "Puls" which means pottage referring to seeds boiled to make porridge or thick soup (Kanavi et al., 2020). The crop is suitable to cultivate under various cropping systems due to its early maturity (within 60–75 days), and tolerance to heat and drought stress (Patil et al., 2021 and Nayak et al., 2022). Known as poor man's meat (Sudhakaran and Bukkan, 2021, Goud et al., 2022 and Kumar et al., 2023) as nearly, 60–70% of carbohydrates and 20–25% of proteins are supplied through various sources of greengram (Nair and Schreinemachers, 2020) and it provides amino acids such as arginine, histidine, lysine, tryptophan, etc (Jayamani et al., 2015 and Chakraborty et al., 2021). It is also rich in total dietary fibre (16.3 g 100 g^{-1}), iron (6.74 mg 100 g^{-1}), zinc (2.68 mg g^{-1}), calcium (132 mg g^{-1}), magnesium (189 mg g^{-1}), phosphorus (367 mg g^{-1}) and potassium (1246 mg g^{-1}) (Sineka et al., 2021). Greengram is said to be involved in soil fertility restoration through atmospheric nitrogen (N_2) fixation by forming a symbiotic connection with Rhizobium species in the soil (Wanga et al., 2017 and Kaur et al., 2021). In Andhra Pradesh, annual production was 5 thousand tonnes from 2.71 thousand hectares, with an average productivity of 541 kg ha^{-1} (Anonymous, 2024). Greengram contributes nearly 16% of the total pulse area in India and is involved in about 11% of the total pulse production.

The greengram breeding program involves generation of genetic material, selecting superior genotypes from available variable genetic sources, and developing superior varieties. There is now a greater focus on enhancing the productivity and overall production of pulses (Sathyamoorthi et al., 2023). The lack of genetic variability for high-yield potential is one of the major constraints for greengram production (Sandhiya and Saravanan, 2018). This is due to numerous limitations, such as a lack of exploitable genetic variability, the effect of biotic and abiotic stresses, the unavailability of superior varieties (Mahla et al., 2024), and absence of suitable ideotype for different cropping systems (Chippy et al., 2021). Genetic diversity among the genotypes is an important asset for any plant breeding program (Kanavi et al., 2020). Understanding the existing genetic variability in a population along with parameters like heritability and genetic advance is crucial for conducting an effective and efficient breeding program (Dey et al., 2021; Tolwani and Shukla, 2022). Analyzing various parameters of genetic variability will help in enhancing the success of a breeding program (Devi et al., 2022). Selecting lines having good good combining ability as parents and crossing them followed by appropriate selection in segregating generations of self-pollinated crops like greengram can lead to development of improved varieties (Patel et al., 2021). Correlation measures the degree and direction of association among variables (dependent and independent). Association analysis evaluates the mutual relationship between various plant traits and determines characters on which selection can be based for breeding programs (Shoba et al., 2018 and Mohammed et al., 2020). Hence, considering the points mentioned above, the current study was planned and carried out to evaluate different greengram genotypes to characterize the genetic variability, estimate heritability, and genetic advancement, and study the correlation among yield and related traits.

2. MATERIALS AND METHODS

The experiment was conducted during *rabi* season (November, 2023–February, 2024) at the Regional Agricultural Research Station (RARS), Lam, Guntur (31.5 meters above mean sea level, 16.18 N and 80.29 E), Andhra Pradesh, India. The seed material used in the study consisted of 83 diverse greengram genotypes obtained from AICRP on Kharif Pulses center, RARS, Lam comprising genotypes procured from different research institutions/stations representing different agro-climatic zones of India. Each genotype was sown in 2 rows of 4 meters in length with following a spacing of 30×10 cm^2 each genotype was sown in 2 rows each of 4 meters in an augmented randomized block design. Plant protection measures and intercultural operations were done at regular intervals during crop growth.

Data on the required traits viz., days to 50% flowering, days to maturity, clusters $plant^{-1}$, pods $plant^{-1}$, seeds pod^{-1}, seed yield $plant^{-1}$ (g), and test weight i.e. 100 seed weight (g) was recorded on five randomly selected plants from each genotype. Statistical analysis was performed based on the mean values of five plants' data. The analysis of variance, parameters related to genetic variability viz., GCV, PCV, heritability, and GAM, was conducted using 'augmented RCBD' R package, and correlation analysis was performed by the "corr_plot" function through 'metan' package in R studio statistics software (Anonymous, 2020).

3. RESULTS AND DISCUSSION

3.1. *Analysis of variance*

The ANOVA results for the studied traits are presented in Table 1 which revealed highly significant differences for all the characters. The mean square attributable to 'Genotypes

Table 1: Analysis of variance for yield and yield related traits in 83 greengram genotypes

Source	Df	DFF	DM	CP	PP	SP	TW (g)	SYP (g)
Treatment (Ignoring Blocks)	82	17.78**	55.77**	6.56**	47.91**	3.09**	0.47**	1.95**
Treatment, check	2	74.62**	615.13**	36.81**	30.09**	17.04**	2.48**	3.55**
Treatment, test	79	16.53**	39.98**	5.64**	47.67**	2.63**	0.43**	1.68**
Treatment, test vs. check	1	2.95**	184.64**	18.63**	102.39**	11.84**	0.03^{ns}	19.76**
Block (Eliminating treatments)	7	0.04^{ns}	0.95^{ns}	0.32^{ns}	0.14^{ns}	0.06^{ns}	0.09^{ns}	0.04^{ns}
Residuals	14	0.29	1.84	0.33	0.14	0.68	0.09	0.17

ns $p>0.05$, $^{*}p<0.05$, $^{**}p<0.01$ and $^{***}p<0.001$; Df: Degree of freedom; DFF: Days to 50% flowering; DM: Days to maturity; CP: Clusters plant^{-1}, PP: Pods plant^{-1}, SP: Seeds pod^{-1}; TW: Test weight (g); SYP: Seed yield plant^{-1} (g)

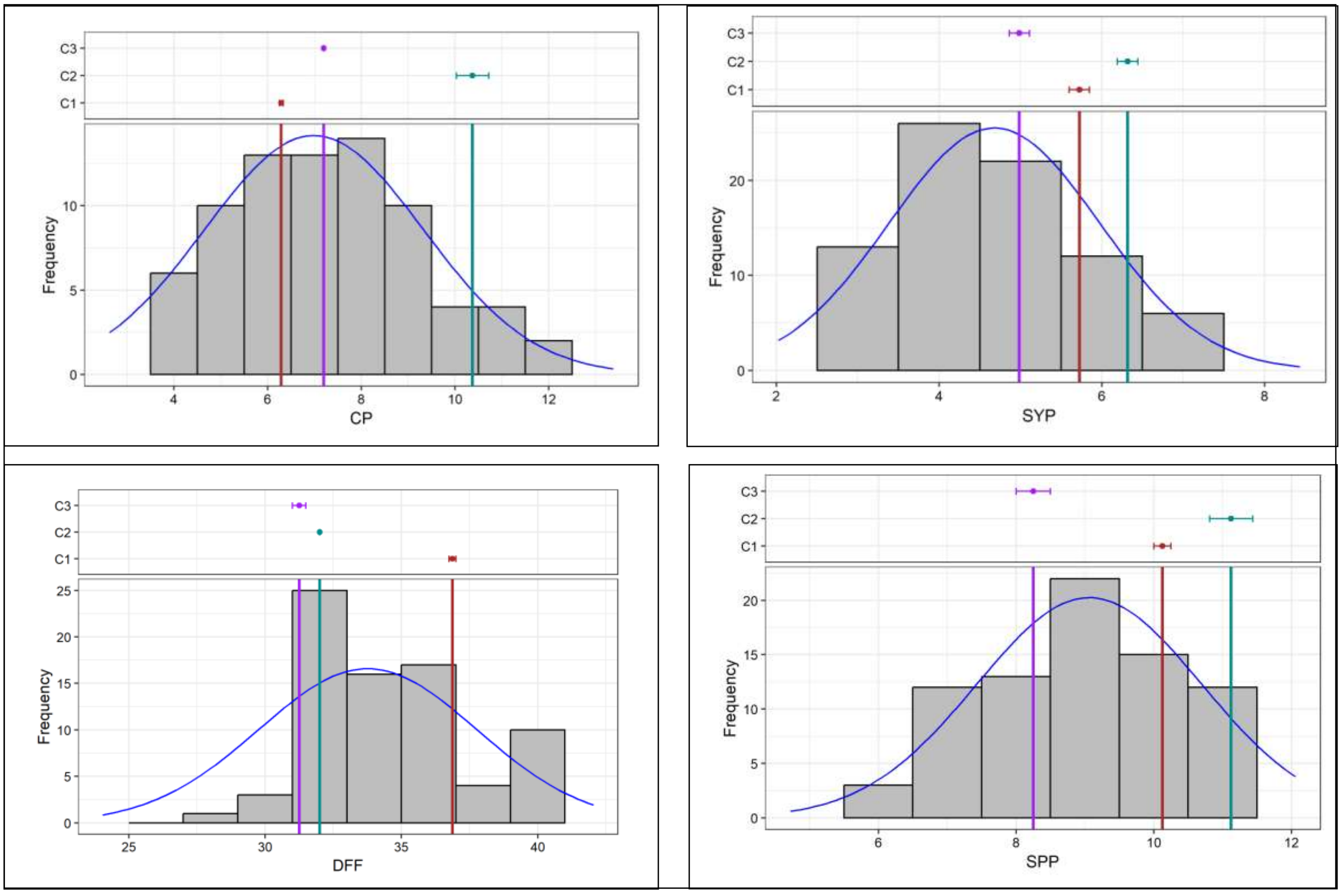
vs check' entries was found to be significant for all the traits except test weight.

3.2. *Descriptive statistics of the studied traits*

A normal distribution curve with a wide range of phenotypic data was observed for most of the traits (Figure 1). Days to 50% flowering varied from 24.00 days to 40.00 days with a mean of 33.27 days. Days to maturity varied from 53.00 days to 79.00 days with a mean of 66.07 days. Clusters plant^{-1} ranged from 3.00 to 14.00, with an average value of 8.00. Pods plant^{-1} varied from 5.00 to 35.00, with a mean value of 19.00. The number of seeds pod^{-1} ranged from 7.00 to 12.00, with an average value of 10.00. The minimum and maximum values for the trait "test weight" were 2.65 g and 4.68 g, with a mean value of 3.49 g. Seed yield plant^{-1} ranged from 1.07 g to 9.05 g, with a mean value of 4.58 g.

3.3. *Phenotypic and genotypic coefficient of variation*

The estimation of coefficients of variability, heritability, and genetic advance for the traits studied are depicted in Table 2. In the study, the PCV values of all traits were higher than the GCV values. Denoting the influence of both genotype and environment factors for variation. This finding was in support of the studies conducted by Raturi et al. (2015),



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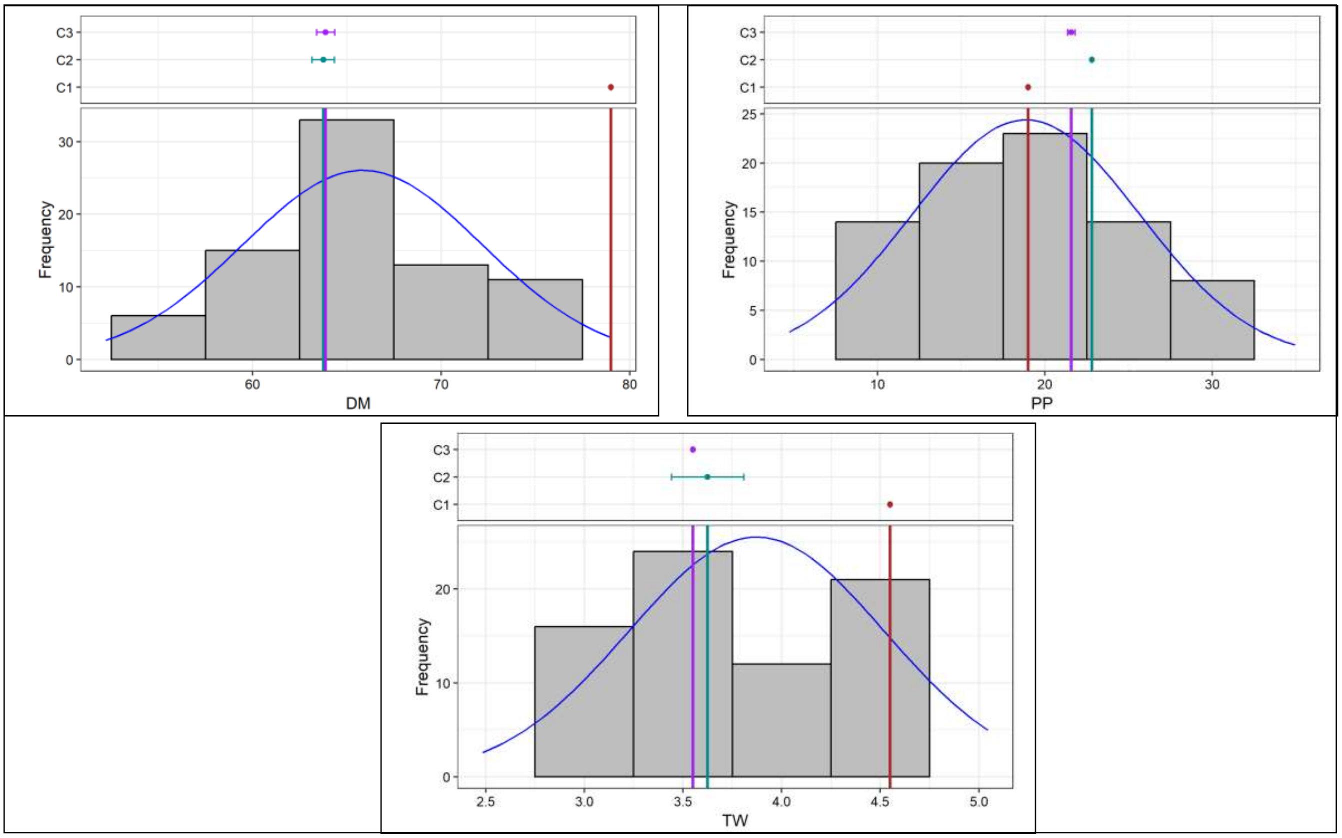

Figure 1: Estimation of frequency distribution; DFF: Days to 50% flowering; DM: Days to maturity; CP: Clusters plant^{-1}; PP: Pods plant^{-1}; SPP: Seeds pod^{-1}; TW: Test weight (g); SYP: Seed yield plant^{-1} (g)

Table 2: Measures of variability parameters in 83 greengram genotypes for traits in the study

Component	DFF	DM	CP	PP	SP	TW	SYP
CV	1.6	2.04	7.95	1.9	8.92	7.7	8.36
CD	1.42	3.56	1.5	0.97	2.16	0.78	1.07
Count	83	83	83	83	83	83	83
Mean	33.27	66.07	8	19	10	3.49	4.58
Std. error	0.44	0.7	0.26	0.74	0.18	0.07	0.14
Std. deviation	3.99	6.36	2.34	6.79	1.63	0.65	1.3
Min	24	53	3	5	7	2.65	1.07
Max	40	79	14	35	12	4.68	9.05
Skewness	-0.31	0.11	0.3	0.23	: 0.14	0.04	0.47
Kurtosis	3.44	2.67	2.83	2.44	2.48	1.88	3.09
GCV (%)	11.94	9.38	33	36.57	15.41	15.03	26.29
PCV (%)	12.04	9.61	34	36.62	17.88	16.9	27.7
H^2bs (%)	98.24	95.4	94.22	99.72	74.23	79.15	90.08
GA (%)	8.24	12.44	4.62	14.2	2.48	1.07	2.41
GAM (%)	24.41	18.9	66.08	75.33	27.39	27.59	51.48

DFF: Days to 50% flowering; DM: Days to maturity; CP: Clusters plant^{-1}; PP: Pods plant^{-1}; SP: Seeds pod^{-1}; TW: Test weight (g); SYP: Seed yield plant^{-1} (g); GCV: Genotypic coefficient variation; PCV: Phenotypic Coefficient Variation; H^2bs: Heritability in a Broad Sense; GA: Genetic advance; GAM: Genetic advance mean

Hemavathy et al. (2015), Anand et al. (2015), Sandhiya and Saravanan (2018), Salman et al. (2023) in greengram. GCV ranged from 9.38% (days to maturity) to 36.57% (pods plant^{-1}). Pods plant^{-1} (36.52% and 36.57%), clusters plant^{-1} (34% and 33%), and seed yield plant^{-1} (27.70% and 26.29%) exhibited high PCV and GCV values. Similar values of high PCV and GCV were revealed for the trait's pods plant^{-1} and seed yield plant^{-1} in studies done by Raturi et al. (2015), Anand et al. (2016), Parimala et al. (2020), Nayak et al. (2022), Salman et al. (2023), Jain et al. (2024). Seeds pod^{-1} (17.88% and 15.41%), test weight (16.90% and 15.03%), and days to 50% flowering (12.04% and 11.94%) exhibited moderate PCV and GCV denoting that these are under influenced by additive gene action. Kumhar and Choudhary (2007), Kanavi et al. (2023) and Jain et al. (2024) also reported similar results for the traits test weight, seeds pod^{-1}, and days to 50% flowering respectively. Days to maturity (9.61% and 9.38%) recorded low values of PCV and GCV. These results i.e lower PCV and GCV values are in correspondence with Perera et al. (2017), Kanavi et al. (2023), and Thonta (2023) with values of 3.75% and 2.79%, 8.84% and 8.74%, 1.83% and 1.63%. The findings pertaining to PCV and GCV indicate a significant potential for further enhancement. Through careful selection of these traits and the development of high-yielding varieties, substantial progress can be achieved.

3.4. Heritability broad sense and genetic advance as % of mean

The heritability broad sense (h^{2}) ranged from 74.23% (seeds pod^{-1}) to 99.72% (pods plant^{-1}). High heritability values combined with high genetic advance as a % of mean (GAM) were observed for maximum number of the traits. Heritability values, along with genetic advance as a % of the mean (GAM), would be more useful in performing selection procedures during breeding programs (Jain et al., 2024). Broad sense heritability estimates and GAM were high for all the characteristics, except for the trait days to maturity in the present study (Figure 2). Therefore, selecting for the characteristics will be rewarding, as these were environmentally less influenced. Similar high broad sense heritability and GAM results was given for the traits clusters plant^{-1}, pods plant^{-1}, and seed yield plant^{-1} in studies conducted by Kanavi et al. (2023), Salman et al. (2023), and Mahla et al. (2024).

3.5. Correlation studies

Analysing the relationships among various traits is important for performing the most efficient selection (Korat et al., 2010). Pearson correlation is a statistical method commonly utilized for analyzing these relations. Out of 6 independent variables studied, 3 traits viz., pods plant^{-1} (0.81***), clusters plant^{-1} (0.64**), and seeds pod^{-1} (0.28*) exhibited a positive and significant association with the trait seed yield plant^{-1}, which is considered as dependent variable (Table 3). A similar association was reported by Srivastava et al. (2024), Harsh and Priyal (2023), Singh et al. (2022) except for the trait seeds pod^{-1}. A significant and positive correlation was observed between days to 50% flowering and days to maturity (0.99***), which was also reported by Harsh and Priyal (2023). Whereas, a non-significant

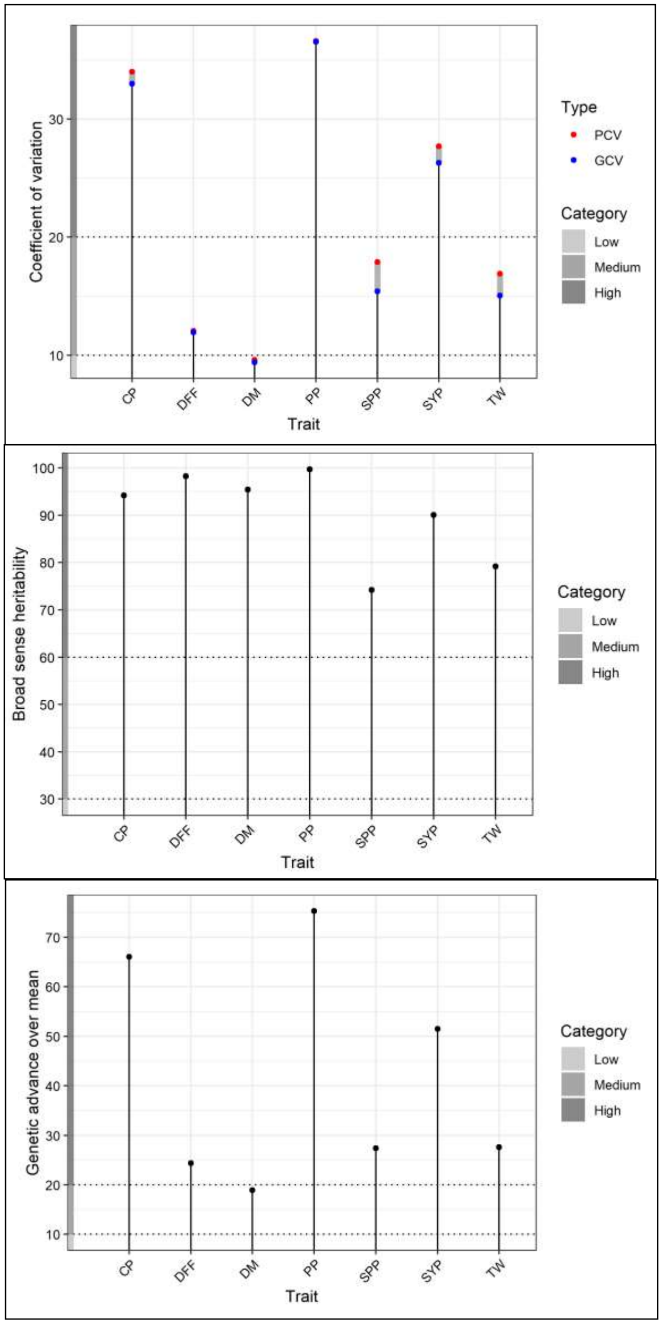

Figure 2: Estimation of variability coefficients, heritability and genetic advance as per mean (GAM); DFF: Days to 50% flowering; DM: Days to maturity; CP: Clusters plant^{-1}, PP: Pods plant^{-1}; SPP: Seeds pod^{-1}, TW: Test weight (g); SYP: Seed yield plant^{-1}

Table 3: Correlation among yield and yield attributing traits

	DFF	DM	CP	PP	SP	TW (g)	SYP (g)
DFF	1	0.98994^{***}	0.0462	-0.0438	0.00764	-0.1751	-0.0499
DM		1	0.0353	-0.0436	0.00118	-0.164	-0.0323
CP			1	0.8163^{***}	0.14513	-0.3443^{**}	0.6423^{***}
PP				1	0.30541^{**}	-0.2696^{*}	0.8148^{***}
SP					1	-0.3709^{***}	0.2812^{*}
TW (g)						1	-0.0986
SYP (g)							1

ns $p>0.05$, $^{*}p<0.05$, $^{**}p<0.01$ and $^{***}p<0.001$; DFF: Days to 50% flowering; DM: Days to maturity; CP: Clusters plant^{-1}; PP: Pods plant^{-1}, SP-Seeds pod^{-1}; TW: Test weight (g); SYP: Seed yield plant^{-1} (g)

relation was observed between the days to maturity and all the other yield-related characters. Test weight exhibited a significant negative association with pods plant^{-1} (-0.27^{*}), clusters plant^{-1} (-0.34^{**}), and seeds pod^{-1} (-0.37^{***}). A positive association was recorded among the trait's pods plant $^{-1}$ and seeds pod^{-1} (0.31^{**}), and clusters plant^{-1} (0.82^{***}). A positive association with non-significance was reported among seeds pod^{-1} by Singh et al. (2022).

4. CONCLUSION

A significant difference was observed for all the characteristics among the 83 genotypes, suggesting the presence of considerable variation among them. A significant positive association was revealed between seed yield plant^{-1} and the traits clusters plant^{-1}, pods cluster^{-1}, and seeds pod^{-1}. Selecting these traits indirectly contributes to the enhancement of seed yield plant^{-1}.

5. ACKNOWLEDGMENT

The authors are sincerely thankful to the RARS, Lam, Guntur, Andhra Pradesh for providing the germplasm resources and the opportunity to carry out this research.

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