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RESEARCH PAPER

Exploitation of crossability in Cowpea [*Vigna unguiculata* (L.) Walp] for enhancing genetic diversity

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Key Message: The study identified highly cross-compatible cowpea parental combinations, particularly P0×P19 and P0×P15, providing valuable opportunities to broaden genetic diversity and support the development of improved cowpea varieties through hybridization and subsequent progeny selection. Furthermore, the identified promising crosses (P0×P6 and P0×P13) offer potential for improving pod length, seed number and important yield-related traits in cowpea.

Abstract

Cowpea (*Vigna unguiculata* [L.] Walp) is an important grain legume that contributes significantly to food security and nutrition, particularly in arid and semi-arid regions. However, its narrow genetic base, resulting from predominant self-pollination, constrains genetic improvement. This study evaluated the crossability of 20 cowpea accessions with the commercial variety *Oloyin* (P0) under controlled conditions to identify compatible parental combinations for subsequent hybridization and progeny evaluation. *Oloyin* served as the pollen donor, while the flowers of the 20 accessions served as pollen recipients. A total of 210 flowers were pollinated, resulting in 64 pods and an overall pod-set percentage of 30.48%. The crossability data were standardized and analyzed using Pearson's correlation analysis, principal component analysis (PCA), and a PCA-based biplot to examine associations among crossability traits and summarize variation among crosses. Crossability varied considerably among parental combinations, with pollinated flowers ranging from 5 to 25 and pod-set success ranging from 0 to 90.9%. P0×P19 had the highest crossability (90.9%), followed by P0×P15 (80.0%), indicating strong parental compatibility. P0×P6 produced the longest pods (23.35 cm) and the highest average number of seeds per pod (20). Positive correlations were observed between number of pods set and pod-set percentage (r=0.94**), and average pod length (r=0.54*) and between pod length and seeds per pod (r=0.89**). PCA showed that number of pods set, pod-set percentage, average pod length, and average seeds per pod contributed strongly to the first principal component, representing overall reproductive success. P0×P15 and P0×P19 showed the highest crossability, while P0×P6 and P0×P13 were promising for pod length and number of seeds per pod. These findings identify cross-compatible parental combinations for further hybridization and progeny evaluation in cowpea breeding programmes. © 2026 The Author(s)

Keywords: Crossability, Cowpea, Genetic base, Hybridization, Parental compatibility, Plant breeding, Progeny evaluation

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Introduction

Cowpea (*Vigna unguiculata* [L.] Walp) is an important grain legume belonging to the family Fabaceae and is widely cultivated in tropical and subtropical regions of the world (Ajayi et al., 2024). It is particularly important in developing countries because of its nutritional, economic, and agricultural significance. Cowpea seeds are an inexpensive source of plant-based protein, carbohydrates, dietary fibre, vitamins, and minerals, making the crop an important component of human diets, particularly in regions where animal protein is relatively expensive (Abebe & Alemayehu, 2022; Shevkani et al., 2025). In addition to its nutritional importance, cowpea contributes to sustainable agricultural production through biological nitrogen fixation, improvement of soil fertility, and its adaptability to diverse environmental conditions (Boukar et al., 2020). Its relatively high tolerance to drought and ability to grow under low-input farming systems make it particularly valuable for smallholder farmers in semi-arid and tropical environments (Affrifah et al., 2022). It is a major grain legume in the dry savannas of Africa, where it provides affordable plant protein for human nutrition and fodder for livestock. Its adaptability, nutritional value, and importance to smallholder farming systems have made it a priority crop for improvement across sub-Saharan Africa (Ajeigbe et al., 2008; Joshi, 2022).

Cowpea is predominantly a self-pollinated diploid species with a chromosome number of 2n = 22. Despite its wide geographical distribution and considerable variation in seed colour, seed size, growth habit, maturity duration, and other

agronomic characteristics, the genetic base of cultivated cowpea remains relatively narrow (Boukar et al., 2020; Chipeta et al., 2025). This limited genetic diversity is partly associated with its reproductive biology, domestication history, restricted gene flow between cultivated and wild populations, and repeated use of a limited number of elite genotypes in breeding programmes (Ajayi et al., 2020a). A narrow genetic base may restrict the availability of desirable alleles required for improving grain yield, nutritional quality, resistance to insect pests and diseases, and tolerance to environmental stresses. Therefore, broadening the genetic diversity of cultivated cowpea is an important objective for developing improved and resilient varieties (Boukar et al., 2019, 2020).

Cowpea improvement through conventional breeding has traditionally relied on selection, hybridization, and recombination among cultivated genotypes. However, the repeated use of genetically related parental materials may limit the development of new genetic combinations (Boukar et al., 2016). In this context, the utilization of genetically diverse germplasm, including landraces, wild relatives, and locally adapted accessions, offers considerable opportunities for broadening the genetic base of cultivated cowpea (Potts et al., 2024; Akinmade et al., 2026). Wild relatives are particularly valuable because they may possess useful genes associated with resistance to insect pests and diseases, drought tolerance, heat tolerance, and other adaptive traits. Incorporating these genetic resources into cultivated backgrounds can generate novel variability and provide valuable parental materials for future breeding programmes (Boukar et al., 2020). Hybridization is therefore an important strategy for broadening cowpea's genetic diversity and combining desirable traits from different genotypes. Controlled crosses can be used to introgress traits such as higher yield, pest and disease resistance, drought tolerance, improved nutritional quality, and preferred seed characteristics into elite backgrounds (Nwosu & Awa, 2013; Patel et al., 2016). However, the success of such programmes depends on identifying parental combinations that are cross-compatible and capable of producing viable pods and seeds. Crossability is influenced by genetic and physiological factors, including pollen pistil interactions, pollen-tube growth, post-fertilization barriers, and the degree of genetic divergence between parents (Bedinger et al., 2017; Broz & Bedinger, 2021).

In addition to agronomic traits, consumer preference can guide the choice of parents in cowpea breeding. The Nigerian commercial variety *Oloyin* is highly preferred by consumers because of its sweet taste (Ojedokun & Yesufu, 2020). A preliminary evaluation showed that *Oloyin* has relatively high seed glucose and fructose concentrations compared with the other accessions used in this study; although its protein content was lower (Oboh et al., 2021; Affrifah et al., 2022; Olowolaju et al., 2024). Seed soluble sugars contribute to sweetness, palatability, cooking quality, and seed storability, and may therefore be valuable targets alongside yield and stress-resistance traits (Weng et al., 2018; Huynh et al., 2024). Crossing *Oloyin* with accessions possessing superior agronomic and nutritional attributes could combine consumer-preferred sweetness with traits such as higher protein content, longer pods, and more seeds per pod. The objective of this study was therefore to assess the crossability of the commercial variety *Oloyin* (P0) with 20 selected cowpea accessions under controlled conditions, and to identify compatible parental combinations that could be used to broaden the genetic base of cowpea breeding programmes.

Materials and Methods

Study site and plant material

The study was conducted in the screen house of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba-Akoko, Nigeria (7.2°N, 5.44°E; 423 m above sea level). Twenty cowpea accessions and one commercial variety, *Oloyin* (P0), were used (Table 1). The 20 accessions were maintained in the Plant Breeding Unit of the Department, of which 14 were originally obtained from the Genetic Resources Centre, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, in 2011. The remaining six accessions (P12, P15, P16, P18, P19, and P20) were M_5 mutants derived from TVu-17327 following treatment with 0.2 or 0.5% (v/v) ethidium bromide (EtBr) for varying durations. *Oloyin* was obtained from a local farmer in Akungba-Akoko, and its seeds were derived from a single plant through single-seed descent to maintain genetic uniformity. The 20 accessions were selected based on their intermediate to semi-erect growth habit, early maturity (39–47 days to first flowering), pod length (115–186 mm), and an average of 2–3 pods per peduncle. Preliminary evaluations (unpublished) also indicated high seed protein content (21.60–26.25%). *Oloyin* was selected because of its strong consumer preference for sweetness and its relatively high seed glucose (265.20 mg g^{-1}) and fructose (328.00 mg g^{-1}) contents, as determined in a preliminary evaluation (unpublished). These values were compared with the overall means of 275.19 and 354.32 mg g^{-1} for glucose and fructose, respectively.

Experimental layout and crop establishment

The experiment was arranged in a completely randomized design (CRD) with three replicates under screen-house conditions. Seeds were sown in plastic pots with drainage holes, each containing 7 kg of sandy loam soil, without fertilizer application. For each accession, five pots were established per replicate, with five seeds sown per pot. Seedlings were thinned to two plants per pot two weeks after emergence.

Hybridization procedure

Hybridization was conducted between *Oloyin* (P0), used as the male parent, and each of the 20 cowpea accessions (P1–P20), used as female parents, following the manual pollination procedure described by Ajayi et al. (2020a). Emasculation and

pollination were performed between 07:00 and 09:00 A.M. Mature, unopened flower buds on the female parents were carefully opened and approximately two-thirds of the corolla was removed with forceps to expose the reproductive organs. The anthers were removed to prevent self-pollination, after which pollen from a newly opened flower of *Oloyin* was transferred to the exposed stigma. Each pollinated flower was tagged with paper tape at the base of the pedicel, indicating the pollination date and cross combination. Hybridization was carried out over 30 days, and the resulting pods were harvested at maturity. For each cross, the number of flowers pollinated, number of pods set, pod-set percentage, mean pod length, and mean number of seeds per pod were recorded. Pod-set percentage was calculated using the following formula:

$$\text{Pod-set percentage} = \frac{Number\ of\ pods\ set}{Number\ of\ flowers\ pollinated} \times 100$$

All emasculation and pollination operations were performed by the same trained pollinator following a standardized procedure to minimize variation arising from handling technique. However, the number of flowers pollinated varied among accessions, ranging from 5 to 25, resulting in an unbalanced crossing dataset. Consequently, differences in pod set and pod-set percentage may reflect the combined effects of parental genotype, pollination handling, flower condition, environmental conditions, and the number of pollination attempts, rather than genetic differences alone. Seeds harvested from successful crosses were kept separately for subsequent evaluation of the F_1 progeny.

Table 1 List of the twenty selected cowpea accessions and *Oloyin* variety evaluated for crossability

Accession ID	Origin	Source	Biological status	Code
TVu-224	USA	IITA	Breeding material	P1
TVu-207	USA	IITA	Breeding material	P2
TVu-218	USA	IITA	Breeding material	P3
TVu-235	Ghana	IITA	Breeding material	P4
TVu-236	Ghana	IITA	Breeding material	P5
TVu-241	USA	IITA	Breeding material	P6
TVu-17327	Nigeria	IITA	Landrace	P7
TVu-17324	Nigeria	IITA	Landrace	P8
TVu-4886	Niger	IITA	Landrace	P9
TVu-9256	Burkina Faso	IITA	Landrace	P10
TVu-7362	Ghana	IITA	Landrace	P11
TVu-17327/0.2% EtBr 8h	Akungba-Akoko	AAUA	Mutant from Tvu-17327	P12
TVu-8660	Benin	IITA	Landrace	P13
TVu-9225	Tanzania	IITA	Landrace	P14
TVu-17327/0.2% EtBr 4h	Akungba-Akoko	AAUA	Mutant from Tvu-17327	P15
TVu-17327/0.2% EtBr 16h	Akungba-Akoko	AAUA	Mutant from Tvu-17327	P16
TVu-11986	Sudan	IITA	Landrace	P17
TVu-17327/0.5% EtBr 8h	Akungba-Akoko	AAUA	Mutant from Tvu-17327	P18
TVu-17327/0.5% EtBr 32h	Akungba-Akoko	AAUA	Mutant from Tvu-17327	P19
TVu-17327/0.5% EtBr 2h	Akungba-Akoko	AAUA	Mutant from Tvu-17327	P20
Oloyin	Akungba-Akoko	Local Farmer	Commercial variety	P0

F_1 progeny evaluation

F_1 seeds obtained from crosses that produced at least 10 seeds were planted and evaluated in a randomized complete block design (RCBD) with two replicates. Crosses with fewer than 10 F_1 seeds were excluded from the progeny evaluation because the available seed quantity was insufficient for a balanced evaluation. The F_1 progeny evaluation assessed hybrid establishment, plant vigour, flowering, fertility, and agronomic performance. Because this evaluation generated a substantial independent dataset and addressed a distinct phase of the breeding programme, its detailed results are reported in a separate manuscript (in preparation).

Data analyses

Crossability data were analyzed using descriptive statistics, including the mean, standard deviation, and coefficient of variation (CV). Pearson's correlation analysis was used to assess pairwise linear associations among the five crossability traits: number of flowers pollinated, number of pods set, pod-set percentage, average pod length, and number of seeds per pod. Correlation coefficients were tested for significance at $P \leq 0.05$ and $P \leq 0.01$. Before principal component analysis (PCA), the five traits were standardized to zero mean and unit variance to eliminate scale effects. PCA was performed on the standardized data using PAST version 4.1, and components with eigenvalues greater than 1 were retained for interpretation. A biplot of the first two principal components was used to visualize relationships among the traits and the distribution of cross combinations. Four crosses (P0×P1, P0×P4, P0×P14, and P0×P20) produced no pods; consequently, pod length and number of seeds per pod was recorded as zero for these crosses, representing the absence of pod formation rather than observed trait values. Therefore, the correlation and PCA results, including the biplot, were interpreted as exploratory summaries of crossability patterns, with due consideration of these structural zeros, rather than as

evidence of causal relationships or definitive rankings of parental superiority.

Results and Discussion

Variation in crossability among cowpea crosses

The results of crossability between *Oloyin* (P0) and 20 cowpea accessions are presented in Table 2. Considerable variation was observed among crosses for all measured parameters, with coefficients of variation ranging from 41.97% for the number of flowers crossed to 88.63% for pod-set percentage. This variation is consistent with previous reports showing that crossability in cowpea differs among parental combinations (Mohammed et al., 2010; Nwosu & Awa, 2013; Ajayi et al., 2020a). The number of flowers crossed ranged from 5 in P0×P1 and P0×P20 to 25 in P0×P16, while the number of pods set ranged from zero in P0×P1, P0×P4, P0×P14, and P0×P20 to 10 in P0×P19. Pod formation was absent in P0×P1, P0×P4, P0×P14, and P0×P20, indicating that these accessions were incompatible, or poorly cross-compatible, with *Oloyin* under the conditions of this study. Similar failures of pod set following controlled hybridization have been reported in cowpea and attributed to reproductive incompatibility between parental genotypes (Mohammed et al., 2010; Nwosu & Awa, 2013). However, the present experiment did not include cytological or histological assessments to determine the stage at which reproductive failure occurred. The absence of pods could have resulted from pre-zygotic failure, such as poor pollen viability, inadequate pollen germination, or arrested pollen-tube growth; alternatively, it could have resulted from post-zygotic failure, including embryo or endosperm abortion after fertilization (Bedinger et al., 2017; Wang & Filatov, 2023). Environmental factors and the limited number of flowers crossed may also have contributed. Future studies should therefore combine pollen-viability testing, aniline-blue fluorescence microscopy of pollinated pistils at sequential time points, and examination of ovules or young seeds after pollination. Such approaches would distinguish failure of pollen germination or pollen-tube growth from post-fertilization embryo or endosperm failure and would provide a more precise explanation for the observed cross-incompatibility (Broz & Bedinger, 2021; Wang & Filatov, 2023).

The pod-set percentage ranged from 0% to 90.90%. The highest pod-set percentage was recorded in P0×P19 (90.90%), followed by P0×P15 (80.00%), indicating strong cross-compatibility between these accessions and *Oloyin* under the experimental conditions. High pod-set success in compatible cowpea crosses has similarly been reported by Mohammed et al. (2010); Ajayi et al. (2020a). A total of 210 flowers were pollinated, producing 64 pods and an overall pod-set percentage of 30.48%. This overall value was lower than the high pod-set rates commonly reported for self-pollinated cowpea (Nameirakpam & Khanna, 2018; Pioltelli et al., 2024), but the performance of P0×P15 and P0×P19 shows that compatible intraspecific combinations can achieve high pod-set success. Average pod length ranged from 8.80 cm in P0×P10 to 23.35 cm in P0×P6, while the average number of seeds per pod ranged from 3.33 to 20. P0×P6 produced the longest pods and the highest number of seeds per pod, although its pod-set percentage was relatively low (14.29%). P0×P13 combined a relatively high pod-set percentage (55.56%) with a long pod (16.30 cm) and 16 seeds per pod. The range of pod length and number of seeds per pod observed here is broadly consistent with previous cowpea studies reporting substantial variation in these reproductive traits (Mohammed et al., 2010; Ogunsola & Igun, 2019). These results indicate that crossability and post-fertilization pod and seed development varied independently among some crosses; thus, a cross with few pods may still produce long pods or many seeds per pod when pod formation occurs.

Associations among crossability traits

Pearson's correlation analysis showed that the number of flowers crossed was positively correlated with the number of pods set (r=0.48*), suggesting that a greater number of pollination attempts may increase the opportunity for pod formation (Table 3). The number of pods set was strongly correlated with pod-set percentage (r=0.94**) and positively correlated with average pod length (r=0.54*). Pod-set percentage was also positively correlated with average pod length (r=0.51*), while average pod length was highly correlated with average number of seeds per pod (r=0.89*). Similar associations among pod and seed traits have been reported in cowpea and other legumes (Kutty et al., 2003; Nigude et al., 2004; Avci & Ceyhan, 2006). These associations indicate that successful pod formation and subsequent pod development are more informative indicators of crossability than the number of flowers crossed alone. However, correlation does not establish causation, and the relationships among traits should be interpreted as patterns of covariation.

Principal component analysis (PCA) of crossability traits

Principal component analysis (PCA) was used to examine the pattern of variation among the five crossability traits (Table 4). The first two principal components had eigenvalues greater than 1 and together explained 81.07% of the total variation, indicating that they provided a useful summary of the major patterns of variation in the dataset. PCA is widely used in plant breeding to reduce correlated traits into a smaller number of independent components and to identify the traits contributing most to observed variation (Gbadamosi et al., 2020; Ajayi et al., 2023). PC1 accounted for 59.92% of the variation and had high positive loadings for number of pods set (0.8735), pod-set percentage (0.8250), average pod length (0.8701), and average number of seeds per pod (0.7391). PC1 can therefore be interpreted as an overall reproductive-success axis, along which crosses with more pods, higher pod-set percentages, longer pods, and more seeds per pod are positioned. This interpretation is consistent with previous multivariate studies in cowpea, in which pod and seed traits contributed strongly to

the principal components describing variation among genotypes (Teodoro et al., 2019; Jain et al., 2022).

PC2 explained a further 21.16% of the variation and was characterized mainly by a strong negative loading for average number of seeds per pod (-0.6523), together with a negative loading for average pod length (-0.4178) and positive loadings for number of pods set (0.4449) and pod-set percentage (0.3087). PC2 therefore primarily contrasted crosses with relatively high pod set but comparatively fewer seeds per pod against crosses with fewer pods but higher seed retention per pod. Because average number of seeds per pod also loaded positively on PC1, it should not be regarded as completely independent of the other reproductive traits. The number of flowers crossed had a moderate positive loading on PC1 (0.4987) but its strongest loading on PC3 (0.7645), indicating that it varied partly independently of the reproductive-success traits. These results should be interpreted as describing covariation among the measured traits rather than causal relationships. The strong association among number of pods set, pod-set percentage, pod length, and number of seeds per pod indicates that crosses successful in early pod formation also tended to show favourable pod and seed characteristics. However, the presence of crosses with no pod set and zero values for pod length and seeds per pod may have amplified the associations among these variables. The PCA is therefore useful for identifying major patterns of variation and highlighting crosses for further evaluation, but it does not by itself establish the genetic or physiological causes of cross-compatibility. The contribution of this study is therefore to apply PCA and biplot analysis to a specific set of crossability traits in cowpea to identify compatible parental combinations and guide further hybridization studies.

Table 2 Level of crossability among *Oloyin* and twenty selected cowpea accessions

Crosses	NFC	NPS	PPS (%)	APL (cm)	ASPP
P0×P1	5	0	0.00	0.00	0.00
P0×P2	11	4	36.36	9.50	3.33
P0×P3	9	3	33.33	12.36	7.67
P0×P4	10	0	0.00	0.00	0.00
P0×P5	15	5	33.33	15.47	10.75
P0×P6	7	1	14.29	23.35	20.00
P0×P7	9	2	22.22	11.65	5.50
P0×P8	10	5	50.00	11.05	7.00
P0×P9	10	4	40.00	11.75	5.00
P0×P10	9	2	22.22	8.80	3.50
P0×P11	16	3	18.75	10.47	7.67
P0×P12	11	1	9.09	10.40	7.00
P0×P13	9	5	55.56	16.30	16.00
P0×P14	7	0	0.00	0.00	0.00
P0×P15	10	8	80.00	11.84	5.00
P0×P16	25	6	24.00	15.03	5.50
P0×P17	13	4	30.77	14.53	9.00
P0×P18	8	1	12.50	9.00	9.00
P0×P19	11	10	90.90	13.73	11.60
P0×P20	5	0	0.00	0.00	0.00
Sum	210	64	573.34	205.23	133.52
GM	10.50	3.20	28.67	10.26	6.68
SD	4.41	2.78	25.41	6.18	5.26
CV (%)	41.97	86.98	88.63	60.20	78.83

NFC = Number of flowers crossed; NPS = Number of pods set; PPS = Pod-set percentage; APL = Average pod length; ASPP = Average seeds per pod; GM = Grand mean; SD = Standard deviation; CV = Coefficient of variation

Table 3 Pearson's correlation for crossing parameters among the standard check and twenty selected cowpea accessions

Trait	NFC	NPS	PPS (%)	APL (cm)	ASPP
NFC	1	0.48*	0.18	0.39	0.12
NPS		1	0.94**	0.54*	0.36
PPS			1	0.51*	0.39
APL				1	0.89**
ASPP					1

** Significant at $P \leq 0.01$; * Significant at $P \leq 0.05$; NFC = Number of flowers crossed; NPS = Number of pods set; PPS = Pod set percentage; APL = Average pod length; ASPP = Average seeds per pod

Table 4 Principal component analysis (PCA) based on crossability traits between a standard check and twenty selected cowpea accessions

Traits	PC 1	PC 2	PC 3	PC 4	PC 5
NFC	0.4987	0.4056	0.7645	0.0422	0.0231
NPS	0.8735	0.4449	-0.1829	0.0367	-0.0647
PSP	0.8250	0.3087	-0.4693	-0.0129	0.0598
APL	0.8701	-0.4178	0.1784	-0.1909	-0.0081
ASPP	0.7391	-0.6523	0.0143	0.1674	0.0037
Eigenvalue	2.9957	1.0578	0.8702	0.0678	0.0084
Percentage of variability (%)	59.915	21.157	17.406	1.356	0.167
Cumulative variability (%)	59.915	81.072	98.478	99.834	100.001

Bold represents traits with high loadings or high contributions; NFC = Number of flowers crossed; NPS = Number of pods set; PPS = Pod-set percentage; APL = Average pod length; ASPP = Average seeds per pod

Biplot analysis of crosses and crossability traits

The PCA biplot visually summarized the relationships among the crossability traits and the relative positions of the crosses (Fig. 1). The similar directions of the vectors for number of pods set and pod-set percentage were consistent with their strong positive correlation (r=0.94**), while the vector for average pod length was broadly aligned with the reproductive-success traits, consistent with its significant correlations with pod set (r=0.54*) and number of seeds per pod (r=0.89**). The number of flowers crossed showed a weaker association with these traits, supporting the interpretation that the number of pollination attempts was not equivalent to successful crossability. In biplot analysis, the angles between trait vectors approximate the correlations among traits, while the positions of genotypes indicate their relative performance for those traits (Yan & Kang, 2002; Atnaf et al., 2017; Ajayi et al., 2020b).

The polygon view identified crosses occupying extreme positions in the two-dimensional PCA space (Fig. 2). P0×P15 and P0×P19 were positioned in the region associated with high pod set and pod-set percentage, consistent with their high crossability success. P0×P6 was separated mainly by its exceptionally long pod and high number of seeds per pod, whereas P0×P13 was associated with a favourable combination of pod set, pod length, and number of seeds per pod. P0×P16 occupied an extreme position largely because of its high number of flowers crossed, but its comparatively low pod-set percentage indicates that this position should not be interpreted as superior overall crossability. This interpretation follows the general principles of PCA-based biplot analysis, in which trait-vector angles approximate trait correlations and genotype positions reflect their relative performance for the displayed traits (Yan & Kang, 2002; Atnaf et al., 2017; Ajayi et al., 2020b).

Crosses located near the origin, or in sectors not associated with favourable trait vectors, showed average or poor performance for the measured traits. P0×P1, P0×P4, P0×P14, and P0×P20 produced no pods and should therefore be regarded as incompatible or poorly cross-compatible with *Oloyin* under the experimental conditions. However, because the study was conducted in one environment and involved a limited number of pollinations per cross, these crosses should be re-evaluated before being permanently excluded from breeding programmes. Overall, the PCA and biplots are useful exploratory tools for grouping crosses according to their crossability profiles and identifying candidates for further hybridization, but they should be used alongside the original crossability data and correlation analysis rather than as standalone evidence of parental superiority (Yan & Kang, 2002; Ajayi et al., 2023).

PCA-based biplots have been used extensively in cowpea and related grain legumes to visualize inter-trait relationships and discriminate genotypes according to their trait profiles (Yan and Kang, 2002; Atnaf et al., 2017; Ajayi et al., 2020b). In this study, the biplots were used as exploratory tools to summarize the crossability data and identify crosses for further evaluation, rather than as definitive evidence of parental superiority. The results of the PCA, biplots, and correlation analysis jointly indicated that the number of pods set, pod-set percentage, average pod length, and average number of seeds per pod were the main traits associated with reproductive success, whereas the number of flowers crossed reflected crossing effort rather than crossability outcome. This study evaluated crossability at the cross-development stage. F_1 seeds obtained from crosses that produced at least 10 seeds were subsequently evaluated in a randomized complete block design with two replicates; the detailed progeny results are reported elsewhere (in preparation). Because crosses with fewer than 10 seeds were excluded from the progeny evaluation, the present study identifies candidate cross-compatible combinations but does not provide a complete assessment of the performance or breeding value of all successful crosses.

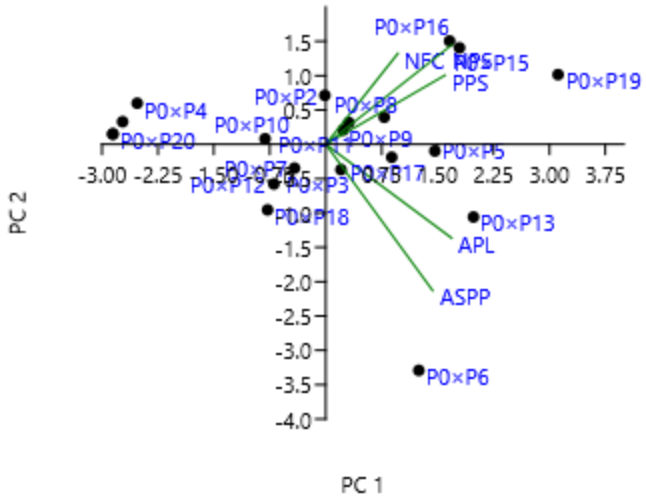


Fig. 1 Biplot of the first two principal component axes (PC1 and PC2) showing the relationships among crossability traits of the standard check and twenty selected cowpea accessions. Crosses are designated as P0×P1 to P0×P20, where P0 represents *Oloyin* (the commercial variety) and P1–P20 represent the selected cowpea accessions. NFC = Number of flowers crossed; NPS = Number of pods set; PPS = Pod-set percentage; APL = Average pod length; ASPP = Average seeds per pod.

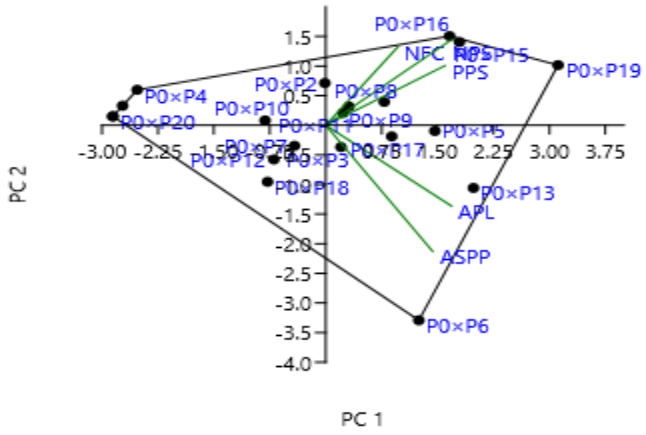


Fig. 2 Polygon view of the genotype x trait biplot of crossability traits of the standard check and twenty selected cowpea accessions. Crosses are designated as P0×P1 to P0×P20, where P0 represents *Oloyin* (the commercial variety) and P1–P20 represent the selected cowpea accessions. NFC = Number of flowers crossed; NPS = Number of pods set; PPS = Pod set percentage; APL = Average pod length; ASPP = Average seeds per pod.

Conclusion

This study demonstrated substantial variation in crossability among the evaluated cowpea accessions. P0×P15 and P0×P19 exhibited the highest crossability success, whereas P0×P6 and P0×P13 showed favourable pod-length and seed-number characteristics. PCA indicated that number of pods set, pod-set percentage, average pod length, and average number of seeds per pod contributed strongly to the main pattern of variation in crossability traits. These results identify P0×P15, P0×P19, P0×P6, and P0×P13 as candidate crosses for further evaluation. F_1 seeds from crosses

that produced at least 10 seeds were evaluated in a randomized complete block design with two replicates; the detailed progeny evaluation is reported elsewhere (in preparation). These progeny data will provide further evidence on hybrid performance, fertility, and the breeding value of the compatible crosses.

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Declarations

i. Ethics approval and consent to participate: This study did not involve human participants, human data, or animal studies; therefore, ethical approval was not required.

ii. Competing interests: The authors declare that there is no conflict of interest regarding the publication of this manuscript.

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