Studies on genetic variability, heritability and genetic advance in cowpea (*Vigna unguiculata* (L.) Walp.) for green pod yield and its component traits

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 Babasaheb Bhimrao Ambedkar University, Lucknow, 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) and it ranged from 0.03 (pod diameter) to 10443.59 (pod yield/plant) for second year. The genotypic variance ranged from 0.03 (pod diameter) to 9873.13 (pod yield/plant), while it ranged from 0.03 (pod diameter) to 10373.99 (pod yield/plant) in second year. During first year, highest magnitude of phenotypic and genotypic coefficient of variation was recorded in pod yield/plant (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 (64.39 and 64.18) followed by pod yield/plot (56.95 and 56.73). Traits like pod yield per plant, pod yield q/ha, 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, variability, GCV, PCV, heritability and genetic advance.

1. Introduction

The eminent leguminous crop recognized among humanity is the cowpea (*Vigna unguiculata* (L.) Walp.). It boasts a chromosomal count of 2n=22 (Darlington and Wylie, 1955) and stands as a constituent of the Fabaceae subfamily within the Leguminosae family (Mackie and Smith, 1935). This plant thrives across the semi-arid tropics, encompassing sectors of Asia, Africa, Southern Europe, the Southern United States, and Central and South America (Timko *et al*., 2007).

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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% (Anonymous, 2022).

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 (Aykroyd, 1963). 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.

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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. Material 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. List of all genotypes and their source of collection used in this experiment are presented here in Table 1.

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 (g), pod yield/plot (kg), pod yield (q/ha), 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 (1962).

The mean value of all the traits were subjected to statistical analyses as analysis of variance following Panse and Sukhatme (1967), Coefficient of variation estimated as per Burton (1952), Heritability in broad sense as per Hanson (1963), Genetic advance and Genetic advance in percent of mean using formula suggested by Johnson *et al*. (1955).

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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 2.a and 2.b. Variability in several quantitative characters of cowpea was also reported by Shanko *et al.* (2014), Mahesh *et al.* (2017) and Patil *et al*. (2021).

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 3.a and 3.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 (2017) for plant height, Satish *et al.* (2017) for primary branches, Shanko *et. al.* (2014) for days to 50% flowering, Ravish *et al.* (2020) for days to maturity, Riddhi and Dhaduk (2019) 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.* (2017) for number of nodes, Singh *et al.* (2018) for number of clusters per plant, Mohan *et al.* (2016) for number of flowers, Tsegaye *et al.* (2018) for number of pods per plant, Manggoel *et al.* (2012) 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*. (2014) for number of pods per plant, Verma *et al.* (2015) for pod weight, Kavyashree *et al*. (2023) for 100-seeds weight, Ajayi (2023) 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^{0}Brix; 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.* (2017) and Tambitkar *et al.* (2020).

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 3.a and 3.b.

During first year (2020-21) the phenotypic variance ranged from 0.03 (pod diameter) to 9947.17 (pod yield/plant) and it ranged from 0.03 (pod diameter) to 10443.59 (pod yield/plant) for second year. The genotypic variance ranged from 0.03 (pod diameter) to 9873.13 (pod yield/plant), while it ranged from 0.03 (pod diameter) to 10373.99 (pod yield/plant) 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 (9947.17 and 9873.13), pod yield q/ha (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 (10443.59 and 10373.99), pod yield q/ha (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.* (2018) and Ravish *et al.* (2020).

3.4 Coefficient of variation

The estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variation (GCV) are presented in Table 3.a and 3.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).

During first year, highest magnitude of phenotypic and genotypic coefficient of variation was recorded in pod yield/plant (63.42 and 63.18) followed by pod yield/plot (55.73 and 55.57), pod yield q/ha (55.30 and 55.13), non-reducing sugars (46.85 and 46.69), number of pods/plant (45.90 and 45.70), total sugars (41.99 and 41.73), whereas, during second year it recorded in pod yield/plant (64.39 and 64.18) followed by pod yield/plot (56.95 and 56.73), pod yield q/ha (55.56 and 55.38), number of pods/plant (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.* (2020), Patil *et al.* (2021) and Kavyashree *et al*. (2023) 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 3.a and 3.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 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 q/ha (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 q/ha, 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*. (1955) 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 (2017) for days to 50 per cent flowering, number of branches per plant, clusters per plant, pods per plant; Krishnaraj *et al.* (2018) for pod yield, green pod yield per plant, seed yield per plant pod length and number of pods per plant; Thangam *et al.* (2020) for pod yield per plant (g) and pod weight (g) and Varanya *et al*. (2022) 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.

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*. (2015) for days to 50% flowering.

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.

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Table 1: List of genotypes and their sources used in present investigation

S.N.	Genotype	Source	S.N.	Genotype	Source
1	IC 628902	IIVR, Varanasi	16	EC 97306	Dr. RPCAU Pusa, Bihar
2	EC 97738	Dr. RPCAU Pusa, Bihar	17	PL 3	Dr. RPCAU Pusa, Bihar
3	IC 628901	IIVR, Varanasi	18	EC 9736	Dr. RPCAU Pusa, Bihar
4	IC 628897	IIVR, Varanasi	19	PL 5	Dr. RPCAU Pusa, Bihar
5	EC 390223	Dr. RPCAU Pusa, Bihar	20	GP 56	Dr. RPCAU Pusa, Bihar
6	IC 628892	IIVR, Varanasi	21	Kashi Shyamal	IIVR, Varanasi
7	IC 390268	Dr. RPCAU Pusa, Bihar	22	EC 9739	Dr. RPCAU Pusa, Bihar
8	GP 3	Dr. RPCAU Pusa, Bihar	23	EC 390252	Dr. RPCAU Pusa, Bihar
9	Kashi Gauri	IIVR, Varanasi	24	Kashi Kanchan	IIVR, Varanasi
10	EC 1738	Dr. RPCAU Pusa, Bihar	25	GP 58	Dr. RPCAU Pusa, Bihar
11	IC 628893	IIVR, Varanasi	26	Kashi Unnati	IIVR, Varanasi
12	PL 2	Dr. RPCAU Pusa, Bihar	27	PL 1	Dr. RPCAU Pusa, Bihar
13	EC 390216	Dr. RPCAU Pusa, Bihar	28	Kashi Nidhi	IIVR, Varanasi
14	EC 9135	Dr. RPCAU Pusa, Bihar	29	IC 628900	IIVR, Varanasi
15	EC 19736	Dr. RPCAU Pusa, Bihar	30	IC 628899	IIVR, Varanasi

Table 2.a: 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 (g)	Pod yield/plot (kg)	Pod yield (q/ha)
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

Table 2.b: 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

Commented [BS5]: The coefficient of variation is very low in some traits. Explain the reason. It seems that it should be at least more than ten, but this has not happened.

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 (g)	Pod yield/plot (kg)	Pod yield (q/ha)
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 3.a: 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 (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 (q/ha)	123.56	32.51	249.51	4640.83	4668.81	99.40	139.91	113.23	55.13	55.30

Table 3.b: 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 (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 (q/ha)	126.44	34.41	260.10	4902.99	4934.22	99.37	143.79	113.72	55.38	55.56

Commented [BS6]: Heritability is high in most traits. Therefore, the additive effects of genes controlling these traits are more prominent. Do you think it is possible to correct the traits you mentioned with high heritability by phenotypic selection?