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Genetic Variability and Heritability Studies in some Cowpea (*Vigna unguiculata*(L.)Walp.) Accessions

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Abstract

Exploring significant variability does broaden the genetic base of domesticated cowpea. To estimate the genetic variability and heritability of some traits in selected cowpea accessions, a trial involving 25 accessions of cowpea was laid out in a randomized complete block design (RCBD) and replicated three times. Analysis of variance (ANOVA) revealed significant variation among the accessions indicating that the planting materials were genetically divergent from each other. High phenotypic and genotypic coefficients of variation (PCV and GCV) observed for traits such as plant height, pod weight per plant, seed per pod, pods per plant, seed weight per pod, weight of 100 seed and pod width, suggest these traits are strongly influenced by genetic factors, making them suitable targets for selection and improvement. The high broad-sense heritability and genetic advance associated with traits like seed weight per pod, weight of 100 seeds, pod width, number pods per plant and seeds per pod highlight their potential for enhancement through breeding. High and positive correlations were noted among yield components. Number of days to first flower, weight of 100 seed, number of seeds per pod and number of pods per plant and other traits were identified as unique contributors to seed yield and could be targeted in cowpea improvement programs. Performers of NGB 07635 and NGB 02183 were notable presenting promising prospects for deliberate crop breeding strategies. This information however justifies the presence of sufficient genetic variability to enable selection for improvement in the cowpea.

Keywords: Genetic factor, Analysis of variance, enhancement, heritability, improvement

Introduction

Cowpea (*Vigna unguiculata L*. [Walp]) is a highly nutritious grain belonging to the family Fabaceae. It ranks next to soybean in plant protein content and therefore serves as a cheap source of protein in human diet and livestock feed formulations (Olayiwola *et. al*., 2015). Cowpea grain contains high proportion of protein (19 to 35%), rich in essential amino acids like, lysine and tryptophan and considerable amounts of β-carotene, thiamin, folic acid riboflavin and zinc (Owade *et al.,* 2020). Alidu *et al.,* 2020 reported that the grains contain about 57% carbohydrate and high in calcium and iron, while the leaves contain up to 27-34% protein, and therefore grown for its cheap source of dietary protein. Cowpea tolerate high temperature and drought compared to other crop species, and performs well in areas with minimum and maximum temperatures between 28 and 30$^{\circ C}$ during the growing season with short rainfall of 500 and 1200mm (Sheidu *et al.,* 2023), it is also grown for improving soil fertility. In Nigeria, cowpea can be processed and eaten as fried or boiled cakes, consumed solely when boiled or along with garri (cassava grains), bread, yam, plantain or boiled along with rice.

Cowpea is an important legume crop widely grown in arid and semi-arid agro-ecologies of the world. In 2024, Nigeria consumed over 3.6 million metric tons with an average per capita consumption of about 23 kg annually. However the domestic production frequently does not cater for the demand, hence necessitating importation (FAOSTAT 2025). Cowpea production in Nigeria faces several significant constraints such as, poor soil fertility, parasitic weed infestation, severe insect and pest attacks and post- harvest losses. Therefore evaluation of genotypes for improved performance, yield potential, and adaptability to varying environmental conditions is important owing to the unpredictable climatic condition. The varietal requirements in terms of plant type, seed type, maturity and use pattern are highly diverse from production regions and these makes cowpea breeding programs more complex (Diriba *et. al.,*.2014). However one of the strategies used to overcome the complexities is the exploration of genetic variability to identify genotypes that show superior adaptability and yield potential in diverse environments. Earlier Ng and Padulosi (1992), reported that continuous evaluations of germplasm broaden's the genetic base of the species resulting to identification of additional genes or alternative sources that control a particular trait useful in a crop improvement programs. Studying the genetic parameters controlling the expression of yield and its components are important in determining the outcome of such genetic parameters in enhancing the seed yield of cowpea (Diriba *et. al.,*2014).An essential factor in plant breeding for developing improved varieties is genetic variability. Fantaye & Kibrom (2021), define Genetic variability as the range of genetic differences present in a population or set of genotypes. This entails, estimating the genetic variability, phenotypic and genotypic coefficients of variation, heritability, genetic advance, and the extent of association between the yield and yield component traits. The Genotypic Coefficient of Variation (GCV) is a statistical measure which assesses the extent of genetic variability in a population. It quantifies the percentage of variation in a trait that is attributed to genetic differences among individuals in the population. Where by Phenotypic Coefficient of Variation (PCV) measures the extent of variation in a trait within a population considering both genetic and environmental factors. Furthermore, high GCV is an indication of possible scope for improvement through selection procedure. Also, high PCV is important in determining the method of selection to improve a particular plant population for a specific trait Omoigui, et.al., (2006). According to Iwuafor and Aba (2017), the extent to which genetic factors contribute to the observed differences in a particular trait within a population is referred to as heritability. Heritability measures the proportion of the variability in a trait that can be attributed to genetic differences amongst individuals. High heritability indicates that genetic factors play a significant role in controlling the trait (Belay & Fiseha, 2020). Furthermore, genetic advance quantifies the potential increase in trait value that can be achieved in a breeding population through

selection (Fantaye & Kibrom, 2021).Therefore, the purpose of the current study is to examine the nature and magnitude of the genetic diversity of various traits in cowpea accessions.

Materials and Methods

Materials

The material for the study comprised of 25 accessions obtained from National Centre for Genetic Resources and Biotechnology (NACGRAB), Moor Plantation, Ibadan, Nigeria.

Table 1. List of the accessions used for the trial

1.	NGB 07629	6.	NGB 05600	11.	NGB 05565	16.	NGB 07633	21.	NGB 08060
2.	NGB 04896	7.	NGB 07655	12.	NGB 08041	17.	NGB 07934	22.	NBG 07640
3.	NGB 05596	8.	NGB 05586	13.	NGB 07606	18.	NGB 05520	23.	NGB 05576
4.	NGB 07663	9.	NGB 07623	14.	NGB 05564	19.	NGB 08040	24.	NGB 07635
5.	NGB 05598	10.	NGB 07665	15.	NGB 05594	20.	NGB 05521	25.	NGB 02183

Methods

The single factor experiment was laid out in a randomized complete block design (RCBD) replicated three times at the teaching and research farm of college of Agriculture, Mokwa, Niger State, Nigeria. Five meter x 3m plot with spacing of 50 cm X 50 cm and 1m between rows was maintained. All othercultural practices were carried out as required.Data on leave length (LL), plant height (PH), number of branches per plant (NBP), number of pods per plant (P/P), number of seeds per pod (NSP), seed yield per plant (SPP), pod length (POL), and pod width (PW)were collected from five randomly selected plants from each plot and the average value was considered per plant basis. Whereas data on days to first flower (NDF), days to 50% flowering (ND 50%), 100-seed weight, seed yield per plant were recorded on plot basis. Data were subjected to analysis of variance. The genetic parameters viz., phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percentage of mean were estimated employing the methods suggested by Johnson *et al.* (1955).

Results and Discussion

Analysis of Variance (ANOVA) and Performance of the accessions

The combined results of analysis of variance revealed the existence of significant differences among all traits studied except number of branches per plant (NBP), pod length (POL) and number of seed per pod (NSP) (table 2). The performance of each genotype across the trait studied as shown in table 2 indicated that different genotype respond differently. The genotype NGB 05520 and NGB 05576 had the longest leave length, while NGB 07640 and NGB 05594 had short leave length. For plant height, NGB 07623 and NGB 07633 produced the tallest plants. The genotype NGB 05596 was the earliest to produce first flower (34.67 days), while it took NGB 07663 and NGB 07934, 51.67 days to produce their first flowers. However it took NGB 05565 and NGB 5596 about 44.67 and 45.00 days respectively for 50% of their plants to flower. Furthermore, genotype NGB 07655 and NGB 07623 produced the largest number of pod per plant (53.00 and 45.00) respectively, while NGB 04896had the least (21.00) number of pods per plant. NGB 08040, NGB 02183 and NGB 05586 produced pods with larger width than other genotypes produced respectively. The genotype

NGB 07665 produced plant with the highest number of seeds per plant (686.33 seeds) and NGB 02183 produced seeds with highest 100 seed weight (31.43g). Furthermore, the genotype NGB 02183 and NGB 07635 produced pods with the highest weight (4.93g per pod and 3.17g) and highest pod weight per plant (143.33g and 129.33g per plant) respectively. The superior yield of these genotypes was primarily driven by their high pod weight per plant, 100 seed weight and fairly large number of seeds per pod. It is interesting to note that NGB 07635 combined high yield with a relatively earlier days to first flowering), higher number of branches, and longer pod length. However, NGB 0556 and NGB 07629 which were characterized by earlier days to first and 50% flowering could not translate it to high yield.The results of this study provide valuable insights into the performance of the genotypes.These findings agrees with the earlier reports by Azumah *et, al*., (2025), Nwosu *et, al*., (2013) and Izmi *et al.* (2026) who reported similar results on cowpea.

Combined Seasons Principal Component Analysis

The results ofCombined Seasons principal component (PC) analysis on table 3 revealed that the first five principal components contributed 73.50% to the total variation observed amongst the population with eigen values >1. The first PC had the highest eigen values (4.24) contributed 30.30% to the total variation observed in the population. This PC was strongly loaded with SWP (0.363), P/P (0.351), PW/P (0.34) and 100w (0.304) reflecting plant's production efficiency, where plants with higher pods per plant, number of seed per pod, weight of 100 seed, seed weight per pod and pod weight per plant traits exhibits their collective impact on the plant's overall productivity potential. This however suggests that the PC is associated with seed production efficiency. On the other hand, PC2 accounted for 14.20% of the total variation with eigen values of 1.99. The PC was highly and loaded with PD (0.50), LL (0.486) and number of seed per pod (0.363) which are the major traits that contributed positively to the observed variations. This suggest that PC2 is associated with plant seed production but with strong negative contribution from plant height (-0.348). Similarly the third PC contributed 11.70% to the total variation and had eigen values of 1.63. PC3 was highly loaded with NBP (0.362), NSP (0.406), SPP (0.381), suggesting that the PC is associated with yield traits. However the PC was also loaded with strong but negative contribution from number of days to first flower (- 0.387) and number of days to 50% flowering (-0.422) indicating that plants with high NBP, NSP and SPP may take longer days to produce first and 50% flower. PC four and five with eigen values 1.40 and 1.01 respectively contributed 1.00% and 0.73% to the total variation, while the fourth PC was loaded with PW/P (0.338), and PH (0.304) and fifth PC was loaded with LL (0.498). The loading of P/P, SWP, 100w and PW/P in the first PC, PD, LL, NSP, NBP and 100w in second PC and NBP, NSP and SPP in PC3 accounted for the variation observed in the population. Suggesting that the maximum variation observed at these PC's were contributed by these traits, these reveal their importance in the maintenance of variability in the population. It further exhibited their importance as traits to be considered for selection during cowpea breeding program.

The percentage contribution made by each trait to the total variation in the population is revealed by the principal component analysis. Result of this study revealed that different traits contributed differently to the total variation in the population. Principal components 1 and 2 were strongly loaded with pods per plant, number of seed per pod, weight of 100 seed, seed weight per pod and pod weight per plant traits reflecting plant's production efficiency, where plants with higher values exhibits collective productivity potential. This therefore suggests that the principal component 1 and 2 were associated with seed production efficiency and the traits can be considered for selection in cowpea improvement program. Similar results have been reported by Azumah *et, al*. (2025). Nwangburuka *et. al*., 2011, reported that traits associated with PC1 and PC2 are implicated for being responsible for the phenotypic divergence observed in the cultivars and can be used for cultivar discrimination.

Table 2. Analysis of variance for 14 character and performance of cowpea accessions

S/NO	TREATMENT	LL (CM)	PH (CM)	NDF (N0)	ND 50%(NO)	FBL (NO)	NBP (NO)	P/P (NO)	POL (CM)	PB (CM)	NSP (NO)	S/P (NO)	100 (G)	SWP (G)	PW/P (G)
1	NGB 07629	10.43	38.33	39.67	47.33	3.67	5.00	20.67	12.78	4.00	13.00	271.00	23.50	1.97	39.83
2	NGB 04896	10.57	35.00	40.33	45.33	2.73	4.67	21.33	13.67	5.33	14.00	304.67	14.00	2.50	72.67
3	NGB 05596	10.17	32.40	34.67	45.00	2.97	5.33	21.67	13.17	6.00	14.67	313.33	25.23	1.67	75.00
4	NGB 07663	9.17	71.33	51.67	55.00	2.77	4.33	40.00	12.83	5.00	13.33	547.00	29.67	4.20	111.50
5	NGB 05598	8.57	29.67	44.67	50.00	2.27	5.00	32.33	16.00	5.67	13.67	450.67	18.60	3.43	56.33
6	NGB 05600	11.77	28.67	42.67	46.00	3.20	5.00	26.00	15.67	6.00	16.00	416.67	17.03	3.07	42.33
7	NGB 07655	11.40	50.67	43.33	53.00	2.90	4.67	53.00	14.00	7.00	15.67	879.33	23.40	3.47	46.83
8	NGB 05586	10.33	70.33	45.00	49.33	3.17	5.00	31.67	14.67	7.67	16.00	524.00	18.67	3.73	71.03
9	NGB 07623	9.60	185.00	49.67	52.00	3.07	4.67	45.00	13.33	5.33	14.00	613.33	19.27	2.57	123.83
10	NGB 07665	10.97	70.00	43.00	46.00	2.93	4.67	43.00	13.89	5.00	15.33	686.33	23.07	2.83	107.83
11	NGB 05565	9.33	110.00	39.33	44.67	2.57	5.00	37.33	13.33	4.67	13.67	523.67	20.00	2.67	80.00
12	NGB 08041	9.87	36.67	41.00	48.33	2.60	4.33	41.33	14.83	6.33	12.33	513.00	18.67	2.57	78.55
13	NGB 07606	9.60	24.33	42.67	47.00	3.15	5.00	24.67	12.07	5.33	13.33	325.33	15.67	2.70	36.03
14	NGB 05564	9.90	55.00	40.67	50.33	2.63	4.67	35.33	11.83	4.33	15.33	545.00	22.33	3.27	70.67
15	NGB 05594	7.57	119.10	35.67	45.33	2.53	5.00	33.33	11.50	6.67	14.00	447.33	26.00	3.40	63.33
16	NGB 07633	12.43	155.77	43.67	50.67	2.57	4.67	24.67	11.50	6.33	15.33	375.33	26.00	3.67	99.00
17	NGB 07934	10.93	31.67	51.67	57.33	2.67	4.67	28.00	12.33	5.33	13.67	397.33	17.50	2.67	53.13
18	NGB 05520	12.90	50.00	46.00	55.00	2.73	5.00	32.00	14.00	7.33	12.67	405.33	23.63	3.60	62.93
19	NGB 08040	11.13	44.67	38.33	51.33	3.40	4.67	27.67	16.00	8.33	15.00	416.33	23.70	3.90	54.50
20	NGB 05521	11.67	51.67	43.00	49.00	2.53	5.33	25.00	12.17	5.67	14.00	350.00	18.67	2.40	69.67
21	NGB 08060	8.33	139.67	44.00	48.67	2.93	4.00	29.33	13.33	5.00	12.00	352.00	20.67	3.33	57.67
22	NBG 07640	6.33	93.60	46.00	49.33	3.13	5.00	27.67	12.67	4.17	11.33	315.33	24.00	2.67	57.17
23	NGB 05576	12.53	25.67	42.00	50.00	3.13	4.67	28.33	11.33	6.50	14.33	408.33	20.33	3.70	66.50
24	NGB 07635	11.67	134.33	41.67	46.67	2.73	5.00	40.67	17.33	6.67	13.33	543.33	29.00	3.17	129.33
25	NGB 02183	10.00	88.67	49.33	53.00	2.87	3.33	40.00	17.55	7.67	15.00	599.00	31.43	4.93	143.33
	Significant	**	**	**	*	**	NS	*	NS	**	NS	*	**	**	**
	SE	0.588	6.819	2.261	2.331	0.158	0.432	5.094	1.607	0.324	0.956	87.643	0.941	0.205	2.418
	LSD	1.671	19.388	6.428	6.629	0.448	1.227	14.483	4.568	0.922	2.717	249.19	2.674	0.584	6.876
	CV(%)	9.9	16.7	9.1	8.2	9.5	15.7	27.2	20.4	9.5	11.8	32.9	7.4	11.4	5.6

SE = Standard Error, LSD = Least Significant Difference and CV = Coefficient of variation. ** = Significant at 1% , * = Significant at 5% level of probability, NS = Not Significant

Table 3.Combined Seasons Principal Component Analysis

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
LL (CM)	0.019	0.486	0.033	-0.065	0.498	-0.051	-0.483	-0.232	-0.07	-0.235	-0.166	0.355	-0.073	-0.022
PH (CM)	0.226	-0.348	0.186	0.304	0.269	-0.151	0.136	0.191	0.53	-0.315	0.16	0.372	-0.077	0.026
NDF (No)	0.283	-0.146	-0.387	-0.321	0.126	-0.145	-0.254	0.34	0.158	0.291	-0.138	-0.112	-0.535	-0.044
ND 50% (N0)	0.288	0.084	-0.422	-0.38	0.179	-0.004	0.103	-0.144	0.148	0.033	0.513	0.025	0.487	0.03
FBL (CM)	-0.106	0.269	-0.215	0.218	-0.257	-0.751	0.007	-0.194	0.325	0.035	-0.149	-0.129	0.091	0.007
NBP (No)	-0.282	0.068	0.362	-0.217	0.276	0.121	0.062	-0.03	0.498	0.562	-0.196	-0.036	0.195	0.017
P/P (N0)	0.351	-0.184	0.296	-0.291	-0.222	-0.059	-0.068	-0.348	0.072	-0.106	-0.155	-0.027	0.037	-0.67
POL (CM)	0.232	0.234	0.044	0.249	-0.517	0.25	-0.432	0.172	0.182	0.302	0.184	0.335	0.103	-0.006
PB (CM)	0.217	0.501	0.071	0.071	-0.026	0.342	0.201	-0.045	0.356	-0.266	0.09	-0.485	-0.302	0.02
NSP (No)	0.109	0.363	0.406	-0.111	0.09	-0.373	0.191	0.527	-0.286	0.102	0.28	-0.004	0.016	-0.215
SPP (No)	0.341	-0.053	0.381	-0.341	-0.201	-0.181	-0.015	-0.199	-0.062	-0.026	-0.055	0.035	-0.078	0.701
100 (g)	0.304	0.007	0.004	0.407	0.23	-0.035	0.248	-0.455	-0.224	0.507	0.168	0.071	-0.277	-0.04
SWP (g)	0.363	0.19	-0.208	0.033	-0.016	0.128	0.44	0.197	-0.065	0.014	-0.636	0.263	0.245	0.019
PW/P (g)	0.344	-0.165	0.109	0.338	0.266	-0.037	-0.382	0.136	-0.093	0.028	-0.153	-0.53	0.417	0.076
Eigen value	**4.2435**	**1.9934**	**1.6388**	**1.4005**	**1.0172**	**0.9018**	**0.7569**	**0.6137**	**0.5424**	**0.4192**	**0.2293**	**0.178**	**0.061**	**0.0044**
Proportion	**0.303**	**0.142**	**0.117**	**0.100**	**0.073**	**0.064**	**0.054**	**0.044**	**0.039**	**0.030**	**0.016**	**0.013**	**0.004**	**0.000**
Cumulative	**0.303**	**0.445**	**0.563**	**0.663**	**0.735**	**0.800**	**0.854**	**0.898**	**0.936**	**0.966**	**0.983**	**0.995**	**1.000**	**1.000**

Table 4.Correlations among traits.

	LL (CM)	*PH (CM)*	*NDF (No)*	*ND 50% (N0)*	*FBL (CM)*	*NBP (No)*	*P/P (N0)*	*POL (CM)*	*PB (CM)*	*NSP (No)*	*SPP (No)*	*100 (g)*	*SWP (g)*	*PW/P (g)*
LL (CM)	1													
PH (CM)	-0.242	1												
NDF (No)	-0.030	0.183	1											
ND 50% (N0)	0.161	0.027	0.717	1										
FBL (CM)	0.131	-0.176	-0.107	-0.067	1									
NBP (No)	0.128	-0.180	-0.377	-0.380	-0.077	1								
P/P (N0)	-0.132	0.358	0.336	0.320	-0.293	-0.245	1							
POL (CM)	0.063	0.021	0.127	0.060	0.048	-0.326	0.254	1						
PB (CM)	0.384	-0.015	-0.043	0.300	0.014	-0.102	0.155	0.472	1					
NSP (No)	0.300	0.001	-0.069	-0.029	0.077	0.111	0.124	0.125	0.335	1				
SPP (No)	-0.023	0.266	0.291	0.292	-0.231	-0.181	0.948	0.258	0.212	0.407	1			
100 (g)	0.045	0.382	0.114	0.256	-0.032	-0.355	0.283	0.239	0.264	0.074	0.260	1		
SWP (g)	0.037	0.187	0.439	0.543	-0.076	-0.500	0.308	0.342	0.550	0.215	0.324	0.494	1	
PW/P (g)	0.070	0.603	0.378	0.129	-0.237	-0.425	0.425	0.337	0.131	0.092	0.360	0.585	0.334	1

Correlations among traits

The results on table 3 shows the relationships that exist among the traits measured. A high correlation between certain variables can serve as an indicator for selecting superior plant. In this result a strong and positive correlation existed between number of pods per plant and seeds per plant(r 0.948) indicating that with more number of pods per plant, the number of seeds per plant increases. Similarly, weight of 100 seeds showed positive correlation with pod weight per plant (r 0.585). Plant height and pod weight per plant showed positive correlation (r 0.603), indicating that taller plant produce heavier pods. More so, number of days to first flower shows strong positive correlation with days to 50% flowering (r 0.717) and with seed weight per pod (r 0.439). Implying that plants that flower early reached 50% flowering earlier, produced heavier seeds matures faster, enabling multiple cropping cycles in tropical agriculture (Mondal et al. 2011). High and positive correlation was found between number of days to when 50% plants in the plot had flowered and seed weight per pod (r 0.543). This implies thatplants that have 50% of their population flower early tend to produce heavier seeds. Similar result was reported by Izmi*et. al*.,(2026) in Purple Winged Bean. Furthermore, pod width shows positive correlation with seed weight per pod (r 0.550), suggesting that pods with wider width are heavier.Positive correlations indicated that as one trait increases, the other trait also increases, and vice versa. Number of pods per plant and seeds per plant, weight of 100 seeds with pod weight per plant, plant height with pod weight per plant exhibited a strong positive correlation. This implies that genotypes with large number pods are most likely to have a greater number of seeds per plant and heavier seed weight. Similar results were reported by Azumah *et al*. (2025). Number of days to first flower correlating strongly with days to 50% flowering, indicates that genotypes with shorter days to flowering reaches maturity earlier and such trait can be considered for selection to improve maturity of cowpea, this result finds support with the findings of Ngalamu *et. al.,* (2012).

Estimates of Variance Components.

Johnson *et al*, 1955 stated, that an understanding of the variability existing in a crop is necessary to formulate and accelerate breeding program. Data given in table 5 showed sufficient genetic variability in most of the traits studied. The phenotypic variance was generally greater than genotypic variance. The result revealed that the Genotypic Coefficient of Variation (GCV) indicated a wide range of variation from 6.67 to 89.10% while the Phenotypic Coefficient of Variation (PCV) ranged from 12.28 to 91.68% for different traits studied. Johnson *et. al*., 1955, classified values of GCV and PCV as low (0-10%), moderate (10-20%) and high (>20%). The maximum coefficient of genotypic and phenotypic variationin this result was recorded in the plant height (89.10 and 91.68) followed by pod weight per plant (54.81 and 55.16), SPP (37.98 and 49.25), P/P (32.74 and 41.85), SWP (31.42 and 33.35), 100w (27.71 and 29.63) and PB (27.50 and 29.00). The narrow difference observed between the GCV and PCV for these traits indicated that they were less influenced by the environment.This finding agrees with the report of Karnwal and Singh (2009), Jandong *et. al*., (2020). Traits with GCV and PCV values greater than 20% indicates that they are influenced by environment and genetic factors, making them ideal candidates for selection in improvement programs (Adebayo *et al*., 2017). Moderate GCV and PCV were recorded for NDF (14.39 and 16.96), FBL (13.96 and 17.46) and POL (12.68 and 25.31) while low estimate was recorded for ND 50% (9.04 and 12.28) and NSP (8.16 and 14.66).Phenotypic variances and phenotypic coefficients of variation were slightly larger than their genotypic counterparts, showing that the environment has an impact in the expression of these traits. The current results correspond with the findings reported by Ngalamu *et. al.,*(2012). However, traits with moderate variability and PCV and GCV values between 10% and 20%, suggest that while genetic factors play a role, environmental influences may also have contributed significantly to the expression of these traits (Yahaya, *et al*., 2021)

Heritability measures the fraction of phenotypic variability that can be attributed to genetic variation, an important concept in quantitative genetics, commonly used in selective breeding.The heritability percentage was grouped as low (0-30%), moderate (31-60%), and high (>60%) as described by Johnson *et,al*., 1955. High heritability values indicate that the traits are primarily governed by genetic factors. In this result, high heritability was measured in LL (80.00)%, PH (94.00)%, NDF (72.00)%, FBL (64.00)%, P/P (61.00)%, PB (90.00)%, 100w (87.00)%, SWP (89.00)% and PW/P (94.00)%. However, moderate heritability was estimated in ND50% (54.00)%, SPP (59.00)% and NSP (31.00)%. These estimates suggest that environmental factors play a considerable role in the traits expression. Furthermore low heritability estimate was recorded in POL (25.00)% and NBP (15.00)%. In this study, a high heritability estimates was obtained for LL, PH, NDF, FBL, P/P, PB, 100w, SWP and PW/P, which indicates that these traits are highly heritable and can be easily transferred from parent to offspring and significantly enhance yield and quality. This also suggests that selection for these traits would be effective for further improvement. These results corroborate those of Idahosa *et. al.,* (2010); Nwosu *et, al*., (2013), Azumah *et, al*. (2025) and Izmi *et. al*.,(2026).

Genetic advance is a measure of the potential for genetic improvement through selection. It suggests that genetic advance percentages exceeding 30% indicates substantial potential for the traits improvement through selection breeding. The result on table 5 detected high genetic advance as percentage of the mean in SWP (60.98), SPP (60.33), 100w (53.38), PB (53.73), P/P (52.76), LL (38.35), NDF (25.14) and FBL (22.98). ND 50% (13.70), and POL (13.09) and NSP (9.35) and NBP (5.26) showed moderate and low genetic advance as a percent of the mean respectively. Heritability estimates along with genetic advance are more important in predicting yield under phenotypic selection than heritability estimate alone (Johnson *et. al*., 1955).The association of high broad-sense heritability and high genetic advance as a percent of the mean as in SWP (89.00 and 60.98)%, 100w (87.00 and 53.38)%, PB (90.00 and 53.73)%, P/P (61.00 and 52.76)%, SPP (59.00 and 60.33)%, and high heritability with moderate genetic advance found in NDF (72.00 and 25.14)%, FBL (64.00 and 22.98)% indicated that these traits were controlled by additive gene action and selection for improvement is possible.These results are supported by the findings of Nwosu *et. al*.,(2013) in a similar experiment. However, Ashkok *et. al*., (2000) suggested mass selection breeding method as a means of improvement of traits controlled by additive gene action.Moderate heritability associated with low genetic advance found in NSP (31.00 and 9.35)% revealed non-additive gene action was prevalent for the traits and the improvement of these traits can be achieved through hybridization as reported by Estakhr et al., (2012).

Table 5. Estimates of general mean, genotypic (GV), phenotypic (PV), genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability in broad sense (h^2) and genetic advance in percent of mean for 14 characters in cowpea

Traits	Means	Genotype variance	Phenotypic variance	Genotypic Coefficient of Variability	Phenotypc coefficient of variation	Heritabilty(h^2)	GAM
LL (CM)	10.26	4.53	5.63	20.75	23.13	0.80	38.35
PH (CM)	69.1	3790.70	4013.10	89.10	91.68	0.94	178.39
NDF (No)	42.95	38.18	53.05	14.39	16.96	0.72	25.14
ND 50% (N0)	49.01	19.62	36.25	9.04	12.28	0.54	13.70
FBL (CM)	2.848	0.16	0.25	13.96	17.46	0.64	22.98
NBP (No)	4.76	0.10	0.69	6.67	17.43	0.15	5.26
P/P (N0)	31.93	109.30	178.60	32.74	41.85	0.61	52.76
POL (CM)	13.73	3.03	12.08	12.68	25.31	0.25	13.09
PB (CM)	5.927	2.66	2.95	27.50	29.00	0.90	53.73
NSP (No)	14.11	1.32	4.28	8.16	14.66	0.31	9.35
SPP (No)	455	29865.00	50225.00	37.98	49.25	0.59	60.33
100 (g)	21.93	36.93	42.22	27.71	29.63	0.87	53.38
SWP (g)	3.146	0.98	1.10	31.42	33.35	0.89	60.98
PW/P (g)	75.02	1690.96	1712.30	54.81	55.16	0.94	112.21

GAM: Genetic advance in percent of mean,

Conclusion

Significant variability was identified among accessions used for this study, exploring them could broaden the genetic base of domesticated cowpea. High phenotypic and genotypic coefficients of variation (PCV and GCV) observed for traits such as plant height, pod weight per plant, seed per pod, pods per plant, seed weight per pod, weight of 100 seed and pod width, suggest these traits are strongly influenced by genetic factors, making them suitable targets for selection and improvement. The high broad-sense heritability combined with genetic advance associated with traits like seed weight per pod, weight of 100 seeds, plant width, pods per plant and seeds per pod is an indication of additive gene action, this highlight their reliability for enhancement through selection. High and positive correlation was noticeable among yield and yield components. Number of days to first flower, weight of 100 seed, number of seeds per pod and number of pods per plant and other traits were identified as unique contributors to seed yield and could be targeted in cowpea improvement programs. Notable performers, such as NGB 07635 and NGB 02183, present promising prospects for tailored crop breeding strategies.

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