



Studies on Genetic Variability, Heritability and Genetic Advance in Cowpea (*Vigna unguiculata* (L.) Walp.) for Green Pod Yield and its Component

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/jeai/2024/v46i72655>

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://www.sdiarticle5.com/review-history/119271>

Original Research Article

Received: 02/05/2024

Accepted: 04/07/2024

Published: 06/07/2024

ABSTRACT

Cowpea (*Vigna unguiculata* (L.) Walp.) is a significant leguminous crop extensively cultivated in tropical and subtropical regions, known for its adaptability and nutritional value. This study, conducted at Horticulture Research Farm, Babasaheb Bhimrao Ambedkar University, Lucknow, (U.P.) India, during 2020-21 and 2021-22, aimed to analyze the genetic variability, heritability, and genetic advance among 30 diverse cowpea genotypes. The experiment utilized a Randomized Block Design (R.B.D.) with three replications, evaluating twenty-six quantitative traits. Analysis of variance revealed significant genetic variation across all traits, indicating potential for effective selection. During first year (2020-21) the phenotypic variance ranged from 0.03 (pod diameter) to 9947.17 (pod yield plant-1) and it ranged from 0.03 (pod diameter) to 10443.59 (pod yield plant-1)

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Cite as: Abha, Ruchika, and M. L. Meena. 2024. "Studies on Genetic Variability, Heritability and Genetic Advance in Cowpea (*Vigna Unguiculata* (L.) Walp.) for Green Pod Yield and Its Component". *Journal of Experimental Agriculture International* 46 (7):1005-15. <https://doi.org/10.9734/jeai/2024/v46i72655>.

for second year. The genotypic variance ranged from 0.03 (pod diameter) to 9873.13 (pod yield plant-1), while it ranged from 0.03 (pod diameter) to 10373.99 (pod yield plant-1) in second year. During first year, highest magnitude of phenotypic and genotypic coefficient of variation was recorded in pod yield plant-1 (63.42 and 63.18) followed by pod yield/plot (55.73 and 55.57), whereas, during second year it recorded in pod yield plant-1 (64.39 and 64.18) followed by pod yield/plot (56.95 and 56.73). Traits like pod yield per plant, pod yield qha-1, pod yield per plot, non-reducing sugar, number of pods per plant, total sugars, plant height, number of branches per plant, average pod weight, weight of 100 seeds, reducing-sugar, number of pods per peduncle, number of green pods per cluster, number of peduncles per plant, number of nodes on main branches, number of seeds per pod, number of clusters per plant, total soluble solids, pod diameter, pod length, number of flowers per cluster, days taken to first flowering showed high heritability and genetic advance, suggesting additive gene action and reliability for selection. The findings underscore the importance of genetic variability in breeding programs, facilitating the selection of superior genotypes to enhance yield and other agronomic traits in cowpea.

Keywords: Cowpea; GCV; genetic advance; heritability PCV and variability.

1. INTRODUCTION

The eminent leguminous crop recognized among humanity is the cowpea (*Vigna unguiculata* (L.) Walp.). It boasts a chromosomal count of $2n=22$ and stands as a constituent of the Fabaceae subfamily within the Leguminosae family [1]. This plant thrives across the semi-arid tropics, encompassing sectors of Asia, Africa, Southern Europe, the Southern United States, and Central and South America [2].

Cowpea, present in 37 countries, contributed 16% to the total area, while peas dry in 96 countries contributed 8%, tur in 24 countries with 7%, and lentil in 43 countries with a contribution of 5% [3].

Cowpea thrives predominantly in tropical and subtropical regions across the globe, serving as a versatile resource as a vegetable, seed source, and, to a lesser degree, fodder. Its smothering attributes, resilience to drought, soil rejuvenation capabilities, and diverse applications render it one of the most adaptable pulse crops. Its tender green pods prove an excellent source of calcium, phosphorus, and iron, boasting a moisture content of 84.9%, 4.3% protein, 8.0% carbohydrates, and 2% fat [4]. Within India, the states of Uttar Pradesh, Punjab, Haryana, Rajasthan, Madhya Pradesh, and Maharashtra are the primary cultivators of cowpea. Often referred to as the "Poor man's meat," it stands as one of the oldest legume varieties.

As yield is a multifaceted trait, influenced by both polygene-controlled qualities and environmental

factors, the success of any plant breeding program hinges on population variability. Hence, research into genetic variability, heritability, and genetic advancement remains paramount, enabling efficient genotype selection and utilization within breeding programs. Indigenous and exotic germplasms lay the foundation for effective breeding initiatives aimed at bolstering yield and yield-contributing traits.

Keeping the above gaps and scopes in view the present study was conducted to analyse the extent of genetic variability and heritability among green pod yield and its attributing traits in cowpea.

2. MATERIALS AND METHODS

The present investigation was carried out during the years 2020-21 and 2021-22 at the Horticultural Research Farm, Department of Horticulture, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya Vihar Raebareli Road, Lucknow U.P.(India). The experiment field was located approximately 10 km away from Lucknow railway station towards southeast and 7 km from Chaudhary Charan Singh International Airport, (Amausi) Lucknow toward North-East direction.

Geographically, Lucknow is situated at an elevation of 123 meter above mean sea level (MSL) in the subtropical climate of central Uttar Pradesh at 26°55' North latitude and 80°59' longitude. The climatic situation of experimental region is subtropical with maximum temperature ranging from 22-45°C in summer, minimum temperature ranging from 1.5-15 °C in

winter relative humidity ranging from 60-80% in different season of the year, with annual rainfall of 110 cm.

The experimental material comprised of 30 diverse genotypes including two checks viz., Kashi Unnati and Kashi Kanchan. The sowing was carried out in Randomized Block Design (R.B.D.) with three replications during *Kharif* of 2020-21 and 2021-22 at the spacing of 60 cm and 30 cm between the rows and plants, respectively. The method of sowing followed was dibbling. One plant per hill was maintained by thinning 10 days after sowing. Individual plot size for each genotype was 2.7 m × 1.20 m for each genotype. The recommended fertilizer dose of nitrogen, phosphorus and potash were applied @ 55 kg, 80 kg and 36 kg per hectare, were respectively. Nitrogen was applied in to split doses; half at the time of sowing and remaining half at the time of vegetative growth and pod formation of cowpea genotypes. All necessary cultural operations were done as and when required during the experimentation trial.

The data were noted on twenty-six quantitative traits as plant height (cm), no. of branches per plant, no. of nodes on main branches, days taken for first flowering, days to 50% flowering, no. of cluster per plant, no. of flower per cluster, no. of green pods per cluster, no. of peduncles per plant, no. of pods per peduncle, days to physiological maturity, days to first picking, no. of pods per plant, pod length (cm), pod diameter (cm), average pod weight (g), no. of seeds per pod, weight of 100 seeds (g), pod yield plant⁻¹ (g), pod yield/plot (kg), pod yield (qha⁻¹), protein content (%), total sugars (mg/g fw), reducing sugar (mg/g fw), non-reducing sugars (mg/g fw) and T.S.S. (mg/g fw). To observe the yield, contributing traits and seed characteristics, five plants were randomly tagged to record these observations. By taking the average, the mean value for the treatment was computed. Total sugar content was estimated by following the method of Hedge and Hofrieter [5].

The mean value of all the traits were subjected to statistical analyses as analysis of variance following Panse and Sukhatme [6], Coefficient of variation estimated as per Burton [7], Heritability in broad sense as per Hanson [8], Genetic advance and Genetic advance in percent of mean using formula suggested by Johnson et al. [9].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

Variances were worked out for all the twenty-six quantitative traits under study. The mean sum of squares due to the genotypes were highly significant for all the characters under study during both years first year (2020-21) and second year (2021-22). This showed considerable amount of variation for all the characters studied. The genotypic and error mean sum of squares were used further for analysis of genotypic and phenotypic variances. Analysis of variance for the different characters presented in Table 1.a and 1.b. Variability in several quantitative characters of cowpea was also reported by Shanko et al. [10], Mahesh et al. [11] and Patil et al. [12].

3.2 Mean Performance and Range of Variability

Genetic variability is the most important parameter to be considered while undertaking breeding programme for crop improvement. Selection of elite genotypes largely depends on extent of genetic variability present in plant population. Direct selection based only on yield will not be much effective as yield generally has low heritability hence it is desirable to select indirectly for yield through other characters. In present investigation, cowpea population showed wide range of variation for all the characters under study in cowpea (Table 2.a and 2.b).

During first year (2020-21) the variation among population for plant height ranged from 47.53 cm to 195.90 cm with the mean value of 118.86 cm. During second year (2021-22) the variation among population for plant height ranged from 45.67 cm to 194.27 cm. The general mean for plant height was 119.55 cm. Number of primary branches per plant ranged from 3.24 to 14.20 for first year, and 3.44 to 14.23 for second year. During first year, number of nodes on main branches ranged from 7.60 to 21.34 and from 7.91 to 21.07 for second year. During first year (2020-21) the variation among population for days taken to first flowering ranged from 31.38 to 49.20 while it ranged from 31.75 to 49.05 for second year. for days to 50% flowering ranged from 45.22 to 61.14 in first year and from 45.32 to 61.04 in second year. During first year (2020-21) the variation among population for days to physiological maturity ranged from 64.67 days to

75.47 days whereas it ranged from 64.87 days to 75.34 days for second year; variation among population for days to first picking ranged from 43.72 days to 61.39 days in first year and from 43.05 days to 60.95 days in second year. Sarath and Reshma [13] for plant height, Satish et al. [14] for primary branches, Shanko et al. [10] for days to 50% flowering, Ravish et al. [15] for days to maturity, Riddhi and Dhaduk [16] for days taken to first picking obtained a high range of variation in their studies on cowpea.

The number of nodes on main branches ranged from 7.60 to 21.34 in first year and 7.91 to 21.07 in second year; the variation among population for number of clusters per plant ranged from 4.66 to 10.53 in first year and from 4.73 to 10.50 in second year; During first year (2020-21) number of flowers per cluster ranged from 3.72 to 6.04 and during second year (2021-22) it ranged from 3.69 to 6.05; number of green pods per cluster ranged from 1.07 to 3.37 and from 1.06 to 3.35 for first year and second year respectively; for number of peduncles per plant the variation ranged from 10.68 to 30.75 in first year and ranged from 10.91 to 30.52 in second year. Similar variation for these valuable traits were observed previously by Jogdhande et al. [17] for number of nodes, Singh et al. [18] for number of clusters per plant, Mohan et al. [19] for number of flowers, Tsegaye et al. [20] for number of pods per plant, Manggoel et al. [21] for number of peduncles.

The number of pods per plant ranged from 4.73 to 30.41 in first year, while it ranged from 5.11 to 31.41 in second year; during first year (2020-21) the variation among population for average pod weight ranged from 3.74 g to 13.94 g whereas 3.95 g to 13.57 g in second year (2021-22); weight of 100 seeds ranged from 5.17 g to 19.50 g in first year and 5.55 g to 19.15 g in second year; the variation among population for pod yield per plant (g) ranged from 17.68 g to 355.50 g and from 20.18 to 370.40g in second year. These results are in accordance with the results noted by Sapara et al. [22] for number of pods per plant, Verma et al. [23] for pod weight, Kavyashree et al. [24] for 100-seeds weight, Ajayi [25] for pod yield per plant.

Protein content ranged from 20.22 % to 25.23 % and 20.10 % to 25.47 %; total soluble solids varied between 3.36 to 7.43 and 3.42 to 7.51^oBrix; reducing sugars ranged from 4.55 to

14.21 and 4.66 to 15.21mg/g; non-reducing sugars (mg/g) ranged from 6.71 to 33.51 and 6.71 to 32.41; total sugars (mg/g) ranged from 11.25 to 51.52 and 11.32 to 48.41 respectively in first year and second year. Similar results of variation were noted by Jogdhande et al. [17] and Tambitkar et al. [26].

3.3 Estimation of Variances

The total variation among the genotypes was partitioned into two components viz. genotypic and phenotypic variance. The estimates of variances due to these two components for twenty-six quantitative characters are given in Tables 2.a and 2.b.

During first year (2020-21) the phenotypic variance ranged from 0.03 (pod diameter) to 9947.17 (pod yield plant-1) and it ranged from 0.03 (pod diameter) to 10443.59 (pod yield plant-1) for second year. The genotypic variance ranged from 0.03 (pod diameter) to 9873.13 (pod yield plant-1), while it ranged from 0.03 (pod diameter) to 10373.99 (pod yield plant-1) in second year. In general, phenotypic variances were higher in magnitude than genotypic variance for all characters.

The phenotypic and genotypic variance was found to be high for pod yield plant-1 (9947.17 and 9873.13), pod yield qha⁻¹ (4668.81 and 4640.43), plant height (2368.42 and 2339.80) in 2020-21 (first year) while the phenotypic and genotypic variance was highest for pod yield plant-1 (10443.59 and 10373.99), pod yield qha⁻¹ (4934.22 and 4902.99), plant height (2324.37 and 2295.23) showed highest magnitude of phenotypic and genotypic variance. Similar results in cowpea were also reported by Sabale et al. [27] and Ravish et al. [15].

3.4 Coefficient of Variation

The estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variation (GCV) are presented in Table 2.a and 2.b.

The amount of genetic variation present in the genotypes was worked out in terms of genotypic coefficient of variation (GCV). In general, phenotypic coefficient of variation (PCV) was greater in magnitude over respective genotypic coefficient of variation (GCV).

Table 1a. Analysis of variance (ANOVA) for 26 traits of cowpea genotypes during 2020-21 (First Year)

Source of variation	DF	Plant Height (cm)	No. of branches per plant	No. of nodes on main branches	Days taken for first flowering	Dyas to 50% flowering	No. of cluster per plant	No. of flower per cluster	No. of green pods per cluster	No. of peduncles per plant	No. of pods per peduncle	Days to physiological maturity	Days to first picking	No. of pods per plant
Replication	2	18.41	0.005	0.053	0.527	0.505	0.002	0.093	0.0001	0.076	0.0001	2.900	0.781	0.024
Genotype	29	7048.02**	31.412**	46.883**	94.588**	68.118**	10.015**	1.512**	1.473**	109.629**	2.189**	32.066**	83.746**	181.035**
Error	58	28.62	0.134	0.479	3.146	4.590	0.116	0.053	0.010	0.906	0.013	8.828	5.195	0.530
Total	89	2315.61	10.323	15.590	32.883	25.198	3.339	0.529	0.487	36.314	0.722	16.266	30.691	59.335

Source of variation	DF	Pod length (cm)	Pod diameter (cm)	Average pod weight (g)	No. of seeds per pod	Weight of 100 seeds (g)	Protein content (%)	T.S.S.	Total sugars (mg/g fw)	Reducing sugar ((mg/g fw)	Non-reducing sugars (mg/g fw)	Pod yield plant-1 (g)	Pod yield/plot (kg)	Pod yield (qha ⁻¹)
Replication	2	18.41	0.005	0.053	0.527	0.505	0.002	0.093	0.0001	0.076	0.0001	2.900	0.781	0.024
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Error	58	28.62	0.134	0.479	3.146	4.590	0.116	0.053	0.010	0.906	0.013	8.828	5.195	0.530
Total	89	2315.61	10.323	15.590	32.883	25.198	3.339	0.529	0.487	36.314	0.722	16.266	30.691	59.335

Table 1b. Analysis of variance (ANOVA) for 26 traits of cowpea genotypes during 2021-22 (Second Year)

Source of variation	DF	Plant Height (cm)	No. of branches per plant	No. of nodes on main branches	Days taken for first flowering	Dyas to 50% flowering	No. of cluster per plant	No. of flower per cluster	No. of green pods per cluster	No. of peduncles per plant	No. of pods per peduncle	Days to physiological maturity	Days to first picking	No. of pods per plant
Replication	2	8.01	0.172	0.194	2.683	0.013	0.021	0.001	0.009	0.322	0.007	0.207	2.253	0.013
Genotype	29	6914.83**	30.663**	46.522**	93.449**	70.043**	9.966**	1.537**	1.449**	107.085**	2.246**	31.714**	86.478**	188.971**
Error	58	29.13	0.136	0.427	2.736	4.896	0.109	0.048	0.011	0.714	0.010	8.594	5.778	0.621
Total	89	2272.31	10.084	15.441	32.293	26.013	3.319	0.532	0.479	35.365	0.739	15.939	31.994	61.980

Source of variation	DF	Pod length (cm)	Pod diameter (cm)	Average pod weight (g)	No. of seeds per pod	Weight of 100 seeds (g)	Protein content (%)	T.S.S.	Total sugars (mg/g fw)	Reducing sugar ((mg/g fw)	Non-reducing sugars (mg/g fw)	Pod yield plant-1 (g)	Pod yield/plot (kg)	Pod yield (qha ⁻¹)
Replication	2	0.022	0.001	0.014	0.114	0.068	0.053	0.049	1.275	0.001	0.01	13.61	0.07	0.14
Genotype	29	66.892**	0.088**	29.468**	21.769**	55.462**	5.699**	4.368**	278.583**	26.250**	142.40**	31191.56**	17.28**	14740.19**
Error	58	1.044	0.001	0.110	0.307	0.244	1.040	0.059	1.072	0.187	0.45	69.60	0.04	31.23
Total	89	22.477	0.029	9.674	7.296	18.233	2.535	1.463	91.502	8.675	46.70	10209.21	5.66	4823.33

Table 2a. The range, mean, variances, coefficient of variation, heritability and genetic advance of cowpea during first year (2020-21)

Characters	Range			Variance		Heritability (%)	Genetic advance		Coefficient of variation	
	Mean	Min	Max	var (g)	var (p)		GA	GA% mean	GCV (%)	PCV (%)
Plant Height (cm)	118.86	47.53	195.90	2339.80	2368.42	98.79	99.04	83.33	40.70	40.94
No.of branches per plant	8.64	3.24	14.20	10.43	10.56	98.73	6.61	76.47	37.36	37.60
No.of nodes on main branches	15.05	7.60	21.34	15.47	15.95	97.00	7.98	53.01	26.13	26.53
Days taken for first flowering	40.71	31.38	49.20	30.48	33.63	90.64	10.83	26.60	13.56	14.24
Dyas to 50% flowering	53.35	45.22	61.14	21.18	25.77	82.19	8.59	16.11	8.63	9.51
No. of cluster per plant	7.65	4.66	10.53	3.30	3.42	96.61	3.68	48.11	23.76	24.17
No. of flower per cluster	4.98	3.72	6.04	0.49	0.54	90.25	1.37	27.40	14.00	14.74
No. of green pods per cluster	2.19	1.07	3.37	0.49	0.50	97.91	1.42	64.87	31.82	32.16
No. of peduncles per plant	19.41	10.68	30.75	36.24	37.15	97.56	12.25	63.10	31.01	31.40
No. of pods per peduncle	2.58	1.17	4.01	0.73	0.74	98.29	1.74	67.38	32.99	33.27
Days to physiological maturity	70.43	64.67	75.47	7.75	16.57	46.74	3.92	5.57	3.95	5.78
Days to first picking	52.66	43.72	61.39	26.18	31.38	83.44	9.63	18.29	9.72	10.64
No. of pods per plant	16.97	4.73	30.41	60.17	60.70	99.13	15.91	93.73	45.70	45.90
Pod length (cm)	21.99	14.14	30.70	20.46	21.50	95.14	9.09	41.32	20.57	21.08
Pod diameter (cm)	0.80	0.52	1.09	0.03	0.03	95.27	0.34	43.14	21.45	21.98
Average pod weight (g)	8.58	3.74	13.94	10.05	10.18	98.74	6.49	75.64	36.95	37.19
No. of seeds per pod	11.75	7.52	18.97	8.19	8.50	96.37	5.79	49.23	24.35	24.80
Weight of 100 seeds (g)	12.32	5.17	19.50	18.68	18.95	98.57	8.84	71.73	35.07	35.33
Protein content (%)	22.42	20.22	25.23	1.70	2.77	61.48	2.11	9.40	5.82	7.42
T.S.S	5.40	3.36	7.43	1.48	1.53	96.66	2.46	45.65	22.54	22.92
Total sugars (mg/g fw)	23.77	11.25	51.52	98.39	99.61	98.78	20.31	85.44	41.73	41.99
Reducing sugar ((mg/g fw)	8.52	4.55	14.21	8.05	8.20	98.21	5.79	67.94	33.28	33.58
Non-reducing sugars (mg/g fw)	14.75	6.71	33.51	47.42	47.75	99.32	14.14	95.85	46.69	46.85
Pod yield plant-1 (g)	157.27	17.68	355.50	9873.13	9947.17	99.26	203.93	129.67	63.18	63.42
Pod yield/plot (kg)	4.18	1.03	8.60	5.40	5.43	99.40	4.77	114.13	55.57	55.73
Pod yield (qha ⁻¹)	123.56	32.51	249.51	4640.83	4668.81	99.40	139.91	113.23	55.13	55.30

Table 2b. The range, mean, variances, coefficient of variation, heritability and genetic advance of cowpea during second year (2021-22)

Characters	Range			Variance		Heritability (%)	Genetic advance		Coefficient of variation	
	Mean	Min	Max	var (g)	var (p)		GA	GA% mean	GCV (%)	PCV (%)
Plant Height (cm)	119.55	45.67	194.27	2295.23	2324.37	98.75	98.07	82.03	40.07	40.33
No.of branches per plant	8.45	3.44	14.23	10.18	10.31	98.68	6.53	77.28	37.77	38.02
No.of nodes on main branches	15.18	7.91	21.07	15.37	15.79	97.30	7.97	52.48	25.83	26.18
Days taken for first flowering	40.62	31.75	49.05	30.24	32.97	91.70	10.85	26.70	13.54	14.14
Dyas to 50% flowering	53.47	45.32	61.04	21.72	26.61	81.60	8.67	16.22	8.72	9.65
No. of cluster per plant	7.65	4.73	10.50	3.29	3.39	96.80	3.67	48.04	23.70	24.09
No. of flower per cluster	4.98	3.69	6.05	0.50	0.54	91.24	1.39	27.84	14.15	14.81
No. of green pods per cluster	2.17	1.06	3.35	0.48	0.49	97.80	1.41	64.92	31.87	32.22
No. of peduncles per plant	19.36	10.91	30.52	35.46	36.17	98.03	12.14	62.73	30.76	31.06
No. of pods per peduncle	2.57	1.24	3.99	0.75	0.76	98.65	1.77	68.78	33.61	33.84
Days to physiological maturity	70.44	64.87	75.34	7.71	16.30	47.28	3.93	5.58	3.94	5.73
Days to first picking	52.38	43.05	60.95	26.90	32.68	82.32	9.69	18.51	9.90	10.91
No. of pods per plant	16.97	5.11	31.41	62.78	63.40	99.02	16.24	95.72	46.70	46.93
Pod length (cm)	21.76	13.95	29.99	21.95	22.99	95.46	9.43	43.34	21.53	22.04
Pod diameter (cm)	0.81	0.52	1.08	0.03	0.03	95.65	0.34	42.37	21.03	21.51
Average pod weight (g)	8.62	3.95	13.57	9.79	9.90	98.89	6.41	74.33	36.28	36.49
No. of seeds per pod	11.53	7.33	16.49	7.15	7.46	95.88	5.40	46.78	23.19	23.69
Weight of 100 seeds (g)	12.42	5.55	19.15	18.41	18.65	98.69	8.78	70.69	34.54	34.77
Protein content (%)	22.41	20.10	25.47	1.55	2.59	59.90	1.99	8.86	5.56	7.18
T.S.S	5.44	3.42	7.51	1.44	1.50	96.08	2.42	44.51	22.04	22.49
Total sugars (mg/g fw)	23.96	11.32	48.41	92.50	93.58	98.85	19.70	82.22	40.14	40.37
Reducing sugar ((mg/g fw)	8.85	4.66	15.21	8.69	8.87	97.89	6.01	67.87	33.30	33.66
Non-reducing sugars (mg/g fw)	15.28	6.71	32.41	47.32	47.77	99.05	14.10	92.32	45.03	45.25
Pod yield plant-1 (g)	158.70	20.18	370.40	10373.99	10443.59	99.33	209.12	131.76	64.18	64.39
Pod yield/plot (kg)	4.22	1.11	8.75	5.74	5.79	99.22	4.92	116.41	56.73	56.95
Pod yield (qha ⁻¹)	126.44	34.41	260.10	4902.99	4934.22	99.37	143.79	113.72	55.38	55.56

During first year, highest magnitude of phenotypic and genotypic coefficient of variation was recorded in pod yield plant-1 (63.42 and 63.18) followed by pod yield/plot (55.73 and 55.57), pod yield qha⁻¹ (55.30 and 55.13), non-reducing sugars (46.85 and 46.69), number of pods plant-1 (45.90 and 45.70), total sugars (41.99 and 41.73), whereas, during second year it recorded in pod yield plant-1 (64.39 and 64.18) followed by pod yield/plot (56.95 and 56.73), pod yield qha⁻¹ (55.56 and 55.38), number of pods plant-1 (46.93 and 46.70), non-reducing sugars (45.25 and 45.03), total sugars (40.37 and 40.14), plant height (40.33 and 40.07). Similar results were also reported by Thangam et al. [28], Patil et al. [12] and Kavyashree et al. [24] in cowpea. It indicates that expression of genotype is affected by environmental factor.

Days to first picking recorded moderate PCV and GCV while lower estimates of phenotypic coefficient of variation were recorded for the characters days to 50% flowering, protein content and days to physiological maturity as shown in Table.

3.5 Heritability (Broad sense) and Genetic Advance

The estimate of heritability, genetic advance and genetic advance as per cent of mean (%) is presented in the Table 2.a and 2.b respectively for both the years.

Estimates of heritability were highest during both the years respectively viz., pod yield per plot and pod yield per hectare (99.40 and 99.37%), non-reducing sugar (99.32 and 99.05%), pod yield per plant (99.26 and 99.22%), number of pods per plant (99.13 and 99.02%), plant height (98.79 and 98.75%), total sugars (98.78 and 98.85%), average pod weight (98.74 and 98.89%), number of branches per plant (98.73 and 98.68%), weight of 100 seeds (98.57 and 98.69%), number of pods per peduncle (98.29 and 98.65%), reducing-sugar (98.21 and 98.89%), number of green pods per cluster (97.91 and 97.80%), number of peduncles per plant (97.56 and 98.03%), number of nodes on main branches (97 and 97.30%), total soluble solids (96.66 and 96.08%), number of clusters per plant (96.61 and 96.80%), number of seeds per pod (96.37 and 95.88%), pod diameter (95.27 and 95.65%), pod length (95.14 and 95.46%), days taken to first flowering (90.64 and 91.70%), number of flowers per cluster (90.25 and 91.24%), days to first picking (83.44 and

82.32%), days to 50% flowering (82.19 and 81.60%), protein content (61.48 and 60.0%).

During first year (2020-21) the range of genetic advance in per cent of mean was from 5.57% to 99.67%. During second year (2021-22) the range of genetic advance in per cent of mean was from 5.58% to 99.76%. High estimates of genetic advance was observed for most of the characters under study in first and second year respectively, pod yield per plant (99.67% and 99.76%), pod yield qha⁻¹ (99.23% and 99.72%), pod yield per plot (99.13% and 99.41%), non-reducing sugar (95.85% and 92.32%), number of pods per plant (93.73% and 95.72%), total sugars (85.44% and 82.22%), plant height (83.33% and 82.03%), number of branches per plant (76.47% and 77.28%), average pod weight (74.64% and 74.33%), weight of 100 seeds (71.73% and 70.69%), reducing-sugar (67.94% and 67.87%), number of pods per peduncle (67.38% and 68.78%), number of green pods per cluster (64.87% and 64.92%), number of peduncles per plant (63.10% and 62.73%), number of nodes on main branches (53.01% and 52.48%), number of seeds per pod (49.23% and 46.78%), number of clusters per plant (48.11% and 48.04%), total soluble solids (45.65% and 44.51%), pod diameter (43.14% and 42.37%), pod length (41.32% and 43.34%), number of flowers per cluster (27.40% and 27.84%), days taken to first flowering (26.60% and 26.70%).

Estimates of heritability coupled with genetic advance is more important for plant breeder than heritability estimates alone for undertaking effective plant breeding programme. High heritability estimates along with high genetic advance were reported pod yield per plant, pod yield qha⁻¹, pod yield per plot, non-reducing sugar, number of pods per plant, total sugars, plant height, number of branches per plant, average pod weight, weight of 100 seeds, reducing-sugar, number of pods per peduncle, number of green pods per cluster, number of peduncles per plant, number of nodes on main branches, number of seeds per pod, number of clusters per plant, total soluble solids, pod diameter, pod length, number of flowers per cluster, days taken to first flowering. Johnson et al. [9] suggested that high heritability combined with high genetic advance is indicative of additive gene action and selection based on these parameters would be more reliable. These results revealed that, these traits are having additive gene action and less influence of environmental factors on expression of traits so

that, these characters can be select for improving seed yield in further generation. Similar results were obtained by Viswanatha and Yogesh [29] for days to 50 per cent flowering, number of branches per plant, clusters per plant, pods per plant; Krishnaraj et al. [30] for pod yield, green pod yield per plant, seed yield per plant pod length and number of pods per plant; Thangam et al. [28] for pod yield per plant (g) and pod weight (g) and Varanya et al. [31] for number of leaves per plant, LAI, green fodder yield per plant, stem dry weight per plant, leaf dry weight per plant, plant height and seed yield per plant [32-35].

The high heritability with moderate genetic advance was recorded by days to first picking and days to 50% flowering while high heritability with low magnitude of genetic advance was observed for characters protein content and days to physiological maturity. High heritability with low genetic advance showing that the expression of traits is more likely to be influenced by environmental factors and controlled by non-additive gene action. Similar results were also reported by Khanpara et al. [36] for days to 50% flowering.

4. CONCLUSION

Based on the overall analysis, it can be concluded that the genotyped involved in the study has a substantial amount of variability for various traits. Most of the economic traits showed additive gene action for its expression. The selection parameters conclude that these genotypes can be used in our breeding program as a parental material/donor.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares 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 manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Chaudhary AR, Solanki SD, Rahevar PM, Patel DA. Genetic Variability, Correlation and Path Coefficient Analysis for Yield and
2. Singh BB, Chambliss OL, Sharma B. Recent advances in cowpea. In: Singh, B.B., Mohan Raj, D.R., Dashiell, and Jackai, L.E.N. Advances in cowpea research. Co-publication of International Institute of Tropical Agriculture (IITA) and Japan International Research Center for Agricultural Sciences (JIRCAS), Ibadan, Nigeria. 1997:30-49
3. Anonymous. Annual Progress Report 2021-22, DPD, Bhopal; 2022.
4. Patil AR, Shinde GC, Awari VR, Tambe SI. Genetic variability studies in seed cowpea (*Vigna unguiculata* L. Walp) genotypes. International Journal of Chemical Studies. 2021;9(4):39-42.
5. Hedge JE, Hofrieter BI. In: Methods in carbohydrate chemistry. Vol. 17, R.L. Whistler and IN. Bc Miller, eds. Academic Press, New York; 1962.
6. Panse VG, Sukhatme PV. Statistical method for agril, workers ICAR, New Delhi, India; 1967.
7. Burton GW. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. Agronomy Journal. 1952;45:478-481.
8. Hanson WD. Heritability. Statistical genetics and plant breeding NAS_NRC, Washington, Publ., 1982: 1963:125-140.
9. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in Soybean and their implication in selection. Agron. J. 1955;47:477-483.
10. Shanko D, Mebeaselassie A, Habtamu Z. Genetic variability and heritability of yield and related characters in cowpea (*Vigna unguiculata* L. Walp.). *Research in Plant Biology*, 2014;4(2):21-26.
11. Mahesh S, Sharma PP, Deva RM, Sharma H. Study of genetic variability parameters in cowpea (*Vigna unguiculata* L.) germplasm lines. *Annals of Plant and Soil Research*. 2017;19(2):185-189.
12. Patil AR, Shinde GC, Awari VR, Tambe SI. Genetic variability studies in seed cowpea (*Vigna unguiculata* L. Walp) genotypes. International Journal of Chemical Studies. 2021;9(4):39-42.
13. Sarath PS, Reshma T. Genetic variability studies in cowpea (*Vigna unguiculata* L. Walp). International Journal of Agricultural

- Science and Research. 2017;7(7):2250-0057.
14. Satish S, Shridhar, Kumar V, Kulkarni NS. Estimation of genetic variability for dual purpose in cowpea (*Vigna unguiculata* L. Walp.). Plant Archive. 2017;17(2):887-891.
 15. Ravish P, Satyawan AS, Satyapal D, Preeti RK. Genetic variability and association studies in cowpea (*Vigna unguiculata* L. Walp) for seed yield and related traits. Forage Research. 2020;46 (3):232-235.
 16. Riddhi K, Dhaduk LK. Correlation and path analysis study in Cowpea (*Vigna unguiculata* (L.) Walp.). Int. J. Chem. Stud. 2019;7(5):3019-3022.
 17. Jogdhande S, Vijay S, Kale, Nagrev PK. Correlation and path analysis study in cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. International Journal of Current Microbiology and Applied Sciences. 2017; 6(6):3305-3313.
 18. Singh OV, 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 Research. 2018;37(5):0250-5371.
 19. Mohan S, Sharma PP, Upadhyay B, Bairwa HL. Study of correlation coefficient and path analysis in cowpea [*Vigna unguiculata* (L.) Walp] germplasm line. International Journal of Development Research. 2016;6(8):9011-9016.
 20. Tsegaye D, Hussein M, Berhanu A. Correlation and path coefficient analysis of yield and yield related traits interactions in Ethiopian cowpea (*Vigna unguiculata* L. Walp) accessions. Academic Research Journal of Agricultural Science and Research. 2018;6(9):526-530.
 21. Manggoel W, Uguru MI., Ndam ON, Dasbak MA. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [*Vigna unguiculata* (L.) Walp] accessions. Journal of Plant Breeding and Crop Science. 2012; 4(5):80-86.
 22. Sapara, G.K., Javia, R.M. and Pokar, M.V. (2014). Genetic variability, heritability and genetic advance in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of plant sciences*, 9 (2): 326-329.
 23. Verma AK, Mehta AK, Gontia AS, Sharma A, Singh RP, Singh P. Genetic variability, heritability and genetic advance studies for yield components in F₂ generation of cowpea (*Vigna unguiculata* L. Walp). International Journal of Chemical Studies. 2015;7(6):3084-3088.
 24. Kavyashree NM, Sanjeev KD, Patil BR, Hegde MG, Shamrao J. Genetic Variability and Character Association Studies on Yield and Yield Attributing Traits in Grain Type Cowpea (*Vigna unguiculata* (L.) Walp.). International Journal of Bio-resource and Stress Management. 2023; 14(1):012-018.
 25. Ajayi AT. Genetic Variability of Quantitative Traits in F₂ Hybrids of Cowpea and Parent Lines. J. Genet. Resour. 2023;9(1):1-10.
 26. Tambitkar NB, Pethe UB, Desai SS, Dhopavkar RV, Kadam JJ. Correlation and path analysis studies in cowpea [*Vigna unguiculata* L. Walp]. The Pharma Innovation Journal. 2020;9(12):314-316.
 27. Sabale GR, Bhave SG, Desai SS, Dalvi MB, Pawar RP. Variability heritability and genetic advance studies in F₂ generation of cowpea (*Vigna unguiculata* sub sp. *unguiculata*). Int. J. Curr. Microbiol. App. Sci. 2018;7(9):3314-3320.
 28. Thangam M, Ramachandrudu K, Kumar AJ, Safeena SA, Priya Devi S. Variability and genetic divergence in vegetable cowpea [*Vigna unguiculata* L. Walp] germplasm of Goa. J. Hortl. Sci. 2020; 15(1):45-51.
 29. Viswanatha KP, Yogeesh LN. Genetic variation and morphological diversity in cowpea (*Vigna unguiculata* L. Walp). Archives of Agriculture and Environmental Science. 2017;2(3):176-180.
 30. Krishnaraj NR, Desai SS. Sawardekar SV, Burudkar MM. Study of genetic variability parameter in F₂ generation of interspecific hybrids in cowpea [*Vigna unguiculata* L. Walp]. International Journal on Pure and Applied Biosciences. 2018;6(1):954-958.
 31. Varanya A, Gayathri G, Arya K, Usha, Thomas C, Pratheesh PG, Priyanka H. Genetic variability and genetic parameters analysis of 143 fodder cowpea [*Vigna unguiculata* (L.) Walp] germplasm accessions for yield and yield attributing traits. The Pharma Innovation Journal. 2022;11(2):2595-2600.
 32. Mofokeng MA, Mashilo J, Rantso P, Shimelis H. Genetic variation and genetic advance in cowpea based on yield and yield-related traits. Acta Agriculturae Scandinavica, Section B—Soil & Plant Science. 2020;70(5):381-91.
 33. Umesh, Singh AK, Lal K, Singh V, Tripathy S, Kumar A, Singh N, Singh A. Studies on

- Estimates of Heritability and Genetic Advance for Certain Quantitative Traits in Fieldpea (*Pisum sativum* L. var. *arvense*). Int. J. Plant Soil Sci. 2024 36(7):393-8. Available:<https://journalijpss.com/index.php/IJPSS/article/view/4744> [Accessed on: 2024 Jun. 17];
34. Aishwarya G, Deepanshu. Investigation on Genetic Variability, Heritability, Correlation Studies in Cowpea (*Vigna unguiculata* L.) Int. J. Environ. Clim. Change. 2023;13(10): 173-82. [Accessed on: 2024 Jun. 17];
- Available:<https://journalijecc.com/index.php/IJECC/article/view/2627>
35. Aykroyd UR. Indian Council of Medical Research, Special Report. Vegetable, National Book Trust India, New Delhi. 1963;42:188-191.
36. Khanpara SV, Jivani LL, Vachhani JH, Kachhadia VH. Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. Electronic Journal of Plant Breeding. 2015;7(2):0975-928.

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Peer-review history:
The peer review history for this paper can be accessed here:
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