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Combining Ability and Reciprocal Effects in Cowpea (*Vigna unguiculata* (L.) Walp.): Identification of Promising Parents and Crosses for Breeding in Côte d'Ivoire

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Authors' contributions

This work was carried out in collaboration among all authors. Author JSKA conceived and designed the study, performed the controlled crosses, developed the experimental protocol, coordinated and supervised the field experiments, conducted the statistical analyses, interpreted the results, and drafted the original manuscript. Author DS contributed to the experimental methodology, statistical interpretation, and critical revision of the manuscript. Authors YB and SDMY contributed to the interpretation of the findings and scientific revision of the manuscript. Author EBZK contributed to the interpretation of the results and critical revision of the manuscript. Author ND contributed to the scientific supervision, interpretation of the findings, and critical revision of the manuscript. All authors read and approved the final manuscript.

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Abstract

Improving cowpea (*Vigna unguiculata* (L.) Walp.) productivity requires the identification of suitable parental lines and promising crosses for breeding programmes. This study aimed to assess general combining ability (GCA), specific combining ability (SCA), and reciprocal effects among four cowpea inbred lines (NBO04, NTE015, NKO03, and NFE011) from the germplasm collection of Peleforo GON COULIBALY University, Côte d'Ivoire. A full diallel comprising four parental lines and twelve F_1 hybrids was evaluated in 2025 using a randomised complete block design with five replications. Seven agromorphological and agronomic traits were analysed according to Griffing's Method 1, Model I (fixed effects). Analysis of variance revealed significant genotypic differences for all traits. GCA accounted for the largest proportions of genotypic variation in seed length (90.75%), leaflet length (84.06%), 100-seed weight (78.47%), and days to maturity (64.37%). Conversely, SCA predominated for the number of pods per plant (76.20%) and grain yield (65.45%). NTE015 exhibited a significant positive GCA effect for grain yield (+729.45 kg ha^{-1}), while the NBO04 × NTE015 parental combination showed a significant positive SCA effect (+2,266.23 kg ha^{-1}). Significant overall reciprocal effects were detected for leaflet width and days to maturity, but not for grain yield. These findings identify NTE015 as a promising parent and NBO04–NTE015 as a priority parental combination for cowpea improvement in Côte d'Ivoire. Further evaluation of segregating generations and multi-environment trials is required to confirm their breeding potential.

Keywords: Vigna unguiculata; general combining ability; specific combining ability; full diallel; reciprocal effects; grain yield; Côte d'Ivoire.

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the major food legumes cultivated in sub-Saharan Africa. It plays an important role in agricultural production systems because it is used for food and feed and provides agronomic benefits. Its protein-rich seeds contribute to improving food and nutritional security, while its ability to fix atmospheric nitrogen helps maintain soil fertility. Its relative tolerance to drought and adaptation to low-fertility soils also make it a crop of particular interest in the Sudano-Sahelian regions, which are characterised by high rainfall variability (Owusu *et al*., 2020; Ezin *et al*., 2023).

Despite these advantages, improving cowpea productivity remains a major challenge for West African agricultural systems. The agronomic performance of this crop is influenced by the genetic characteristics of cultivated varieties, environmental constraints, and their interactions. Water deficits, irregular rainfall patterns, and differences in yield potential among genotypes may substantially limit grain yield. Ezin *et al*. (2023) demonstrated that the agronomic performance and combining ability of cowpea genotypes may vary under different water availability conditions, highlighting the need for suitable genetic materials and appropriate breeding strategies.

Recent multi-environment evaluations have also documented variation among cowpea accessions in drought response and yield stability, reinforcing the importance of considering environmental conditions when assessing candidate breeding materials (Sansa *et al*., 2025; Iseki & Olaleye, 2025).

In this context, exploiting genetic diversity and identifying parental lines with desirable traits are essential steps in the development of improved varieties. However, the individual performance of an inbred line does not necessarily predict its performance as a parent in a breeding programme. It is therefore necessary to assess its ability to transmit desirable traits to its progeny and its performance in specific parental combinations.

Recent studies have reported variation in morphological and nutritional traits among cowpea genotypes (Mishra, 2026) and exploitable variability in yield-related traits in advanced segregating populations (Job *et al*., 2026), supporting the use of complementary characterisation and selection approaches in breeding programmes.

Combining ability analysis is a particularly relevant approach for achieving this objective. Within diallel crossing systems, it allows researchers to distinguish between general combining ability (GCA), which reflects the average contribution of a parent to the performance of its progeny, and specific combining ability (SCA), which represents deviations associated with particular parental combinations (Griffing, 1956). In classical genetic terms, GCA is primarily associated with additive genetic effects, whereas SCA is generally associated with non-additive genetic effects. However, their interpretation depends on the statistical model and the genetic materials under investigation.

In cowpea, several recent studies have confirmed the relevance of this approach for improving agronomic traits. In Ghana, Owusu *et al*. (2020), using a full diallel involving five parental lines, demonstrated the importance of GCA and SCA effects in the expression of grain yield, yield components, and maturity-related traits. Their findings showed that the relative contributions of these effects varied depending on the traits considered. Similarly, in Benin, Ezin *et al*. (2023) identified parental lines and crosses exhibiting favourable combining ability for physiological and agronomic traits under both well-watered and water-deficit conditions. These findings confirm that diallel analysis can guide the selection of parents and promising crosses in breeding programmes.

Beyond GCA and SCA effects, full diallel crossing designs also allow the assessment of reciprocal effects, which represent differences in performance when two parental lines are crossed in opposite directions. Identifying such effects is particularly important because it helps determine whether using a given genotype as the female or male parent influences trait expression in the resulting progeny. Owusu *et al*. (2020) reported reciprocal effects for several cowpea traits, highlighting the potential importance of cross direction in genetic improvement strategies. Nevertheless, the detection of reciprocal effects alone does not establish the maternal or cytoplasmic mechanisms responsible for the observed differences.

In Côte d'Ivoire, particularly in the northern part of the country, cowpea genetic improvement requires more effective use of local plant genetic resources. Research conducted at Peleforo GON COULIBALY University (UPGC), Korhogo, has led to the establishment and characterisation of a collection of cowpea lines exhibiting diversity in agromorphological traits. In this regard, Assouman *et al*. (2024) investigated the homogeneity and agromorphological characteristics of six cowpea lines from the UPGC germplasm collection, contributing to the identification of plant materials suitable for breeding programmes.

Studies of cowpea germplasm in other sub-Saharan African settings have also combined morphological and molecular characterisation to describe population structure and identify marker–trait associations relevant to breeding programmes (Chipeta *et al*., 2025).

Among these genetic resources, the NBO04, NTE015, NKO03, and NFE011 lines are of particular interest for developing new genetic combinations. However, their value as breeding parents cannot be assessed solely on the basis of their individual characteristics. Evaluating their combining ability and the effects associated with cross direction is necessary to identify the most promising parents and parental combinations for improving agronomic traits.

Despite the existing agromorphological characterisation of the UPGC collection, the combining ability of NBO04, NTE015, NKO03, and NFE011 and the possible influence of cross direction on their progeny have not been jointly established. This leaves a practical need to distinguish parents with favourable average contributions from specific parental combinations that may merit further evaluation for the agronomic traits considered here.

Therefore, the present study was undertaken to evaluate the combining ability of four cowpea lines from the UPGC plant genetic resources collection using a full diallel crossing design that included both direct and reciprocal crosses.

The findings are expected to provide useful information to guide crossing and selection strategies within the Cowpea Improvement Programme in Côte d'Ivoire (PANCI).

The originality of this study lies in the experimental evaluation of combining ability and reciprocal effects among four locally selected cowpea inbred lines from the UPGC germplasm collection. Using a full diallel crossing design, the study specifically aimed to: (i) assess agromorphological and agronomic variability among the parental lines and their F_1 hybrids; (ii) estimate general and specific combining ability effects for seven agronomically important traits; (iii) determine the relative contributions of GCA, SCA, and reciprocal effects to the observed variation; and (iv) identify promising parents and parental combinations for improving grain yield, earliness, and morphological traits in cowpea.

2. Materials and Methods

2.1 Study Site and Experimental Period

The study was conducted at the Botanical Garden of Peleforo GON COULIBALY University (UPGC), Korhogo, northern Côte d'Ivoire. The study comprised two successive experimental phases. The first phase, conducted from August to October 2024, involved controlled hybridisation among four parental lines of cowpea (*Vigna unguiculata* (L.) Walp.). The second phase, conducted from July to September 2025, involved the evaluation of the four parental lines and their twelve F_1 hybrids to estimate general combining ability (GCA), specific combining ability (SCA), and reciprocal effects.

2.2 Plant Materials

The plant materials consisted of four cowpea inbred lines, NBO04, NTE015, NKO03, and NFE011, obtained from the plant genetic resources collection of UPGC. These lines had previously undergone purification and agromorphological characterisation (Assouman *et al*., 2024).

The four lines were selected from the available genetic resources for their evaluation as potential breeding parents. The study was designed to assess their combining ability within a defined set of locally maintained genetic materials rather than to estimate genetic parameters representative of the entire cowpea population.

The four parental lines were used in a full diallel crossing scheme that included direct and reciprocal crosses. The twelve resulting F_1 hybrids, together with the four parental lines, constituted the sixteen genotypes evaluated in this study.

2.3 Diallel Crosses and Controlled Pollination

Controlled hybridisations were performed from August to October 2024 using a full diallel crossing scheme involving the four parental lines. Each line was successively used as both the female and male parent in crosses with each of the other three lines, resulting in six distinct parental combinations and their six reciprocal crosses, for a total of twelve F_1 hybrids.

According to Griffing's (1956) Method 1, a full diallel includes the parental entries and both crossing directions for each pair of parents. Consequently, the four-parent diallel used in this study comprised sixteen entries: four parents, six direct crosses, and six reciprocal crosses. Although the number of parents was limited, all the required combinations among the selected lines were represented, allowing the estimation of GCA, SCA, and reciprocal effects within this specific genetic set.

Manual pollination was performed using Technique C described by Assouman *et al*. (2021). This technique involves completely removing the keel and stamens from the flower selected as the female parent. The emasculated flower is then pollinated by directly covering it with a portion of the keel collected from a male-parent flower, together with the flower's complete set of pollen-bearing stamens. This procedure allows pollen from the male parent to contact the female reproductive structures of the emasculated flower.

Crosses were designated according to the female × male convention, with the first genotype denoting the female parent and the second denoting the male parent. This notation was consistently maintained throughout the analyses to distinguish direct crosses from their reciprocals.

2.4 Experimental Design and Crop Management

The agronomic evaluation was conducted from July to September 2025 in a randomised complete block design (RCBD) with five replications. Each block contained the sixteen genotypes, which were randomly allocated to experimental plots, giving a total of 80 microplots.

Each microplot consisted of three rows of four planting hills, corresponding to twelve hills per microplot. Inter-row and intra-row spacings were 0.75 m and 0.50 m, respectively. Two to three seeds were sown per hill, followed by thinning to retain one plant per hill. The theoretical planting density was therefore 26,667 plants ha^{-1}, with twelve plants per microplot. A theoretical plot area of 4.50 m^2 was used for grain yield calculations. Crop management practices were applied uniformly across all experimental units.

Five plants were selected from each microplot for agromorphological, phenological, and yield-component measurements. Grain yield was determined from the harvest of all plants within each microplot. The microplot, rather than each sampled plant, was considered the experimental unit for statistical analyses.

2.5 Agronomic Traits Evaluated

Seven traits were evaluated. For the first six traits, each microplot value represented the mean of observations recorded on five selected plants, whereas grain yield was determined from the total harvest of the microplot.

- **Leaflet length (LL):** Mean leaflet length, expressed in centimetres (cm).
- **Leaflet width (LW):** Mean leaflet width, expressed in centimetres (cm).
- **Days to maturity (DM):** Number of days from sowing to the appearance of the first dry pod on a plant, expressed as days after sowing (DAS).
- **Number of pods per plant (NP):** Number of pods produced per plant.
- **Seed length (SL):** Mean seed length, expressed in millimetres (mm).
- **100-seed weight (100SW):** Weight of 100 seeds, expressed in grams (g).
- **Grain yield (GY):** Total grain weight harvested per microplot, converted into kilograms per hectare (kg ha^{-1}).

Grain yield was calculated using the theoretical microplot area of 4.50 m^2:

$$GY\ (kg\ ha^{-1}) = [W\ (kg) \times 10{,}000] / A\ (m^2)$$

where GY is grain yield (kg ha^{-1}), W is the total grain weight harvested from the microplot (kg), and A is the theoretical microplot area (4.50 m^2).

For each trait, statistical analyses were based on 80 experimental observations (16 genotypes × 5 blocks).

2.6 Statistical Analyses

2.6.1 Analysis of Variance for the Evaluated Traits

Data were subjected to analysis of variance (ANOVA) under the randomised complete block design. The statistical model was:

$$Y_{ij} = \mu + B_i + G_j + \varepsilon_{ij}$$

where Y_{ij} is the observed value of genotype j in block i, μ is the overall mean, B_i is the effect of block i, G_j is the effect of genotype j, and ε_{ij} is the experimental error. Differences among genotypes were tested using Fisher's F-test at the 5% significance level. The degrees of freedom were 4 for blocks, 15 for genotypes, and 60 for experimental error.

The coefficient of variation was calculated as:

$$CV\ (\%) = \frac{\sqrt{MS_e}}{\bar{Y}} X100$$

where MS_e is the residual mean square and $\bar{Y}$ is the overall mean of the trait.

2.6.2 Diallel Analysis According to Griffing's Model

Diallel analysis was performed according to Griffing's (1956) Method 1, Model I (fixed effects), which includes the four parental lines, six direct crosses, and six reciprocal crosses. The statistical model was:

$$Y_{ijk} = \mu + B_k + g_i + g_j + s_{ij} + r_{ij} + \varepsilon_{ijk}$$

where Y_{ijk} is the observed value of cross i × j in block k, μ is the overall mean, B_k is the effect of block k, g_i and g_j are the GCA effects of the parental lines, s_{ij} is the SCA effect of the parental combination, r_{ij} is the reciprocal effect, and ε_{ijk} is the experimental error. The genotype sum of squares was partitioned into GCA (3 degrees of freedom), SCA (6 degrees of freedom), and reciprocal effects (6 degrees of freedom). Each component mean square was tested against the residual mean square using an F-test at the 5% significance level.

2.6.3 Estimation of GCA, SCA, and Reciprocal Effects

GCA effects were estimated for the four parental lines, whereas SCA effects were estimated for the six parental combinations by jointly considering both crossing directions. A positive GCA effect indicates an average contribution towards increasing the trait value, whereas a negative GCA effect indicates a contribution towards decreasing it. A positive SCA effect indicates a positive deviation from the value expected based on parental GCA effects. Whether an effect is considered favourable or unfavourable depends on the breeding objective, particularly when selecting for early maturity.
Reciprocal effects were estimated as:

$$\hat{r}_{ij} = \frac{\bar{Y}_{ij} - \bar{Y}_{ji}}{2}$$

where $\bar{Y}_{ij}$ and $\bar{Y}_{ji}$ are the mean performances of the two crossing directions. The first parent denotes the female parent. A significant reciprocal effect indicates a difference between crossing directions but does not, by itself, establish the presence of maternal or cytoplasmic genetic mechanisms.

2.6.4 Relative Contributions of Diallel Components

The relative contribution of each diallel component (GCA, SCA, or reciprocal effects) to the total genotype sum of squares was calculated as:

$$CR(\%) = \frac{SS_c}{SSG} X100$$

where SSc is the sum of squares associated with the component considered and SS_G is the total genotype sum of squares. Under the fixed-effects model used in this study, these percentages do not represent direct estimates of additive or non-additive genetic variance components.

2.6.5 Significance Testing of Individual Effects

Individual effects were assessed using two-sided Student's t-tests:

$$t = \hat{\theta} / SE(\hat{\theta})$$

with 60 residual degrees of freedom, where $\hat{\theta}$ is the estimated effect and $SE(\hat{\theta})$ is its standard error. For four parental lines and five replications, the standard errors were calculated as follows:

$$SE(GCA) = \sqrt{\frac{3MS_e}{160}}$$

$$SE(SCA) = \sqrt{\frac{MS_e}{16}}$$

$$SE(r) = \sqrt{\frac{MS_e}{10}}$$

The resulting p-values were adjusted using Holm's (1979) sequential multiple-testing procedure, separately for each trait and each family of effects (four GCA effects, six SCA effects, and six reciprocal effects). Statistical significance was assessed at the 5 % level using adjusted p-values.

2.6.6 Assessment of Statistical Assumptions and Sensitivity Analyses

Residual normality was assessed using the Shapiro–Wilk test, whereas homogeneity of variances was evaluated using the median-centred Levene's test. Studentised residuals were also examined to identify potentially influential observations.

An unusually high observation was recorded for the NTE015 × NBO04 cross in the fourth block, particularly for the number of pods per plant and grain yield. Because its experimental authenticity had been confirmed, this observation was retained in the primary analyses.

Sensitivity analyses were considered to assess the influence of this observation; however, their results are not reported in the present manuscript.

2.6.7 Statistical Software

All statistical analyses were performed using R statistical software (R Core Team, n.d.). The analyses included analysis of variance under the randomised complete block design; diallel analysis using Griffing's (1956) Method 1, Model I (fixed effects); estimation and significance testing of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects; adjustment of p-values using Holm's procedure; and assessment of statistical assumptions through residual diagnostics.

3. Results

3.1 Variability in Agronomic Traits and Grain Yield Among Cowpea Genotypes

The analysis of variance of the sixteen cowpea genotypes, comprising four parental lines and twelve F_1 hybrids, revealed significant genotypic differences for all seven traits investigated (Table 1).

Genotypic effects were highly significant ($P < 0.01$) for leaflet length, leaflet width, days to maturity, seed length, and 100-seed weight. Significant differences ($P < 0.05$) were also observed for the number of pods per plant and grain yield.

Block effects were significant for the number of pods per plant ($P = 0.009$) and grain yield ($P = 0.021$), but not for the other five traits.

The coefficients of variation ranged from 4.29% for days to maturity to 53.37% for grain yield. Relatively low coefficients of variation were recorded for days to maturity (4.29%), seed length (5.22%), and leaflet length (5.71%). In contrast, the number of pods per plant (43.70%) and grain yield (53.37%) exhibited high residual variability, indicating lower experimental precision for these two traits.

Table 1. Overall analysis of variance for seven agronomic traits in 16 cowpea genotypes

Trait	Block MS	Genotype MS	Error MS	Genotype F	CV (%)
LL	0.167	19.026	0.529	35.951***	5.71
LW	0.218	0.966	0.319	3.025**	8.07
DM	11.500	184.827	6.860	26.943***	4.29
NP	3,022.519	1,634.370	812.272	2.012*	43.70
LGr	0.248	6.083	0.183	33.191***	5.22
100SW	3.430	41.725	1.720	24.262***	8.98
GY	13,874,300.470	10,239,149.576	4,449,223.069	2.301*	53.37

*MS: mean square; CV: coefficient of variation; df: blocks = 4, genotypes = 15, error = 60. * p < 0.05; ** p < 0.01; *** p < 0.001*

3.2 Analysis of Variance for Combining Ability and Reciprocal Effects

Partitioning genotypic variation according to Griffing's Method 1, Model I (fixed effects), revealed significant general combining ability (GCA), specific combining ability (SCA), and reciprocal effects, whose relative importance varied across the traits investigated (Table 2).

GCA effects were significant for six of the seven traits. Highly significant effects ($P < 0.001$) were observed for leaflet length, days to maturity, seed length, and 100-seed weight, whereas significant effects ($P < 0.05$) were detected for leaflet width and grain yield. In contrast, GCA effects were not significant for the number of pods per plant.

SCA effects were significant for six traits, with highly significant effects ($P < 0.001$) for leaflet length, days to maturity, seed length, and 100-seed weight. Significant SCA effects were also detected for the number of pods per plant ($P < 0.01$) and grain yield ($P < 0.01$). However, no significant SCA effect was observed for leaflet width.

Reciprocal effects were significant only for leaflet width ($P < 0.001$) and days to maturity ($P < 0.01$). No significant overall reciprocal effects were detected for leaflet length, number of pods per plant, seed length, 100-seed weight, or grain yield.

Table 2. Mean squares for general and specific combining ability and reciprocal effects in cowpea

Trait	GCA (3 df)	SCA (6 df)	Reciprocal (6 df)	Error (60 df)
LL	79.970***	6.596***	0.984 ns	0.529
LW	1.221*	0.207 ns	1.597***	0.319
DM	594.850***	137.108***	27.533**	6.860
NP	1,848.083 ns	3,113.350**	48.533 ns	812.272
LGr	27.604***	1.290***	0.117 ns	0.183
100SW	163.703***	19.077***	3.384 ns	1.720
GY	16,528,107.859*	16,752,627.728**	581,192.284 ns	4,449,223.069

*ns: not significant; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$*

3.2.1 Relative Contributions of GCA, SCA, and Reciprocal Effects

The partitioning of genotypic sums of squares revealed marked differences in the relative contributions of GCA, SCA, and reciprocal effects among the seven traits investigated (Table 3).

GCA accounted for the largest proportion of genotypic variation in seed length (90.75%), leaflet length (84.06%), 100-seed weight (78.47%), and days to maturity (64.37%). These results indicate that GCA was the predominant source of variation for these traits within the evaluated set of parental lines and hybrids.

Conversely, SCA contributed the largest proportion of genotypic variation in the number of pods per plant (76.20%) and grain yield (65.45%), exceeding the corresponding contributions of GCA (22.62% and 32.28%, respectively).

For leaflet width, reciprocal effects accounted for 66.16% of the genotypic sum of squares, compared with 25.28% for GCA and 8.56% for SCA. This finding highlights the importance of crossing direction in the expression of leaflet width among the evaluated genotypes.

Table 3. Relative contributions of diallel components to the genotypic sum of squares

Trait	GCA (%)	SCA (%)	Reciprocal effects (%)
LL	84.06	13.87	2.07
LW	25.28	8.56	66.16
DM	64.37	29.67	5.96
NP	22.62	76.20	1.19
LGr	90.75	8.48	0.77
100SW	78.47	18.29	3.24
GY	32.28	65.45	2.27

Percentages represent the proportions of the genotypic sum of squares attributable to each diallel component. They are not direct estimates of additive or non-additive genetic variance components

3.3 Estimation and Significance of Individual Combining Ability Effects

3.3.1 General Combining Ability of the Parental Lines

The estimation of individual general combining ability (GCA) effects revealed differences among the four parental lines for the seven traits investigated (Table 4).

For leaflet length, NTE015 exhibited the highest positive GCA effect (+2.02 cm), whereas NKO03 (−0.92 cm) and NFE011 (−1.04 cm) showed significant negative effects. The effect of NBO04 (−0.06 cm) was not significant. For leaflet width, NBO04 exhibited a significant positive GCA effect (+0.22 cm), while the effects of the other parental lines were not significant after Holm's correction. Regarding days to maturity, NBO04 showed a highly significant positive GCA effect (+5.77 days), indicating a contribution towards delayed maturity. Conversely, NTE015 (−2.15 days), NFE011 (−2.00 days), and NKO03 (−1.63 days) exhibited highly significant negative effects, indicating favourable contributions towards earlier maturity.

For the number of pods per plant, NTE015 recorded the highest positive GCA effect (+7.90), followed by NFE011 (+2.60). However, none of the individual GCA effects for this trait remained significant after Holm's correction.

For seed length, NBO04 exhibited a highly significant positive GCA effect (+1.19 mm), whereas NKO03 (−0.57 mm) and NFE011 (−0.58 mm) showed highly significant negative effects. The effect of NTE015 (−0.03 mm) was not significant.

For 100-seed weight, NBO04 (+2.39 g) and NTE015 (+0.92 g) exhibited highly significant positive GCA effects, while NKO03 (−2.00 g) and NFE011 (−1.31 g) showed highly significant negative effects.

Finally, for grain yield, NTE015 exhibited a significant positive GCA effect (+729.45 kg ha^{-1}; adjusted P = 0.0426), identifying it as a promising parent for improving grain yield. Conversely, NKO03 showed a significant negative GCA effect (−807.91 kg ha^{-1}; adjusted P = 0.0277). The effects of NBO04 (+200.02 kg ha^{-1}) and NFE011 (−121.57 kg ha^{-1}) were not statistically significant.

Table 4. Individual general combining ability effects of the four parental lines and their significance after Holm's correction

Trait	NBO04	NTE015	NKO03	NFE011	SE(GCA)
LL	−0.06 ns	+2.02***	−0.92***	−1.04***	0.100
LW	+0.22*	−0.15 ns	+0.07 ns	−0.13 ns	0.077
DM	+5.77***	−2.15***	−1.63***	−2.00***	0.359
NP	−2.57 ns	+7.90 ns	−7.93 ns	+2.60 ns	3.903
LGr	+1.19***	−0.03 ns	−0.57***	−0.58***	0.059
100SW	+2.39***	+0.92***	−2.00***	−1.31***	0.180
GY	+200.02 ns	+729.45*	−807.91*	−121.57 ns	288.830

*SE(GCA): standard error of an individual GCA effect. ns: not significant; * adjusted p < 0.05; ** adjusted p < 0.01; *** adjusted p < 0.001. Holm's correction was applied to the four individual GCA effects for each trait*

3.3.2 Specific Combining Ability of the F_1 Hybrids

The analysis of individual specific combining ability (SCA) effects revealed differences among the six parental combinations for the seven traits investigated (Table 5).

For leaflet length, the highest significant positive SCA effects were observed for NBO04 × NTE015 (+1.00 cm) and NTE015 × NFE011 (+0.79 cm). Conversely, NBO04 × NFE011 (−0.67 cm) and NBO04 × NKO03 (−0.53 cm) exhibited significant negative effects.

For leaflet width, none of the individual SCA effects remained significant after Holm's correction.

Regarding days to maturity, three parental combinations involving NBO04 exhibited highly significant negative SCA effects: NBO04 × NTE015 (−3.33 days), NBO04 × NFE011 (−3.07 days), and NBO04 × NKO03 (−3.05 days). These effects indicate favourable deviations towards earlier maturity relative to expectations based on parental GCA effects. Conversely, NKO03 × NFE011 exhibited a significant positive SCA effect (+2.23 days), indicating a deviation towards delayed maturity.

For the number of pods per plant, NBO04 × NTE015 exhibited the highest positive SCA effect (+28.35; adjusted $P < 0.01$), whereas NBO04 × NKO03 showed a significant negative effect (−21.43). The remaining parental combinations did not exhibit significant individual SCA effects for this trait.

For seed length, NTE015 × NFE011 exhibited a significant positive SCA effect (+0.37 mm), while NBO04 × NFE011 showed a significant negative effect (−0.33 mm). For 100-seed weight, significant positive SCA effects were recorded for NBO04 × NTE015 (+1.43 g) and NTE015 × NKO03 (+0.89 g).

Finally, for grain yield, NBO04 × NTE015 exhibited the highest positive SCA effect (+2,266.23 kg ha^{-1}; adjusted $P < 0.001$). This was the only parental combination showing a statistically significant individual SCA effect for grain yield after Holm's correction. The remaining combinations did not exhibit significant SCA effects for this trait.

Overall, NTE015 emerged as a promising parent based on its favourable GCA effects for grain yield, 100-seed weight, and earlier maturity. The NBO04–NTE015 parental combination was particularly promising because of its significant positive SCA effects for grain yield, number of pods per plant, and 100-seed weight, together with its negative SCA effect for days to maturity. These findings support the prioritisation of this parental combination for further breeding evaluations.

Table 5. Individual specific combining ability effects and their significance after Holm's correction

Parental combination	LL	LW	DM	NP	SL	100SW	GY
NBO04 × NTE015	+1.00***	+0.12 ns	−3.33***	+28.35**	+0.25 ns	+1.43***	+2,266.23***
NBO04 × NKO03	−0.53*	+0.15 ns	−3.05***	−21.43*	+0.01 ns	−0.47 ns	−1,280.25 ns
NBO04 × NFE011	−0.67**	−0.03 ns	−3.07***	+3.15 ns	−0.33*	+0.66 ns	+181.82 ns
NTE015 × NKO03	−0.39 ns	−0.19 ns	+0.98 ns	−2.10 ns	+0.18 ns	+0.89*	−149.90 ns
NTE015 × NFE011	+0.79***	+0.12 ns	+0.65 ns	−12.03 ns	+0.37**	+0.83 ns	−545.65 ns
NKO03 × NFE011	+0.42 ns	+0.03 ns	+2.23**	+0.70 ns	+0.16 ns	−0.10 ns	+47.53 ns
SE(SCA)	0.182	0.141	0.655	7.125	0.107	0.328	527.330

*SE(SCA): standard error of an individual SCA effect. ns: not significant; * adjusted p < 0.05; ** adjusted p < 0.01; *** adjusted p < 0.001. Holm's correction was applied to the six individual SCA effects for each trait. SCA effects were estimated by considering both directions of each parental combination*

3.4 Estimation and Significance of Reciprocal Effects

The analysis of reciprocal effects revealed differences between crossing directions for certain traits (Table 6). After Holm's correction for multiple comparisons, three individual reciprocal effects remained statistically significant, involving leaflet width, leaflet length, and days to maturity. However, the overall analysis of variance indicated significant reciprocal effects only for leaflet width and days to maturity (Table 2).

3.4.1 Reciprocal Effects on Morphological Traits

For leaflet width, the NTE015 × NKO03 combination exhibited a highly significant positive reciprocal effect (+0.810 cm; adjusted P = 0.00017), corresponding to a mean difference of 1.62 cm between the two crossing directions. The NTE015 ♀ × NKO03 ♂ cross therefore exhibited greater leaflet width than its reciprocal, NKO03 ♀ × NTE015 ♂.

For leaflet length, the same parental combination exhibited a significant positive reciprocal effect (+0.630 cm; adjusted P = 0.0487), corresponding to a mean difference of 1.26 cm between the two crossing directions. However, because the overall reciprocal effect was not significant for leaflet length, this individual result should be interpreted cautiously.
For seed length and 100-seed weight, none of the individual reciprocal effects remained statistically significant after Holm's correction.

3.4.2 Reciprocal Effects on Days to Maturity

For days to maturity, the NKO03 × NFE011 combination exhibited a significant positive reciprocal effect (+2.600 days; adjusted P = 0.0158), corresponding to a mean difference of 5.2 days between the two crossing directions.

The NKO03 ♀ × NFE011 ♂ cross therefore exhibited a longer time to maturity than its reciprocal, NFE011 ♀ × NKO03 ♂. This result indicates that crossing direction influenced maturity within this particular parental combination.

The other parental combinations did not exhibit significant individual reciprocal effects for days to maturity after Holm's correction.

3.4.3 Reciprocal Effects on Pod Number and Grain Yield

For the number of pods per plant, reciprocal effects ranged from −2.000 to +3.100, and none of the individual comparisons remained significant after Holm's correction.

For grain yield, reciprocal effects ranged from −331.34 kg ha^{-1} for NTE015 × NKO03 to +277.75 kg ha^{-1} for NBO04 × NKO03. However, none of these effects was statistically significant after adjustment for multiple comparisons.

For the NBO04 × NTE015 parental combination, the reciprocal effect was −142.81 kg ha^{-1}, indicating a numerically higher grain yield when NTE015 was used as the female parent. Nevertheless, this difference was not statistically significant.

Overall, no significant individual reciprocal effects were detected for grain yield, indicating that the observed differences between crossing directions were insufficient to establish a statistically significant directional effect on this trait under the experimental conditions.

Table 6. Individual reciprocal effects and Holm-adjusted p-values for the seven traits investigated

A. Estimates of reciprocal effects

Cross (♀ × ♂)	LL	LW	DM	NP	SL	100SW	GY
NBO04 × NTE015	+0.100	−0.030	−1.700	+2.900	−0.077	+0.440	−142.81
NBO04 × NKO03	+0.007	+0.090	+1.700	+3.100	+0.076	+0.468	+277.75
NBO04 × NFE011	+0.227	+0.310	+1.700	+1.000	−0.032	−1.060	−278.89
NTE015 × NKO03	+0.630	+0.810	−1.000	+1.300	−0.146	−0.670	−331.34
NTE015 × NFE011	−0.030	−0.060	−0.300	+2.100	−0.161	−0.180	+205.58
NKO03 × NFE011	−0.362	−0.440	+2.600	−2.000	−0.100	−0.114	−146.12
SE(Reciprocal)	0.230	0.179	0.828	9.013	0.135	0.415	667.025

B. Holm-adjusted p-values

Cross (♀ × ♂)	LL	LW	DM	NP	SL	100SW	GY
NBO04 × NTE015	1.000	1.000	0.222	1.000	1.000	1.000	1.000
NBO04 × NKO03	1.000	1.000	0.222	1.000	1.000	1.000	1.000
NBO04 × NFE011	1.000	0.352	0.222	1.000	1.000	0.079	1.000
NTE015 × NKO03	0.0487	0.00017	0.464	1.000	1.000	0.557	1.000
NTE015 × NFE011	1.000	1.000	0.718	1.000	1.000	1.000	1.000
NKO03 × NFE011	0.604	0.0835	0.0158	1.000	1.000	1.000	1.000

A positive value indicates a higher mean in the indicated crossing direction. Bold Holm-adjusted p-values indicate significance at the 5% level. Holm's correction was applied to the six reciprocal comparisons for each trait

3.5 Mean Performance of Parental Lines and F_1 Hybrids

The mean performance of the sixteen cowpea genotypes, comprising four parental lines and twelve F_1 hybrids, revealed considerable variation in morphological, phenological, and yield-related traits (Table 7).

Among the parental lines, NBO04 exhibited the longest time to maturity (82.0 days), whereas NFE011 showed the shortest (57.2 days). Among the F_1 hybrids, days to maturity ranged from 57.0 days for NFE011 × NKO03 to 63.8 days for NBO04 × NKO03. The NBO04 × NTE015 and NTE015 × NBO04 hybrids reached maturity at 59.6 and 63.0 days, respectively.

For the number of pods per plant, the highest mean values were recorded for NBO04 × NTE015 (101.8 pods) and its reciprocal NTE015 × NBO04 (96.0 pods). These values exceeded those observed for all four parental lines, whose mean pod numbers ranged from 50.0 for NBO04 to 78.6 for NFE011.

Regarding seed characteristics, NBO04 exhibited the greatest seed length among the parental lines (10.65 mm) and the highest parental 100-seed weight (17.76 g). Among the hybrids, NBO04 × NTE015 recorded the highest 100-seed weight (19.78 g), followed by its reciprocal NTE015 × NBO04 (18.90 g).

Mean grain yield varied substantially among the sixteen genotypes, ranging from 1,786.18 kg ha^{-1} for NKO03 × NBO04 to 7,290.58 kg ha^{-1} for NTE015 × NBO04. Among the parental lines, NFE011 exhibited the highest numerical grain yield (4,025.24 kg ha^{-1}), followed by NTE015 (3,840.29 kg ha^{-1}), NKO03 (3,718.86 kg ha^{-1}), and NBO04 (3,184.31 kg ha^{-1}).

The two reciprocal hybrids derived from NBO04 and NTE015 exhibited the highest numerical grain yields, with 7,004.96 kg ha^{-1} for NBO04 × NTE015 and 7,290.58 kg ha^{-1} for NTE015 × NBO04. These high mean yields were consistent with the significant positive SCA effect previously identified for this parental combination. However, the numerical difference in grain yield between the two crossing directions was not statistically significant after Holm's correction.

Overall, the NBO04–NTE015 parental combination exhibited promising performance for grain yield, pod number, and 100-seed weight under the experimental conditions, supporting its prioritisation for further evaluation in cowpea breeding programmes.

Table 7. Mean performance of four parental lines and twelve F_1 hybrids for the seven traits investigated

Genotype (♀ × ♂)	LL	LW	DM	NP	SL	100SW	GY
NBO04	12.82	7.20	82.0	50.0	10.65	17.76	3,184.31
NTE015	15.38	6.64	58.4	66.8	7.33	13.30	3,840.29
NKO03	11.42	7.14	57.6	72.2	6.71	10.28	3,718.86
NFE011	10.12	6.62	57.2	78.6	6.82	10.60	4,025.24
NBO04 × NFE011	11.20	7.36	63.4	69.4	8.44	15.28	3,933.45
NFE011 × NBO04	10.75	6.74	60.0	67.4	8.50	17.40	4,491.22
NBO04 × NTE015	15.80	7.16	59.6	101.8	9.52	19.78	7,004.96
NTE015 × NBO04	15.60	7.22	63.0	96.0	9.67	18.90	7,290.58
NKO03 × NFE011	10.84	6.52	62.2	58.6	7.11	11.07	2,924.00
NFE011 × NKO03	11.56	7.40	57.0	62.6	7.31	11.30	3,216.23
NKO03 × NBO04	11.23	7.34	60.4	30.2	8.74	14.04	1,786.18
NBO04 × NKO03	11.24	7.52	63.8	36.4	8.89	14.98	2,341.68
NKO03 × NTE015	12.82	5.92	59.2	61.8	7.92	15.08	4,055.05
NTE015 × NKO03	14.08	7.54	57.2	64.4	7.63	13.74	3,392.37
NFE011 × NTE015	14.54	6.90	57.8	61.6	8.12	15.22	3,808.73
NTE015 × NFE011	14.48	6.78	57.2	65.8	7.80	14.86	4,219.88

Mean values from five replications per genotype. LoFo: leaflet length (cm); LaFo: leaflet width (cm); TMa: days to maturity (DAS); NGo: number of pods per plant; LGr: seed length (mm); P100Gr: 100-seed weight (g); Rend: grain yield (kg ha^{-1})

4. Discussion

4.1 Agromorphological and Agronomic Variability Among the Studied Genotypes

Analysis of variance revealed significant differences among the sixteen cowpea genotypes for all seven traits investigated, indicating substantial phenotypic variability within the evaluated genetic materials. This variability demonstrates the potential value of the four parental lines, NBO04, NTE015, NKO03, and NFE011, for generating new genetic combinations and identifying promising materials for cowpea improvement.

These findings are consistent with those of Owusu *et al*. (2020), who reported significant genotypic differences for grain yield, yield components, and maturity-related traits in a five-parent full diallel of cowpea in Ghana. Similarly, Ezin *et al*. (2023) identified considerable variation among cowpea parental lines and their hybrids under both well-watered and water-deficit conditions. Matjeke *et al*. (2025) also reported differences in grain yield and morphological traits among cowpea genotypes. More recently, da Silva *et al*. (2026) demonstrated the usefulness of diallel crosses involving local cowpea accessions for identifying promising genetic combinations under semiarid conditions.

However, the magnitude of residual variability differed considerably among the traits investigated. Relatively low coefficients of variation were observed for days to maturity (4.29%), seed length (5.22%), and leaflet length (5.71%), suggesting greater experimental precision for these traits. In contrast, the number of pods per plant (43.70%) and grain yield (53.37%) exhibited substantially higher coefficients of variation, indicating greater residual variability and lower precision in estimating genotypic differences for production-related traits.

The relatively high variability observed for grain yield and pod number warrants particular attention because these traits are central to the identification of promising breeding materials. Ezin *et al*. (2023) demonstrated that the expression of yield-related traits and combining ability in cowpea can vary according to water availability, while Njihia *et al*. (2026) emphasised the importance of experimental conditions when evaluating productivity-related traits.

Although significant genotypic differences were detected for all traits, the high residual variability associated with pod number and grain yield indicates that conclusions concerning these traits should be interpreted cautiously and confirmed through additional experimental evaluations.

4.2 Relative Importance of GCA, SCA, and Reciprocal Effects

Partitioning the genotypic sums of squares revealed marked differences in the relative contributions of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects among the traits investigated.

GCA accounted for the largest proportions of genotypic variation in seed length (90.75%), leaflet length (84.06%), 100-seed weight (78.47%), and days to maturity (64.37%). This predominance indicates that average differences among the parental lines contributed substantially to the expression of these traits within the evaluated diallel set. In classical quantitative genetic interpretation, GCA is generally associated with additive genetic effects, although its relative contribution in a fixed-effects diallel should not be interpreted as a direct estimate of additive genetic variance.

These findings are partially consistent with those of Owusu *et al*. (2020), who reported a predominance of GCA for 100-seed weight and several maturity-related traits in cowpea. Ezin *et al*. (2023) also demonstrated the importance of additive genetic effects for several traits under contrasting water regimes. Similarly, Salunke *et al*. (2024), using a line × tester mating design, reported a relatively greater contribution of additive effects for certain traits, including days to maturity and 100-seed weight, despite the predominance of non-additive effects for several other quantitative characters.

Conversely, SCA accounted for the largest proportions of genotypic variation in the number of pods per plant (76.20%) and grain yield (65.45%). These results indicate that differences among specific parental combinations played a particularly important role in the expression of production-related traits. This pattern is compatible with an important contribution of non-additive genetic effects, commonly associated with dominance and epistatic interactions.

Comparable findings were reported by Njihia *et al*. (2026), who observed a relatively greater importance of SCA for grain yield. Emmanuel *et al*. (2026) also reported substantial non-additive contributions to several agronomic traits in cowpea. In contrast, Ezin *et al*. (2023) identified a predominance of additive effects for several traits under the water regimes investigated. Such differences among studies may reflect variation in parental genetic backgrounds, environmental conditions, traits evaluated, and statistical approaches.

Leaflet width exhibited a distinct pattern, with reciprocal effects accounting for 66.16% of the genotypic sum of squares, compared with 25.28% for GCA and 8.56% for SCA. This finding indicates that crossing direction contributed substantially to the observed variation in leaflet width among the evaluated genotypes.

Nevertheless, the percentages reported in the present study represent the relative contributions of GCA, SCA, and reciprocal effects to the genotypic sums of squares. Because the analysis was performed using Griffing's Method 1, Model I (fixed effects), these percentages should not be considered direct estimates of additive, dominance, or cytoplasmic genetic variance components.

4.3 General Combining Ability of the Parental Lines

The estimation of individual GCA effects identified parental lines exhibiting favourable average contributions to several agronomic traits. For grain yield, NTE015 showed a significant positive GCA effect (+729.45 kg ha^{-1}; Holm-adjusted P = 0.0426), whereas NKO03 exhibited a significant negative effect (−807.91 kg ha^{-1}; Holm-adjusted P = 0.0277). The GCA effects of NBO04 and NFE011 were not statistically significant for this trait.

These results identify NTE015 as a promising parent for improving grain yield within the evaluated genetic materials. Its favourable contribution was not restricted to yield, since this line also exhibited a significant positive GCA effect for 100-seed weight (+0.92 g) and a significant negative effect for days to maturity (−2.15 days). The latter suggests that NTE015 may contribute to the development of earlier-maturing progenies.

The usefulness of GCA for parental selection has been demonstrated in previous cowpea studies. Owusu *et al*. (2020) identified parental lines with favourable GCA effects for grain yield and maturity-related traits, including IT86D-610. Ezin *et al*. (2023) similarly identified promising parents for productivity and water-deficit-related traits. Salunke *et al*. (2024) reported favourable combining ability for selected parental materials, including PL 4 and NIC 23105, while Matjeke *et al*. (2025) highlighted the usefulness of GCA estimates for identifying promising cowpea parents.

However, the breeding value of a parental line depends on the specific traits targeted and the genetic backgrounds in which it is evaluated. Thus, the significant negative GCA effect of NKO03 for grain yield does not necessarily indicate an absence of breeding value. This line exhibited a significant negative GCA effect for days to maturity (−1.63 days), suggesting potential usefulness in breeding for earliness, although its unfavourable contributions to seed length and 100-seed weight should also be considered.

Similarly, NBO04, despite its nonsignificant GCA effect for grain yield, exhibited favourable positive effects for seed length (+1.19 mm) and 100-seed weight (+2.39 g). These results emphasize the importance of considering several complementary traits when selecting parents rather than relying exclusively on grain yield.

4.4 Specific Combining Ability and Identification of Promising Crosses

The analysis of individual SCA effects identified the NBO04–NTE015 parental combination as particularly promising for improving grain yield. This combination exhibited a significant positive SCA effect of +2,266.23 kg ha^{-1} (Holm-adjusted $P < 0.001$), representing the only statistically significant individual SCA effect for grain yield among the six parental combinations evaluated.

In addition to grain yield, the same parental combination exhibited favourable SCA effects for the number of pods per plant (+28.35), 100-seed weight (+1.43 g), and days to maturity (−3.33 days). These results suggest that the combination may be useful for simultaneously improving productivity-related traits and promoting earlier maturity.

The mean grain yields recorded for the two reciprocal hybrids, NBO04 × NTE015 (7,004.96 kg ha^{-1}) and NTE015 × NBO04 (7,290.58 kg ha^{-1}), were the highest numerical values observed in the experiment. These mean yields are consistent with the favourable SCA effect estimated for the parental combination. Nevertheless, the high residual variability observed for grain yield and the presence of an unusually high experimental observation require cautious interpretation of these mean values.

The identification of favourable specific parental combinations agrees with the findings of Owusu *et al*. (2020), who reported significant SCA effects for grain yield and maturity-related traits in cowpea. Ezin *et al*. (2023) also identified promising crosses for productivity and adaptation to water-deficit conditions. Similar observations were reported by Salunke *et al*. (2024) and Matjeke *et al*. (2025), emphasizing the importance of evaluating specific crosses rather than relying exclusively on the average combining ability of parental lines
.
More recently, Njihia *et al*. (2026) reported differences in combining ability among cowpea parental combinations for grain and biomass yield, while da Silva *et al*. (2026) identified promising crosses among local cowpea accessions evaluated under semiarid conditions.

From a breeding perspective, the favourable SCA effects observed for NBO04–NTE015 support the prioritisation of this combination for further genetic improvement activities. However, a favourable SCA effect in the F_1 generation does not necessarily guarantee the fixation of superior performance in subsequent generations. The expression and transmission of desirable traits will depend on the underlying genetic effects and segregation patterns.

Consequently, evaluation of F_2 and subsequent generations will be necessary to identify promising segregants combining high grain yield, favourable seed characteristics, and early maturity. Further trials will also be required to determine whether the performance observed in the present experiment can be reproduced under different environmental conditions.

4.5 Reciprocal Effects and the Influence of Crossing Direction

The diallel analysis revealed significant overall reciprocal effects for leaflet width and days to maturity, indicating that the direction of crossing influenced the expression of these traits within the evaluated genetic materials. In contrast, no significant overall reciprocal effect was detected for grain yield.

For leaflet width, the NTE015 × NKO03 parental combination exhibited a highly significant positive reciprocal effect (+0.810 cm; Holm-adjusted $P = 0.00017$), corresponding to a mean difference of 1.62 cm between the two crossing directions. This result indicates that the NTE015 ♀ × NKO03 ♂ hybrid exhibited greater leaflet width than its reciprocal.

For days to maturity, NKO03 × NFE011 exhibited a significant positive reciprocal effect (+2.600 days; Holm-adjusted $P = 0.0158$), corresponding to a difference of 5.2 days between the two crossing directions. Thus, the NKO03 ♀ × NFE011 ♂ hybrid matured later than NFE011 ♀ × NKO03 ♂.

These findings are consistent with the broader importance of reciprocal effects reported in cowpea diallel studies. Owusu *et al*. (2020) observed reciprocal effects for several agronomic traits, while da Silva *et al*. (2026) reported significant reciprocal effects for several characters in a full diallel involving local cowpea accessions. Together, these studies suggest that crossing direction can be an important consideration when designing hybridisation strategies.

An individual reciprocal effect was also significant for leaflet length in the NTE015 × NKO03 combination (+0.630 cm; Holm-adjusted $P = 0.0487$). However, because the overall reciprocal effect was not significant for this trait, this isolated result should be interpreted with caution.

For grain yield, the NTE015 ♀ × NBO04 ♂ hybrid exhibited a numerically higher mean than its reciprocal. Nevertheless, this difference was not statistically significant after Holm's correction. Therefore, the present findings do not provide sufficient evidence to recommend one crossing direction over the other specifically for grain yield.

Biologically, reciprocal differences may arise from several mechanisms, including maternal influences, cytoplasmic inheritance, or other processes associated with seed development and early plant growth. However, the experimental design and statistical analyses employed in this study do not allow these mechanisms to be distinguished or confirmed independently.

Consequently, the significant reciprocal effects observed for leaflet width and days to maturity demonstrate the importance of crossing direction for certain traits, without establishing the underlying biological mechanisms responsible for these differences.

4.6 Implications for Cowpea Genetic Improvement and Study Limitations

The findings of this study provide useful information for guiding cowpea breeding strategies in northern Côte d'Ivoire. The predominance of GCA for leaflet length, seed length, 100-seed weight, and days to maturity suggests that selecting parents with favourable average combining ability may be particularly useful for improving these traits.

Conversely, the relatively high contribution of SCA to grain yield and the number of pods per plant highlights the importance of evaluating specific parental combinations when targeting productivity improvement. These findings support breeding strategies that combine the selection of promising parents with the evaluation of their hybrid progenies.

Within the evaluated genetic materials, NTE015 emerged as a promising parent for grain yield improvement, while NBO04 contributed favourable effects for seed length and 100-seed weight. Their parental combination exhibited particularly favourable SCA effects for grain yield, pod number, 100-seed weight, and earlier maturity.

These results could contribute to the activities of the Cowpea Improvement Programme in Côte d'Ivoire (PANCI), particularly through the selection of suitable parental lines, the planning of new crosses, and the evaluation of segregating generations.

Nevertheless, several limitations should be considered. First, the study involved only four selected parental lines. Although this number is sufficient for conducting a full diallel analysis, the estimated combining ability effects are specific to the evaluated parental set and should not be generalised to the broader cowpea germplasm without additional evidence.

Second, the genotypes were evaluated in a single environment during one growing season. Therefore, the stability of the estimated combining ability effects across locations, years, and contrasting environmental conditions remains unknown.

Third, the high coefficients of variation observed for the number of pods per plant (43.70%) and grain yield (53.37%) indicate substantial residual variability and reduced precision for these traits. The unusually high observation recorded for NTE015 × NBO04, retained after confirmation of its experimental authenticity, further highlights the importance of assessing the robustness of yield-related conclusions through sensitivity analyses and independent trials.

Fourth, the analysis was conducted using Griffing's fixed-effects Model I. Consequently, the relative contributions of GCA, SCA, and reciprocal effects represent the partitioning of variation within the selected genetic materials and should not be interpreted as direct estimates of genetic variance components in a randomly sampled population.

Future research should therefore include multi-location and multi-year evaluations, together with the assessment of F_2 and subsequent segregating generations. Such investigations will be essential for identifying stable, high-performing genotypes and determining whether the favourable effects observed in the present experiment can be exploited in the development of improved cowpea varieties.

Overall, the complementary information provided by GCA, SCA, and reciprocal effects offers a useful foundation for developing more targeted crossing and selection strategies within PANCI, with the long-term objective of improving cowpea productivity and adaptation to the agroecological conditions of northern Côte d'Ivoire.

5. Conclusion

This study evaluated general combining ability (GCA), specific combining ability (SCA), and reciprocal effects among four cowpea (*Vigna unguiculata* (L.) Walp.) parental lines from the germplasm collection of Peleforo GON COULIBALY University (UPGC), using a full diallel crossing design. Significant genotypic differences were detected for all seven agromorphological and agronomic traits investigated, demonstrating the potential of these genetic materials for cowpea improvement.

The partitioning of genotypic sums of squares revealed that GCA predominated for seed length (90.75%), leaflet length (84.06%), 100-seed weight (78.47%), and days to maturity (64.37%), whereas SCA accounted for the largest proportions of variation in the number of pods per plant (76.20%) and grain yield (65.45%). These findings highlight the complementary importance of parental combining ability and specific parental combinations in the expression of the evaluated traits.

Among the four parental lines, NTE015 exhibited a significant positive GCA effect for grain yield (+729.45 kg ha^{-1}), identifying it as a promising parent for yield improvement. The NBO04–NTE015 parental combination exhibited the highest positive SCA effect for grain yield (+2,266.23 kg ha^{-1}), together with favourable effects for pod number, 100-seed weight, and earlier maturity. This combination therefore represents a priority for further breeding evaluations.

Significant overall reciprocal effects were detected for leaflet width and days to maturity, indicating that crossing direction influenced the expression of these traits. However, no significant overall reciprocal effect was observed for grain yield.

From a breeding perspective, these results support the use of NTE015 as a promising parent and the prioritisation of the NBO04–NTE015 combination for developing and evaluating segregating populations. Nevertheless, the limited number of parental lines, the single-environment evaluation, and the high residual variability observed for yield-related traits require cautious interpretation of the findings. Further evaluation of F_2 and subsequent generations, together with multi-location and multi-year trials, will be essential to confirm the breeding potential and stability of the identified materials.

Overall, this study provides a scientific basis for improving parental selection and crossing strategies within the Cowpea Improvement Programme in Côte d'Ivoire (PANCI), contributing to the long-term development of productive and adapted cowpea varieties for northern Côte d'Ivoire.

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Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. ChatGPT, Claude and Perplexity were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that no competing interests exist.

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