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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE OF IMPROVED COWPEA GENOTYPES (*Vigna unguiculata* L.)

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ABSTRACT

Field experiments were conducted at the Teaching and Research Farm of the Faculty of Agriculture to evaluate the genetic variability, heritability, and genetic advance of some selected agronomic traits of fifteen (15) newly developed promising cowpea genotypes. Cowpea, a crucial legume crop, is widely grown in arid and semi-arid regions for its early maturity, drought and heat tolerance, and nutritional value. This study assessed genetic variation among newly developed cowpea genotypes and determined agronomic traits' heritability and genetic advance. Genetic variability is crucial for improved varieties, while heritability measures phenotypic variation caused by genetic differences. Genetic advancement measures the potential increase in trait value through selection in breeding populations. The study reveals significant genetic variation among 15 cowpea genotypes, indicating a wide range of agronomic traits for selective breeding. Four traits-leaf length, leaf weight, days until first flowering, and 50% flowering-demonstrated high heritability and genetic advancements. These traits may be promising for targeted breeding efforts because they respond well to selection pressure and can be improved through phenotypic selection. Cowpea varieties with improved performance, yield potential, and adaptability to varying environmental conditions can be developed by focusing on these traits, contributing to food security and agricultural sustainability.

Keywords: Cowpea, Genetic advance, Heritability, GCV, PCV

INTRODUCTION

Cowpea (*Vigna unguiculata* L.) is a diploid species (2n=22), and it is one of Africa's most-grown crops (Sheidu and Igyuve, 2023). Cowpea grains contain 21–33 % protein, 57 % carbohydrate, and are high in calcium and iron, while the leaves contain 27-34% protein (Alidu *et al.*, 2020). The grains contain reasonable amounts of β-carotene, thiamin, folic acid riboflavin, and zinc (Owade *et al.*, 2020). Cowpea provides income for smallholder farmers, improves soil fertility through nitrogen fixation, and nutritious fodder for livestock (Sheidu and Igyuve, 2023; Muindi *et al.*, 2021). The crop is grown in the tropical regions of West Africa for its drought tolerance and nitrogen fixation (Naab *et al.*, 2009; Timko and Singh, 2008; El-Amin, 2018). However, salinity is a major abiotic stress that negatively impacts cowpea production and quality (Eric *et al.*, 2018; Hall, 2004; Zaid and Radwan, 2022). It performs well in areas with short rainfall of 500 and 1200m (Madamba et al., 2006), with minimum and maximum temperatures between 28 and 30^{0}C during the growing season (Craufaud *et al.*, 1996).

Souza et al. (2011) define genetic variability as genetic differences. Genetic variability is the range of genetic differences present in a population or set of genotypes, and it is an essential factor in plant breeding for developing improved varieties (Fantaye & Kibrom, 2021). Heritability, however, quantifies the proportion of phenotypic variation in a trait caused by genetic differences between individuals (Fantaye & Kibrom, 2021). High heritability indicates that genetic factors play a significant role in controlling the trait, making it amenable to improvement through selection and breeding (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). The study aimed to assess genetic variation among newly developed cowpea genotypes and determine agronomic traits' heritability and genetic advance.

MATERIALS AND METHOD

The experiment includes fifteen (15) newly developed promising cowpea genotypes developed at the Institute of Agricultural Research (IAR), the International Institute of Agricultural Research (IITA), and the Federal University of Agriculture, Makurdi (FUAM). The experiment was carried out in a complete randomized block design (RCBD) with three replications at the teaching and research farm faculty of agriculture Shabu-Lafia campus during the off-season and wet season of 2021-2022. Each plant was planted in three rows of three metres each, with a row-to-row distance of 45cm (about 1.48 ft) and a plant-to-plant distance of 5 cm (about 1.97 in). Weeding was done by hand at 20 and 45 days after sowing. Two insecticide sprayings were carried out to control the leaf miner and other insect pests. At 4, 6, and 8 weeks, yield contributing and morphological characteristics such as yield per plant, number of leaves, number of branches, plant height, leaf length, and leaf weight were measured. Days to first flowering and 50% flowering were recorded for each plot. The analysis of variance for a complete randomised block design was performed using Panse and Sukhame's method (1955). The obtained data were analysed for genotypic and phenotypic coefficients of variation, heritability (in the broad sense), and expected genetic advance as a percentage of the mean. The genotypic and phenotypic (GCV and PCV) variables were calculated using Burton's method (1952). Heritability (in the broad sense) was calculated using Allard's method (1960). The genetic advance (at 5% selection intensity) was calculated for each character using the formula proposed by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences between the studied traits, as shown in Table 2, which displays the mean performance of the studied traits. The number of leaves at 4 weeks indicates that all studied traits had similar mean performance across the genotype. At 6 weeks, fuampea1 had the highest mean performance of the number of leaves (41.50), while UAM 15-118-5 (18.38) had the lowest. The number of leaves at 4 weeks shows that UAM 15-2154 (11.50) had the highest mean performance while CLS 39-11-3 (38.44) had the lowest. At 6 and 8 weeks, fuampea 1 (12.50 and 26.81) had the highest mean performance of the number of branches while UAM 15-118-5 (5.50) had the lowest. Plant height at 4 weeks Indicates that all studied traits had a similar mean performance. Plant height at 6 weeks indicates Sampea 19 (16.45) had the highest mean performance while UAM 15-2157-4 had the lowest. Plant height at 8 weeks indicates that Fuampea 1 had the highest mean performance (14.26) while fuampea 4 had the lowest. Leave length at 4 weeks indicated that CLS 39-11-3 (14.36) had the highest mean performance while UAM 15-2157.4 (8.32) had the lowest. Leave length at 6 weeks indicates that UAM-126-127 (11.53) had the highest mean performance while UAM 15-2157.4 (8.32) had the lowest. Leave length at 8 weeks indicates that Fuampea 1 (13.00) had the highest while F4 (9.21) had the lowest. Leave width at 4 weeks indicates that UAM 15-2157.4 (5.56) had the highest mean performance while sampea 18 (2.49) had the lowest. Leave width at 8 weeks indicates that Fuampea 1 (11.43) had the highest mean performance while F-4 (8.10) had the lowest. Vine length at 6 weeks, Indicates high performance in all the studies traits. Days to first flowering indicate high performance in Sampea 19 (49.33), while F-3 recorded the lowest (38.00). Crop yield had high mean performance across the genotype.

Genetic parameters of the studied traits are presented in Table 3. The result showed that most of the studied traits had a high phenotypic coefficient of variation. This conforms with the findings of Malik *et al.,* (2011) and Islam *et al.,* (2015). However, for NB at 8 weeks (0.00), PH at 8 weeks (7.90), leave weight at 8 weeks (0.00), days to flowering (8.19), days to 50 % flowering (7.85) and crop yield (5.77) recorded low PCV. More so, leave length at 6 and weeks (15.91 and 12.29 respectively) recorded moderate PCV. High genotypic coefficient of variation was observed for number of leaves at 6 weeks (25.45), number of leaves at 8 leaves (22.96), vine length at 6 weeks (43.03) and crop yield (25.90). This result is in accordance with the findings of Malik *et al.,* (2011) and Islam *et al.,* (2015). However, most of the studied traits recorded moderate to low GCV as presented in Table 3. High heritability estimates were observed for leave length at 8 weeks (0.56), leave weight at 8 weeks (0.54), days to first flowering, (0.78) and days to 50 % flowering, (0.84). This result is in accordance with the findings of Idahosa et al., (2010); Omoigui *et al.,* (2005); Xu *et al.,* (2009); and Lesly (2005). However, most of the studied traits recorded moderate to low heritability estimate as presented in Table 3. High heritability accompanied with high genetic advance was recorded for leave length at week 6, days to flowering and days to 50 % flowering, indicating the presence of additive gene action for the expression of these traits. Similar findings were reported by Islam *et al.,* (2015) and Kushwantoro (2017).

CONCLUSION

From the result of this study, it can be concluded that there is high genetic heterogeneity among genotypes, including both genotypic and phenotypic variation. The results further revealed that four of the traits viz., leave length, leave weight, number of days to first flowering and 50 % flowering, had higher heritability with high expected genetic advance, indicating additive gene action and predicting that phenotypic selection may be more effective for these traits. These traits may be promising for targeted breeding efforts because they respond well to selection pressure and can be improved through phenotypic selection. Cowpea varieties with improved performance, yield potential, and adaptability to varying environmental conditions can be developed by focusing on these traits, contributing to food security and agricultural sustainability.

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Table 1: ANOVA for the Studied Traits of Cowpea

SOV	Df	NL-4	NL-6	NL-8	NB-4	NB-6	NB-8	PH-4	PH-6	PH-8	LL-4	LL-6	LL-8	LW-4	LW-6	LW-8	VL-6	DF	50% F	CROP-Y
Rep	2	89.68	710.76	344.71	12.52	91.71	31.86	10.9	0.39	0.33	19.53	4.07	0.16	0.93	51.69	0.17	158.66	1.27	11.02	454.3
Variety	14	19.05^{ns}	134.16**	198.83**	12.37**	12.59**	59.57**	3.24^{ns}	12.34**	4.21**	12.49**	2.02*	3.44**	1.94**	33.36*	2.07**	19.89^{ns}	38.25**	35.88**	2975.90^{ns}
Error	28	31.54	134.16	130.47	10.48	8.1	59.57	6.5	5.07	1.37	10.26	2.27	0.72	1.8	41.26	0.46	65.32	3.24	2.09	3495.9

*,**sig at 5% and 1% ,NL-4(number of leaves at 4 weeks), NL-6(number of leaves at 6 weeks), NL-8(number of leaves at 8 weeks), NB-4(number of branches at 4 weeks), NB-6(number of branches at 6 weeks), NB-8(number of branches at 8 weeks), PH-4(plant height at 4 weeks), PH-6(plant height at 6 weeks), PH-8(plant height at 8 weeks), LL-4(leave length at 4 weeks), LL-6(leave length at 6 weeks), LL-8(leave length at 8 weeks), LW-4(leave weight at 4 weeks), LW-6(leave weight at 6 weeks), LW-8(leave weight at 8 weeks), VL-6(vine length at 6 weeks), DF(days to first flowering) 50%F(days to 50% flowering), CROP Y (crop yield)

Table 2: Means Performance for the Studied Traits Of Cowpea

Variety	NL-4	NL-6	NL-8	NB-4	NB-6	NB-8	PH-4	PH-6	PH-8	LL-4	LL-6	LL-8	LW-4	LW-6	LW-8	VL-6	DF	50% F	CROP-Y
F-3	16.92a	22.50bc	39.73b	5.92ab	6.33bc	13.18d	10.71a	10.25c	10.67c	8.13b	8.33b	9.47de	3.92ab	4.82b	8.69bcd	13.42a	38.00d	42.00h	262.37a
U152157-4	15.33a	26.00abc	38.57b	11.50a	9.75abc	12.39d	8.06a	8.48c	10.72c	7.48b	8.32b	9.47de	5.56a	17.70a	8.51cd	17.25a	38.00d	42.33gh	274.50a
CLS3911-3	21.700a	28.75abc	38.44b	7.08ab	7.67abc	12.55d	7.97a	11.39c	11.57bc	14.36a	8.85ab	9.55de	3.53ab	4.46b	8.50cd	18.82a	41.67bc	47.00de	249.03a
SAM-14	18.58a	30.50abc	49.33ab	5.08b	11.58ab	17.41bcd	8.71a	12.25bc	11.58bc	7.55b	8.80ab	9.81cde	3.67ab	5.37b	9.33bcd	17.63a	41.67bc	47.00de	213.57a
U15118-5	11.08a	18.58c	47.10ab	3.08b	5.50c	16.45cd	7.02a	10.83c	11.97bc	6.26b	9.17ab	10.00cde	3.06ab	5.58b	8.80bcd	18.42a	41.33bcd	47.33de	261.17a
SAM-18	13.42a	32.83abc	43.83b	3.92b	10.42abc	14.96cd	8.68a	11.87c	13.55ab	6.26b	8.88ab	11.27bc	2.49b	5.07b	9.27bcd	18.83a	46.33a	52.00ab	225.27a
SAM-17	15.25a	36.25ab	50.31ab	4.00b	10.25abc	22.58abc	7.67a	11.38c	13.50ab	6.15b	9.50ab	10.90bcd	2.64b	5.50b	9.93b	22.74a	42.67b	49.33cd	159.77a
FU-1	15.25a	41.50a	50.63ab	4.17b	12.50a	26.81a	9.67a	15.96ab	14.26a	5.96b	8.92ab	13.00a	4.31ab	5.72b	11.43a	24.83a	48.00a	50.33bc	192.50a
SAM-19	13.08a	25.83abc	57.50ab	3.75b	8.17abc	23.25abc	8.33a	16.45a	13.57ab	6.13b	10.09ab	10.90bcd	2.80b	4.46b	9.93b	19.25a	49.33a	53.33a	236.40a
U-126L27	14.50a	18.17c	48.13ab	5.25b	6.70bc	14.57cd	8.68a	11.51c	13.38ab	7.15b	11.53a	11.96ab	4.03ab	4.87b	9.57bc	19.25a	40.67bcd	46.00ef	255.03a
F-4	13.42a	31.00abc	54.33ab	4.33b	9.83abc	19.41abcd	7.39a	11.85c	10.67c	7.13b	9.04ab	9.21e	3.83ab	6.01b	8.10d	18.88a	42.00bc	46.33ef	222.30a
U15L10-3	16.58a	25.17abc	49.24ab	3.67b	7.98abc	17.10bcd	6.47a	10.02c	12.00bc	6.63b	9.37ab	9.62de	4.64ab	4.88b	8.77bcd	16.62a	38.67cd	44.00fgh	251.90a
F-2	15.08a	35.25abc	68.60a	5.25b	10.75abc	25.67ab	8.93a	12.12bc	12.25abc	8.08b	9.02ab	10.67bcde	3.78ab	9.22ab	10.00b	17.30a	40.33bcd	45.00efg	199.20a
U-14126L34	16.92a	30.17abc	59.23ab	5.50b	9.67abc	20.40abcd	8.76a	11.16c	13.23ab	7.68b	10.28ab	9.67cde	3.72ab	6.24b	8.73bcd	19.02a	38.67cd	43.67fgh	213.43a
SAM-15	14.83a	21.08bc	51.15ab	5.00b	7.17abc	17.27bcd	8.18a	11.88c	11.98bc	6.94b	9.32ab	10.22cde	3.09ab	5.79b	8.90bcd	19.51a	38.67cd	43.00gh	207.40a
GM	15.46	28.24	49.74	5.17	8.95	18.07	8.35	11.83	12.33	7.46	9.29	10.38	3.67	6.38	9.21	18.78	41.73	46.58	228.26
CV	36.32	31.39	22.96	62.66	31.8	24.67	30.54	19.04	9.48	42.94	16.2	8.18	36.49	100.71	7.39	43.03	4.32	3.11	25.9
MS error	31.54	78.59	130.47	10.48	8.1	19.88	6.5	5.07	1.37	10.26	2.27	0.72	1.8	41.26	0.46	65.32	3.24	2.09	3495.94

Means with the same alphabet are not significantly different

Table 3: Genetic Parameters of the Studied Traits of Cowpea

Traits	**NL-4**	**NL-6**	**NL-8**	**NB-4**	**NB-6**	**NB-8**	**PH-4**	**PH-6**	**PH-8**	**LL-4**	**LL-6**	**LL-8**	**LW-4**	**LW-6**	**LW-8**	**VL-6**	**DF**	**50% F**	**CROP-Y**
GM	15.46	28.24	49.74	5.17	8.95	0.00	8.35	11.83	12.33	7.46	9.29	10.38	3.67	6.38	0.00	18.78	41.73	46.58	228.26
SEm	3.24	5.12	6.59	1.87	1.64	2.57	1.47	1.30	0.67	1.85	0.87	0.49	0.77	3.71	0.39	4.67	1.04	0.84	34.14
CD 5%	9.39	14.83	19.10	1.87	4.76	7.47	4.26	3.77	1.95	5.36	2.52	1.42	2.24	10.74	1.14	13.52	3.01	2.42	98.89
CD 1%	12.67	20.00	25.77	1.87	4.76	10.09	5.75	5.08	2.64	7.23	3.40	1.92	3.02	14.49	1.54	18.23	4.06	3.26	133.40
	31.54	78.59	130.47	10.48	8.10	19.88	6.50	5.07	1.37	10.26	2.27	0.72	1.80	41.26	0.46	65.32	3.24	2.09	3495.93
	-4.16	18.52	22.79	0.63	1.50	13.23	-1.09	2.42	0.95	0.74	-0.08	0.91	0.05	-2.63	0.54	-15.14	11.67	11.26	-173.34
	27.38	97.11	153.26	11.11	9.60	33.11	5.41	7.49	2.31	11.00	2.19	1.63	1.84	38.62	1.00	50.17	14.91	13.36	3322.60
	36.32	31.39	22.96	62.66	31.80	0.00	30.54	19.04	9.48	42.94	16.20	8.18	36.49	100.71	0.00	43.03	4.32	3.11	25.90
	13.20	15.24	22.96	15.36	13.66	0.00	12.49	13.16	7.90	11.54	3.09	9.18	6.08	25.45	0.00	20.72	8.19	7.20	5.77
	33.84	34.90	24.89	64.51	34.61	0.00	27.87	23.15	7.90	44.47	15.91	12.29	37.00	97.44	0.00	37.71	9.25	7.85	25.25
	-0.15	0.19	0.15	0.06	0.16	0.40	-0.20	0.32	0.41	0.07	-0.04	0.56	0.03	-0.07	0.54	-0.30	0.78	0.84	-0.05
	-1.64	3.87	3.79	0.39	0.99	4.74	-0.96	1.82	1.28	0.46	-0.11	1.47	0.08	-0.87	1.11	-4.40	6.22	6.35	-6.19
	-10.60	13.71	7.62	7.53	11.11	0.00	-11.52	15.41	10.41	6.17	-1.23	14.12	2.06	-13.69	0.00	-23.44	14.92	13.63	-2.71

PCV: Phenotypic coefficient of variation; **GCV**: Genotypic coefficient of variation, **PV (p):** Phenotypic variance, **GV (g)**: Genotypic variance, **GA**: Genetic advance, **GA (%)**: Percentage genetic advance; **h2b**; Heritability in broad sense., **CD:** Critical Difference