



The Effect of Genetic Variation and Trait Association in Cowpea [*Vigna unguiculata* (L.) Walp]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/ijpss/2025/v37i85643>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/140777>

Original Research Article

Received: 12/05/2025

Accepted: 24/07/2025

Published: 02/08/2025

ABSTRACT

A field experiment was conducted for estimate the genetic variability and trait association for yield and yield attributing characters among eighteen genotypes of cowpea [*Vigna unguiculata* (L.) Walp] in a Randomized Complete Block Design (RCBD) with three replications at Research Farm, College of Agriculture, Fatehpur-Shekhawati, Sikar during *kharif* 2024. The analysis of variance in

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Cite as: Seemar, Mahendra Kumar, Champa Lal Khatik, Kailash Chandra, and Mujahid Khan. 2025. "The Effect of Genetic Variation and Trait Association in Cowpea [*Vigna Unguiculata* (L.) Walp]". *International Journal of Plant & Soil Science* 37 (8):414-22. <https://doi.org/10.9734/ijpss/2025/v37i85643>.

genotypes for all the character revealed the significant genetic variability. The high magnitudes of phenotypic coefficient of variance (PCV) were observed for characters like plant height and pods per cluster. While, moderate magnitude of genotypic coefficient of variance (GCV) were observed plant height, branches per plant, pods per plant, pods per cluster and 100-seed weight. The high heritability was estimated for plant height, 100-seed weight and pods per cluster. The high genetic advance was estimated for plant height, 100-seed weight and pods per cluster. Trait association estimate of grain yield per plant had significant and positive association with plant height, branches per plant, clusters per plant, pods per cluster and pods per plant at genotypic level and branches per plant, pods per cluster and seed per pod at phenotypic levels.

Keywords: Genetic variability; correlation; phenotypic coefficient of variance (PCV); genotypic coefficient of variance (GCV); heritability.

1. INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important legume crop and forms an important component of farming systems throughout the tropics and warm sub-tropics. Cowpea is a self-pollinated crop and belongs to the family Fabaceae and genus *Vigna* with chromosome number, $2n = 22$. Cowpea cultivars grown for grain, green pods and fodder which is used as vegetable are known as snake bean and yard-long bean. This crop is recognized for its drought tolerance; its wide and droopy leaves keep soil and soil moisture conserved due to shading effect. It is also called as southern pea and black-eyed pea and has multiple uses like; food, feed, fodder, green manuring and vegetable. Cowpea seed is a nutritious component in the human diet and cheap livestock feed.

It is native to Africa and is an important legume crop in eastern, southern, central and western Africa. According to (Vavilov, 1951), Africa and India are the centre of origin/native of cowpea. The secondary centre of origin of cowpea is considered China. The semi-arid tropical region depends heavily on the cowpea crop because of its resistance to drought and capacity to grow in poor soils. As a result, it becomes "the crop of choice" for the arid region (Manisha et al., 2018).

The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance are key biometrical parameters used to evaluate genetic variability within a germplasm collection Sharma et al., (2017). "Assessment and utilization of existing genetic variability among genotype acts as a major raw material for plant breeders in exercising effective selection for evolving new

and superior genotypes. So, a proper thorough understanding and adequate evaluation of genotype under a particular environment for different yield attributing traits is a prerequisite for improving productivity and identifying superior donors as well as developing better performing varieties with desirable traits in any crop breeding programmers" (Abha & Meena, 2024).

Correlation analysis provides insights into the nature and strength of the association between two or more quantitative traits Singh et al. (2022). "It measures the mutual relationship between yield and its contributing traits, thereby assisting in the selection of better performance genotypes from a diverse genetic population. The correlation coefficient between a pair of characters is either positive or negative and it may be high or low. Estimating correlation coefficients among yield contributing variables is crucial for understanding the direction of selection and accelerating yield improvement efficiently. Thus, correlation play important role in the selection of superior genotype from divers genetic populations" (Jogdhande et al., 2017).

2. MATERIALS AND METHODS

2.1 Experimental Site

The experiment was conducted during *kharif*, 2024 at Research farm of College of Agriculture, (Sri Karan Narendra Agriculture University, Jobner) Fatehpur- Shekhawati, Sikar (Rajasthan). It is situated between 27° 04.01' N to 27° 55' 43.59" N latitude and 74° 58' 47.47" E to 74° 59' 45.97" E longitude with an altitude of 321 to 330 meters above mean sea level.

List 1. Details of genotypes and checks used in experiment

Genotypes					Checks
1.CPD-229	4.CPD-273	7.CPD-307	10.IC-0650821	13. CF4-1-4	16.RC-19(C)
2.CPD-260	5.CPD-302	8.CPD-317	11. CF1-1-1	14. CF9-1-9	17.RC-101(C)
3.CPD-269	6.CPD-305	9.CPD-330	12.CF2-1-2	15. CF10-1-10	18. TC-901(C)

Source: - Department of Genetics and Plant Breeding, ARS, Fatehpur-Shekhawati, Sikar

2.2 Experimental Details

The experiment was conducted fifteen genotypes with three checks in RCB Design of cowpea crop for estimate genetic variability and correlation analysis. Each genotype was sown in 4 m length with four rows per plot. The spacing use in cowpea is 30 X 10 cm². The observation was recorded five randomly selected plant for plant height (PH), branches per plant (BP), pods per cluster (PC), pod per plant (PP), pod length (PL), seeds per pod (SP), 100-seed weight (SW) and grain yield per plant (GY) except days to 50 % flowering (DFF) and days to maturity (DM).

2.3 Statistical Analysis

The ANOVA for Randomized Complete Block Design of experiment were carried out using the method suggested by Panse and Sukhatme (1985). The Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated using the standard formulas proposed by Burton and Devane (1953). Heritability in broad sense that the genetic advance percent mean was calculated by using the formula given by Johnson *et al.*, (1955). The correlation among the various characters of genotypic and phenotypic correlation coefficients was worked out by

assuming the method described by Singh and Chaudhary (1985).

3. RESULTS AND DISCUSSION**3.1 Analysis of Variance (ANOVA)**

The ANOVA was highly significant for all traits these are presented in Table 1. Analysis of variance for the experiment involving a set of 18 genotypes of cowpea for 10 character namely days to 50 % flowering, days to maturity, plant height, branches per plant, pods per cluster, pods per plant, pod length, seed per pods, 100-seed weight and grain yield per plant revealed than mean sum of square were highly significant all characters indicating the presence of considerable genetic variation in the experiment source. The significant variation for grain yield and its related traits in cowpea were also observed earlier workers like Singh *et al.* (2022), Hulsure *et al.* (2022) and Kiran *et al.* (2020).

3.2 Genetic Variability

The various quantitative characters were studied in cowpea genotypes for evaluating genetic variability parameters such as phenotypic coefficient of variance.

Table 1. Analysis of variance for various characters of cowpea genotypes

Characters	Mean Sum of Square (MSS)		
	Replication (2df)	Genotypes (17df)	Error(34df)
DFF	1.351	43.668**	20.116
DM	1.500	32.990**	16.460
PH (cm)	4.062	246.562**	5.347
BP	0.091	2.739**	0.688
PP	4.846	19.370**	4.913
PC	0.375	0.667**	0.117
PL (cm)	2.969	5.356**	2.473
SP	0.216	4.319**	2.040
SW (g)	0.361	3.466**	0.260
GY (g)	0.828	4.100**	2.0516

*, ** Significant at 5% and 1% level of significance, respectively

Table 2. Estimate mean, range, phenotypic and genotypic coefficient of variance, heritability and genetic advance of different characters of cowpea

Characters	Mean	Range	PCV	GCV	Heritability (%)	Genetic advance
DFF	47.41	42.67 - 54.67	11.16	5.91	28.10	6.45
DM	65.17	58.67 - 70.00	7.19	3.60	25.10	3.71
PH (cm)	45.19	35.81 - 59.75	20.49	19.84	93.80	39.57
BP	7.27	5.47 - 9.53	16.11	11.37	49.80	16.53
PP	18.64	13.27 - 21.80	16.73	11.77	49.50	17.06
PC	2.71	2.13 - 4.00	20.24	15.79	60.90	25.37
PL (cm)	13.4	10.47 - 15.87	13.83	7.31	28.00	7.97
SP	11.89	9.27 - 13.93	14.08	7.33	27.10	7.86
SW (g)	9.07	7.77 - 11.50	12.71	11.39	80.40	21.04
GY (g)	12.47	10.07 - 14.00	13.27	6.62	25.00	6.82

Genotypic coefficient of variance, heritability and genetic advance as percent mean and details are presented in the Table 2. The overall magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variance for all the characters.

3.2.1 Phenotypic and genotypic coefficient of variance

High PCV were recorded for plant height (20.49%) and pods per cluster (20.24%). Moderate PCV was observed for pods per plant (16.73%), branches per plant (16.11%), pods per plant (14.08%), pod length (13.83%), grain yield per plant (13.27%), 100-seed weight (12.71%) and days to 50 % flowering (11.16%). However, low value of PCV were noted for days to maturity (7.19%), indicating low variability for this character. Moderate GCV was recorded for plant height (19.84%) pods per cluster (15.79%) pods per plant (11.77%), 100-seed weight (11.39%) and branches per plant (11.37%). Low GCV was observed for pods per plant (7.33%), pod length (7.31%), grain yield per plant (6.62%), days to 50 % flowering (5.91%) and days to maturity (3.60%) indicating low variability for this character. Similar result was found by Koraddi and Basavaraja (2019) reported high PCV values for plant height, Gowsalya *et al.*, (2016) for pods per clusters. The high PCV and GCV suggest the scope for direct selection for these traits. Similar findings were delineated by Singh *et al.*, (2020) for clusters per plant, moderate GCV were observed for grain yield per plant which implies negligible influence of environment on these traits. Similar results were obtained by Singh *et al.* (2020) Moderate GCV was recorded for plant height and 100-seed weight. This specifies the presence of variations, such that these traits can be improved as the external environment effect is considerably low.

Dinesh *et al.*, (2017) reported similar results for plant height and Sharma *et al.*, (2017) for test weight. Moderate PCV and low GCV were noticed for pod length which indicates the more significant influence of the environment on these traits, and the results were similar to the findings of Hulsure *et al.*, (2022). The low magnitude of PCV and GCV were noticed for days to 50% flowering and days to maturity. Low estimates of GCV and PCV implies that the selection based on these traits would not be appropriate in a crop improvement program. Similar results were reported by Sharma *et al.*, (2017). The PCV values were greater than the GCV values for all characters examined in the current experiment. These conclusions mostly matched those of the studies by and Shanko *et al.* (2014), Khan *et al.* (2015), Dinesh *et al.* (2017), Sabale *et al.* (2018).

3.2.2 Heritability and genetic advance

High heritability was observed for plant height (93.80%), 100-seed weight (80.40%) and pods per cluster (60.90%). Moderate heritability was recorded for the character viz., branches per plant (49.80%) and pods per plant (49.50%). Low heritability was observed days to 50% flowering (28.10%), pod length (28%), seed per pods (27.10%), days to maturity (25.10%) and grain yield per plant (25%). The high genetic advance expressed as percentage of mean is used to relate genetic advance for many traits. In the present study, the high value of genetic advance as percentage of mean was observed for plant height (39.57%), pods per cluster (25.37%) and 100-seed weight (21.04%). Moderate genetic advance percentage of mean was registered pods per plant (17.06%), branches per plant (16.53%). However, low genetic advance percent of mean pod length (7.97%), seeds per pod (7.86), grain yield per plant (6.82%), days to 50% flowering (6.45%) and days to maturity (3.17%).

Table 3. Estimation of genotypic correlation coefficient of different characters of cowpea

Characters	DFF	DM	PH (cm)	BP	PP	PC	PL (cm)	SP	SW (g)	GY (g)
DFF	1	0.905**	-0.162	-0.307*	-0.027	-0.366**	0.510**	-0.033	-0.161	-0.330*
DM		1	0.447**	0.013	-0.117	-0.306*	0.556**	-0.591**	0.986**	-0.109
PH (cm)			1	-0.181	-0.174	-0.160	0.423**	-0.088	0.463**	0.465**
BP				1	0.448**	0.561**	-0.702**	0.052	-0.157	0.726**
PP					1	0.660**	-0.175	0.215	-0.359**	0.359**
PC						1	-0.565**	-0.083	-0.301*	0.451**
PL (cm)							1	0.470**	0.443**	-0.261
SP								1	0.030	0.442**
SW (g)									1	0.177
GY (g)										1

*, ** Significant at 5% and 1% level of significance, respectively

Table 4. Estimation of phenotypic correlation coefficient of different characters of cowpea

Characters	DFF	DM	PH (cm)	BP	PP	PC	PL (cm)	SP	SW (g)	GY (g)
DFF	1	0.064	-0.049	-0.019	0.012	-0.091	-0.031	-0.170	-0.058	0.198
DM		1	0.258	-0.117	-0.107	-0.197	0.146	-0.136	0.382**	-0.092
PH (cm)			1	-0.098	-0.080	-0.085	0.242	-0.025	0.404**	0.215
BP				1	0.260	0.316*	-0.159	0.053	-0.040	0.338*
PP					1	0.371**	-0.066	0.191	-0.243	0.147
PC						1	-0.024	0.188	-0.280*	0.286*
PL (cm)							1	0.582**	0.216	-0.019
SP								1	-0.108	0.276*
SW (g)									1	-0.019
GY (g)										1

*, ** Significant at 5% and 1% level of significance, respectively

Similar result was found for the high genetic advance as of per cent mean values, the result is in accordance with Shanko *et al.* (2014), Patel *et al.* (2016), Chaudhary *et al.* (2020). High GAM values for plant height were also observed by Patel *et al.* (2016) and showed high heritability coupled with high genetic advance as per cent has been noticed in the parameters like plant height and hundred 100-seed weight. Meena *et al.* (2015) showed high estimates of heritability along with high genetic advance as per cent of mean for the characters 100-seed weight and plant height. Other character was showing low heritability were found similar result Dinesh *et al.* (2017), Gogoi *et al.*, (2024), Deeksha and Krishna (2024).

3.3 Trait Association

The association between all possible combinations of characters was estimated at genotypic and phenotypic levels both and is showed in Table 3 and Table 4. Examination of the table reveals that the magnitude of the genotypic correlation coefficient was grater for most character pairs compared to their respective phenotypic correlation coefficients, indicating a low effect of the environment on character expression. For most characters, the differences in the magnitude and direction of the correlation coefficients between phenotypic and genotypic levels were negligible. The degree of association was quantified based on the phenotypic and genotypic correlation coefficients.

In the investigation were fond results with its similar finding for the character like plant height, branches per plant, Ningwal *et al.* (2023), for the pods per plant and pods per cluster Manggoel *et al.*, (2012) followed by Patel *et al.* (2016), and seed per pod Bhanu *et al.*, (2017) followed by Dinesh *et al.* (2017), were show positive and significant association at genotypic level. While, days to 50% flowering were show negative and significant correlation at genotypic level. At phenotypic level, pods per cluster Gautam *et al.* (2017) followed by Kalambe *et al.* (2019), and seed per pods Nalajala *et al.* (2022) and Kumari *et al.*, (2024) were show positive and significant correlation. Similar result was found Paghadar *et al.* (2019) followed by Das *et al.* (2020).

4. CONCLUSION

High estimates of heritability coupled with high genetic advance as per cent of mean were detected for plant height, clusters per plant and

100-seed weight. The traits days to 50% flowering, plant height, branches per plant, pods per cluster, pods per plant, seeds per pods and 100-seed weight exhibited positive and direct effect on grain yield per plant as well as showed positive relationship with grain yield per plant. So, selection based on among the genotypes studied were found to be high yielding and may be evaluated in future breeding programme.

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 this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Appendix-I

Mean weekly weather parameter recorded during crop season (*Kharif*, 2024)

Standard Meteorological Week	Period		Temperature (°C)		R.H. (%)		Wind	Bright Sunshine	Total Rainfall	No. of Rainy days*
	From	To	Max.	Min.	Max.	Min.	(km/hrs.)	(hrs.)	(mm.)	
26	25/06	01/07	38.4	24.7	80	58	1.5	4.8	5.7	1
27	02/07	08/07	35.7	25.8	84	66	2.0	2.9	14.6	2
28	09/07	15/07	37.3	26.8	79	60	1.7	6.6	10.4	2
29	16/07	22/07	40.3	28.4	83	52	1.1	8.2	2.8	1
30	23/07	29/07	36.1	26.7	83	72	1.2	4.6	63.9	2
31	30/07	05/08	34.7	26.5	88	67	1.1	6.9	40.6	1
32	06/08	12/08	30.3	25.2	92	85	1.9	0.7	29.3	4
33	13/08	19/08	32.8	25.3	90	72	0.7	4.3	52.5	3
34	20/08	26/08	35.7	25.8	89	73	0.9	6.7	4.6	1
35	27/08	02/09	34.5	24.9	90	74	14.0	5.8	2.4	0
36	03/09	09/09	32.9	24.4	94	83	0.6	4.1	81.8	4
37	10/09	16/09	34.2	24.3	93	66	1.1	6.8	7.6	2
38	17/09	23/09	34.6	22.9	90	70	0.8	6.5	2.2	0
39	24/09	30/09	37.4	23.9	86	52	0.5	8.4	0	0
40	01/10	07/10	37.9	22.7	82	43	1.6	9.0	0	0
41	08/10	14/10	36.0	18.8	86	41	0.6	8.2	7.2	1
42	15/10	21/10	36.8	16.5	80	44	0.4	7.9	0	0
43	22/10	28/10	36.0	16.9	89	39	0.5	8.1	0	0
44	29/10	04/11	36.9	15.9	88	59	0.7	8.6	0	0
AV.			35.71	23.49	86.68	61.96	1.74	6.27	325.60	24.00

*Total Rainy Days Source: Agricultural Research Station, Fatehpur-Shekhawati, Sikar

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