



COMPARING RECIPROCAL F₁ PROGENIES IN SELECTED COWPEA (*Vigna unguiculata* (L) WALP) CROSSES

Adewuyi A. P¹. and O. B. Kehinde²

1School of Agriculture and Environmental Sciences, University of The Gambia

2 Federal University of Agriculture, Abeokuta, Nigeria: kehindeob@funaab.edu.ng

Received 12th April, 2026; Accepted 9th July, 2026

ABSTRACT: Genetic variation is essential for designing crop breeding programmes that achieve desired breeding objectives. This study evaluated variations in pod, seed, and leaf characteristics among F₁ hybrids derived from five purebred cowpea (*Vigna unguiculata* (L.) Walp.) lines. The experiment was conducted at the Federal University of Agriculture, Abeokuta (FUNAAB) using a completely randomized design with five replicates, giving a total of 25 experimental units. Both qualitative and quantitative traits were assessed. Qualitative traits were classified into phenotypic categories, while quantitative data were analyzed using analysis of variance (ANOVA) at $\alpha = 0.05$. No maternal or cytoplasmic effects were detected in the inheritance of seed coat texture, petiole formation, peduncle type, pod shattering, or the inverted V-shaped leaf mark. However, maternal effects significantly influenced quantitative traits, including seed weight, number of seeds per pod, ovules per pod, pod length, and leaf size, with seed weight showing the strongest maternal influence. No significant differences were observed between parental lines and F₁ progenies for ovules per pod, pod length, 100-seed weight, seeds per pod, and leaf size. Smooth seed coat, dehiscent pods, non-branching peduncles, and petiolate leaves exhibited dominance over their respective alternative traits. The findings highlight the importance of considering maternal effects when developing cowpea breeding strategies for improved quantitative traits.

Keywords: Reciprocal crosses, Maternal effect, Branching peduncle, Cowpea lines, Pod length.

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important grain legume widely cultivated in tropical and subtropical regions of the world. It belongs to the family Fabaceae (Patel et al., 2009) and is considered one of the most valuable food legumes in sub-Saharan Africa. The widespread distribution of wild cowpea in West Africa provides strong evidence supporting the

region as its centre of origin (Pandey & Singh, 2015). Cowpea is a warm-season, herbaceous annual crop that is highly sensitive to cold temperatures and severe frost (Pandey & Singh, 2015).

Cultivated cowpea exhibits considerable morphological diversity, including variations in growth habit, pod length, seed size, seed colour, and seed texture. Growth forms range from erect, determinate, and indeterminate types to profusely branching, non-branching, prostrate, and climbing forms. The species is diploid ($2n = 22$), and members within the species are generally interfertile (Ezin et al., 2023). Although cowpea is predominantly self-

* Corresponding Author E-mail: paademola@utg.edu.gm
Tel: +220-3650027

This article remains permanently open access under the terms of the Creative Commons Attribution License 4.0, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

pollinated, varying levels of natural outcrossing have been reported depending on pollinator activity (Kebede & Bekeko, 2020).

Cowpea is the most important pulse crop in tropical Africa and is cultivated extensively along the southern fringes of the Sahara, from West to East Africa and into southern regions of the continent. Africa accounts for over 75% of global cowpea production, with major production occurring in countries such as Nigeria, Niger, Uganda, and Senegal (Kebede & Bekeko, 2020). Under favourable environmental conditions, cowpea can produce yields of 1,500–2,000 kg/ha within 60–70 days after planting (Lelou et al., 2011). However, production is constrained by several abiotic and biotic factors, including inadequate insolation, erratic moisture distribution, temperature stress, poor soil fertility, low organic matter content, insect pests such as aphids, and diseases including anthracnose (Tewodros et al., 2021).

Beyond its agronomic importance, cowpea plays a critical role in human nutrition and livestock production. The seeds contain approximately 23.4% protein and contribute substantially to dietary protein intake, particularly in West Africa where they serve as an affordable protein source for many households (Kebede & Bekeko, 2020). The green pods, seeds, and young leaves are consumed as vegetables, while cowpea flour is used in the preparation of traditional foods such as *akara* and *moin-moin* (Tewodros et al., 2021). In addition, cowpea haulms provide valuable feed resources for livestock.

Cowpea is also environmentally important due to its ability to tolerate drought conditions and utilize limited soil nutrients more efficiently than many cereal crops (Manda et al., 2020). Through biological nitrogen fixation, cowpea improves soil fertility and contributes to sustainable crop production, particularly among smallholder farmers with limited access to external inputs. Its use as a cover crop and mulch material further enhances its role in sustainable agricultural systems.

The wide range of uses and adaptability of cowpea highlight the need for continuous genetic improvement. Crop improvement programmes rely largely on breeding strategies aimed at increasing

yield potential and enhancing resistance or tolerance to major production constraints, including pests, diseases, drought, and adverse climatic conditions. However, achieving genetic improvement depends on the identification of suitable parental lines capable of producing superior progenies. The challenge of predicting parental performance and identifying desirable gene combinations makes the understanding of inheritance patterns essential in breeding programmes.

Diallel and reciprocal cross analyses are important biometrical approaches used to evaluate the combining ability of parental lines and to determine the nature of gene action controlling important traits. Reciprocal crosses, in particular, provide an opportunity to detect maternal and/or cytoplasmic effects by comparing progenies derived from different directions of crossing. Understanding these effects is important for selecting appropriate parental combinations and improving breeding efficiency. In most breeding programmes, little attention has been given to the importance of female parents in the inheritance of some characters in self-pollinated protandrous plants like cowpea (*Vigna unguiculata* L. Walp). Different cowpea traits are preferred for specific production and market purposes. For example, cowpea varieties with rough seed coats are easier to wash and are therefore preferred by processors and vendors of traditional foods such as *akara* and *moin-moin*, whereas farmers generally prefer high-yielding varieties to maximize productivity and profitability. Consequently, understanding the inheritance of these desirable traits is essential for developing improved cultivars that meet the needs of both producers and consumers. Therefore, this study was conducted to determine the influence of maternal effects on the inheritance of selected qualitative and quantitative traits in cowpea (*Vigna unguiculata* (L.) Walp.) for crop improvement and enhanced economic production.

Materials and Methods

Study location

The study was conducted at the mini-campus of the University of Agriculture, Abeokuta (UNAAB), now Federal University of Agriculture, Abeokuta (FUNAAB), located in Isale-Igbein, Abeokuta, Ogun

State, Nigeria. Abeokuta lies within latitude 7.150° N and longitude 3.350° E in the tropical rainforest agro-climatic zone of south-western Nigeria, characterized by high rainfall and humidity conditions suitable for agricultural activities (NiMet, 2022).

Planting materials and experimental procedures

The genotypes used in this study consisted of five pure-breeding cowpea lines obtained from the Genetics Unit, Department of Agricultural Biology, University of Ibadan, Nigeria. The lines and their distinguishing characteristics were: TVU 1 (red, medium-sized seeds), G2497 (white, smooth-textured seeds), POPSE 2 (non-branching peduncle with large leaves), IFE BPC (brown, rough seed coat), and POPSE 1 (determinate growth habit, non-branching peduncle, and trifoliate leaves).

The experiment was laid out in a completely randomized design (CRD) comprising the five selected cowpea lines, each replicated five times, giving a total of 25 experimental units. Two seeds were sown per pot at a depth of 2–3 cm using topsoil as the growth medium.

A complete diallel mating design, including reciprocal crosses, was employed to evaluate maternal and/or cytoplasmic effects on selected qualitative and quantitative traits. At flowering, controlled hand pollinations were carried out among the parental lines to produce F_1 progenies. The parental lines and their corresponding F_1 progenies were subsequently evaluated for selected morphological characters.

Qualitative traits assessed included seed coat texture, seed colour, petiole formation, peduncle type (branching or non-branching), pod dehiscence, and the presence or absence of an inverted V-shaped leaf mark. Quantitative traits evaluated included leaf size, pod length, number of seeds per pod, number of ovules per pod, and 100-seed weight. Pod dehiscence was assessed under field conditions, while vegetative traits were recorded during plant growth. At physiological maturity, representative plants from each parental line, F_1 plants and seeds were randomly selected for data collection. For the determination of seed weight, a random sample of 100 mature seeds was collected from each line and weighed with analytical balance.

Data analysis

Data were collected on the number of ovules per pod, Peduncle type (branching or non-branching), Pod length (cm), Leaf size (cm²), seed weight (g), Number of seeds per pod, seed coat texture, petiolation, V-shape mark on the leaf, peduncle type and pod dehiscence. Data was analyzed using descriptive and inferential statistics. T-test and ANOVA were done and significance was determined at α 0.05, means were separated using Duncan Multiple Range Test.

The T - test procedure:

$$S_p = \sqrt{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2 / (n_1 + n_2 - 2)}$$

$$S_{\bar{x}} = S_p / \sqrt{n}$$

$$S(x_1 - x_2) = \sqrt{[S_{x_1}^2 + S_{x_2}^2]}$$

$$T = \bar{x}_1 - \bar{x}_2 / S(x_1 - x_2)$$

where S_p = pooled estimate of the standard deviation for both populations.

S_x = standard error of each sample.

$S(x_1 - x_2)$ = sampling error of the distribution of the difference in sample mean.

T = T – test

n = Size of the sample

$n_1 + n_2 - 2$ = Degree of freedom.

The coefficient of variation was calculated to estimate the extent of variation in the quantitative characters between the F_1 progenies and the parentals in the diallel experiment.

$$CV = S / \bar{X} \times 100$$

where S = standard deviation $\bar{X}$ = mean value. CV = Co-efficient of variation (%).

Duncan's multiple range test (DMRT):

$$R_p = Q_p \sqrt{MSE/n}$$

R_p is the shortest significant range,

Q_p is a critical value found in Duncan's table

MSE is the mean square error from the ANOVA, and

n is the number of replicates per group.

RESULTS

Variation in pod, seed, and leaf characteristics in parental lines

Parental lines used in this project work vary with respect to pod, seed, and leaf characteristics (Table 1). The mean ovules per pod did not differ in POPSE 2, POPSE 1, and TVU 1. Also, there was no significant difference in the mean ovules per pod between IFE BPC and G2497. But there were significant differences in the mean ovules per pod between TVU 1, POPSE 1, POPSE 2, and IFE BPC and G2497. POPSE 1 had the highest mean value with respect to ovules per pod. There were significant differences in the mean seeds per pod between POPSE 1 and G2497. There were no significant differences in the mean seeds per pod between TVU 1 and the rest of the lines. Also, the mean seeds per pod did not significantly differ between POPSE 1 and POPSE 2. TVU 1 and POPSE 2 differ significantly in their mean pod length. There were significant differences among G2497, IFE BPC, and POPSE 1 in terms of their mean pod length.

Table 1: Variation in pod, seed, and leaf characteristics in parental lines

Line	Mean number of Ovules per Pod	Mean number of Seeds per pod	Mean Pod length (cm)	Mean leaf Size (cm ²)	Mean 100 Seed Weight (g)
POPSE 2	14.6 ^a	12.2 ^{ab}	16.68 ^{ac}	98.8 ^a	12.24 ^b
IFE BPC	11.8 ^b	10.6 ^{bc}	13.00 ^e	50.6 ^b	16.1 ^a
POPSE 1	15.2 ^a	12.4 ^a	15.06 ^{ad}	50.0 ^b	11.93 ^{bc}
G2497	11.2 ^b	10.4 ^b	13.34 ^{de}	90.8 ^a	11.40 ^c
TVU 1	14.7 ^a	12.0 ^{abc}	14.72 ^{cd} _e	51.2 ^b	9.44 ^d

Values within the same column followed by different superscript letters are significantly different at the 5% level of significance

There was no significant difference in the mean leaf size between IFE BPC and POPSE 1. Significant differences were observed for leaf size between G2497 and IFE BPC and POPSE 1. POPSE 2 had the highest mean leaf size. Significant differences were observed for 100 - seed weight between G 2497 and TVU 1, and IFE BPC. There was no significant difference between POPSE 1 and G2497 for 100 - seed weight. IFE BPC had the highest mean value for 100 - seed weight.

Reciprocal experiment

The F₁ progenies from reciprocal crosses were not different from each other in qualitative characters such as peduncle type, presence of an inverted V-shape mark on the leaf, seed coat texture, petiole type, and dry pod dehiscence (Table 2). Data on reciprocal F₁ progenies obtained for quantitative traits are shown in Table 3. Significant differences were observed for 100 - seed weight in all the reciprocal F₁ progenies except in IFE BPC X POPSE 2 and its reciprocal. Also, significant differences were observed between the mean values of reciprocal F₁ progenies in all the crosses for the leaf size, except in the crosses G2497 x POPSE 1 and TVU 1 x POPSE 1. No reciprocal difference in the F₁ progenies for pod length in the following crosses: IFE BPC x TVU 1; IFE BPC x POPSE 2; G2 497 X POPSE 2, and IFE BPC x POPSE 1 and their reciprocals. On the other hand, significant differences were observed in the reciprocal F₁ progenies of the crosses: G2497 x POPSE 1; TVU 1 x POPSE 1, and POPSE 2 x TVU 1 for mean pod length. Also, reciprocal differences were observed in F₁ progenies for mean seeds per pod in all the crosses except in IFE BPC x POPSE 2 and TVU 1 x POPSE 1. Significant differences were also observed in the reciprocal F₁ progenies for the ovules per pod in the crosses IFE BPC x POPSE 2, G2497 x POPSE 1, IFE BPC x POPSE 1, and G2497 x POPSE 2, while the crosses IFE BPC x POPSE 2, TVU 1 x POPSE 1, and POPSE 2 x TVU 1 did not show significant reciprocal differences in their F₁ progenies for ovules per pod.

Table 2: Comparison of reciprocal F₁ progenies for five qualitative characters

CROSSES	Peduncle Type	Phenotype Observed	Inverted V-Shaped Mark	Phenotype Observed	Seed Coat Texture	Phenotype Observed	Petiole Formation	Phenotype Observed	Dry Pod Dehiscence	Phenotype Observed
IFE BPC X TVU1 TVU1 X IFE BPC	NBP NBP	NBP	Absent Absent	A	Smooth Smooth	Smooth	Present Present	Petiolate	Dehiscent Dehiscent	Dehiscent
IFE BPC X POPSE 2 POPOSE 2 X IFE BPC	NBP NBP	NBP	Absent Absent	A	Rough Rough	Rough	Present Present	Petiolate	ND ND	ND ND
G2497 X POPSE 1 POPOSE 1 X G2497	NBP NBP	NBP	Absent Absent	A	Smooth Smooth	Smooth	Present Present	Petiolate	ND ND	ND ND
IFE BPC X POPSE 1 POPOSE 1 X IFE BPC	NBP NBP	NBP	Absent Absent	A	Smooth Rough	Rough	Present Present	Petiolate	ND ND	ND ND
G2497 X POPSE 2 POPOSE 2 X G2497	NBP NBP	NBP	Absent Absent	A	Rough Smooth	Smooth	Present Present	Petiolate	ND ND	ND ND
TVU1 X POPSE 1 POPOSE 1 X TVU 1	NBP NBP	NBP	Absent Absent	A	Smooth Smooth	Smooth	Present Present	Present	Dehiscent Dehiscent	Dehiscent
POPOSE 2 X TVU1 TVU1 X POPSE 2	NBP NBP	NBP	Absent Absent	A	Smooth Smooth	Smooth	Present Present	Petiolate	Dehiscent Dehiscent	Dehiscent

NBP = Non-branching Peduncle; A = Absence of inverted V-shaped mark; ND = Non-dehiscent Pod

Table 3: Comparison of reciprocal F₁ progenies for ovules per pod, seeds per pod, pod length, leaf size and 100-seed weight

CROSSES	Mean Ovules per pod	t-test	Mean Length cm) SE	Pod cm) t-test	Mean Seeds Per Pod	t-test	Mean Leaf Size (cm ²)	t- test	Mean 100-Seed Weight (g)	t-test
	SE				SE		SE		SE	
IFE BPC X TVU1	14.42 ± 0.28		13.74 ± 0.07		12.63a ± 0.28		62.77a ± 3.68		14.79b ± 0.08	
TVU1 X IFE BPC	13.67 ± 0.28	NS	13.38 ± 0.10	NS	11.18b ± 0.30	S	51.38b ± 4.00	S	18.90a ± 0.08	S
IFE BPC X POPSE 2	17.34a ± 0.50		14.84 ± 0.10		12.32 ± 0.32		55.66b ± 3.48		15.71 ± 0.15	
POPOSE 2 X IFE BPC	13.96b ± 0.17	S	15.14 ± 0.28	NS	12.84 ± 0.28	NS	61.71a ± 4.12	S	15.75 ± 0.24	NS
G2497 X POPSE 1	13.96b ± 0.39		15.98 ± 0.26		12.47a ± 0.54		76.40 ± 4.34		14.18b ± 0.01	
POPOSE 1 X G2497	15.19a ± 0.27	S	15.09b ± 0.20	S	11.45b ± 1.70	S	79.33 ± 2.01	NS	15.73a ± 0.18	S
IFE BPC X POPSE 1	14.21b ± 0.19		15.40a ± 0.29		14.16a ± 0.24		68.00a ± 1.76		15.01b ± 0.09	
POPOSE 1 X IFE BPC	14.60a ± 0.28	S	14.94 ± 0.37	NS	11.00b ± 6.52	S	62.00b ± 2.31	S	15.87a ± 0.01	S
G2497 X POPSE 2	14.82a ± 0.17		16.33 ± 0.27		12.56a ± 0.54		87.85a ± 2.78		13.86a ± 0.54	
POPOSE 2 X G2497	12.60 b ± 0.89	S	16.12 ± 0.33	NS	11.45b ± 0.31	S	70.54b ± 2.85	S	12.93b ± 0.02	S
TVU1 X POPSE 1	14.90 ± 0.22		13.69b ± 0.36		13.69a ± 0.25		57.93 ± 2.22		13.79a ± 0.53	
POPOSE 1 X TVU 1	15.44 ± 0.23	NS	15.81a ± 0.36	S	13.77b ± 0.46	NS	53.36 ± 3.89	NS	11.88b ± 0.12	S
POPOSE 2 X TVU1	14.95 ± 0.39		11.87b ± 0.33		10.31a ± 0.87		43.13a ± 2.80		9.66a ± 0.10	
TVU1 X POPSE 2	14.48 ± 0.23	NS	15.04a ± 0.27	S	8.96b ± 0.34	S	63.00b ± 1.90	S	11.75b ± 0.30	S

NS = Not significant at 5% significant level; S = Significant at 5% significant level; SE = Standard error

Diallel experiment

Data on pod length, seeds per pod, leaf size, ovules per pod, and 100 - seed weight for the parental lines and all the possible cross

combinations (excluding reciprocals) are presented in Table 4. The coefficient of variation for these traits was generally low, with the pod length having the lowest value.

Table 4: Pod, seed and leaf characteristics of parentals and F₁ hybrids in diallel experiment

Parental lines and Crosses	Mean Ovules per pod	Mean seed per pod	Mean Leaf size (cm ²)	Mean Pod Length (cm)	Mean 100- seed weight (g)
Parental lines					
IFE BPC	11.54	10.55	49.10	12.82	15.99
TVU1	14.73	12.19	50.00	14.55	9.43
POPSE 2	14.44	12.52	92.38	16.00	12.25
G2497	11.33	10.00	96.08	12.88	11.43
POPSE 1	15.39	12.09	49.14	12.09	11.93
Crosses					
IFE BPC X TVU1	14.42	12.62	62.97	13.73	14.61
IFE BPC X POPSE 2	17.35	12.31	55.06	14.84	15.71
IFE BPC X G2497*	-	-	-	-	-
IFE BPC X POPSE 1	14.21	14.16	68.94	15.40	15.01
TVU1 X POPSE 2	14.48	8.96	63.00	15.04	11.75
TVU1 X G2497*	-	-	-	-	-
TVU1 X POPSE 1	14.90	12.26	57.93	13.69	13.79
POPSE 2 X G2497	12.60	10.44	70.54	16.12	12.93
POPSE 2 X POPSE 1*	-	-	-	-	-
G2497 X POPSE 1	13.96	12.47	76.40	15.98	14.18
Overall mean	14.12	11.64	64.99	14.29	13.17
Standard error	±0.48	±0.43	±4.70	±0.39	±0.59
Coeff of variation (%)	11.73	12.71	25.05	9.41	15.50
Standard deviation	1.66	1.48	16.28	1.35	2.04

*Unsuccessful crosses

Inheritance pattern of five Qualitative Characters in Selected Diallel Crosses in F₁ Progenies

The data obtained with respect to F₁ for the five selected crosses from the diallel experiment is presented in Table 5. The results were used to test the validity of the earlier studies in the inheritance of seed coat texture, presence of V-shape mark on the leaf, dry pod dehiscence, petiole formation and peduncle type in F₁. The following observation was deduced from the results for each of the following traits:

Seed Coat Texture: Crosses between smooth and rough-seeded coat cowpeas always result in a smooth seed coat, which suggests that smooth-seeded coat may be dominant over rough-seeded coat. Example TVU 1 (smooth-seeded coat) x

POPSE 2 (rough-seeded coat) results in smooth seed coat cowpea.

Peduncle Type: It was observed that crosses between the branching peduncle type and the non-branching peduncle cowpea always result in a non-branching peduncle cowpea. Example IFE BPC (branching peduncle) x POPSE 1 (Non-branching peduncle) results in a non-branching peduncle as indicated in the Table 5.

Inverted V-Shape Mark: Crosses between lines without the mark and those that bear it always result in progenies without the mark. Example G2497 (V-shape mark present) x POPSE 1 (No V-shape mark), the progenies as shown in Table 5 are without the mark in F₁.

Table 5: Inheritance pattern of five Qualitative Characters in Selected Diallel Crosses in F₁ Progenies

Crosses	Peduncle Type	Phenotype Observed	Inverted V-Shaped Mark	Phenotype Observed	Seed Coat Texture	Phenotype Observed	Petiole or Non- Petiolate	Phenotype Observed	Dry Pod Dehiscence	Phenotype Observed
IFE BPC	Branching		Absent		Rough		Petiolate		ND	
X		Non-branching		Absent		Rough		Petiolate		ND
POPSE 1	Non-branching		Absent		Rough		Petiolate		ND	
TVU1	Non-branching		Absent		Smooth		Petiolate		Dehiscent	
X		Non-branching		Absent		Smooth		Petiolate		Dehiscent
POPSE 2	Non-branching		Absent		Rough		Petiolate		ND	
TVU1	Non-branching		Absent		Smooth		Petiolate		Dehiscent	
X		Non-branching		Absent		Smooth		Petiolate		ND
POPSE 1	Non-branching		Absent		Rough		Petiolate		ND	
POPSE 2	Non-branching		Present		Rough		Petiolate		ND	
X		Non-branching		Absent		Rough		Petiolate		ND
G2497	Non-branching		Absent		Rough		NP		ND	
G2497	Non-branching		Present		Rough		NP		ND	
X		Non-branching		Absent		Rough		Petiolate		ND
POPSE 1	Non-branching		Absent		Rough		Petiolate		ND	

ND = non-dehiscent, NP= non-petiolate

Pod Dehiscence: From Table 5, crosses between a dehiscent pod line and a non-dehiscent line always result in dehiscent pods type. e.g TVU 1 (dehiscent pod) x POPSE2 (Non-dehiscent) results in dehiscent pod type.

Petiole Formation: Crosses involving petiole and non-petiole lines always results in petiolate type. Example POPSE 2 (petiolate) x G2497 (Non-petiolate) results in petiolate cowpea.

DISCUSSION

The parental mean separation results obtained in this study revealed considerable genetic variability among the characters of the parental lines evaluated. This finding agrees with the report of Mofokeng and Gerrano (2021), who observed substantial variation among cowpea genotypes for yield and yield-related traits, thereby providing opportunities for effective selection in breeding programmes. The presence of such genetic diversity among the parental lines provides a favourable genetic foundation for the expression and recombination of desirable gene combinations in the resulting progenies (Patel *et al.*, 2009; Mukri *et al.*, 2022).

Results from the reciprocal crossing experiment revealed no significant differences among reciprocal F_1 progenies for all the qualitative characters evaluated, including seed coat texture, petiole formation, peduncle type, pod dehiscence, and inverted V-shaped mark. The absence of reciprocal effects suggests that the inheritance of these traits was not influenced by the maternal parent, indicating the lack of maternal and/or cytoplasmic effects. This observation may be attributed to the involvement of multiple genes and their interaction effects in the expression of some qualitative traits in cowpea. The finding is consistent with the report of Oladejo *et al.* (2021), who demonstrated that the inheritance of certain qualitative traits, such as seed coat colour, can be influenced by epistatic interactions among genes. Therefore, since the direction of crossing did not affect the expression of these traits, any of the parental lines evaluated could be used as either male or female parents in breeding programmes targeting improvement of these qualitative characters.

On the other hand, reciprocal differences were obtained for quantitative characters in some crosses, while some crosses did not show any significant reciprocal difference in their F_1 progenies. The reciprocal differences observed in 100-seed weight among all F_1 progenies resulting from reciprocal crosses in this study are consistent with the findings of Patel *et al.* (2009), who reported maternal effects on the inheritance of certain seed traits in cowpea. This implies that if the seed weight is the breeding goal, maternal effects should be examined, and where it is suspected and/or confirmed, maternal parents should be selected from such lines. Since there were no reciprocal differences in F_1 progenies for seed weight in the cross IFE BPC x POPSE 2, either of the lines can be used as maternal parents in breeding for seed weight (Aliyu, 2005). Also, all the crosses revealed significant differences in reciprocal F_1 progenies with respect to the number of seeds per pod, except the reciprocals of IFE BPC x POPSE 2 and TVU 1 x POPSE 1. This is in agreement with the report of Pandey and Singh (2015) that maternal effects contribute to the inheritance of certain seed-related traits in cowpea, emphasizing that the direction of crossing influences progeny performance. Their findings suggest that careful selection of the female parent is important in cowpea breeding programmes aimed at improving seed and pod characteristics.

Hence, maternal parents should be selected from those crosses that showed significant differences in their reciprocal F_1 progenies if the number of seeds per pod is desired in the hybrids. The crosses that indicated maternal and/or cytoplasmic effect in their reciprocal F_1 progenies agree with the report of (Patel *et al.*, 2009). He reported that if subspecies *mensensis* is the female parent in crosses with *dekindtiana*, seeds are produced, but they are shriveled and weigh only 12 mg each compared to 21 and 26 mg in the female and male parents, respectively (Ezin *et al.*, 2023). The crosses that did not exhibit reciprocal difference in their F_1 progenies are in line with the experimental results obtained by involving reciprocal crosses among four cultivars, two wild varieties, and one weedy

type of cowpea (Patel *et al.*, 2009). Gomes *et al.* (2021) observed that there were no significant differences in the mean values of F_1 reciprocal progenies for pod length, number of ovules per pod, number of seeds per pod, and 100 - seed weight.

Crosses like G2497 x POPSE 1, TVU 1 x POPSE 1, and POPSE 2 x TVU 1 showed reciprocal differences in their F_1 progenies for the number of ovules per pod, pod length, and leaf size Owusu *et al.* (2020), respectively. This implies that the inheritance of each of these characters in each of the respective crosses was influenced by the female or maternal parents (Ezin *et al.*, 2023). Therefore, breeding for hybrids for any of these characters required the use of the lines as the maternal parents. On the other hand, any of the lines may be used as maternal parents for the crosses that did not show maternal effect for the character(s) under consideration (Boukar *et al.*, 2020).

The results of the diallel experiments indicated that there were no significant differences among the parental lines and the F_1 progenies for all the quantitative characters studied, such as: ovules per pod, pod length, seeds per pod, seed weight, and leaf size (Lelou and Van Damme, 2006). This implies that there were no significant improvements or depression in the F_1 progenies. This agrees with the report by Ezin *et al.* (2023) that there is no practicable improvement in the grain yield of cowpea because of its low heritability and complex quantitative characteristics.

The F_1 results obtained from critical experiments in selected diallel crosses seem to be in general agreement with earlier studies that some traits were dominant over others in the F_1 (Barro *et al.*, 2018 ; Lelou *et al.*, 2011).

Dry pod shattering was observed to be likely dominant over non-shattering because all the crosses involving a dehiscent dry pod always result in dehiscent dry pod progenies. This agrees with the report of Barro *et al.* (2018) that the tough cowpea type is dominant over the soft.

Smooth-seeded lines also seem to be dominant over the rough seeded (Ayo-Vaughan *et al.*, 2013). This is due to the fact that all the crosses involving

smooth-seeded coat result in smooth-seeded coat F_1 progenies. Ezin *et al.* (2023) reported that two anatomically different macrosclerid arrangements in the seed coat, perpendicular and parallel with respect to the cotyledon. Ayo-Vaughan *et al.* (2013) also asserted that the perpendicular arrangement is responsible for smooth coat and the vertical arrangement for rough seed coat, with the former being dominant and a single gene controlling the two macrosclerid.

Non-branching peduncle was phenotypically observed to be dominant over the branching peduncle type because all the crosses involving the non-branching line always resulted in non-branching peduncle progenies. Lelou and Van Damme (2006) reported that whenever a cross involves a branching peduncle and a non-branching peduncle of cowpea varieties, the resulting offspring is the non-branching type. The same authors also stressed that this has been attributed to a recessive gene that conditions a branching peduncle capable of producing 2 - 10 seeds/peduncle.

A petiolate leaf was also observed to be dominant over the non-petiolate, as the crosses between non-petiolate and petiolate result in petiolate leaves (Ezin *et al.*, 2023). Also, the lines without the inverted V-shape mark dominate those that bear the mark in all the crosses involving the two lines, respectively.

CONCLUSION

The study revealed that seed weight, number of seeds per pod, and pod length, were influenced by maternal parents. Therefore, the choice of female parent should be considered in breeding programmes targeting improvement of these traits. The identified parental lines may be utilized as maternal parents to enhance the expression of desirable characteristics in subsequent generations.

RECOMMENDATION

Further research should be conducted to include more cowpea lines and additional quantitative traits to explore the potential of maternal effects in cowpea breeding programmes.

REFERENCES

- Aliyu, B. (2005). Crossability of *Vigna rhomboidea* Burtt. Davy with cowpea (*V. unguiculata* (L.) Walp.). *Genetic Resources and Crop Evolution*, 52(4). <https://doi.org/10.1007/s10722-005-2254-0>
- Ayo-Vaughan, M. A., Ariyo, O. J., & Alake, C. O. (2013). Combining ability and genetic components for pod and seed traits in cowpea lines. *Italian Journal of Agronomy*, 8(2). <https://doi.org/10.4081/ija.2013.e10>
- Barro, A., Batieno, T. B. J., Sawadogo, N., Tignegre, J. B. D. L. S., Nanema, K. R., Traore, R. E., & Sawadogo, M. (2018). Resistance evaluation of five varieties of cowpea and their F₁ descendants from a diallel crossing to cowpea aphid-borne mosaic virus in Burkina Faso. *International Journal of Biological and Chemical Sciences*, 12(2). <https://doi.org/10.4314/ijbcs.v12i2.5>
- Boukar, O., Abberton, M., Oyatomi, O., Togola, A., Tripathi, L., & Fatokun, C. (2020). Introgression Breeding in Cowpea [*Vigna unguiculata* (L.) Walp.]. In *Frontiers in Plant Science* (Vol. 11). <https://doi.org/10.3389/fpls.2020.567425>
- Ezin, V., Tossou, T. A. W., Chabi, I. B., & Ahanchede, A. (2023). Diallel analysis of cowpea (*Vigna unguiculata* (L.) Walp.) genotypes under water deficit stress. *BMC Plant Biology*, 23(1). <https://doi.org/10.1186/s12870-023-04508-0>
- Gomes, A. M. F., Draper, D., Nhantumbo, N., Massinga, R., Ramalho, J. C., Marques, I., & Ribeiro-Barros, A. I. (2021). Diversity of cowpea [*Vigna unguiculata* (L.) Walp.] landraces in mozambique: New opportunities for crop improvement and future breeding programs. *Agronomy*, 11(5). <https://doi.org/10.3390/agronomy11050991>
- Kebede, E., & Bekeko, Z. (2020). Expounding the production and importance of cowpea (*Vigna unguiculata* (L.) Walp.) in Ethiopia. In *Cogent Food and Agriculture* (Vol. 6, Issue 1). <https://doi.org/10.1080/23311932.2020.1769805>
- Lelou, B., Diatewa, M., & Van Damme, P. (2011). A study of intraspecific hybrid lines derived from the reciprocal crosses between wild accessions and cultivated cowpeas (*Vigna unguiculata* (L.) Walp.). *African Journal of Plant Science*, 5(6).
- Lelou, B., & Van Damme, P. (2006). ProductiPBAon of intraspecific F₁ hybrids between wild and cultivated accessions of cowpea (*Vigna unguiculata* (L.) Walp.) using conventional methods. *Communications in Agricultural and Applied Biological Sciences*, 71(4).
- Manda, J., Alene, A. D., Tufa, A. H., Feleke, S., Abdoulaye, T., Omoigui, L. O., & Manyong, V. (2020). Market participation, household food security, and income: The case of cowpea producers in northern Nigeria. *Food and Energy Security*, 9(3). <https://doi.org/10.1002/fes3.211>
- Mofokeng, M. A., & Gerrano, A. S. (2021). Efforts in breeding cowpea for aphid resistance: a review. *Acta Agriculturae Scandinavica Section B: Soil and Plant Science*, 71(6). <https://doi.org/10.1080/09064710.2021.1923797>
- Nigerian Meteorological Agency (NiMet). (2022). *Climate review bulletin*. Abuja, Nigeria: NiMet. Retrieved from <https://nimet.gov.ng/>
- Oladejo, A. S., Bolaji, A. O., Okuniyi, E. O., & Gidado, R. M. (2021). Segregation of genes controlling seed coat color in cowpea (*Vigna unguiculata* [L.] Walp.). *Genetics & Biodiversity Journal*, 5(2), 198–206. <https://doi.org/10.46325/gabj.v5i2.86>
- Owusu, E. Y., Mohammed, H., Manigben, K. A., Adjebeng-Danquah, J., Kusi, F., Karikari, B., & Sie, E. K. (2020). *Diallel analysis and heritability of grain yield, yield components, and maturity traits in cowpea (Vigna unguiculata (L.) Walp.)*. The Scientific World Journal, 2020, Article 9390287. <https://doi.org/10.1155/2020/9390287>
- Pandey, B., & Singh, Y. V. (2015). Heterosis for yield and yield contributing characters in cowpea genotypes. *Legume Research*, 38(5). <https://doi.org/10.18805/lr.v38i5.5931>
- Patel, S. J., Desai, R. T., Bhakta, R. S., Patel, D. U., Kodappully, V. C., & Mali, S. C. (2009). Heterosis studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 32(3). <https://doi.org/10.20546/ijcmas.2017.607.191>
- Tewodros, A., Melese, L., & Yoseph, T. (2021). Assessment Of The Production And Importance Of Cowpea [*Vigna unguiculata* (L.) Walp]: Cases From Selected Districts Of Southern Ethiopia. *African Journal of Food, Agriculture, Nutrition and Development*, 21(7). <https://doi.org/10.18697/ajfand.102.19630>

HOW TO CITE THIS ARTICLE:

Adewuyi and Kehinde (2026) Comparing Reciprocal F₁ Progenies in Selected Cowpea (*Vigna unguiculata* (L.) Walp) Crosses. *Nigeria Journal Of Plant Breeding* (<https://pbanjournal.org/>), 3(2), 112-122. ISSN: 2814-3531