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Research Article

Evaluation of cowpea [*Vigna unguiculata* (L.) Walpers] lines developed through backcross breeding method for early maturity and high grain yield

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Abstract
Cowpea [*Vigna unguiculata* (L.) Walpers] is a herbaceous annual crop predominantly grown in the dry agro-ecologies of the tropics in Latin America, Africa and South Asia. It is an essential crop in Botswana, valued for its nutritional importance and adaptability to the country's semi-arid climate. The purpose of this study was to evaluate the genetic variability of the cowpea lines developed through backcross breeding method for early maturity and high grain yield. The offsprings were developed between August 2022 and April 2024 using B138 and ER7 as parental lines. Four F_1, 9 reciprocal F_1, 4 BC_1, 6 reciprocal BC_1, 8 BC_2 and 13 reciprocal BC_2 were produced and evaluated for various traits. Days to flowering ranged from 31 (EB-5F_1) to 37.00 days (EB9-9-3BC_2) while days to 50% flowering ranged from 34 days (EB-5F_1) to 40 days (BE3-2-1BC_2). The results of this study indicated that EB-5F_1, EB8-7-1BC_2 and EB8-7-2BC_2 can be exploited in breeding programmes targeting earliness and adaptation to short growing seasons. Seed yield per plant ranged from 16.10 g (EB-3F_1) to 134.62 g (EB4-1BC_1), with BE2-1-2BC_2 and EB5-6-1BC_2 yielding higher than ER7 but lower than B138. These lines are promising recombinants for further selection and improvement.

Keywords: Conventional breeding, backcrossing, cowpea, flowering, maturity, yield

INTRODUCTION

The productivity of cowpea is reported to be low in Sub-Saharan Africa, despite its importance in the diets of many households, with less than 600 kg/ha produced compared to a genetic potential grain yield of over 2000 kg/ha (Boukar *et al*., 2019). Cowpea production in Botswana averages 300 kg/ha against a potential yield of 2500 kg/ha, making it difficult for farmers to meet the demand of the growing human population (Molosiwa and Makwala, 2020). Even though cowpea is considered a drought-tolerant crop that can grow in harsh climatic conditions with limited water, it is affected by a range of climatic factors that frequently result in low yields. The use of unimproved varieties, insufficient input application, and poor agronomic practices during crop production further contribute to reduced yield (Horn *et al*., 2022).

Improvement of cowpea for yield and earliness in Botswana has been pursued through integrated breeding and agronomic measures that combine evaluation of local germplasm, advanced selection methods, and optimized cultivation practices. Molosiwa and Makwala (2020) conducted a field evaluation in Botswana that identified exceptional local genotypes such as B137B which exhibited high seed yield and desirable agronomic traits.

In another study by Molosiwa *et al.* (2016), phenotypic characterization of Botswana's cowpea germplasm was undertaken to present genetic diversity based on agro-ecological zones. The variation in traits across districts may have been caused by the climatic conditions as they differ from each district. These evaluation provide the critical baseline information for breeding programs aimed at enhancing early maturing and high-yielding lines well adapted to the Botswana growing conditions.

A clear understanding of this genetic variability of cowpea is important to design and accelerate conventional breeding programs. Accurate assessment of genetic variability plays a role in the preservation and utilization of germplasm resources and improvement of cultivars. The genetic variability present among cowpea genotypes gives breeders the opportunity to select parental lines for hybridization with higher levels of desirable traits. Genetic variability is a pre-requisite in crop improvement programme as the breeders must quantify the fixable and non-fixable components of variation for an actual selection programme. Cowpea exhibits important forms of variations in qualitative traits such as plant type, seed coat colour and quantitative agronomic traits such as yield, maturity or stress tolerance (Boukar **et** *al*., 2019).

Conventional plant breeding methods have been used for hundreds of years and remain widely used today to create new plant varieties. The backcross breeding method has been effectively employed in cowpea breeding programs (Owusu **et** *al.,* 2018) and the method allows breeders to enhance specific traits such as earliness and yield. Previous research conducted has demonstrated that cowpea varieties that mature in less than 60 days after planting can significantly contribute to early harvests, thereby improving food security (Metwally **et** *al.,* 2021; Owusu **et** *al.,* 2018). These early maturing varieties require minimal irrigation and are compatible with mechanized harvesting techniques (Aishwarya *et al.,* 2025; Khojambergenov *et al.,* 2025) . Therefore, the purpose of this study was to evaluate the genetic variability of the cowpea lines developed through backcross breeding method for early maturity and high grain yield.

MATERIALS AND METHODS

The research experiment was conducted at the Botswana University of Agriculture and Natural Resources (BUAN) content farm, Sebele (altitude of 992 m, latitude of 24.33.40 S, and longitude of 25.56.37 E), Botswana under greenhouse condition. The two parental lines were selected based on their contrasting maturity periods and yield potential: B138, a late-maturing landrace requiring 91 days after sowing and yielding approximately 426.79 kg/ha, and ER7, an early-maturing variety that matures in 61 days and yields about 297.06 kg/ha. B138 produces reddish-brown seeds, whereas ER7 has cream-white seeds with a brown eye (**Fig. 1**). B138 was hybridized with ER7 to generate the F_1 generation and backcrossed with B138 as the recurrent parent to create BC_1 and BC_2 populations during 2022 and 2024. Reciprocal crosses were also made to assess the maternal effects on the traits under study. The developed offsprings along with their parents were planted in the plastic pots replicated three times using a completely randomized design and evaluated in the greenhouse for physiological, morphological and yield performance. Agronomic practices were followed to raise healthy crops and fertilizers were applied as per the crop requirement.

Crossing program:
B138 (♀) × ER7 (♂): F_1
ER7 (♀) × B138 (♂): Reciprocal F_1 (RF_1)

F_1 (B138 x ER7) (♀) × B138 (♂): Backcross one (BC_1)
RF_1 (ER7 x B138) (♀) × B138 (♂): Reciprocal backcross one (RBC_1)

BC_1 (♀) × B138 (♂): Backcross two (BC_2)
RBC_1 (♀) × B138 (♂): Reciprocal backcross two (RBC_2)

Data Collection and Analysis: Data were collected on growth, yield and yield-related traits using cowpea descriptors (IBPGR Executive Secretariat, 1983) for plant height , number of branches, number of leaves, leaf area, days to first flowering, days to 50% flowering, days to first pod maturity, days to 90% pod maturity, days to maturity, number of pods per plant, pod length, pod width, number of seeds per pod, 100 seed weight, seed yield per plant and seed yield per plot . Data were collected from tagged plants in each replication and analyzed using the variability package in R programming language software.

RESULTS AND DISCUSSION

Genetic variation in cowpea is essential for cowpea improvement programs as a narrow genetic base can limit genetic gains in improved varieties. Previous studies have shown that genetic variation in cowpea is vital for expression of various traits, such as seed size, plant height and leaf area, which are closely linked to adaptation in plants (Herniter *et al.,* 2019). Further, genetic variability among cowpea landraces is crucial for conserving local varieties and serves as a foundation for developing improved varieties (Carvalho *et al.,* 2017). The present study revealed significant variation among the genotypes for growth, physiological yield and yield related characters .

Growth characters: Significant differences were observed for plant height where ER7 consistently taller than B138 and their offspring across all days after sowing (**Table 1**). All F_1 progenies were taller than B138 but shorter than ER7. The first backcross generations were taller than B138 but shorter than ER7 while BE3-1BC_1 was shorter compared to ER7 and B138 across all observation days All RBC_1 generations were taller than B138 but remained

Table 1. Evaluation of parents, F$_1$, BC$_1$ and BC$_2$ population for plant height (cm)

GENOTYPES	PEDIGREE	14 DAS	28 DAS	42 DAS	56 DAS
B138	Landrace	41.13 b	44.00	46.47	44.27
ER7	Variety	115.70 a	111.30	110.17	106.50
BE-1F$_1$	B138 X ER7	78.40 ab	77.40	82.60	80.63
BE-2F$_1$	B138 X ER7	76.87 ab	72.60	76.77	76.13
BE-3F$_1$	B138 X ER7	82.23 ab	84.07	76.00	71.23
BE-4F$_1$	B138 X ER7	73.93 ab	75.53	79.50	71.67
EB-1F$_{1,}$	ER7 X B138	71.97 ab	74.90	78.03	75.70
EB-2F$_1$	ER7 X B138	63.37 ab	58.50	67.40	65.37
EB-3F$_1$	ER7 X B138	43.70 b	43.60	40.83	39.83
EB-4F$_1$	ER7 X B138	72.10 ab	75.90	68.37	73.27
EB-5F$_1$	ER7 X B138	102.03 ab	98.53	107.97	100.37
EB-6F$_1$	ER7 X B138	57.97 ab	62.30	58.20	62.33
EB-7F$_1$	ER7 X B138	57.07 ab	53.97	55.23	55.87
EB-8F$_1$	ER7 X B138	68.80 ab	68.03	70.17	67.37
EB-9F$_1$	ER7 X B138	66.17 ab	72.40	73.93	73.83
BE2-1BC$_1$	BE-2F$_1$ X B138	74.43 ab	74.13	75.00	74.90
BE3-1BC$_1$	BE-3F$_1$ X B138	38.23 b	40.00	41.73	36.80
BE3-2BC$_1$	BE-3F$_1$ X B138	63.20 ab	64.00	65.57	67.50
BE3-3BC$_1$	BE-3F$_1$ X B138	72.97 ab	75.43	80.53	73.93
EB4-1BC$_1$	EB-4F$_1$ X B138	69.70 ab	74.03	71.47	69.67
EB5-1BC$_1$	EB-5F$_1$ X B138	68.27 ab	74.23	71.57	72.00
EB8-1BC$_1$	EB-8F$_1$ X B138	77.37 ab	74.60	78.27	70.87
EB8-2BC$_1$	EB-8F$_1$ X B138	63.37 ab	64.37	65.00	66.60
EB9-1BC$_1$	EB-9F$_1$ X B138	60.43 ab	62.63	66.97	65.90
EB9-2BC$_1$	EB-9F$_1$ X B138	52.90 ab	54.33	57.67	54.57
BE2-1-1BC$_2$	BE2-1BC$_1$ X B138	41.90 b	43.93	49.73	43.90
BE2-1-2BC$_2$	BE2-1BC$_1$ X B138	65.50 ab	68.83	69.37	66.40
BE2-1-3BC$_2$	BE2-1BC$_1$ X B138	39.43 b	35.30	44.77	41.10
BE2-1-4BC$_2$	BE2-1BC$_1$ X B138	38.80 b	38.63	37.07	36.47
BE2-1-5BC$_2$	BE2-1BC$_1$ X B138	46.40 ab	46.07	46.33	45.77
BE2-1-6BC$_2$	BE2-1BC$_1$ X B138	56.83 ab	60.77	59.67	59.03
BE3-1-1BC$_2$	BE3-1BC$_1$ X B138	34.67 b	32.93	35.37	36.03
BE3-3-1BC$_2$	BE3-3BC$_1$ X B138	55.20 ab	51.90	52.23	51.17
EB5-1-1BC$_2$	EB5-1BC$_1$ X B138	58.17 ab	57.07	57.30	60.73
EB8-1-1BC$_2$	EB8-1BC$_1$ X B138	56.13 ab	53.90	57.50	57.00
EB8-1-2BC$_2$	EB8-1BC$_1$ X B138	57.17 ab	53.90	56.07	55.73
EB9-1-1BC$_2$	EB9-1BC$_1$ X B138	50.03 ab	53.63	49.13	52.03
EB9-1-2BC$_2$	EB9-1BC$_1$ X B138	46.70 ab	41.17	45.60	44.20
EB9-1-3BC$_2$	EB9-1BC$_1$ X B138	42.03 b	44.27	41.87	41.47
EB9-2-1BC$_2$	EB9-2BC$_1$ X B138	64.67 ab	64.67	69.00	71.10
EB9-2-2BC$_2$	EB9-2BC$_1$ X B138	43.60 b	41.53	39.00	39.70
EB9-2-3BC$_2$	EB9-2BC$_1$ X B138	41.73 b	46.53	54.83	51.97
EB9-2-4BC$_2$	EB9-2BC$_1$ X B138	43.13 b	41.40	40.80	44.07
EB9-2-5BC$_2$	EB9-2BC$_1$ X B138	68.23 ab	74.53	66.70	77.60
EB9-2-6BC$_2$	EB9-2BC$_1$ X B138	38.90 b	40.47	41.93	42.67
EB9-2-7BC$_2$	EB9-2BC$_1$ X B138	44.07 b	47.67	48.47	49.07
R^2		0.18	0.18	0.18	0.17
GM		59.69	60.22	61.48	60.53
LSD (0.05)		71.18	71.14	72.12	70.41

NOTE: DAS (Days After Sowing), R^2 (Coefficient of determination), GM (Grand Mean), LSD (Least Significant Difference)

B138

ER7

Fig. 1. Seeds of B138 used as a recurrent parent and ER7 used as a non-recurrent parent for the development of improved cowpea lines

shorter than ER7 across all the days of data collection. In the BC$_2$ and RBC$_2$ generations, genotypes such as BE2-1-3BC2, BE2-1-4BC2 and BE3-1-1BC2, EB9-1-2BC2, EB9-1-3BC2, EB9-2-2BC2, EB9-2-4BC2 and EB9-2-6BC2 were shorter than both the ER7 and B138. Plant height at 56 DAS ranged from 36.03 cm (BE3-1-1BC$_2$) to 106.50 cm (ER7) with several genotypes being significantly shorter than ER7 and B138. Among the offspring that were shorter than the parents, most originated from crosses where ER7 served as the female parent in the initial crossing population.

Within each generation, certain genotypes were significantly taller than others, indicating scope for further selection to improve plant height. Plant height is an important trait as it influences the competitive ability of cowpea genotypes . Studies have shown that taller plants often exhibit better resilience to water scarcity, making plant height a key factor in determining the drought tolerance of cowpea varieties (Karuwal *et al.,* 2017). In another study to evaluate the genetic differences and correlation of characters in F$_2$ population of cowpea from IT98K-205-8 cross with IT98K-555-1 (Ajayi, 2023), the highest plant height (22.29 cm) was recorded in parental line IT98K-555-1. In contrast, the present study recorded , ER7 as the tallest parental line compared to B138 and their offspring.

The F$_1$ and RF$_1$ generations had more branches compared to ER7 but less compared to B138 across all the days of data collection (**Table 2**). In the BC$_1$ generation, BE2-1BC$_1$ recorded more branches than both ER7 and B138 at 14 and 28 DAS but fewer branches at 42 and 56 DAS than B138. BE3-1BC$_1$ had the highest number of branches compared to ER7 but less compared to B138. BE3-2BC$_1$ and BE3-3BC$_1$ had higher number of branches compared to both ER7 and B138. With the RBC$_1$ generation, EB4-1BC$_1$ had more branches compared to both ER7 and B138. BE2-1-1BC$_2$ and BE2-1-5BC$_2$ displayed the highest number of branches compared to both B138 and ER7. RBC$_2$ generation, had high number of branches compared to ER7. EB5-1-1BC$_2$ and EB8-1-1BC$_2$ had the highest number of branches than B138 at 56 DAS. Number of branches at 56 DAS ranged from 3.67 (B138) to 13.00 (BE2-1-1BC$_2$).

Number of branches at 56 DAS showed a significant variation among genotypes with BC$_1$, RBC$_1$, BC$_2$ and RBC$_2$ lines recording significantly higher values than both parental lines indicating genetic improvement for this trait in the offspring. BE2-1-1BC$_2$ (13.00) recorded the highest number of branches at 56 DAS compared to all the generations studied. The number of branches in cowpea is an important trait that significantly influences yield potential and agronomic traits. Studies have demonstrated that the number of branches per plant is positively correlated with pod yield in cowpea, indicating that an increased number of branches can lead to higher yields (Gerrano *et al.,* 2022). This relation was supported by the present study, wherein EB5-1-1BC$_2$ recorded the highest number of branches (11.67) followed by EB8-1-1BC$_2$ (11.00) and EB8-1-2BC$_2$ (9.33).

Physiological characters: Significant differences were observed among the genotypes for days to 50% flowering, and days to pod maturity (**Table 3**). The F$_1$ generation flowered later than ER7 but earlier than B138 except for BE-4F$_1$ (35.00) that flowered later than both the parental lines. Among the reciprocal F$_1$s, EB-5F$_1$ flowered earlier than both the parental lines. In the reciprocal BC$_1$ generation, EB4-1BC$_1$ flowered earlier than B138. Similarly, in the reciprocal BC$_2$ generation, EB8-7-2BC$_2$, EB9-10-1BC$_2$, EB9-10-2BC$_2$, EB9-10-3BC$_2$, EB9-10-5BC$_2$ and EB9-10-7BC$_2$ flowered earlier than B138. Days to first flowering ranged from 30.50 (EB-5F$_1$) to 37.00 days (EB9-9-3BC$_2$) while days

Table 2. Evaluation of parents, F_1, BC_1 and BC_2 population at 56 days after sowing for number of branches

GENOTYPES	PEDIGREE	56 DAS	GENOTYPES	PEDIGREE	56 DAS
B138	Landrace	9.33 ab	BE2-1-1BC_2	BE2-1BC_1 X B138	13.00 a
ER7	Variety	3.67 b	BE2-1-2BC_2	BE2-1BC_1 X B138	11.00 ab
			BE2-1-3BC_2	BE2-1BC_1 X B138	11.00 ab
BE-1F_1	B138 X ER7	5.33 ab	BE2-1-4BC_2	BE2-1BC_1 X B138	10.67 ab
BE-2F_1	B138 X ER7	5.33 ab	BE2-1-5BC_2	BE2-1BC_1 X B138	11.00 ab
BE-3F_1	B138 X ER7	4.67 b	BE2-1-6BC_2	BE2-1BC_1 X B138	11.67 ab
BE-4F_1	B138 X ER7	5.67 ab	BE3-1-1BC_2	BE3-1BC_1 X B138	11.33 ab
			BE3-3-1BC_2	BE3-3BC_1 X B138	11.00 ab
EB-1F_1	ER7 X B138	6.00 ab			
EB-2F_1	ER7 X B138	5.33 ab	EB5-1-1BC_2	EB5-1BC_1 X B138	11.67 ab
EB-3F_1	ER7 X B138	6.33 ab	EB8-1-1BC_2	EB8-1BC_1 X B138	11.00 ab
EB-4F_1	ER7 X B138	4.67 b	EB8-1-2BC_2	EB8-1BC_1 X B138	9.33 ab
EB-5F_1	ER7 X B138	7.33 ab	EB9-1-1BC_2	EB9-1BC_1 X B138	7.00 ab
EB-6F_1	ER7 X B138	5.33 ab	EB9-1-2BC_2	EB9-1BC_1 X B138	7.67 ab
EB-7F_1	ER7 X B138	5.33 ab	EB9-1-3BC_2	EB9-1BC_1 X B138	8.33 ab
EB-8F_1	ER7 X B138	6.33 ab	EB9-2-1BC_2	EB9-2BC_1 X B138	6.67 ab
EB-9F_1	ER7 X B138	6.67 ab	EB9-2-2BC_2	EB9-2BC_1 X B138	8.33 ab
			EB9-2-3BC_2	EB9-2BC_1 X B138	7.00 ab
BE2-1BC_1	BE-2F_1 X B138	9.00 ab	EB9-2-4BC_2	EB9-2BC_1 X B138	5.67 ab
BE3-1BC_1	BE-3F_1 X B138	4.33 b	EB9-2-5BC_2	EB9-2BC_1 X B138	7.00 ab
BE3-2BC_1	BE-3F_1 X B138	9.67 ab	EB9-2-6BC_2	EB9-2BC_1 X B138	7.00 ab
BE3-3BC_1	BE-3F_1 X B138	10.33 ab	EB9-2-7BC_2	EB9-2BC_1 X B138	6.00 ab
EB4-1BC_1	EB-4F_1 X B138	10.33 ab	R^2		0.25
EB5-1BC_1	EB-5F_1 X B138	10.33 ab	GM		8.01
EB8-1BC_1	EB-8F_1 X B138	8.33 ab	LSD (0.05)		8.29
EB8-2BC_1	EB-8F_1 X B138	9.00 ab			
EB9-1BC_1	EB-9F_1 X B138	9.00 ab			
EB9-2BC_1	EB-9F_1 X B138	7.67 ab			

Note: DAS (Days After Sowing), R^2 (coefficient of determination), GM (Grand mean), LSD (Least Significant Difference). Different lowercase letters indicate $p \leq 0.05$, as determined by analysis of variance

to 50% flowering ranged from 33.50 days (EB-5F_1) to 40.25 days (BE3-2-1BC_2). Days to first pod maturity ranged from 44 to 49 days after sowing. Among the F_1 generation, BE-2F_1 and BE-4F_1 reached first pod maturity earlier than ER7 but were not significantly different from B138 (44.00 days). The reciprocal F_1s, EB-1F_1, EB-2F_1, EB-4F_1, EB-7F_1 and EB-9F_1 matured earlier than ER7. Early flowering in cowpea is a crucial as it significantly impacts plant development and yield potential. The reciprocal F_1, EB-5F_1 flowered (31 days) earlier than both the parental lines. Similarly, reciprocal BC_1, EB4-1BC_1 and reciprocal BC_2 generation, EB8-7-2BC_2, EB9-10-1BC_2, EB9-10-2BC_2, EB9-10-3BC_2, EB9-10-5BC_2 and EB9-10-7BC_2 flowered earlier than B138 indicating the superiority of reciprocal crosses over direct crosses for early flowering. Similar studies also recorded a wide range in variation in flowering time as (Owusu, 2020) observed the means of days to 50% flowering and days to first flower initiation of the cowpea F_1 progeny were lower than their mid- parent mean values and closer to the early maturing parent (Sanzi). Further, Ajayi (2023) reported that parent IT98K-205-8 flowered first with a mean value of 45 days, followed by IT98K-205- 8 × IT98K-555-1 (47 days), 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. Early flowering is particularly important in cowpea breeding for enhancing agricultural resilience to climate change, optimizing yields under drought conditions and pest management. According to Doumbia *et al.* (2013), early flowering varieties can significantly mitigate the adverse effects of climate change, allowing for timely harvesting and improved food security.

Table 3. Evaluation of parents parents, F_1, BC_1 and BC_2 population for duration

GENOTYPES	PEDIGREE	DF	DFF	DFPM	DNPM	DM
B138	Landrace	34.75 cdef	37.50 cdefg	44.00 f	50.00 c	58.00 a
ER7	Variety	31.75 jk	34.75 jk	46.00 d	49.00 d	53.00 d
BE-1F_1	B138 X ER7	34.50 cdefg	38.25 abcde	47.00 c	50.00 c	53.00 d
BE-2F_1	B138 X ER7	32.25 hijk	36.00 fghij	44.00 f	46.00 g	50.00 f
BE-3F_1	B138 X ER7	32.00 ijk	35.00 ijk	48.00 b	51.00 b	56.00 b
BE-4F_1	B138 X ER7	35.00 bcdef	38.00 bcdef	44.00 f	46.00 g	50.00 f
EB-1F_1	ER7 X B138	34.00 efghi	37.00 efghi	44.00 f	50.00 c	58.00 a
EB-2F_1	ER7 X B138	35.50 abcde	38.50 abcde	44.00 f	46.00 g	50.00 f
EB-3F_1	ER7 X B138	35.00 bcdef	38.00 bcdef	48.00 b	51.00 b	58.00 a
EB-4F_1	ER7 X B138	35.75 abcde	38.75 abcde	44.00 f	46.00 g	50.00 f
EB-5F_1	ER7 X B138	30.50 k	33.50 k	48.00 b	51.00 b	56.00 b
EB-6F_1	ER7 X B138	35.50 abcde	38.50 abcde	48.00 b	51.00 b	56.00 b
EB-7F_1	ER7 X B138	36.00 abcde	39.00 abcde	44.00 f	50.00 c	58.00 a
EB-8F_1	ER7 X B138	34.25 defgh	37.25 defgh	45.00 e	48.00 e	54.00 c
EB-9F_1	ER7 X B138	36.25 abcd	39.25 abcd	44.00 f	46.00 g	50.00 f
BE2-1BC_1	BE-2F_1 X B138	35.00 bcdef	38.00 bcdef	47.00 c	50.00 c	56.00 b
BE3-1BC_1	BE-3F_1 X B138	36.00 abcde	38.75 abcde	49.00 a	52.00 a	56.00 b
BE3-2BC_1	BE-3F_1 X B138	34.75 cdef	37.75 cdef	45.00 e	48.00 e	54.00 c
BE3-3BC_1	BE-3F_1 X B138	34.00 efghi	38.00 bcdef	47.00 c	50.00 c	53.00 d
EB4-1BC_1	EB-4F_1 X B138	31.50 jk	34.50 jk	47.00 c	50.00 c	53.00 d
EB5-1BC_1	EB-5F_1 X B138	35.00 bcdef	38.25 abcde	47.00 c	50.00 c	53.00 d
EB8-1BC_1	EB-8F_1 X B138	34.50 cdefg	37.50 cdefg	47.00 c	50.00 c	56.00 b
EB8-2BC_1	EB-8F_1 X B138	34.25 defgh	37.75 cdef	47.00 c	50.00 c	53.00 d
EB9-1BC_1	EB-9F_1 X B138	36.00 abcde	40.00 ab	47.00 c	50.00 c	53.00 d
EB9-2BC_1	EB-9F_1 X B138	34.75 cdef	38.00 bcdef	47.00 c	50.00 c	53.00 d
BE2-1-1BC_2	BE2-1BC_1 X B138	35.75 abcde	38.75 abcde	49.00 a	52.00 a	56.00 b
BE2-1-2BC_2	BE2-1BC_1 X B138	31.75 jk	34.75 jk	46.00 d	49.00 d	53.00 d
BE2-1-3BC_2	BE2-1BC_1 X B138	34.50 cdefg	37.50 cdefg	46.00 d	49.00 d	53.00 d
BE2-1-4BC_2	BE2-1BC_1 X B138	35.50 abcde	39.50 abc	46.00 d	49.00 d	58.00 a
BE2-1-5BC_2	BE2-1BC_1 X B138	35.50 abcde	39.50 abc	46.00 d	49.00 d	53.00 d
BE2-1-6BC_2	BE2-1BC_1 X B138	32.50 ghijk	35.50 ghijk	46.00 d	49.00 d	53.00 d
BE3-2-1BC_2	BE3-1BC_1 X B138	37.25 a	40.25 a	49.00 a	52.00 a	56.00 b
BE3-4-1BC_2	BE3-3BC_1 X B138	32.00 ijk	35.00 ijk	49.00 a	52.00 a	56.00 b
EB5-6-1BC_2	EB5-1BC_1 X B138	36.50 abc	39.00 abcde	47.00 c	51.00 b	58.00 a
EB8-7-1BC_2	EB8-1BC_1 X B138	35.00 bcdef	38.00 bcdef	44.00 f	47.00 f	51.00 e
EB8-7-2BC_2	EB8-1BC_1 X B138	32.50 ghijk	35.00 ijk	44.00 f	46.00 g	50.00 f
EB9-9-1BC_2	EB9-1BC_1 X B138	35.50 abcde	39.00 abcde	46.00 d	49.00 d	53.00 d
EB9-9-2BC_2	EB9-1BC_1 X B138	36.25 abcd	39.25 abcd	46.00 d	49.00 d	53.00 d
EB9-9-3BC_2	EB9-1BC_1 X B138	37.00 ab	40.00 ab	49.00 a	52.00 a	56.00 b
EB9-10-1BC_2	EB9-2BC_1 X B138	32.00 ijk	35.00 ijk	49.00 a	52.00 a	56.00 b
EB9-10-2BC_2	EB9-2BC_1 X B138	34.50 cdefg	38.00 bcdef	44.00 f	48.00 e	53.00 d
EB9-10-3BC_2	EB9-2BC_1 X B138	34.50 cdefg	37.75 cdef	44.00 f	48.00 e	53.00 d
EB9-10-4BC_2	EB9-2BC_1 X B138	34.75 cdef	38.00 bcdef	47.00 c	50.00 c	56.00 b
EB9-10-5BC_2	EB9-2BC_1 X B138	32.25 hijk	35.25 hijk	46.00 d	49.00 d	53.00 d
EB9-10-6BC_2	EB9-2BC_1 X B138	36.00 abcde	39.00 abcde	47.00 c	51.00 b	58.00 a
EB9-10-7BC_2	EB9-2BC_1 X B138	33.25 fghij	37.25 defgh	46.00 d	49.00 d	53.00 d
R^2		0.06	0.61	1.00	1.00	1.00
GM		34.42	37.59	46.26	49.41	54.15
LSD (0.05)		2.09	2.15	0.00	0.00	0.00

Note: DF (days to flowering), DFF (days to 50% flowering), DFPM (days to first pod maturity), DNPM (days to 90% pod maturity), DM (days to maturity), R^2 (coefficient of determination), GM (grand mean), LSD (least significant difference). Different lowercase letters indicate $p \le 0.05$, as determined by analysis of variance

Ninety percent (90%) pod maturity occurred between 46 to 52 days after sowing (**Table 3**). Among the F_1 genotypes, BE-2F_1 and BE-4F_1 were the earliest to reach days to 90% pod maturity compared to both parental lines. The reciprocal F_1 progenies; EB-2F_1, EB-4F_1, EB-8F_1 and EB-9F_1 reached 90% pod maturity earlier than both their parental lines. With BC_1 generation, BE3-2BC_1 reached 90% pod maturity earlier than both the parental lines. The reciprocal BC_2 crosses; EB8-7-1BC_2, EB8-7-2BC_2, EB9-10-2BC_2 and EB9-10-3BC_2 reached days to 90% pod maturity earlier than both the parental lines . The genotypes reached physiological maturity between 50 and 58 days after sowing. The F_1 progenies, BE-2F_1 and BE-4F_1 reached physiological maturity (50.00 days) earlier than B138 and ER7. The reciprocal F_1 progenies, EB-2F_1, EB-4F_1 and EB-9F_1 were also the earliest to mature compared to both the parental lines at 50 days after sowing, while reciprocal BC_2 generation, EB8-7-1BC_2 and EB8-7-2BC_2 reached days to maturity earlier than both the parental lines (**Table 3**).

The harvest period for cowpea pods typically ranges from 5 to 9 weeks after sowing, with semi-early varieties becoming harvest readiness around the 7th week (Barro *et al.,* 2023). Previous studies have also shown that crossing cowpea lines with early flowering traits can lead to progenies to combine desirable attributes, such as early flowering and determinate maturing characteristics (Lazaridi *et al.,* 2023). In addition to optimizing yield under drought conditions, early flowering plays a vital role in pest management. Dzemo *et al.* (2010) emphasize that flowering and podding stages are critical periods where cowpea is vulnerable to pest infestations limiting increased and sustainable cowpea grain production. By developing early flowering varieties, breeders can strategically time flowering to avoid peak pest populations, thereby reducing the reliance on chemical pest control methods and promoting sustainable agricultural practices (Dzemo *et al.,* 2010).

The number of days to maturity indicated that there was an improvement in the F_1, RF_1, BC_1, RBC_1, BC_2 and RBC_2 progenies as compared to ER7 and B138 parental lines. Most progenies matured earlier than the late maturing parental genotype (B138). Early maturity provide harvesting before the drought season approaches allowing improved yield productivity. Similar study by Owusu (2020) observed the means of days to 90% pod maturity and days to first pod maturity of the F_1 progeny were lower than their mid- parent mean values and closer to the early maturing parent (Sanzi).

Yield and yield related characters: Significant differences were observed among the genotypes for number of pods per plant, pod length, pod width, number of seeds per pod, 100 seed weight, seed yield per plant and seed yield per plot (**Table 4).** Number of pods per plant ranged of 5.25 (EB9-10-7BC_2) to 21.75 (EB4-1BC_1). The F_1 generation has less number of pods per plant compared to both the parental lines with BE-1F_1 (20.00) recording same number of pods with B138. All the reciprocal F_1s had less number of pods compared to both the parental lines. Similarly, BC_1 generation, had fewer pods than both the parents, although BE3-2BC_1 (20.00) was not significantly different from B138. The RBC_1 generation recorded less number of pods per plant except for EB4-1BC_1 (21.75) and EB8-BC_1 (21.50) not significantly different from ER7 but more than B138 (20.00). For the BC_2 and RBC_2 generations, all progenies had less number of pods per plant compared to both the parental lines, except for EB8-7-1BC_2 (20.00) and EB9-10-3BC_2 (20.25) that were not significantly different from B138 (**Table 4**).

Overall, most developed offsprings recorded fewer pods per plant than their parental lines. The reciprocal BC_1, EB4-1BC_1 (21.75) recorded non-significantly higher number of pods compared to ER7 (21.50) and B138 (20.00). This observation may indicate additive genetic effects, genetic relatedness, environmental conditions and the heritability of the trait. These factors collectively influence the expression of pod number in cowpea breeding programs, guiding selection strategies for improved yield. Similar variability in pod number was reported by Zaki and Radwan (2022) who observed the mean number of pods per plant of the developed crosses differed from 21.50 for the cross Cr7 x Al to 71.00 for the cross D331 x Al in F_1s, and from 38.70 for the cross Cr7 x Com1 to 48.20 for the cross Cr7 x Al in F_2s.

Pod length among the studied genotypes ranged from 15.28 cm (BE2-1-5BC_2) to 21.00 cm (BE3-3BC_1) (**Table 4**). The F_1 progenies; BE-1F_1 (17.28 cm) was longer than B138 but shorter than ER7. BE-2F_1 (15.40 cm) was shorter compared to both the parental lines whereas BE-3F_1 (16.75 cm) was not significantly different from B138 but shorter than ER7. BE-4F_1 (18.30 cm) was longer than B138 but short compared to ER7. In the RF_1, EB-4F_1 (16.28 cm) was shorter than both parents, while the remaining genotypes were longer than B138 but shorter than ER7. The BC_1 and RBC_1 progenies were longer in pod sizes than B138 but shorter than ER7, except for BE3-3BC_1 (21.00 cm) that was longer than both the parental lines. EB8-2BC_1 (15.58 cm) was shorter compared to both the parental lines. Similarly, most of the BC_2 and RBC_2 progenies were longer than B138 but shorter than ER7 except for BE2-1-1BC_2 (16.08 cm), BE2-1-5BC_2 (15.28 cm), BE2-1-6BC_2 (16.18 cm), EB9-9-2BC_2 (16.45 cm) and EB9-10-2BC_2 (16.25 cm) that were shorter than both the parental lines. BE3-4-1BC_2 (19.13 cm) was longer than B138 but not significantly different from ER7.

Significant variation was observed for pod length among parents, their F_1 crosses, backcross 1 and backcross 2 generations studied, where only BE3-4-1BC_2 (19.13 cm) recorded more pod length compared to all the studied

Table 4. Evaluation of parents, F$_1$, BC$_1$ and BC$_2$ population for yield and yield contributing characters

Genotypes	PEDIGREE	NOPP	PL	PW	NOSP	HSW	SYP	SYPP
B138	Landrace	20.00 ab	16.53 pqrstu	2.30 cde	17.25 cdefgh	10.84 r	124.40 c	0.12 b
ER7	Variety	21.50 a	19.08 b	2.25 e	17.00 defghi	9.21 l	101.68 j	0.10 d
BE-1F$_1$	B138 X ER7	20.00 ab	17.28 ijklmnop	2.35 bcde	17.75 bcdef	10.93 q	88.48 o	0.09 e
BE-2F$_1$	B138 X ER7	16.25 efg	15.40 wx	2.40 abcde	14.00 m	12.01 e	73.17 y	0.07 g
BE-3F$_1$	B138 X ER7	13.50 ijk	16.75 opqrstu	2.35 bcde	16.75 efghi	11.43 j	83.97 t	0.08 f
BE-4F$_1$	B138 X ER7	12.00 kl	18.30 cdef	2.38 abcde	16.75 efghi	11.85 f	80.15 w	0.08 f
EB-1F$_1$	ER7 X B138	6.25 p	17.30 hijklmno	2.33 cde	16.00 hijk	10.17 e	34.93 o	0.03 k
EB-2F$_1$	ER7 X B138	15.50 fghij	18.05 cdefgh	2.43 abcd	16.75 efghi	10.78 u	45.39 l	0.05 i
EB-3F$_1$	ER7 X B138	9.00 mno	17.08 klmnopq	2.38 abcde	16.50 fghij	10.42 a	16.10 t	0.02 l
EB-4F$_1$	ER7 X B138	16.00 fgh	16.28 rstuv	2.53 a	18.00 bcde	11.25 n	83.91 u	0.08 f
EB-5F$_1$	ER7 X B138	9.00 mno	18.45 bcde	2.45 abc	18.25 bcd	11.18 p	64.01 d	0.06 h
EB-6F$_1$	ER7 X B138	9.75 lmn	16.90 mnopqrst	2.38 abcde	17.00 defghi	9.15 m	52.42 j	0.05 i
EB-7F$_1$	ER7 X B138	10.00 lm	17.03 klmnopqr	2.30 cde	16.50 fghij	10.11 g	38.61 n	0.04 j
EB-8F$_1$	ER7 X B138	16.25 efg	18.48 bcd	2.38 abcde	15.75 ijkl	10.05 h	62.28 g	0.06 h
EB-9F$_1$	ER7 X B138	11.50 kl	17.95 defghi	2.30 cde	17.25 cdefgh	10.22 d	82.50 v	0.08 f
BE2-1BC$_1$	BE-2F$_1$ X B138	18.75 bcd	17.10 jklmnopq	2.43 abcd	16.75 efghi	10.79 t	107.40 e	0.11 c
BE3-1BC$_1$	BE-3F$_1$ X B138	11.75 kl	17.73 defghijkl	2.45 abc	17.50 bcdefg	13.06 a	29.75 p	0.03 k
BE3-2BC$_1$	BE-3F$_1$ X B138	20.00 ab	16.93 mnopqrst	2.30 cde	17.75 bcdef	11.77 h	131.43 b	0.13 a
BE3-3BC$_1$	BE-3F$_1$ X B138	19.75 abc	21.00 a	2.33 cde	17.00 defghi	11.38 l	104.27 h	0.10 d
EB4-1BC$_1$	EB-4F$_1$ X B138	21.75 a	18.13 cdefg	2.30 cde	16.25 ghijk	12.04 d	134.62 a	0.13 a
EB5-1BC$_1$	EB-5F$_1$ X B138	17.50 cdef	17.65 fghijklm	2.40 abcde	17.75 bcdef	10.66 x	108.35 d	0.11 c
EB8-1BC$_1$	EB-8F$_1$ X B138	21.50 a	16.98 lmnopqrs	2.38 abcde	16.50 fghij	9.13 n	98.52 l	0.10 d
EB8-2BC$_1$	EB-8F$_1$ X B138	17.50 cdef	15.58 vwx	2.43 abcd	17.50 bcdefg	10.58 y	100.40 k	0.10 d
EB9-1BC$_1$	EB-9F$_1$ X B138	19.50 abc	16.90 mnopqrst	2.35 bcde	18.00 bcde	8.83 o	64.53 b	0.06 h
EB9-2BC$_1$	EB-9F$_1$ X B138	15.75 fghi	17.85 defghij	2.38 abcde	18.25 bcd	10.83 s	101.77 i	0.10 d
BE2-1-1BC$_2$	BE2-1BC$_1$ X B138	7.00 op	16.08 uvw	2.28 de	18.75 ab	7.23 p	19.41 s	0.02 l
BE2-1-2BC$_2$	BE2-1BC$_1$ X B138	15.25 fghij	17.93 defghi	2.43 abcd	14.50 lm	10.71 w	107.09 f	0.11 c
BE2-1-3BC$_2$	BE2-1BC$_1$ X B138	14.75 ghij	17.63 fghijklmn	2.45 abc	11.50 n	9.87 i	64.09 c	0.06 h
BE2-1-4BC$_2$	BE2-1BC$_1$ X B138	16.75 defg	16.88 nopqrst	2.40 abcde	18.00 bcde	10.05 h	86.27 r	0.09 e
BE2-1-5BC$_2$	BE2-1BC$_1$ X B138	8.75 mno	15.28 x	2.40 abcde	16.00 hijk	11.79 g	47.33 k	0.05 i
BE2-1-6BC$_2$	BE2-1BC$_1$ X B138	13.25 jk	16.18 tuv	2.43 abcd	15.75 ijkl	11.41 k	54.71 i	0.05 i
BE3-2-1BC$_2$	BE3-1BC$_1$ X B138	13.25 jk	17.35 hijklmno	2.38 abcde	18.25 bcd	9.45 j	45.22 m	0.05 i
BE3-4-1BC$_2$	BE3-3BC$_1$ X B138	16.25 efg	19.13 b	2.40 abcde	17.00 defghi	11.58 i	86.55 q	0.09 e
EB5-6-1BC$_2$	EB5-1BC$_1$ X B138	15.75 fghi	17.98 defghi	2.33 cde	15.25 jklm	11.43 j	106.22 g	0.11 c
EB8-7-1BC$_2$	EB8-1BC$_1$ X B138	20.00 ab	17.03 klmnopqr	2.53 a	15.00 klm	11.27 m	64.83 a	0.06 h
EB8-7-2BC$_2$	EB8-1BC$_1$ X B138	18.50 bcde	17.70 efghijkl	2.43 abcd	14.00 m	12.49 b	93.18 m	0.09 e
EB9-9-1BC$_2$	EB9-1BC$_1$ X B138	7.50 nop	17.25 ijklmnop	2.38 abcde	17.25 cdefgh	11.24 o	26.01 q	0.03 k
EB9-9-2BC$_2$	EB9-1BC$_1$ X B138	14.50 ghij	16.45 qrstu	2.50 ab	17.75 bcdef	10.52 z	92.23 n	0.09 e
EB9-9-3BC$_2$	EB9-1BC$_1$ X B138	14.50 ghij	17.38 ghijklmno	2.33 cde	17.00 defghi	10.41 b	87.23 p	0.09 e
EB9-10-1BC$_2$	EB9-2BC$_1$ X B138	13.75 hijk	18.78 bc	2.43 abcd	18.25 bcd	11.25 n	71.57 z	0.07 g
EB9-10-2BC$_2$	EB9-2BC$_1$ X B138	15.00 ghij	16.25 stuv	2.33 cde	17.75 bcdef	9.29 k	59.10 h	0.06 h
EB9-10-3BC$_2$	EB9-2BC$_1$ X B138	20.25 ab	17.65 fghijklm	2.53 a	18.25 bcd	10.34 c	84.92 s	0.08 f
EB9-10-4BC$_2$	EB9-2BC$_1$ X B138	15.75 fghi	17.15 jklmnopq	2.28 de	18.75 ab	9.21 l	62.49 f	0.06 h
EB9-10-5BC$_2$	EB9-2BC$_1$ X B138	10.25 lm	18.38 bcdef	2.53 a	18.50 abc	12.41 c	78.37 x	0.08 f
EB9-10-6BC$_2$	EB9-2BC$_1$ X B138	15.25 fghij	18.38 bcdef	2.30 cde	19.75 a	10.74 v	63.11 e	0.06 h
EB9-10-7BC$_2$	EB9-2BC$_1$ X B138	5.25 p	17.78 defghijk	2.45 abc	16.75 efghi	10.15 f	21.11 r	0.02 l
R^2		0.91	0.83	0.30	0.73	1.00	1.00	1.00
GM		14.82	17.42	2.38	16.93	10.69	74.65	0.07
LSD (0.05)		2.26	0.75	0.17	1.45	0.00	0.00	0.00

Note: NOPP (Number of pods per plant), PL [Pod length (cm)], PW [Pod width(cm)], NOSP (Number of seed per pod), HSW [100 seed weight(g)], SYP [Seed yield per plant(g)], SYPP [Seed yield per plot(kg)], R^2 (coefficient of determination), GM (grand mean), LSD (least significant difference. Different lowercase letters indicate $p \le 0.05$, as determined by analysis of variance genotypes **(Table 4)**. Most progenies recorded pod length that was not significantly different from ER7 and B138 parental lines. Pod width exhibited a significant variation for all the genotypes studied. There was an improvement in some of the progenies developed as they recorded significantly more pod width compared to both the parental lines. Pod length and width are key yield-determining traits, as longer and wider pods can accommodate more seeds, thereby increasing grain yield (Molosiwa and Makwala, 2020). Zaki and Radwan (2022) similarly reported longer and thicker pods in several F_1 and F_2 cowpea crosses compared to their parents.

Pod width ranged from 2.25 cm (ER7) to 2.53 cm (EB-4F_1) for the studied genotypes. The F_1 and RF_1 progenies were significantly wider compared to both the parental lines except for EB-1F_1 (2.33 cm), EB-7F_1 (2.30 cm) and EB-9F_1 (2.30 cm) that were wider than ER7 but not significantly different from B138 **(Table 4)**. The BC_1 and RBC_1 generations were wider than both the parental lines except BE3-2BC_1 (2.30 cm), BE3-3BC_1 (2.33 cm) and EB4-1BC_1 (2.30 cm), that were significantly wider than ER7 but not significantly from B138. A more significant variation was recorded amongst the BC_2 progenies compared to both the parental lines with BE2-1-1BC_2 (2.28 cm) lesser than B138 but wider ER7. The RBC_2 generations were significantly wider compared to both the parental lines except for EB5-6-1BC_2 (2.33 cm), EB9-9-3BC_2 (2.33 cm), EB9-10-2BC_2 (2.33 cm) and EB9-10-2BC_2 (2.30 cm) which were not significantly different from B138 but wider than ER7. EB9-10-4BC_2 (2.28 cm) was significantly wider than ER7 but less than B138.

The reciprocal F_1; EB-4F_1 and EB-5F_1 had a greater number of seeds per pod compared to the two parental lines. With the RBC_1 generation, EB9-1BC_1 and EB9-2BC_1 having a greater number of seeds per pod than B138 and ER7. The BC_2 and RBC_2 progenies; BE2-1-1BC_2, BE2-1-4BC_2, BE3-2-1BC_2, EB9-10-1BC_2, EB9-10-3BC_2, EB9-10-4BC_2, EB9-10-5BC_2 and EB9-10-6BC_2 recorded a greater number of seeds per pod than B138 and ER7. Number of seeds per pod ranged from 14.00 (BE-2F_1 and EB8-7-2BC_2) to 19.75 (EB9-10-6BC_2) across all the studied genotypes. Hundred (100) seed weight for the genotypes studied ranged from 7.23 g (BE2-1-1BC_2) to 13.06 g (BE3-1BC_1) (**Table 4**). The F_1 progenies weighed significantly more compared to the two parental genotypes. With the RF_1 progenies, EB-4F_1 and EB-5F_1, weighing more compared to the two parental lines. The BC_1 generations weighed significantly more compared to both parental lines, except for BE2-1BC_1 which weighed less than B138 but more than ER7. EB4-1BC_1 weighed more than B138 and ER7. With BC_2 progenies, BE2-1-5BC_2, BE2-1-6BC_2 and BE3-4-1BC_2 weigh more compared to the two parental lines. The RBC_2 generation; EB5-6-1BC_2, EB8-7-1BC_2, EB8-7-2BC_2, EB9-9-1BC_2, EB9-10-1BC_2 and EB9-10-5BC_2 weighed more than B138 and ER7.

Data recorded for number of seeds per pod across the studied genotypes; the reciprocal F1; EB-4F_1 (18.00) and EB-5F_1 (18.25), RBC_1 generation; EB9-1BC_1 and EB9-2BC_1, BC_2 and RBC_2 progenies; BE2-1-1BC_2, BE2-1-4BC_2, BE3-2-1BC_1, EB9-10-1BC_2, EB9-10-3BC_2, EB9-10-4BC_2, EB9-10-5BC_2 and EB9-10-6BC_2 recorded a greater number of seeds per pod than both the parental lines (B138 and ER7). These genotypes could be selected for improvement as they indicated a great potential that may contribute to grain yield (Table 4). In another cowpea study by Zaki and Radwan (2022), F_1 and F_2: Col x Al, Col x Com1, Cr7 x Al, Cr7 x Com1, D331 x Al, and D331 x Com1. 'Al' and 'Com1' had superior number of seeds per pod and seed weight per pod.

Seed yield per plant ranged from 16.10 g (EB-3F_1) to 134.62 g (EB4-1BC_1) (**Table 4**). The F_1 and RF_1 progenies yield significantly less compared to the two parental lines. For the BC_1 generations, only BE3-2BC_1 was more yielding compared to the two parental lines. BE2-1BC_1 and BE3-3BC_1 yielded more than ER7 but less than B138. The reciprocal BC_1 had less seed yield compared to the two parental lines except for EB4-1BC_1 which yielded more compared to the two parental lines. EB5-1BC_1 and EB9-2BC_1 had less seed yield compared to B138 but more than ER7. The BC_2 and RBC_2 progenies significantly yielded less compared to the two parental lines, with BE2-1-2BC_2 and EB5-6-1BC_2 yielding more than ER7 but less than B138. The same trend for seed yield per plot (g) was observed for the studied genotypes.

The 100 seed weight for the genotypes studied, F_1 progenies, RF_1 progenies, EB-4F_1 and EB-5F_1, BC_1 generations, BC_2 progenies, BE2-1-5BC_2, BE2-1-6BC_2 and BE3-4-1BC_2 recorded more seed weight compared to the two parental lines (Table 4). The RBC_2 generation; EB5-6-1BC_2, EB8-7-1BC_2, EB8-7-2BC_2, EB9-9-1BC_2, EB9-10-1BC_2 and EB9-10-5BC_2 recorded more 100 seed weight than both B138 and ER7. Since 100-seed weight is a reliable indicator of seed size and yield potential, it remains a crucial selection criterion in cowpea breeding.

Zaki and Radwan (2022) recorded a significant variation in seed weight per plant produced by the cowpea F_1 and F_2 generations of crossings. Crosses in F_1 had a higher seed weight than crosses in F_2, except Cr7 x Al cross, which had the lowest seed weight of all the crosses. D331 x Al cross exceeded the parental genotypes as well as the other crosses in F_1 with an average of 80.7 g per plant. Ajayi (2023) also reported higher yield traits in reciprocal crosses, although these remained lower than the superior parent IT98K-555-1.

From this study, the reciprocal BC_2 generation (EB8-7-1BC_2 and EB8-7-2BC_2) showed a reduction in days to maturity reaching maturity at 51 and 50 days after sowing, respectively, which was earlier than the early-maturing parent that matured at 53 days after sowing.

Yield improvement was also observed in the backcross 2 generation (BE2-1-2BC$_2$ and EB5-6-1BC$_2$) as BE2-1-2BC$_2$ and EB5-6-1BC$_2$ recorded increases in seed yield per plant of 5.41 g and 4.54 g, respectively, compared to ER7 (101.68 g). This increase indicates genetic improvement in the offspring and supports their selection for further breeding. Among the developed BC$_2$ offsprings, EB8-7-1BC$_2$, EB8-7-2BC$_2$, EB9-10-1BC$_2$, EB9-10-2BC$_2$, EB9-10-3BC$_2$, EB9-10-5BC$_2$ and EB9-10-7BC$_2$ showed improved earliness by reaching maturity earlier than both parents. For number of seed per pod, BE2-1-1BC$_2$, BE2-1-4BC$_2$, BE3-2-1BC$_2$, EB9-10-1BC$_2$, EB9-10-3BC$_2$, EB9-10-4BC$_2$, EB9-10-5BC$_2$ and EB9-10-6BC$_2$ performed better than both parental lines. Thus, these backcross 2 offsprings can be effectively utilized for further breeding programs for improvement of early maturity and yield. Present study concluded that backcross breeding method was successfully used to develop improved cowpea offspring in terms of early maturity and increased yield.

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