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Article

Genetic variability in exotic cowpea (*Vigna unguiculata* L.) genotypes

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Abstract: Genetic variability plays a crucial role in hybridization and the development of crops with desirable traits. This study, conducted at the Regional Agricultural Research Station of the Bangladesh Agricultural Research Institute in Chattogram, focused on assessing genetic diversity, correlations, and path coefficients related to yield and other traits in 31 cowpea genotypes. The experiment, designed as a randomized complete block with three replications, revealed significant differences among the genotypes for all traits measured, as confirmed by analysis of variance. While most traits showed minimal differences between phenotypic and genotypic variances, plant height and yield per plant were more significantly influenced by environmental factors. The coefficients of variation were low for days to first flowering, days to 50% flowering, days to maturity, and days to harvesting; moderate for seeds per plant; and high for other traits. Plant height, thousand-seed weight, and yield per plant exhibited high heritability and substantial genetic advance, suggesting that direct selection for these traits would be effective due to their additive genetic control. The correlation analysis indicated significant positive relationships between yield per plant and several flowering and maturity traits at both the genotypic and phenotypic levels. Path analysis identified plant height, days to 50% flowering, days to harvesting, seeds per plant, pods per plant, and thousand-seed weight as having positive direct effects on yield per plant, implying that selection for these traits could enhance cowpea yield. Among the evaluated genotypes, E25 stood out as the highest yielding with 533.33 g yield per plant, early maturity at 84 days after sowing, moderate thousand-seed weight (124.33 g), seeds per plant (13.87), and plant height (103.33 cm), making it a promising candidate for hybridization. This research provides valuable insights for cowpea breeding programs, highlighting the importance of selecting specific traits like plant height, flowering time, and thousand-seed weight to develop high-yielding, resilient cowpea varieties adaptable to diverse agricultural conditions.

Keywords: correlation; heritability; genetic advance; yield traits; phenotypic variation

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1. Introduction

Cowpea, scientifically known as *Vigna unguiculata* L. (Walp), is a significant herbaceous leguminous crop cultivated for several purposes such as seed production, vegetable consumption, feed for animals, green manure, medicinal uses, and as a mulching material. This legume crop is commonly cultivated in arid tropical regions of Africa, South Asia, and Latin America (Boukar *et al*., 2019). Although cowpea has gained recognition, it has not attained a prominent status among the top-ranked pulse crops worldwide, with its demand remaining relatively lower compared to other legume crops. Cowpea is a widely farmed pulse crop in Bangladesh, particularly in the greater Chattogram, Bhola, and Feni regions (Akter *et al*., 2022). Additionally, smaller-scale cowpea production takes place in other locations. The need for this grain legume is steadily increasing with the rapid expansion of the population in Bangladesh (Jiang *et al*., 2021). To meet the growing demand and popularity, Bangladesh Agricultural Research Institute developed a few cowpea varieties that have high performance in yield, pest, and disease resistance. But still, cowpea cultivation in Bangladesh encounters challenges like weather suitability, soil fertility, land constraints, and released varieties that are inadequate to satisfy the product demand. Farmers have access to some exotic varieties for cultivation but they are not enough to fill up the requirements and demands.

Hybridization plays a vital role in increasing genetic diversity to achieve improved crops with the desired characteristic(s). Successful plant breeding programs and yield enhancements require knowledge regarding the nature and scale of variation in the existing germplasm, the relationships between yield and other agronomic traits, as well as the level of environmental effect on the expression of these characteristics (Edukondalu *et al*., 2017; Thapa *et al*., 2021). The study of genetic diversity is essential for the development of new crops with desired traits and is critical for evaluating, preserving, and utilizing germplasm resources (Delfina *et al*., 2016). Genetically diversified parents are prone to segregate and generate high heterotic crosses, with greater variety increasing the likelihood of obtaining high heterotic offspring. Prior to hybridization, it is crucial to comprehend the genetic diversity present among the existing accessions.

Genetic correlation analysis is a useful tool that quantifies the degree of relationship between significant quantitative characteristics. The investigations on correlation are antiquated and comprehensive, although regrettably, there are no established guidelines regarding the extent to of a character influences the manifestation of other character(s) in a plant population. Path analysis is a statistical technique used to quantify the direct and indirect influence of a causal factor on an outcome factor (Ahmed *et al*., 2020).

In line with this, the research questions guiding this investigation include, what is the extent of genetic and phenotypic variability among cowpea genotypes for key agronomic traits, particularly yield per plant and associated morphological characteristics? To what degree do genetic and environmental factors influence these traits, and which traits exhibit high heritability, making them ideal for selection in breeding programs? Additionally, how do various morphological traits correlate with yield, and which traits exert the most direct impact on yield per plant through direct and indirect pathways? Based on these research questions, the study hypothesizes that significant genetic variability exists among the cowpea genotypes studied, with high heritability in several traits, indicating their suitability for selection. It is further hypothesized that traits such as plant height, pods per plant, seeds per pod, and thousand seed weight exhibit strong positive correlations with yield per plant and that these traits contribute directly to yield enhancement. The study aims to enhance efficient and swift selection in crop enhancement by assessing the performance of exotic cowpeas. Specific objectives include assessing the association between traits, determining direct and indirect effects on fruit yield per plant, and identifying suitable cowpea genotypes for future hybridization programs. The findings of this research provide valuable insights for breeding programs aimed at enhancing cowpea yield, suggesting that targeted selection of specific traits like plant height, flowering time, and thousand-seed weight could accelerate the development of high-yielding, resilient cowpea varieties suitable for diverse agricultural environments.

2. Materials and Method

2.1. Ethical approval

No ethical approval was required to conduct the study.

2.2. Experimental site and planting material

The experiment was conducted at the Regional Agricultural Research Station in Hathazari, Chattogram, Bangladesh situated at coordinates 22°30'03"N and 91°47'35"E (Figure 1).

The study, which lasted from March to July 2022, took place in a flood-free and elevated site. The soil varies from clay loam to sandy loam and has a pH of 5.5-6.5. For the study, 31 distinct genotypes of cowpea seeds were obtained from the Bangladesh Agricultural Research Institute (Table 1).

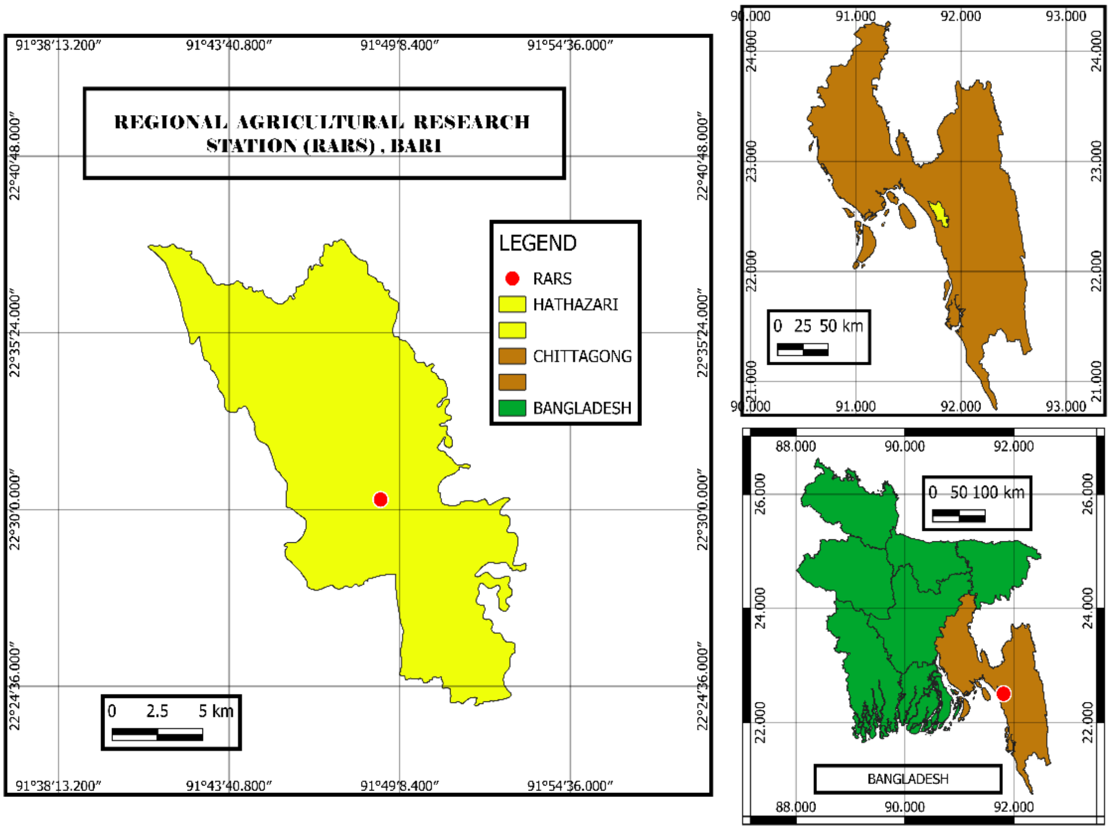

Figure 1. Map showing location of the experimental site.

Table 1. Name of the planting materials used in the study.

Genotypes	Accession	Source	Genotypes	Accession	Source
E1	TVU2252	BARI	E17	TVU165	BARI
E2	TVU6782	BARI	E18	TVU16253	BARI
E3	TVU1417	BARI	E19	TVU1886	BARI
E4	TVU1637	BARI	E20	TVU2598	BARI
E5	TVU5307	BARI	E21	TVU1477	BARI
E6	TVU1059	BARI	E22	TVU1036	BARI
E7	TVU1650	BARI	E23	TVU1811	BARI
E8	TVU7642	BARI	E24	TVU53	BARI
E9	TVU6365	BARI	E25	TVU870	BARI
E10	TVU884	BARI	E26	TVU473	BARI
E11	TVU201	BARI	E27	TVU15692	BARI
E12	TVU1280	BARI	E28	TVU15315	BARI
E13	TVU84	BARI	E29	TVU15391	BARI
E14	TVU2398	BARI	E30	TVU4622	BARI
E15	TVU15445	BARI	E31	BARI Felon-1	BARI
E16	TVU4894	BARI			

* BARI = Bangladesh Agricultural Research Institute, Joydebpur, Gazipur, Bangladesh

2.3. Land preparation, fertilizer application, and experimental design and layout

The land was irrigated properly at first, then it was ploughed using a tractor-drawn disc plough and further refined through additional ploughing, cross-ploughing, harrowing, and laddering to achieve the desired fine tilth. During the final preparation of the land, Urea, TSP, MOP, gypsum, and zinc sulphate were all used at the recommended rates of 30, 45, 30, 110, and 7 kg/ha, respectively. The experiment was conducted in plots measuring 4 m × 1.2 m, with a plant spacing of 10 cm and a row spacing of 40 cm. A randomized complete block design with three replications was used, with each replication separated by 1 meter between blocks and 0.5 meters between plots.

2.4. Seed sowing and Intercultural operations

Seeds were sown at a depth of 2-3 cm in the mid of March 2022, with two rounds of thinning at 25 and 30 Days after Sowing (DAS). Two irrigations were provided for vegetative growth and whenever necessary, and weeding was also performed as per needed. Pest control included addressing early-stage worms (*Agrotis ipsilon*) and fungus (*Fusarium oxysporum*) and controlling pod borers (*Marucate stulalis*) with Malathion and Ripcord 10 EC. Pods were harvested in June 2022, after allowing pods to mature.

2.5. Data collection and statistical analysis

Data of nine different agronomic traits such as days to first flowering (DFF), days to 50% flowering (DFPF), days to maturity (DM), days to harvesting (DH), plant height at maturity (PH) (cm), pods per plant (PPP), seeds per pod (SPP), thousand seed weight (TSW) (g), and yield per plot (YPP) (g) were collected from 10 randomly chosen plants from each genotype within each replicate. Some data were recorded in the field, while others were noted in the field laboratory after harvesting. All quantitative data related to agronomic traits were analyzed using ANOVA through the R-software to determine significant differences among the cowpea genotypes. The variability among the accessions was evaluated by calculating the genotypic variance and coefficients of variation, using the approach outlined by Burton and De Vane (1953). The phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated following the method of Singh and Chaudhary (1985). Genetic advance (GA) was determined based on the formula by Robinson *et al*. (1949), and the genetic advance as a percentage of the mean (GAM) was classified according to Johnson *et al*. (1955). Path coefficient analysis was carried out using the techniques proposed by Dewey and Lu (1959) and Dabholkar (1992).

3. Results and Discussion

3.1. Variability analysis for agronomic traits

The ANOVA analysis showed highly significant variations ($P \leq 0.01$) for all the traits assessed. Significant mean sum of squares were observed for DFF (64.51^{**}), DFPF (57.65^{**}), DM (66.19^{**}), DH (45.98^{**}), PH (2579.96^{**}), PPP (22.86^{**}), SPP (11.71^{**}), TSW (2004.63^{**}), and YPP (42868.30^{**}), indicating substantial genotypic variation among the evaluated genotypes (Table 2). This indicates genotypic differences among the studied genotypes. The significant variation highlighted the substantial potential for breeding and provided essential genetic information for selecting desirable traits. The genetic and phenotypic variances also demonstrated inherent genetic diversity among various cowpea genotypes. Nkhoma *et al.* (2020) also revealed that highly significant differences among different phenotypic traits of cowpea germplasms under study.

Table 2. Analysis of variance for nine traits across 31 cowpea genotypes.

Source of variance	DF	DFF	DFPF	DM	DH	PH (cm)	PPP	SPP	TSW	YPP
Replication	2	68.26	4.72	58.27	52.91	196.71	81.67	32.73	562.87	8727.70
Genotype	30	64.51^{**}	57.65^{**}	66.19^{**}	45.98^{**}	2579.96^{**}	22.86^{**}	11.71^{**}	2004.63^{**}	42868.30^{**}
Error	60	0.26	2.23	0.81	1.00	43.16	2.56	1.77	3.76	3342.10
CV (%)		0.67	1.87	1.00	1.04	12.38	24.15	9.83	1.63	20.74

******indicates 1% level of significant; TSW (g) and YPP (g)

3.2. Mean performance of yield and yield related traits

The mean performance of yield and yield-related traits reveals significant differences among the studied genotypes. The highly significant genotypic variations in yield and related traits indicate a wide range of diversity among the examined genotypes (Table 3). DFF ranged from 59.00 to 83.00 days, with E19 exhibiting the shortest duration and E14 the longest. The remaining genotypes displayed intermediate flowering durations. DFPF varied from 65.00 to 88.00 days, with E19 (65.00) again showing the shortest duration, and E10 the longest followed by E5 (85.00). In the case of DM, the minimum duration was observed in E31 (80.00), followed by E7 (84.00) and E25 (84.00), while the maximum duration was recorded in E12 (97.00) and E14 (97.00). Regarding the time for harvesting (DH) recorded on cowpea genotypes showed considerable variation. The genotype E19 took the shortest time to mature, while E14 required the longest. PH ranged from 80.00 to 125.00, with E12 being the tallest and E31 the shortest. PPP ranged from 2.87 to 13.60, with E31 being the highest and E9 being the lowest. SPP varied from 9.80 to 16.67, with E24 having the most and E27 the least. TSW ranged from 79.00 to 171.67, with E21 having the heaviest and E3 the lightest seeds. Finally, YPP varied from 95.00 to 533.33, with E25 having the highest, followed by E21 (460.00), E5 (446.67), E22 (436.67), and

E28 (436.67) and E16 with the lowest yields, as reported in Table 3. These results offer important insights into how various cowpea genotypes perform across several parameters. The observed differences in phenotypic traits reveal substantial genetic diversity among the genotypes studied. This variation could assist breeders in developing new populations through hybridization, with a focus on improving traits of interest, particularly yield, for both small-scale and commercial production (Begum *et al*., 2016; Shoyeb *et al*., 2017; Sayadat *et al*., 2019; Mofokeng *et al*., 2020; Nkhoma *et al*., 2020).

Table 3. Average performance of nine traits in 31 cowpea genotypes.

Characters	DFF	DFPF	DM	DH	PH	PPP	SPP	TSW	YPP
E1	79.00^{e}	82.00^{cd}	90.00^{g}	100.00^{bc}	38.47^{i-n}	6.33^{f-m}	11.53^{i-m}	83.67^{mn}	270.00^{f-i}
E2	75.00^{f}	78.33^{e-g}	91.00^{fg}	96.00^{fg}	37.67^{i-n}	3.20^{op}	11.33^{j-m}	85.67^{m}	96.67^{k}
E3	82.00^{b}	83.00^{bc}	90.00^{g}	95.00^{g}	38.93^{h-n}	7.40^{d-k}	10.67^{lm}	79.00^{o}	103.33^{k}
E4	75.00^{f}	78.33^{e-g}	92.33^{ef}	96.00^{fg}	56.77^{ef}	4.40^{l-p}	16.53^{a}	101.00^{k}	236.67^{hi}
E5	80.00^{d}	85.00^{b}	91.00^{fg}	97.00^{ef}	22.47^{o}	10.00^{cd}	10.87^{k-m}	136.00^{e}	446.67^{a-c}
E6	80.00^{d}	85.00^{b}	91.00^{fg}	96.00^{fg}	33.33^{k-n}	5.13^{i-p}	11.93^{h-m}	166.00^{b}	336.67^{d-g}
E7	74.00^{g}	79.00^{ef}	84.00^{h}	91.00^{i}	33.87^{k-n}	8.73^{c-f}	9.87^{m}	113.67^{j}	101.67^{k}
E8	82.00^{b}	84.00^{bc}	96.00^{ab}	101.00^{b}	61.00^{e}	4.93^{k-p}	14.33^{b-g}	123.67^{hi}	116.67^{jk}
E9	82.00^{b}	84.00^{bc}	96.00^{ab}	101.00^{b}	39.00^{h-n}	2.87^{p}	13.33^{e-j}	113.00^{j}	101.67^{k}
E10	82.00^{b}	88.00^{a}	95.00^{bc}	101.00^{b}	41.57^{h-l}	5.07^{j-p}	13.27^{e-j}	103.67^{k}	313.33^{e-h}
E11	74.00^{g}	76.67^{fg}	91.00^{fg}	101.00^{b}	31.33^{l-o}	7.33^{e-k}	13.27^{e-j}	95.67^{l}	253.33^{g-i}
E12	81.00^{c}	83.00^{bc}	97.00^{a}	98.33^{de}	125.00^{a}	3.87^{m-p}	16.20^{ab}	165.67^{b}	310.00^{e-h}
E13	80.00^{d}	85.00^{b}	91.00^{fg}	96.00^{fg}	40.33^{h-m}	7.73^{d-i}	16.00^{a-c}	113.00^{j}	236.67^{hi}
E14	83.00^{a}	85.00^{b}	97.00^{a}	104.00^{a}	124.67^{a}	3.20^{op}	12.73^{g-l}	129.33^{f}	200.00^{ij}
E15	74.00^{g}	79.00^{ef}	84.00^{h}	91.00^{i}	45.00^{g-j}	7.33^{e-k}	12.80^{g-l}	131.00^{f}	280.00^{f-i}
E16	80.00^{d}	83.00^{bc}	96.33^{ab}	103.00^{a}	49.40^{f-h}	3.93^{m-p}	12.87^{g-k}	125.33^{gh}	95.00^{k}
E17	74.00^{g}	79.00^{ef}	93.00^{de}	99.00^{cd}	54.00^{e-g}	10.67^{bc}	12.80^{g-l}	81.67^{no}	283.33^{f-i}
E18	75.00^{f}	80.00^{de}	85.00^{h}	92.00^{hi}	47.00^{f-i}	8.33^{c-h}	16.60^{a}	121.00^{i}	230.00^{hi}
E19	59.00^{i}	65.00^{i}	85.00^{h}	89.00^{j}	30.67^{m-o}	12.67^{ab}	13.00^{f-k}	80.67^{no}	303.33^{e-h}
E20	75.00^{f}	77.33^{fg}	85.00^{h}	92.00^{hi}	98.33^{c}	4.67^{l-p}	13.40^{d-j}	125.67^{gh}	386.67^{b-e}
E21	74.00^{g}	79.00^{ef}	94.00^{cd}	100.00^{bc}	30.00^{m-o}	5.67^{i-o}	15.20^{a-e}	171.67^{a}	460.00^{ab}
E22	74.00^{g}	76.33^{g}	90.00^{g}	94.67^{g}	63.00^{e}	9.67^{c-e}	14.20^{b-g}	125.00^{h}	436.67^{bc}
E23	74.00^{g}	79.00^{ef}	90.00^{g}	96.67^{f}	77.00^{d}	6.00^{h-n}	14.07^{b-h}	121.00^{i}	336.67^{d-g}
E24	74.00^{g}	79.00^{ef}	90.00^{g}	96.00^{fg}	34.33^{j-n}	3.20^{op}	16.67^{a}	151.00^{c}	236.67^{hi}
E25	74.00^{g}	76.33^{g}	84.00^{h}	96.00^{fg}	103.33^{bc}	6.33^{f-m}	13.87^{c-h}	124.33^{h}	533.33^{a}
E26	75.00^{f}	77.00^{fg}	85.00^{h}	93.00^{h}	31.33^{l-o}	8.67^{c-g}	16.20^{ab}	81.67^{no}	420.00^{b-d}
E27	75.00^{f}	80.00^{de}	96.00^{ab}	97.00^{ef}	28.33^{no}	6.93^{f-l}	9.80^{m}	145.67^{d}	266.67^{f-i}
E28	75.00^{f}	77.33^{fg}	91.00^{fg}	92.00^{hi}	40.00^{h-m}	6.07^{g-n}	15.13^{a-f}	128.33^{fg}	436.67^{bc}
E29	79.00^{e}	81.67^{cd}	95.00^{bc}	96.00^{fg}	113.00^{b}	3.67^{n-p}	12.53^{g-l}	145.00^{d}	353.33^{c-f}
E30	75.00^{f}	80.00^{de}	85.00^{h}	92.00^{hi}	33.00^{k-no}	7.60^{d-j}	13.53^{d-i}	124.00^{hi}	236.67^{hi}
E31	72.00^{h}	73.00^{h}	80.00^{i}	91.00^{i}	42.33^{h-k}	13.60^{a}	15.53^{a-d}	104.00^{k}	223.33^{hi}
Min	59.00	65.00	80.00	89.00	22.47	2.87	9.80	79.00	95.00
Max	83.00	88.00	97.00	104.00	125.00	13.60	16.67	171.67	533.33
Mean	76.03	79.74	90.23	96.26	54.30	6.72	13.53	119.60	280.91
SE	0.41	1.22	0.74	0.82	5.36	1.31	1.09	1.58	47.20
LSD (0.05)	0.83	2.44	1.47	1.64	10.73	2.61	2.18	3.17	94.42

*PH (cm), TSW (g) and YPP (g)

3.3. Variability and genetic parameters

The phenotypic variance (PV) was higher than the corresponding genotypic variance (GV) for all traits studied (Table 4). However, the small differences between them for most traits suggest a limited environmental influence on these parameters, except for PH and YPP, where larger differences indicated a significant environmental impact. Similar cases were also observed for phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). PCV and GCV both showed various parameters from low to high. GCV and PCV were low for DFF, DFPF, DM, and DH, but high for the PPP, TSW, PH, and YPP. For the SPP, both values were moderate.

Heritability ranged from 99.44 and 65.13 for TSW and SPP, respectively. All traits demonstrated moderate to high heritability coupled with a broad range of genetic advance (GA) and genetic advance as percentage of mean (GAM%). The high heritability with low GA and a moderate GAM% were found in cases of DFF, DFPF, DM, and DH traits. High heritability coupled with moderate genetic advance as a percentage of the mean indicates the scope of these traits for improvement through selection. Similar results were observed by Belay and Fisseha (2021) for days of first flowering, Pandiyan *et al*. (2020) for days of 50% flowering, Meena *et al*. (2015) for days of maturity, and Devi and Jayamani (2018) for days of harvesting in cowpeas. Conversely, PPP, SPP, TSW, PH, and YPP all showed high heritability and high GAM% suggesting additive gene action for these parameters, allowing for simple direct selection. Similar outcomes were reported by Belay and Fiseha (2021) for plant height, by Gupta *et al.* (2019) and Sharma *et al.* (2019) for pod yield per, by Gupta *et al.* (2019) for pods per plant, and Belay and Fiseha (2021) for thousand seed weight.

Table 4. Genetic parameters of nine traits in 31 cowpea genotypes.

Characters	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability	(GA)	(GAM%)
DFF	21.42	21.68	6.09	6.12	98.81	9.48	12.46
DFPF	18.47	20.70	5.39	5.71	89.22	8.36	10.49
DM	21.79	22.61	5.17	5.27	96.40	9.44	10.46
DH	14.99	15.99	4.02	4.15	93.73	7.72	8.02
PH	845.60	888.76	53.55	54.90	95.14	58.43	107.61
PPP	6.77	9.32	38.73	45.45	72.59	4.57	67.97
SPP	3.31	5.09	13.45	16.67	65.13	3.03	22.36
TSW	666.96	670.72	21.59	21.65	99.44	53.05	44.36
YPP	13175.40	16517.50	40.86	45.75	79.77	211.18	75.18

3.4. Correlation analysis of morphological traits

DFF showed a highly significant and positive correlation with DFPF, DM, DH, PH, and TSW. Similarly, DFPF was significantly and positively correlated with DM, DH, and TSW. Such findings revealed the enhancement of one character will improve the positively correlated character. Conversely, both DFF and DFPF showed a non-significant and negative correlation with SPP and a significant but negative correlation with PPP and YPP. The DM correlated positively with DH, PH, and TSW but a strong negative correlation with PPP and non-significant and negative correlation with SPP and YPP. In addition, the DH exhibited a strong positive correlation with PH, negative with PPP and YPP and non-significant with TSW and SPP. The PH was significantly correlated with TSW (Table 5). Positive and significant relationships between plant height and pod yield were also noted by Kalambe *et al.* (2019). Both PPP and SPP showed significant positive correlations with yield per plant, consistent with the findings of Mofokeng *et al.* (2020) and Ajayi and Gbadamosi (2020). Thousand seed weight was also significantly correlated with yield per plant, a trend also observed by Kalambe *et al.* (2019).

Table 5. Genotypic and phenotypic correlation coefficients among various yield components of cowpea.

Characters		DFF	DFPF	DM	DH	PH	PPP	SPP	TSW
DFPF	r_g	0.962^{**}							
	r_p	0.910^{**}							
DM	r_g	0.596^{**}	0.624^{**}						
	r_p	0.595^{**}	0.580^{**}						
DH	r_g	0.640^{**}	0.634^{**}	0.827^{**}					
	r_p	0.634^{**}	0.594^{**}	0.805^{**}					
PH	r_g	0.253^{*}	0.126	0.230^{*}	0.205^{*}				
	r_p	0.249^{*}	0.111	0.223^{*}	0.217^{*}				
PPP	r_g	-0.611	-0.577	-0.657	-0.571	-0.417			
	r_p	-0.524	-0.508	-0.552	-0.505	-0.349			
SPP	r_g	-0.127	-0.185	-0.116	-0.114	0.169	-0.067		
	r_p	-0.096	-0.139	-0.083	-0.073	0.159	-0.013		
TSW	r_g	0.238^{*}	0.314^{**}	0.303^{**}	0.133	0.283^{**}	-0.417	0.156	
	r_p	0.237^{*}	0.292^{**}	0.297^{**}	0.128	0.273^{**}	-0.347	0.117	
YPP	r_g	-0.270	-0.253	-0.201	-0.21	0.195	0.212^{*}	0.278^{**}	0.328^{**}
	r_p	-0.220	-0.194	-0.157	-0.163	0.172	0.175^{NS}	0.176^{NS}	0.297^{**}

r_p = phenotypic correlation coefficient, r_g = genotypic correlation coefficient, *=5% level of significance; **=1% level of significance; NS= non-significance; PH (cm), TSW (g) and YPP (g).

3.5. Path co-efficient analysis of yield-influencing traits

The path coefficient analysis indicated that TSW had the most substantial positive direct effect on seed yield (0.440), with PPP (0.402) following closely behind. This suggests that selecting for these traits could lead to a notable improvement in seed yield in cowpea breeding programs. Additionally, traits such as PH (0.276), SPP (0.177), DFPF (0.168), and DH (0.137), demonstrated smaller positive direct effects on seed yield. Conversely, DFF (-0.354) and DM (-0.122) exhibited negative direct effects. In this study, TSW, SPP, and PPP had significant positive correlations with YPP at 0.328^{**}, 0.278^{**}, and 0.212^{*} respectively, indicating that selecting these traits could improve yield. These results are in line with findings from Manggoel *et al.* (2012) and Mishra and Dash (2009) suggested, the residual effect was 0.1320, meaning 86.80% of the variability was explained by the traits studied, while the remaining 13.20% could be attributed to other factors not included in this analysis (Table 6).

Table 6. Partitioning of genotypic effects into direct and indirect effects of morphological traits in 31 cowpea genotypes based on path coefficient analysis.

Traits	DFF	DFPF	DM	DH	PH	PPP	SPP	TSW	YPP
DFF	**-0.354**	0.162	-0.072	0.088	0.070	-0.246	-0.023	0.105	-0.270^{**}
DFPF	-0.341	**0.168**	-0.076	0.087	0.035	-0.232	-0.033	0.138	-0.253^{*}
DM	-0.211	0.105	**-0.122**	0.114	0.063	-0.264	-0.021	0.133	-0.201^{NS}
DH	-0.226	0.107	-0.101	**0.137**	0.057	-0.229	-0.020	0.059	-0.217^{*}
PH	-0.090	0.021	-0.028	0.028	**0.276**	-0.168	0.030	0.125	0.195^{NS}
PPP	0.216	-0.097	0.080	-0.078	-0.115	**0.402**	-0.012	-0.184	0.212^{*}
SPP	0.045	-0.031	0.014	-0.016	0.047	-0.027	**0.177**	0.069	0.278^{**}
TSW	-0.084	0.053	-0.037	0.018	0.078	-0.168	0.028	**0.440**	0.328^{**}

Residual effect = 0.1320; *=5% level of significance **= 1% level of significance NS=non-significance; PH (cm), TSW (g) and YPP (g).

3.6. Selection

Out of the 31 cowpea genotypes evaluated, four were chosen based on their mean performance, each exhibiting distinct characteristics. E25 stood out as the top performer with the highest YPP at 533.33 g, coupled with moderate values for TSW (124.33 g), SPP (13.87), PH (103.33 cm), and a shorter maturity period of 84 DAS. E21 displayed a noteworthy performance with a high YPP of 460g, the highest TSW (171.67 g), and a high number of SPP (13.87). However, it exhibited a longer maturity period of 94 DAS. E5 demonstrated a high YPP at 446.67g, second only to E25, along with a moderate TSW (136 g), fewer SPP (10.87), and a high number of PPP (10). It had a longer maturity period of 91 DAS. E22 showcased a high YPP (436.67 g), low TSW (125 g), high SPP (14.20), and a maturity period of 90 DAS. Each of these genotypes presents a unique set of characteristics, and the selection among them would depend on specific breeding goals and environmental considerations. The selected cowpea genotypes each demonstrated unique strengths, with some excelling in yield combined with favorable maturity periods, while others showed high seed weight or pod counts. This diversity in traits offers valuable options for breeders to target specific goals, such as yield enhancement or adaptability to varying growing seasons (Dorvlo *et al*., 2022; Atakora *et al*., 2023).

4. Conclusions

In the evaluation of selected cowpea genotypes, the primary objective was to identify the highest-yielding genotype. E25 emerged as the most promising, demonstrating superior seed yield and favorable traits such as moderate time to maturity and balanced growth characteristics. Its exceptional performance suggests that E25 is a strong candidate for further breeding programs. However, certain gaps in understanding the genotype's adaptability to diverse environmental conditions remain unaddressed. Future studies should focus on evaluating E25 under different environmental and stress conditions to fully explore its potential for widespread agricultural use.

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Data availability

Data from the experiment that underpins the study's findings can be obtained from the authors upon request.

Conflict of interest

None to declare.

Authors’ contribution

Abul Kashem Chowdhury, Md. Mainul Islam Rashad, Md. Muktadir Alam: conceptualization, methodology; Shuvo Jit Saha, Md. Mainul Islam Rashad, Md. Muktadir Alam, Sheikh Md. Mohsen Farhan: data collection, analysis, and manuscript writing; Abul Kashem Chowdhury: supervision; Abul Kashem Chowdhury, Md. Mainul Islam Rashad, Md. Muktadir Alam: reviewing, and editing. All authors have read and approved the final manuscript.

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