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Genetic Variability of Quantitative Traits in F2 Hybrids of Cowpea and Parent Lines

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ABSTRACT

The grain yield of cowpea across the producing countries falls below expectation due to diverse production constraints. Hence, it seems that broadening its genetic base for sustainable yield improvement and tolerance to environmental stresses in the context of global climate change is necessary. Therefore, the objectives of the present study are to evaluate the genetic differences and correlation of characters in F_2 hybrids of cowpea and their parent lines. The present study was performed in the field during the rainy season. The obtained data were subjected to various statistical analyses. The hybrids and the parents exhibited significant variation for all the traits studied, including the seed yield. High variability among the offspring and parents suggests better chances of producing the desired recombinants in the successive generation. Emergence ranged between 53.04% in offspring of IT98K-555-1 × IT98K-205-8 and 73.68% in IT98K-555-1. Parents exhibited higher main branches (4.72 and 4.80). IT98K-555-1 was superior for most traits, including the seed yield per plant (288.64 g). However, IT98K-205-8 flowered first at day 45 while IT98K-555-1 flowered last at day 56. Traits such as emergence percentage, days to first flowering, pods/plant, and seed yield/plant exhibiting a combination of high broad-sense and narrow-sense heritability (> 60%) and high genetic advance as a percent of the mean (> 20%) indicated that they were under genetic control and responsive to the improvement. Traits such as plant height, seeds/pod, pods/plant, and seeds/plant with a high positive genotypic correlation ($r \geq 0.99$) to seed yield/plant could be considered the core selection indices in cowpea improvement programs. Nonetheless, further studies into F_3 and later generations are required to exploit the relationships between the high yields, seed coat color, and drought tolerance among the cowpea hybrids.

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Introduction

Cowpea (*Vigna unguiculata* L. Walp) has been of high importance in Nigerian nutrition and the nutrition of other tropical and subtropical countries (Nkomo *et al*., 2021). This importance lies in its high protein content (about 25%), tremendous capacity to replenish soils through nitrogen fixation (between 70–350 kg of nitrogen per hectare), rapid maturity (around 55 days), extraordinary adaptability to drought conditions and soils of diverse pH range compared to cereals and other legumes (Pereira, 2016; Cui *et al*., 2020). These attributes make it a choice crop for cultivation among resource-poor farmers. Moreover, cowpea has different uses across different subtropical and tropical countries. These uses are influenced by consumer preferences that are based on different combinations of phenotypic traits exhibited by the crop (Shwetha *et al*., 2021; Ajayi *et al*., 2020).

Nigeria has consistently topped the list of cowpea-producing countries globally, and in the year 2020, it produced 2.61 tons out of the estimated 7.23 tons (FAOSTAT, 2020). However, the grain yield of cowpea in Nigeria and other African countries falls below expectation due to many production constraints. These constraints are classified as abiotic limitations such as salinity, drought, soil acidity, and toxicity which are mostly the consequences of climate change, and biotic constraints, such as infestation by diseases and attack by pests (Adetumbi *et al*., 2019; Ajayi *et al*., 2022). Cowpea is predominantly a self-pollinating crop (Shwetha *et al*., 2021), and as a consequence, it has a narrow genetic base that underlies its vulnerability to the dangers posed by various environmental constraints (Garcia-Oliveira *et al*., 2020; Lazaridi *et al*., 2016). Hence, there is an urgent need to broaden the genetic base of the available cowpeas for sustainable yield improvement and tolerance to adverse the environmental stresses.

The commencement of any plant breeding program relies on genetic variation. The potential contribution of genotypes in any breeding program depends on the knowledge of their genetic variability and interactions of their traits. This information is crucial in genetic improvement programs for the identification of useful genes as well as for understanding their behavior in breeding schemes (Adetumbi *et al*., 2019; Ajayi *et al*., 2020). Furthermore, consideration must be given to genotypes of diverse origins in germplasm assemblage intended as parental stocks. This takes into account their adaptability to specific constraints which is vital for sourcing the genes to breed improved varieties. There are significant genetic differences between cowpea genotypes in tropical countries, which can be studied as a source of hybrid development for specific restrictions (Ajayi *et al*., 2020). Therefore, an appropriate choice of parental lines is critical to an effective breeding plan for cowpea.

Some important characteristics of the accessions IT98K-205-8 and IT98K-555-1 used in this study have been reported (Ajayi *et al*., 2020). Hence, another key step to be taken is to cross IT98K-205-8 as a drought tolerant genotype with IT98K-555-1 to produce promising genotypes with improved drought tolerance while preserving other superior traits of IT98K-555-1 such as high seed yield. Therefore, this study aims to produce high-yielding, drought-tolerant hybrids capable of making promising genotype selections. Hence, the objectives of the present study are to evaluate the genetic differences and correlation of characters in F_2 hybrids of cowpea from IT98K-205-8 cross with IT98K-555-1.

Materials and Methods

Source of seeds and hybrids

Parent Lines: IT98K-555-1 and IT98K-205-8 were obtained from the International Institute of Tropical Agriculture (IITA) in Nigeria. The hybrids were generated by direct and reciprocal crossing in the screen house and F_1 was evaluated in the field; these were done between October 2017 and August 2018. The crossing details, subsequent evaluation, and the important traits of the accessions are published in (Ajayi *et al*., 2020). The F_2 hybrids and their parental lines are presented in Table 1.

Table 1. Parent lines and F_2 hybrids of cowpea.

Number	Generation
1	IT98K–205–8 (Parent 1)
2	IT98K-555-1 (Parent 2)
3	IT98K-205-8 × IT98K-555-1 (F_2)
4	IT98K-555-1 × IT98K-205-8 (F_2)

Location and procedure

The study was done at Adekunle Ajasin University, Plant Breeding Experimental Field, Department of Plant Science and Biotechnology. A few characteristics of the environment are mentioned in Ajayi *et al*. (2022). The set-up was performed during the rainy season between August and December 2019. The evaluation of the genotypes was done by adopting a Randomized Complete Block Design (RCBD) in the field with four replicates. In each replicate, there were four plots for the genotypes, each with a dimension of 8 m × 0.6 m. Each plot was 1 m away from the other and each replicate was done in an interval if 2 m. Two rows on each plot were utilized for the planting of the seeds per genotype with an intra-row space of 30 cm and inter-row space of 50 cm. Two seeds were sown per hill for each genotype, and two weeks after seedling emergence, seedlings were thinned to one per hill after the data on emergence percentage had been taken, making the final number of plants per genotype. Per replicate, the final number was fifty, while the number across the four replicates was two hundred per genotype. Furthermore, few hills in which no seedlings emerged were transplanted, through removing one seedling from hills where two seedlings emerged.

Data collection

Data on morphological parameters were collected five weeks after sowing, including the quantitative traits of plant height and number of main branches. The number of days to first flowering was recorded as genotypes flowered. Data such as the number of peduncles per plant, peduncle length, and pods per plant, pod length, seeds per pod, and seeds per plant, one hundred seeds weight, and seed yield per plant were recorded at maturity (when pods dried and were harvested). Data were subjected to statistical analysis. As cited by Ajayi *et al*. (2014), estimates of genetic parameters were done as follows: Genotypic (Vg) and phenotypic (Vp) Variances were estimated as $Vg = (MSg - MSe) \div r$ and $Vp = Vg + MSe$ where MSg, MSe, and r represented square genotype, mean square error, and the number of replicates, respectively. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated as $PCV = (\sqrt{Vp} \div GX) \times 100$ and $GCV = (\sqrt{Vg} \div GX) \times 100$ where Vp, Vg, and GX represented Vp, Vg, and grand mean of the trait under consideration, respectively. They were classified as low (0 – 10%), moderate (10- 20%) and high (above 20%). Broad sense heritability (h^2B) was estimated through $h^2B = (Vg \div Vp) \times 100$ and grouped as low (0- 30%), moderate (30-60%), and high (above 60%). Genetic advance (GA) was calculated through

$GA = h^2B \times K \times \sqrt{Vp}$ where K was a constant (2.06) at 50% selection intensity. Genetic advance was the percent of the mean (GAM) which was calculated as $GAM = (GA \div GX) \times 100$, and ranked as low (0-10%), moderate (10-20%) and high (above 20).

Narrow-sense heritability was analyzed by parent-offspring regression. Genotypic and phenotypic correlations of the quantitative traits were performed with version 4.1 of the plant breeding tools (2014), and coefficients were compared against the "t" table correlation values (at 0.05 and 0.01) at n–2 degrees of freedom (Fisher and Yates, 1963).

Results

Genotypic differences

ANOVA revealed significant differences between parents and hybrids for all quantitative traits. Significant differences were also observed among the replicates for all traits except for the emergence percentage, seed yield, plant height, number of main branches, seed weight, pod length, and pods per plant. The range of the Coefficient of Variation (CV) was from the lowest (1.11%) in the number of seeds per plant to the highest (5.25%) in the number of pods per plant (Table 2).

Table 2. Mean square values of quantitative traits of parent lines and F_2 hybrids of cowpea.

Source of Variance	DF	EMP (%)	PH (cm)	NMB	DFF	PEDL (cm)	PDL (cm)	SPP	PDP	100-SW (g)	SDPL	SYD (g)
Treatment	3	294.72*	5.11*	0.06*	127.53*	3.04*	2.31*	2.14*	4925.56*	0.83*	1287361.94*	42367.94*
Replication	3	0.01^{ns}	0.50^{ns}	0.02^{ns}	1.14*	1.52*	0.15^{ns}	0.54*	3.84^{ns}	0.00^{ns}	140.51*	4.75^{ns}
Error	9	1.18	1.10	0.04	0.40	0.75	0.69	0.42	7.05	0.28	70.61	7.75
CV (%)		1.76	5.08	4.27	1.23	2.88	4.60	4.47	5.25	2.99	1.11	2.07

**: Significant at $P \leq 0.05$; ns: not significant*; DF: Degree of Freedom; CV: Coefficient of Variation.

EMP: Emergence Percentage; PH: Plant Height; NMB: Number of Main Branches; DFF: Days to First Flowering; PEDP: Peduncles Per Plant; PEDL: Peduncle Length; PDP: Pods per Plant; PDL: Pod Length; SPP: Seeds per Pod; 100-SW: One Hundred Seeds Weight; SDPL: Seeds per Plant; SYD: Seed Yield per Plant.

Mean Performance

The mean performance for quantitative traits among the parent lines and the F_2 hybrid of cowpeas are presented in Table 3. Emergence percentage ranged from the lowest (53.04%) in IT98K-555-1 × IT98K-205-8 to the highest (73.68%) in IT98K-555-1 (P_2). The comparison between the parents and the hybrids showed that the parents exhibited higher main branches (4.72 and 4.80). The highest plant height (22.29 cm), peduncles per plant (4.66), seeds per pod (16.55), pods per plant (103.25), seeds per plant (1603.56), and seed yield per plant (288.64 g) were obtained in parent IT98K-555-1 (P2), while parent IT98K-205-8 (P1) had the lowest seed yield per plant, peduncle length, seeds per plant, pod length, pods per plant, and seed weight. Parent IT98K-205-8 (P1) flowered first with a mean value of 45 days, followed by IT98K-205-8 × IT98K-555-1 (47 days), while the last flowering parent was IT98K-555-1 with a mean of 56 days (Table 3).

Table 3. Mean performance of parent lines and F_2 hybrids of cowpea for quantitative traits.

Genotype	**EMP (%)**	**PH (cm)**	**NMB**	**DFF**	**PEDL (cm)**	**PDL (cm)**
IT98K–205–8 (P_1)	59.94±0.33^{b}	19.96±0.85^{a}	4.72±0.01^{a}	45.24±0.23^{a}	28.95±0.30^{a}	16.95±0.19^{a}
IT98K-555-1 (P_2)	73.68±0.73^{d}	22.29±0.30^{b}	4.80±0.38^{a}	56.19±0.24^{c}	30.65±0.66^{b}	18.37±0.44^{b}
IT98K–205–8× IT98K-555-1	61.67±1.09^{c}	20.65±0.26^{a}	4.69±0.16^{a}	47.31±0.40^{b}	30.69±0.63^{b}	18.67±0.49^{b}
IT98K-555-1 × IT98K–205–8	53.04±0.08^{a}	19.83±0.27^{a}	4.51±0.05^{a}	55.69±0.56^{c}	30.73±0.11^{b}	18.22±0.29^{b}
Grand Mean	62.08±7.72	20.68±0.33	4.68±0.05	51.11±1.27	30.25±0.29	18.05±0.24

Genotype	**SPP**	**PDP**	**100-SW (g)**	**SDPL**	**SYD (g)**
IT98K–205–8 (P_1)	14.40±0.26^{a}	30.67±0.71^{a}	17.25±0.25^{a}	441.14±0.25^{a}	76.08±1.15^{a}
IT98K-555-1 (P_2)	15.55±0.33^{b}	103.25±2.04^{c}	18.00±0.00^{bc}	1603.56±3.64^{d}	288.64±0.66^{c}
IT98K–205–8× IT98K-555-1	13.80±0.26^{a}	33.83±0.62^{ab}	18.25±0.25^{c}	466.49±5.09^{b}	85.12±1.17^{b}
IT98K-555-1 × IT98K–205–8	14.40±0.45^{a}	35.00±1.09^{b}	17.50±0.29^{ab}	502.53±3.21^{c}	87.97±1.97^{b}
Grand Mean	14.54±0.22	50.69±7.89	17.75±0.14	753.43±126.89	134.45±23.02

Within a column, mean values with the same superscript are not significantly different from one another at $P \leq 0.05$ based on DMRT. EMP: Emergence Percentage; PH: Plant Height; NMB: Number of Main Branches; DFF: Days to First Flowering; PEDL: Peduncle Length; PDL: Pod Length; SPP: Seeds per Pod; PDP: Pods per Plant; 100-SW: One Hundred Seeds Weight; SDPL: Seeds per Plant; SYD: Seed Yield per Plant.

Genetic Parameters

Table 4 presents the estimates of the genetic parameters. Genotypic Variance (GV) and Phenotypic Variance (PV), respectively, ranged from the lowest (0.005 and 0.045) in the number of the main branches to the highest (321822.83 and 321893.44) in the number of the seeds per plant. The existence of low Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) (≤ 10%) were observed in the plant height, pod length, the number of main branches, seeds per pod, peduncle length, and seed weight. Moderate (10 – 20%) GCV and PCV were observed in the emergence percentage and days to first flowering. However, both GCV and PCV were found to be high (≥ 30%) in the seed yield per plant, seeds per plant, and number of pods per plant. Furthermore, broad-sense heritability was low in the number of the main branches (11.11%), and moderate in the seed weight, plant height, seeds per pod, peduncle length, and pod length with the range falling between 33.33 and 50.59%. Nevertheless, traits such as the emergence percentage, seed yield per plant, days to first flowering, seeds per plant, and the number of pods per plant exhibited a high broad-sense heritability, ranging between 98.42 and 99.98%. Genetic Advance as a percent of the Mean (GAM) was high (between 22.62 and 157.61%) in traits such as the emergence percentage, seed yield per plant, days to first flowering, seeds per plant, and pods per plant, while it was low (< 10%) in the rest of the traits. Traits such as the emergence percentage, days to first flowering, seed yield per plant, pod length, seed weight, and pods per plant exhibited a high narrow-sense heritability (between 61.55 and 100%). However, narrow-sense heritability was low (< 10%) in traits such as the plant height, peduncle length, the number of main branches, and number of seeds per plant, while seeds per pod exhibited a moderate narrow-sense heritability (47.86%).

Correlation of Quantitative Traits

All significant correlations at both levels (genotypic and phenotypic) were positive (Table 5). Within the genotypic level, the emergence percentage exhibited a highly significant correlation (1.00**) with traits such as the number of main branches and plant height. The plant height exhibited a highly significant correlation (1.00**) with traits such as the pods per plant, seeds per plant, and seed yield. The peduncle length correlated with the pod length, while the pod length displayed a highly significant correlation (1.00**) with the seed weight. Traits such as the seed yield and the seeds per plant in conjunction with the pods per plant exhibited a highly significant correlation (1.00**) with the seeds per pod. However, while the pods per plant at both levels (genotypic and phenotypic) displayed a highly significant correlation with the seeds per plant (1.00** and 0.99**) and seed yield (1.00** and 1.00**), the seeds per plant also displayed a highly significant correlation (0.99** and 0.99**) with the seed yield. Furthermore, at the phenotypic level, the plant height and emergence (0.96*), the plant height and seed yield (0.95), the peduncle length, and the pod length (0.97) were each positively correlated.

Table 4. Genetic parameters estimation of quantitative traits of parent lines and F_2 hybrids of cowpea.

Trait	Min	Max	Mean	GV	PV	GCV (%)	PCV (%)	H^2B (%)	GAM (%)	h^2b (%)
EMP	53.00	75.47	62.08	73.39	74.57	13.80	13.92	98.42	28.09	82.79
PH	18.16	22.97	20.68	1.00	2.10	4.84	7.01	47.62	6.87	13.07
NMB	4.20	4.92	4.68	0.005	0.045	1.51	4.53	11.11	1.04	11.67
DFF	44.71	56.83	51.11	31.78	32.18	11.03	11.09	98.76	22.62	66.11
PEDL	28.32	32.58	30.25	0.57	1.32	2.49	3.80	43.18	3.38	2.53
PDL	16.60	19.78	18.05	0.41	1.10	3.55	5.80	37.27	4.46	99.92
SPP	13.2	16.20	14.54	0.43	0.85	4.51	6.34	50.59	6.61	47.86
PDP	29.33	107.67	50.69	1229.63	1236.68	69.18	69.38	99.43	142.10	93.93
100-SW	17.00	19.00	17.75	0.14	0.42	2.11	3.64	33.33	2.51	100.00
SDPL	432.35	1610.72	753.43	321822.83	321893.44	75.29	75.30	99.98	155.09	0.57
SYD	73.50	289.93	134.45	10590.05	10597.80	76.54	76.57	99.93	157.61	61.55

GV: Genotypic Variance; PV: Phenotypic Variance; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; H^2B: Heritability in the Broad sense; GAM: Genetic Advance as percent of the Mean; H^2N: Heritability in the Narrow sense; EMP: Emergence Percentage; PH: Plant Height; NMB: Number of Main Branches; DFF: Days to First Flowering; PEDL: Peduncle Length; PDP: Pods per Plant; PDL: Pod Length; SPP: Seeds per Pod; 100-SW: One Hundred Seeds Weight; SDPL: Seeds per Plant; SYD: Seed Yield per Plant.

Discussion

Global climate change is also a major challenge to cowpea cultivation in Nigeria and other tropical and subtropical countries. Therefore, the demand for more diverse and tolerant genotypes can encourage breeding programs in an effort to ameliorate the issues of increased heat and drought. The rate of cultivar improvement in cowpea depends on the degree to which the desirable genes can introgress into varieties that are vulnerable to adverse environmental constraints (Adetumbi *et al*., 2019). Also, suitable techniques must be deployed to assess the performance of crosses in their early segregating generations for breeding potential and isolation of superior segregates (Shwetha *et al*., 2021). The major research objective for various tropical crops is the improvement of seed yield (Edematie *et al*., 2021) in the context of the consequences imposed by the present climate change. Therefore, breeding plans intended at increasing productivity in cowpea and leading to generating climate-smart varieties will benefit from information on the inheritance of traits that contribute to yield. Hence, the present study assessed the genetic differences and correlation of characters in the F_2 hybrids of cowpea.

Highly significant differences revealed by ANOVA among the parent and the hybrids for all traits measured indicated a sufficient level of differences among the genotypes. A similar degree of differences for quantitative traits has been reported in cowpea (Olunloyo *et al*., 2019), and snake beans (Sn andThomas, 2021). A similar wider range of mean in the F_2 generation among traits such as the seed yield per plant and number of pods per plant was reported in crosses of greengram and blackgram (Mahalingam and Manivannan, 2021). This high variability among the genotypes suggests better chances of producing desired recombinants in the successive generation (Roy & Shil, 2020; Sobda *et al*., 2018).

Table 5. Genotypic (upper) and phenotypic (below) correlation of quantitative traits of parent lines and F_2 hybrids of cowpea.

Trait	EMP (%)	PH (cm)	NMB	DFF	PEDL (cm)	PDL (cm)	SPP	PDP	100-SW (g)	SDPL	SYD (g)
		1.00**	1.00**	0.22	0.15	0.27	0.81	0.88	0.59	0.89	0.89
EMP (%)		0.96*	0.89	0.22	0.13	0.22	0.72	0.88	0.51	0.88	0.89
			1.00**	0.52	0.56	0.64	0.93	1.00**	0.71	1.00**	1.00**
PH (cm)			0.74	0.45	0.39	0.45	0.75	0.94	0.62	0.94	0.95*
				-0.32	0.02	-0.07	0.73	0.89	0.43	0.82	0.90
NMB				-0.21	-0.25	-0.09	0.49	0.62	0.34	0.57	0.63
					0.79	0.57	0.73	0.63	0.17	0.63	0.63
DFF					0.69	0.51	0.66	0.63	0.15	0.63	0.63
						1.00**	-0.01	0.41	0.94	0.38	0.40
PEDL (cm)						0.97*	0.09	0.35	0.71	0.33	0.35
							-0.02	0.37	1.00**	0.36	0.37
PDL (cm)							-0.00	0.32	0.86	0.31	0.32
								1.00**	-0.11	1.00**	1.00**
SPP								0.92	-0.01	0.92	0.92
									0.45	1.00**	1.00**
PDP									0.39	0.99**	1.00**
										0.43	0.44
100-SW (g)										0.37	0.39
											0.99**
SDPL											0.99**

*** Significant at $P \leq 0.01$; * Significant at $P \leq 0.05$.*

EMP: Emergence Percentage; PH: Plant Height; NMB: Number of Main Branches; DFF: Days to First Flowering; PEDL: Peduncle Length; PDP: Pods per Plant; PDL: Pod Length; SPP: Seeds per Pod; 100-SW: One Hundred Seeds Weight; SDPL: Seeds per Plant; SYD: Seed Yield per Plant.

In parent lines, the mean performance for all the quantitative traits was higher in parent IT98K-555-1, and this attribute was also reflected among the crosses for traits such as the emergence percentage, plant height, number of main branches, pod length, and seed weight, where IT98K-555-1 was used as the maternal parent (direct cross), indicating maternal effect. However, all the yield traits were higher in the reciprocal crosses, yet lower than what was obtained in parent IT98K-555-1. These results also ratify those acquired by Sobda *et al.* (2018) for the number of pods and seeds weight among the F_2 hybrids of cowpea obtained by reciprocal crosses. Nevertheless, the mean values among the hybrids for all quantitative traits were in most cases substantially lower than the mid-parent values except in peduncle length, pod length, and seed weight. Such transgressive segregation was found among the $F_{2:3}$ intraspecific hybrids of cowpea for the pod length, the number of peduncles, and the peduncle length (Garcia-Oliveira *et al*., 2020). Furthermore, parent IT98K-205-8 flowered earlier than the others on day 45 after planting followed by IT98K-205-8 × IT98K-555-1 on day 47, while IT98K-555-1 and IT98K-555-1× IT98K-205-8 flowered late respectively at day 56 and day 55, which means that IT98K-555-1 can be considered responsible for late flowering when used as the male parent. The earliness in the flowering of the offspring compared to IT98K-555-1 can be regarded as a maternal effect. Therefore, this observation can be regarded that the direction of crosses influences the success rate, and hence, careful selection of the male and female parents must be made before crossing in the designing of any hybridization program as suggested by Mondo *et al*. (2022). The results obtained for quantitative traits in this study are similar to the reports in Shwetha *et al*. (2021), Lachyan *et al*. (2016), Edematie *et al*. (2021), and Lachyan & Dalvi (2015).

The higher PCV compared to GCV among the genotypes suggest the influence of the environment on the studied traits. However, minimal differences between the PCV and GCV across the traits (Table 4) can be considered to have marginal environmental influences on these traits. Hence, this will make the selection on a phenotypic basis worthwhile (Roy & Shil, 2020; Soomro, 2020). Nevertheless, the seed weight, plant height, pod length, number of main branches, seeds per pod, and peduncle length that exhibited low GCV and PCV with higher differences between the two coefficients make them less responsive to the improvement through selection. Traits such as the number of pods, seed yield, and the number of seeds per plant exhibiting the highest mark of GCV and PCV indicate that the genotypes may possess a broad genetic base for these attributes. Furthermore, the number of days to first flowering and emergence percentage that exhibited moderate GCV and PCV suggest that moderate variation may exist among the genotypes for the studied traits. It is critically indicated that fruitful selection is only achievable if a high mean performance with high variability and high mean performance with a moderate variation of traits are considered, because producing a higher number of suitable extreme phenotypes is impossible in low variation (Soomro, 2020; Bamaniya *et al*., 2020).

The effectiveness of a character selection is premised on heritability estimation accompanied by an established GAM (Roy & Shil, 2020; Carvalho *et al*., 2017) as many factors, such as environment, trial material, the size of the sample, and generation of hybrid and biometrical methods affect the heritability estimates. The consequence of high GAM with high heritability, and high GAM with low heritability is an additive gene effect that can lead to an effective selection. An indication of non-additive gene effects comes into play when low GAM accompanies high heritability. However, low GAM with low heritability designates a high influence of environmental fluctuations on the character making the selection ineffective (Ajayi & Gbadamosi, 2020). Apart from the number of main branches, most traits showed moderate to high broad-sense heritability which indicates that they are less influenced by the fluctuations in the environmental conditions while being effectively transmitted to the progeny. Traits such as the emergence percentage, days to first flowering, seed yield, and the number of pods per plant exhibiting the combination of high broad-sense heritability, high narrow-sense heritability, and high GAM suggest that genuine progress in the improvement of yield can be made through selection. The number of the main branches which combined low heritability estimates with low GAM indicates that selection based on this trait will be ineffective because of being highly influenced by the environmental fluctuation. Olunloyo *et al*. (2019) reported a high heritability on such traits as days to first flowering and seed yield among the F_2 hybrids of cowpea in line with the present study. However, their GAM on these traits ranged from low to moderate. In agreement with the present study, they also reported a moderate to high heritability for pod length, and low to moderate GAM for pod length and seeds per pod. The present study also confirms the results obtained by Sobda *et al.* (2018) regarding the high and moderate broad-sense heritability for pods per plant and seed weight, respectively. The results are contrary to Sobda et al (2018), however, because of showing a high narrow-sense heritability among the hybrids for these traits. Garcia-Oliveira *et al.* (2020) reported similar high broad-sense heritability among the $F_{2:3}$ hybrids of cowpea in traits such as the peduncle length, seeds per pod, and pods per plant, while Amusa *et al.* (2019) reported a high broad-sense heritability among the F_2 hybrids of cowpea for pod length and seed weight. Their findings are in contrast to the present findings.

The knowledge of relationships between various traits is required for making an indirect selection for enhancing economic significant characters. This is achieved through correlation (genotypic and phenotypic) analysis by paving the way for understanding the relationships among significant economic characters with highly heritable traits and their contributions to the crop's genotype. For phenotypic correlation, the true genetic relationship of any no two characters can be depicted due to the interaction between the heritability and the environmental influences. However, the superiority of genotypic correlations lies in their propensity to provide the estimate of the inherent relationship among the genes governing the two characters and their effectiveness in the formulation of an effective selection scheme (Ajayi & Gbadamosi, 2020). Higher genotypic correlation compared to the phenotypic level observed across most traits in the present study indicates a high restriction of the environmental effects on the traits making their interactions highly heritable. Similar results were obtained amongst tomato hybrids (Bamaniya *et al*., 2020). Highly significant correlations between the plant height and yield traits such as seed yield, pods per plant, and seeds per plant are indicative of the possibility of enhancing the seed yield in cowpea if the hybrids are selected based on the plant height. Also, the selection for pods per plant, seeds per pod, and seeds per plant will enhance the seed yield. The peduncle length and pod length selection will enhance the pod length and seed weight, respectively. These results confirm those obtained by Garcia-Oliveira *et al*. (2020) and Edematie *et al*. (2021). For Garcia-Oliveira *et al*. (2020), the relevance of the seeds per pod on cowpea productivity was emphasized. Stating that genes controlling peduncle length and pod length belong to the same genomic regions, they emphasized how the correlation between the peduncle length and pod length can enhance the yield in cowpea. However, as Edematie *et al*. (2021) noted, the importance of pod length to seed weight as well as the importance of pods per plant and seeds per plant to seed yield should be emphasized.

Conclusions

The cowpea F_2 hybrids together with their parental lines exhibited significant variation for all the traits studied, including the seed yield. Estimates of the genetic parameters for the studied traits indicated that the substantial variation among the genotypes was under the influence of genetic control, especially for traits such as the emergence percentage, days to first flowering, seed yield, and the number of pods per plant exhibiting a combination of high broad-sense heritability, narrow-sense heritability, and GAM. Traits such as the plant height, seeds per pod, pods per plant, and seeds per plant with a high positive genotypic correlation to seed yield should be considered as core selection indices in cowpea improvement programs. Nonetheless, further studies into the F_3 and later generations are required to exploit the relationships between the high yields, drought tolerance, and other important traits among the cowpea hybrids. This knowledge will help to the improvement of the breeding programs of cowpea despite the environmental constraints.

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Conflicts of interest

There was no conflict of interest in the report.

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