



International Journal of Horticulture and Food Science

E-ISSN: 2663-1067

P-ISSN: 2663-1075

NAAS Rating: 4.74

www.hortijournal.com

IJHFS 2025; 7(7): 51-55

Received: 06-05-2025

Accepted: 07-06-2025

Kiran K Jakhotra

M.Sc., Student, Department of Vegetable Science, College of Horticulture, Junagadh Agricultural University, Junagadh, Gujarat, India

SM Makwana

Professor and Head, Department of Basic Science, College of Horticulture, Junagadh Agricultural University, Junagadh, Gujarat, India

Dharvi P Madhani

M.Sc., Student, Department of Vegetable Science, College of Horticulture, Junagadh Agricultural University, Junagadh, Gujarat, India

Lata J Raval

Associate Research Scientist, Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh, Gujarat, India

Genetic variability, heritability and genetic advance studies in vegetable cowpea *Vigna unguiculata* (L.) Walp

Kiran K Jakhotra, SM Makwana, Dharvi P Madhani and Lata J Raval

DOI: <https://www.doi.org/10.33545/26631067.2025.v7.i7a.337>

Abstract

A field trial was conducted to estimate “Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]” using 40 genotypes. The variability parameters like coefficient range, GCV, PCV, heritability and genetic advance were estimated for 14 different characters. The result revealed that analysis of variance showed that the mean squares for all traits were significantly influenced by genotypes, indicating substantial genetic variability in the experimental material. The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) slightly for all the traits examined, suggesting a relatively low influence of environmental factors on the expression of these traits. The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for green pod yield per plant, ten pod weight, hundred fresh seeds weight, pod length, plant height, number of pods per cluster, pod width and number of pods per plant, while high heritability (broad sense) values were observed for all the twelve characters except for the two characters days to first green pod picking and days to last picking. The genetic advance expressed as percentage of mean was found high for green pod yield per plant followed by days to 50% flowering, ten pod weight, hundred fresh seeds weight, pod length and number of pods per cluster.

Keywords: GCV, PCV, cowpea, Genetic variability, heritability, genetic advance

1. Introduction

Cowpea (*Vigna unguiculata* [L.] Walp.) is a highly important vegetable crop, originally native to West Africa (Vavilov, 1951) [31]. However, Steele (1976) proposed Ethiopia as its primary center of origin, with the rest of Africa serving as a secondary center of diversity. Taxonomically, cowpea belongs to the order *Rosales*, family *Fabaceae*, and genus *Vigna*. It is a diploid species with a somatic chromosome number of $2n=22$ (Darlington and Wylie, 1955) [8]. The genus *Vigna* includes approximately 160 species, predominantly found across Asia and Africa.

A logical way to start any breeding programme is to assess the variation existing in the available materials. It is said that genetic variability is the “sine qua non” of any such programme. Selection is said to be effective in a population having large heritable variability. The genetic variability and its components are the genetic fractions of observed variability that provides measures of transmissibility of the variation and response to selection. The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop. The breeder's choice of the material for any improvement work consequently depends on the amount of genetic variability present. The phenotype is often not true indicator of its genotype. The phenotypic variability is the result of the effect of environment and genotype interaction. Attempts have been made to determine the magnitude of heritable and non-heritable components and genetic parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance as percentage of mean in some of the quantitative characters of cowpea.

The availability of sufficient genetic variability is a fundamental prerequisite for any successful crop improvement program.

Corresponding Author:

Kiran K Jakhotra

M.Sc., Student, Department of Vegetable Science, College of Horticulture, Junagadh Agricultural University, Junagadh, Gujarat, India

The effectiveness of a breeding strategy largely depends on the extent of genetic variation present within the experimental material. Therefore, it is crucial for plant breeders to assess this variability using quantitative parameters such as the Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability, and genetic advance. These metrics provide valuable insights into the nature and magnitude of genetic variability for various traits within the germplasm, thereby guiding the selection process and enhancing the efficiency of breeding efforts.

To investigate these effects, the present experiment was conducted with the following objective:-

To estimate the genetic variability, heritability and genetic advance for green pod yield and yield contributing traits

2. Materials and Methods

The present investigation was undertaken to evaluate the Genetic variability, heritability, and genetic advance in vegetable cowpea (*Vigna unguiculata* [L.] Walp.). The experiment was conducted during the summer season of 2024 at the Instructional Farm, Jambuvadi, Department of Vegetable Science, College of Horticulture, Junagadh Agricultural University, Junagadh. The experimental site is characterized by a semi-arid, tropical climate. Weather conditions during the growing period were favorable for the normal growth and development of the crop. A total of 40 cowpea genotypes were evaluated using a Randomized Block Design (RBD) with three replications. Each genotype was sown at a spacing of 60 × 30 cm, and the genotypes were randomly assigned to plots within each replication. Standard agronomic practices and plant protection measures were followed to ensure successful crop establishment and growth. Observations were recorded on five randomly selected plants per genotype in each replication. Data were collected on the following traits: days to 50% flowering, days to first green pod picking, number of primary branches per plant, plant height (cm), pod length (cm), pod width (cm), number of pods per plant, number of seeds per pod, number of pods per cluster, ten-pod weight (g), hundred fresh seed weight (g), green pod yield per plant (g), days to last picking and number of pickings.

Analysis of variance for the Randomized Block Design (RBD) was performed for each trait following the procedure described by Panse and Sukhatme (1985) [17]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formulas proposed by Burton and De Vane (1952). Additionally, heritability and genetic advance were estimated according to the methods outlined by Allard (1960) [2].

3. Results and Discussions

The analysis of variance for all the characters studied has been presented in Table 1. It is revealed that mean squares due to genotypes were highly significant for all the characters which indicated that the presence of variability in cowpea genotypes.

The estimates of mean genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability and genetic advance over mean (GAM) for different characters are presented in Table 2. The results showed that phenotypic variance and phenotypic coefficient of variation were higher than genotypic variance and

genotypic coefficient of variation for all traits. This means the environment played an important role in affecting how these traits were expressed.

The high magnitude of GCV and PCV was observed for green pod yield per plant, ten pod weight and hundred fresh seeds weight. This is in relation with the earlier reports of Barik *et al.* (2023) [4], Vinay *et al.* (2022) [33] for green fruit yield per plant and ten pod weight; Singh *et al.* (2020) [21] and Sogalad *et al.* (2022) [22] for green pod yield per plant; Abiola and Alaba (2020) [1] and Gupta *et al.* (2023) [11] for hundred fresh seeds weight; Swathi *et al.* (2024) [25] for ten pod weight.

The moderate magnitude of GCV and PCV was observed for pod length, plant height, number of pods per cluster, pod width and number of pods per plant. This is in accordance with the earlier reports of Purohit *et al.* (2020) [18], Thangam *et al.* (2020) [26] and Ugale *et al.* (2020) [29] for plant height, number of pods per cluster and number of pods per plant; Imandi and Depanshu (2019) [12] and Abiola and Alaba (2020) [1] for number of pods per plant, plant height and pod length and Sogalad *et al.* (2022) [22] for plant height and pods per plant; Yadav *et al.* (2019) [35] for plant height and pod width.

However, low magnitudes of GCV and PCV were recorded for days to last picking, days to 50% flowering and days to first green pod picking. The main reason could be that these traits show more phenotypic plasticity. This means the traits change more due to the environment than genetic variation. This also shows that selection for these traits is not effective. The reason is that they have a narrow genetic variation. Lower magnitude of GCV and PCV were also reported by Chaudhary *et al.* (2020) [6] and Thouseem *et al.* (2018) [28] for days to 50% flowering; Barik *et al.* (2023) [4], Gupta *et al.* (2023) [11] and Swathi *et al.* (2024) [25] for days to first green pod picking and last picking; Thapa *et al.* (2021) [27] and Singh *et al.* (2022) [20] for first pod picking.

The result indicated that the heritability estimates were high for the characters *viz.*, hundred fresh seeds weight (98.22%), green pod yield per plant (98.01%), ten pod weight (97.56%), pod width (97.34%), number of pod per cluster (97.20%), plant height (95.60%), pod length (93.72%), number of seeds per pod (91.61%), number of pods per plant (89.78%), days to 50% flowering (88.06%), number of picking (87.19%) and number of primary branches per plant (82.23%). Similar results of high heritability was reported Gupta *et al.* (2023) [11] for plant height, days to 50% flowering, 100 seeds weight and yield per plant; Manju and Jayamani (2018) [14] for character pods per plant, pod weight, seeds per pod, pod length; Datthi *et al.* (2022) [9] for 50% flowering, plant height and pods per plant; Vinay *et al.* (2022) [33], for pod length, 50% flowering, 100 seeds weight, pods per plant; Singh *et al.* (2020) [21], for plant height, seeds per pod.

The estimates of heritability were moderate for days to first green pod picking and days to last picking. Similar results of moderate heritability were also reported by Gupta *et al.* (2023) [11], Singh *et al.* (2022) [20] days to last picking; Sarath and Reshma (2017) [19], Srinivas *et al.* (2017b) [23] for first green pod picking.

The expected genetic advance value was high for characters green pod yield per plant, days to 50% flowering and ten pod weight. The result was in agreement with the findings of Verma *et al.* (2019) [32] and Barik *et al.* (2023) [4] for green pod yield per plant and ten pod weight; Gupta *et al.*

(2023) ^[11] and Dahiya *et al.* (2024) ^[7] for pod yield per plant. Low genetic advance was observed for pod width, number of primary branches per plant, number of pods per cluster, number of picking, number of seeds per pod, days to last picking, pod length, days to first green pod picking, hundred fresh seeds weight and number of pods per plant. The results are in agreement with the findings of Abiola and Alba (2020), for number of pods per cluster and number of seeds per pod; Singh *et al.* (2020) ^[21] for days to last picking; Thapa *et al.* (2021) ^[27] for pod length; Swathi *et al.* (2024) ^[25] for days to first picking and days to last picking; Dahiya *et al.* (2024) ^[7] for pod length and seeds per pod; Chaudhary *et al.* (2020) ^[6] for number of branches per plant; Panchta *et al.* (2020) ^[15], Singh *et al.* (2022) ^[20] for number of seeds per pod; Pandiyan *et al.* (2020) ^[16] for pods per plant and pod length.

Highest genetic advance as percent of mean was exhibited by green pod yield per plant followed by days to 50% flowering, ten pod weight, hundred fresh seeds weight and pod length, number of pods per cluster and pod width. The result was in agreement with the findings of Verma *et al.* (2019) ^[32] for green pod yield, pods per cluster, ten pod weight, pod length and 100 seed weight; Dahiya *et al.* (2024) ^[7] Singh *et al.* (2022) ^[20] for pod yield per plant, pod length and 100 seeds weight; Lonare *et al.* (2024) ^[13] for pod yield; Vir and Singh (2014) ^[34] for 100 seed weight, pod

length and number of pod per cluster.

However, the moderate genetic advance as per cent of mean was observed for number of pods per plant, plant height and number of picking. The result was in agreement with the findings of Gawande *et al.* (2024) ^[10] for pods per plant and Gupta *et al.* (2023) ^[11] for pods per plant and plant height; Ugale *et al.* (2020) ^[29] for pods per plant.

Low genetic advance as percent of mean was observed for days to last picking, days to first green pod picking. The result was in agreement with the findings of Vavilapalli *et al.* (2013) ^[30] for first pod picking; Thapa *et al.* (2021) ^[27], Gawande *et al.* (2024) ^[10] for days to last picking; and Swathi *et al.* (2024) ^[25] for days to last picking and days to first green pod picking.

High heritability coupled with high genetic advance as percent of mean observed for green pod yield per plant and days to 50 per sent flowering indicated additive gene action for the character. The result was in agreement with the findings of Purohit *et al.* (2020) ^[18] for days 50 per sent flowering; Barik *et al.* (2023) ^[4] for pod yield and 50 per cent flowering. While, low heritability with low genetic advance as per cent of mean observed for days to last picking and days to first green pod picking indicated non-additive gene action. The similar result revealed by Swathi *et al.* (2024) ^[25].

Table 1: Analysis of variance showing mean squares of 14 characters in 40 genotypes of cowpea

	Mean sum of square		
	Replication (DF=2)	Genotypes (DF=39)	Error (DF=78)
Days to 50 % flowering	3.42	15.76**	1.88
Days to first green pod picking	23.77	38.76**	8.86
Number of primary branches per plant	0.03	0.37**	0.06
Plant height	10.13	276.40**	12.17
Pod length	3.80	25.62**	1.61
Pod width	0.001	0.03**	0.001
Number of pods per plant	15.87	188.66**	19.28
Number of seeds per pod	0.37	4.12**	0.35
Number of pods per cluster	0.04	0.75**	0.02
Ten pod weight	30.04	782.92**	19.11
Hundred fresh seeds weight	0.22	114.71**	2.04
Green pod yield per plant	38.60	11964.99**	238.43
Days to last picking	3.17	45.72**	17.74
Number of picking	0.88	2.70**	0.35

*,** significant at 5% and 1% levels, respectively

Table 2: Range, Coefficient of range (%), Mean, GCV (%), PCV (%), Heritability, GA and GA expressed as % of mean for various characters in cowpea

Characters	Range	Coefficient of range (%)	Mean	Genotypic Coefficients of Variance (GCV %)	Phenotypic Coefficients of Variance (PCV %)	Heritability in broad sense h^2_{bs} (%)	Genetic Advance (GA)	Genetic advance as % of mean (GAM %)
Days to 50 per cent flowering	45.40-54.47	9.08	51.87	4.15	4.42	88.06	41.58	80.16
Days to first green pod picking	56.07-70.40	11.33	65.70	4.81	5.47	77.14	5.71	8.69
Number of primary branches per plant	1.67-3.67	37.45	2.61	12.12	13.36	82.23	0.59	22.63
Plant height (cm)	37.27-74.13	33.09	58.11	16.15	16.52	95.60	18.90	32.53
Pod length (cm)	10.48-23.08	37.52	14.33	19.74	20.39	93.72	5.64	39.36
Pod width (cm)	0.36-0.83	39.50	0.56	17.89	18.14	97.34	0.20	36.36
Number of pods per plant	28.67-57.80	33.69	46.42	16.19	17.08	89.78	14.67	31.60
Number of seeds per pod	8.53-14.20	24.95	11.47	9.78	10.22	91.61	2.21	19.29
Number of pods per cluster	1.73-4.13	40.95	2.71	18.14	18.40	97.20	1.00	36.84
Ten pod weight (g)	31.97-96.57	50.26	60.98	26.17	26.49	97.56	32.47	53.24
Hundred fresh seeds weight (g)	17.00-37.53	37.65	27.33	22.43	22.63	98.22	12.51	45.79
Green pod yield per plant (g)	55.20 – 245.10	63.23	150.97	41.41	41.83	98.01	127.50	84.46
Days to last picking	76.53 – 91.13	8.71	81.98	3.73	4.76	61.20	4.92	6.00
Number of picking	5.53 – 9.33	25.57	7.40	11.97	12.82	87.19	1.70	23.02

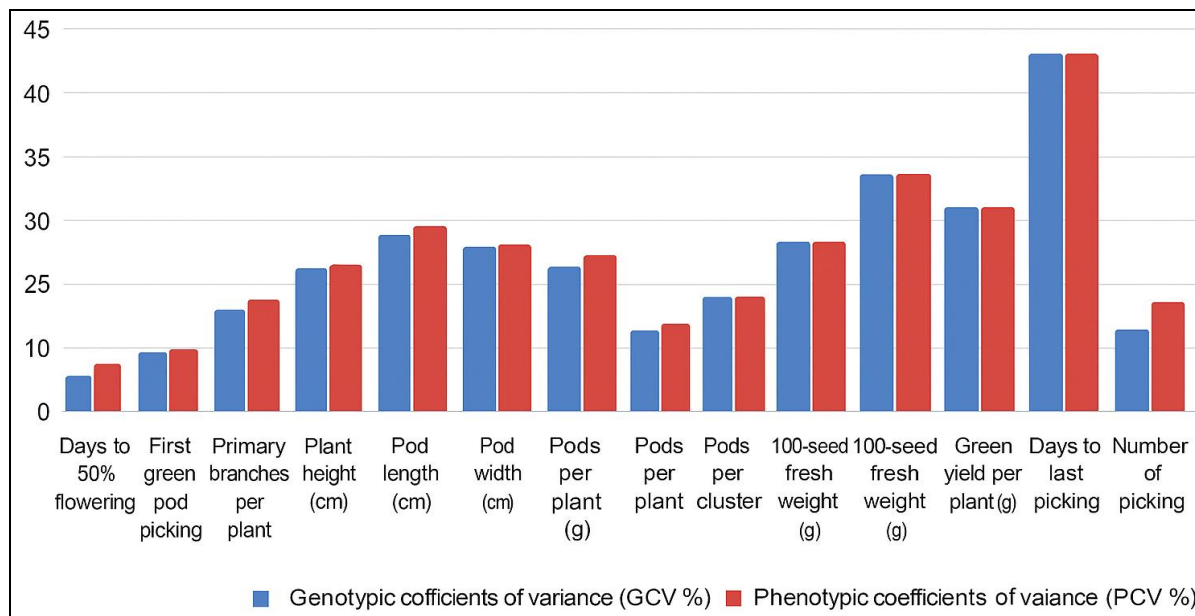


Fig 1: Genotypic coefficients of variation and phenotypic coefficient of variance of fourteen characters in cowpea

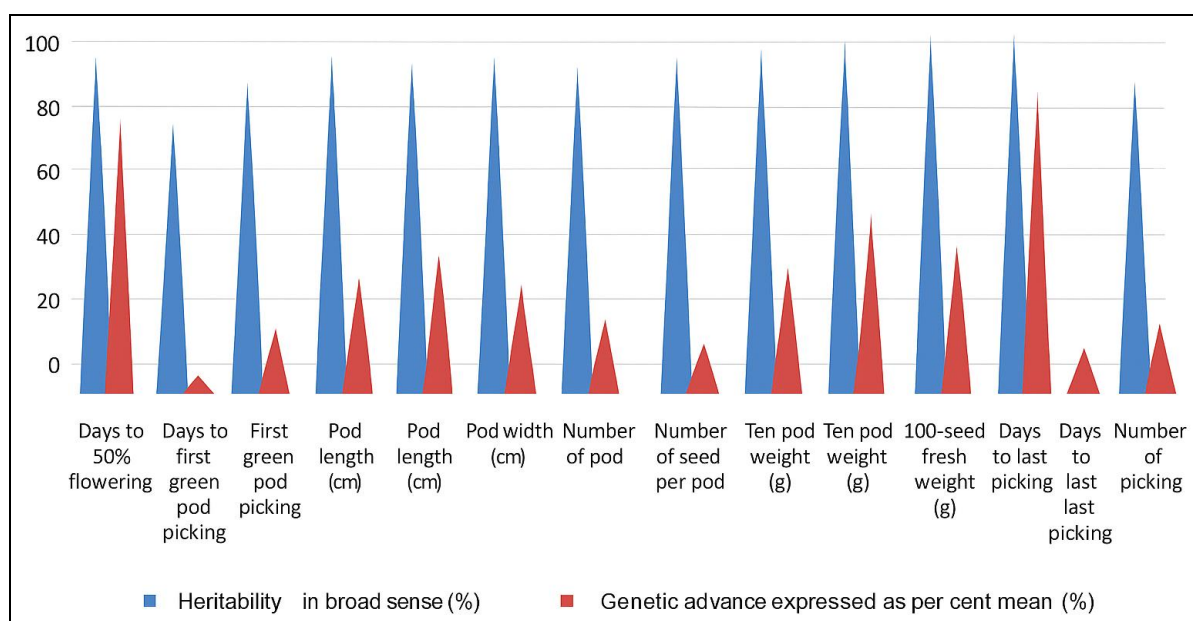


Fig 2: Heritability and genetic advance expressed as per cent of mean for fourteen characters in cowpea

4. Conclusion

The analysis of variance showed that the mean squares for all traits were significantly influenced by genotypes, indicating substantial genetic variability in the experimental material. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all the traits studied, indicating a minimal environmental influence on trait expression. This suggests that phenotypic variation can serve as a reliable indicator of genetic variation. The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for green pod yield per plant, ten pod weight, hundred fresh seeds weight, pod length, plant height, number of pods per cluster, pod width and number of pods per plant. The high heritability (broad sense) values were observed for all the twelve characters except for the two characters days to first green pod picking and days to last picking. The genetic advance expressed as percentage of

mean was found high for green pod yield per plant followed by days to 50% flowering, ten pod weight, hundred fresh seeds weight, pod length and number of pods per cluster.

5. References

1. Abiola AB, Alaba AE. Genetic variability, character association and yield potentials of twenty-five accessions of cowpea (*Vigna unguiculata* (L.) Walp). Pure Appl Agric. 2020;5(2):1-16.
2. Allard RW. Principles of plant breeding. New York: John Wiley and Sons, 1960, p. 485.
3. Bambhaniya UB, Makwana SM, Patoliya A, Raval LJ. Studies on genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). Int J Adv Biochem Res. 2024;8(7):536-40.
4. Barik D, Chatterjee S, Nayak P. Study on morphological and genetic variations among vegetable cowpea (*Vigna unguiculata* (L.) Walp.) genotypes in

- north-eastern ghat region of India. *Bio Forum Int J*. 2023;15(5):1247-55.
5. Burton GW. Quantitative inheritance in grasses. *Proc 6th Int Grassland Congr*. 1952;1:277-83.
 6. Chaudhary AR, Solanki SD, Rahevar PM, Patel DA. Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in cowpea *Vigna unguiculata* (L.) Walp accessions. *Int J Curr Microbiol Appl Sci*. 2020;9(2):1281-93.
 7. Dahiya A, Arya S, Panchta R, Jogender. Delineating the genetic variability in cowpea *Vigna unguiculata* (L.) Walp under the summer season. *Int J Res Agron*. 2024;7(12):88-92.
 8. Darlington CD, Wylie AP. Chromosome atlas of flowering plants. London: George Allen and Unwin, 1955, p. 132-4.
 9. Datthi S, Deepanshu, Bahadur V. Study on genetic variability, heritability and correlation studies in cowpea (*Vigna unguiculata* (L.) Walp). *Int J Horti Food Sci*. 2022;4(1):10-17.
 10. Gawande Y, Rathore NR, Sinha A. Genetic variability, character association and path analysis studies in cowpea *Vigna unguiculata* (L.) Walp. *Int J Curr Microbiol Appl Sci*. 2024;13(12):250-257.
 11. Gupta S, Intwala CG, Sree Ganesh S. Genetic variability, correlation and path analysis in cowpea (*Vigna unguiculata* (L.) Walp). *Indian J Agric Res*. 2023;57(5):573-578.
 12. Imandi I, Deepanshu H. Genetic analysis in cowpea (*Vigna unguiculata* (L.) Walp) under Prayagraj agroclimatic condition. *J Pharm Phytochem*. 2019;8(4):1271-1274.
 13. Lonare KM, Pethe UB, Kunkerkar RL, *et al*. Genetic variability, heritability and genetic advance studies in F2 generation of cowpea *Vigna unguiculata* (L.) Walp. *Int J Adv Biochem Res*. 2024;8(10):1091-1095.
 14. Manju SM, Jayamani P. Genetic variability, heritability, genetic advance studies in cowpea germplasm (*Vigna unguiculata* (L.) Walp). *Electr J Plant Breed*. 2018;9(2):476-481.
 15. Panchta R, Preeti, Arya S. Variability, correlation and path analysis studies in grain cowpea *Vigna unguiculata* (L.) Walp. *Int J Pure Appl Biosci*. 2020;8:169-172.
 16. Pandiyan M, Vaithilingan A, Krishnaveni P, *et al*. Genetic variability studies on cowpea genotypes. *Int J Curr Microbiol Appl Sci*. 2020;9(6):3794-3797.
 17. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: ICAR, 1985.
 18. Purohit P, Nautiyal MK, Bhatt L, *et al*. Estimation of genetic advance, heritability, genetic gain and genetic diversity of elite genotypes of grain cowpea [*Vigna unguiculata* (L.) Walp.]. *Int J Chem Stud*. 2020;8(4):631-637.
 19. Sarath P, Reshma T. Genetic variability studies in cowpea *Vigna unguiculata* (L.) Walp. *Int J Agric Sci Res*. 2017;7(3):129-132.
 20. Singh A, Deepanshu, Bahadur V. Genetic variability, heritability, correlation studies and path coefficient in cowpea (*Vigna unguiculata* (L.) Walp). *Pharm Innov J*. 2022;11(5):1318-1324.
 21. Singh O, Shekhawat N, Singh K, Gowthami R. Assessment of genetic variability and inter-character association in the germplasm of cowpea (*Vigna unguiculata* L. Walp) in hot arid climate. *Legume Res Int J*. 2020;43(3):332-336.
 22. Sogalad MS, Deshpande SK, Kavyashree NM. Genetic variability, correlation and path analysis studies in grain cowpea (*Vigna unguiculata* (L.) Walp subsp. *unguiculata*). *J Pharm Innov*. 2022;11(12):3749-3754.
 23. Srinivas J, Kale VS, Nagre PK. Study of genetic variability, heritability and genetic advance in cowpea *Vigna unguiculata* (L.) Walp. *Int J Curr Microbiol Appl Sci*. 2017;6:3314-3318.
 24. Steele WM. Cowpeas [*Vigna unguiculata* (L.) Walp.]. In: Sunumerfield RJ, Bunting AH, editors. Evolution of crop plants. London: HMSO, 1976, p. 183-5.
 25. Swathi S, Joseph J, Sindhumole P, Mathew D. Genetic variability and heritability studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *J Trop Agric*. 2024;62(1):14-21.
 26. Thangam M, Ramachandrudu K, Kumar AJ, *et al*. Variability and genetic divergence in vegetable cowpea germplasm of Goa. *J Horti Sci*. 2020;15:45-51.
 27. Thapa B, Adhikari N, Darai R, Kandel B. Genetic variability of exotic cowpea genotypes for agromorphological traits in mid-western region of Nepal. *Alinteri J Agric Sci*. 2021;36(1):47-54.
 28. Thouseem N, Thomas B, Elizabeth N. Genetic parameters in seed yield components of cowpea (*Vigna unguiculata* (L.) Walp). *Int J Curr Microbiol Appl Sci*. 2018;7(2):2268-2274.
 29. Ugale PN, Wankhade MP, Bagade AB. Genetic variability studies in cowpea (*Vigna unguiculata* L.). *J Pharm Phytochem*. 2020;9(6):476-479.
 30. Vavilapalli S, Celine VA, Duggi S, *et al*. Genetic variability and heritability studies in bush cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Genom Genet*. 2013;4(4):4-8.
 31. Vavilov NI. The origin, variation, immunity and plant breeding of cultivated plants. New York: Ronald Press Co., 1951, p. 256-257.
 32. Verma AK, Mehta AK, Gontia AS, *et al*. Genetic variability, heritability and genetic advance studies for yield components in F2 generation of cowpea (*Vigna unguiculata* (L.) Walp). *Int J Chem Stud*. 2019;7(6):3084-3088.
 33. Vinay K, Rao PJM, Sandhya Kishore N, Hari Y. Genetic variability studies for seed yield and yield component traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *Electr J Plant Breed*. 2022;13(2):544-548.
 34. Vir O, Singh AK. Genetic variability and inter-character association studies in the germplasm of cowpea (*Vigna unguiculata* L. Walp) in fragile climate of western Rajasthan, India. *Legume Res*. 2014;37(2):126-132.
 35. Yadav BN, Duddukur R. Genetic variability, trait association and path analysis in cowpea (*Vigna unguiculata* L. Walp). *Int J Curr Microbiol Appl Sci*. 2019;8(12):1979-1986.