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Phenotypic evaluation of gene-pyramided cowpea lines for resistance to *Striga gesnerioides* using multi-origin inoculum from Nigeria

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Abstract

Cowpea (*Vigna unguiculata* (L.) Walp.) is a major source of dietary protein in sub-Saharan Africa, but its productivity is severely constrained by the parasitic weed *Striga gesnerioides*. This study evaluated 140 BC_3F_2 cowpea lines developed through marker-assisted gene pyramiding for resistance to S. gesnerioides. Two segregating populations were assessed: Population 1 derived from {(IT90K-277-2 × B301) × (IT90K-277-2 × TVu-1272)} and Population 2 from {(IT90K-277-2 × TVu-16514) × (IT90K-277-2 × TVu-1272)}. The BC_3F_2 lines were screened in a replicated pot experiment using a mixed Striga seed inoculum collected from three major cowpea-producing areas in northern Nigeria. Analysis of variance revealed highly significant genetic variation ($p < 0.0001$) among lines for both agronomic traits and Striga resistance parameters. Broad-sense heritability estimates ranged from moderate to high, indicating strong genetic control of the evaluated traits. Hierarchical clustering and heatmap analyses identified a subset of BC_3F_2 lines combining low Striga infestation with favourable yield components, while strong negative correlations were observed between Striga infestation parameters and yield traits. Segregation analysis conformed to a two-gene dominant inheritance model for Striga resistance, with observed ratios fitting the expected 1:1:1:1 distribution ($\chi^2 = 2.34$). The results demonstrate the effectiveness of marker-assisted pyramiding in combining resistance alleles from multiple donor parents and identify BC_3F_2 lines suitable for advancement towards the development of cowpea cultivars with stable resistance to S. gesnerioides in Striga-endemic production systems.

1 Introduction

Cowpea (Vigna unguiculata (L.) Walp.) is a vital food and forage legume widely cultivated in tropical and subtropical regions, particularly in sub-Saharan Africa, where it serves as a major source of dietary protein [28]. With an average protein content of approximately 24% on a dry weight basis, cowpea provides an affordable and nutritionally important staple for millions of households in West and Central Africa [15]. Beyond

its nutritional value, cowpea contributes to soil fertility through biological nitrogen fixation, fits well into intercropping systems, and serves as an important cash crop for smallholder farmers [10, 19]. Its ability to produce reasonable yields on poor, sandy soils with minimal fertiliser input further enhances its importance in low-input farming systems [28].

West Africa accounts for approximately 95% of global cowpea production, underscoring the crop's regional importance [23, 25]. Nigeria is the world's largest producer and consumer of cowpea [27], producing about 3.63 million metric tonnes from 4.7 million hectares in 2021, followed by Niger Republic with 2.66 million metric tonnes from 5.97 million hectares [12]. Other African countries with substantial cowpea production include Burkina Faso, Cameroon, Ghana, Kenya, Uganda, and Tanzania [18]. Despite its importance, average cowpea yields across the region remain low, largely due to persistent biotic and abiotic constraints.

Among the biotic stresses affecting cowpea production, the parasitic weed Striga gesnerioides (Willd.) Vatke represents one of the most severe yield-limiting factors in the dry savannas of West and Central Africa [13, 21]. S. gesnerioides is an obligate root hemiparasite that attaches to cowpea roots, siphoning water and nutrients from the host plant. This interaction results in chlorosis, stunted growth, and, in severe cases, complete crop failure, with yield losses ranging from 80% to 100% in susceptible cultivars [20]. Conventional control measures, including cultural practices and chemical methods, have had limited success under smallholder farming conditions, making host plant resistance the most sustainable and economically viable control strategy [27].

However, reliance on single-gene resistance has proven unstable due to the existence of diverse Striga races and the parasite's capacity to overcome resistance genes over time [6]. The occurrence of multiple S. gesnerioides races across cowpea-growing regions necessitates the deliberate stacking of resistance genes to enhance durability and reduce the risk of resistance breakdown [22]. Marker-assisted selection (MAS), particularly marker-assisted backcrossing (MABC), offers an efficient approach for pyramiding resistance genes into elite genetic backgrounds. This approach allows precise introgression of multiple resistance loci while accelerating recovery of the recurrent parent genome, thereby shortening breeding cycles compared with conventional methods [9].

In cowpea, B301 has historically been the principal source of resistance to S. gesnerioides across several regions [26]. However, the identification of additional resistance sources in accessions such as TVu-16,514 and TVu-1272 [21] provides an opportunity to broaden the genetic base of resistance and enhance its durability. Pyramiding resistance genes from these diverse sources into farmer-preferred cultivars is therefore a promising strategy for developing cowpea varieties with broad-spectrum resistance to S. gesnerioides.

This study evaluates the performance of gene-pyramided elite cowpea lines for resistance to S. gesnerioides under controlled screening conditions. Rather than conducting multi-location field trials at this stage, a mixed Striga inoculum sourced from major cowpea-growing ecologies in Nigeria was used to simulate diverse parasite pressure within a single experimental environment. This approach enables early-generation identification of genotypes exhibiting broad-spectrum resistance prior to resource-intensive field validation. By integrating resistance genes from multiple donor parents into an elite genetic background, the study aims to provide a foundation for the development

of high-yielding, Striga-resistant cowpea varieties suitable for sustainable production in Striga-endemic regions.

2 Materials and methods

2.1 Experimental materials, design and location

Preliminary F_1 crosses were conducted at the International Institute of Tropical Agriculture (IITA), Kano State, Nigeria, between September and December 2022. Subsequent backcrossing (BC_1F_1 to BC_3F_2) and molecular screening were carried out at the Molecular Biology Laboratory, Federal University of Agriculture, Makurdi, Nigeria, now Joseph Sarwuan Tarka University (JOSTUN), between November and December 2023. The average temperature at both locations was approximately 28 °C, while mean relative humidity was 38% in Kano and 79% in Makurdi during the respective periods of operation.

Two BC_3F_2 cowpea populations pyramided with resistance genes against Striga gesnerioides were developed and used for phenotypic evaluation. Resistance genes were introgressed from three donor genotypes, namely B301, TVu-16,514, and TVu-1272, into the susceptible but agronomically elite recurrent parent IT90K-277-2. A total of 140 BC_3F_2 lines, comprising 70 lines from each population, were evaluated in this study.

Descriptions of the parental genotypes, their origin, resistance status, and associated Striga races are presented in Table 1.

Population 1 was generated from {(IT90K-277-2 × B301) × (IT90K-277-2 × TVu-1272)}, while.

Population 2 was generated from {(IT90K-277-2 × TVu-16514) × (IT90K-277-2 × TVu-1272)}.

2.2 Simultaneous pyramiding of resistance genes and population development

A simultaneous gene pyramiding strategy based on marker-assisted backcrossing was employed to introgress resistance genes from donor parents while recovering the genetic background of the recurrent parent. Crosses were performed by emasculation following the procedure described by Myers (1996).

For Population 1, the susceptible recurrent parent IT90K-277-2 was crossed separately with the resistant donor parents B301 and TVu-1272 to generate two independent F_1 populations. These F_1s were subsequently intercrossed to obtain a pyramided F_1 carrying resistance alleles from both donors. The resulting F_1 was backcrossed to IT90K-277-2 up to the BC_3F_1 generation. At each backcross generation, foreground selection was conducted using the SSR1 marker (Table 2), which is associated with resistance to S. gesnerioides [21]. Only plants carrying the desired resistance alleles were advanced to subsequent backcrosses.

Table 1 Parental Material used in the Study

Cowpea genotypes	Origin	Gene	Response to Striga	SG Races
IT90K-277-2	Improved variety from IITA Breeding Program Nigeria	n/a	S	n/a
Tvu-16,514	Landrace from Burkina Faso	Rsg2	R	SG2
Tvu-1272	Landrace from Nigeria	Rsg1	R	SG1
B301	Landrace from Botswana	Rsg3	R	SG3

Key: R=Resistant Cultivar S=Susceptible Cultivar, SG= Races of *Striga gesnerioides*,

Table 2 Description of the SSR1 Marker Associated with *Striga gesneriodes* Resistance in Cowpea

Marker Name	Marker Sequence	Trait associated with
SSR1 Forward Primer	CCT AAG CTT TTC TCC AAC T CAA GAA GGA GGA GGC	***Striga gesneriodes*-Resistance**
SSR1 Reverse Primer	CAA GAA GGA GGC GGC GAA GAC T CAA GAA GGA GGA GGC	***Striga gesneriodes*-Resistance**

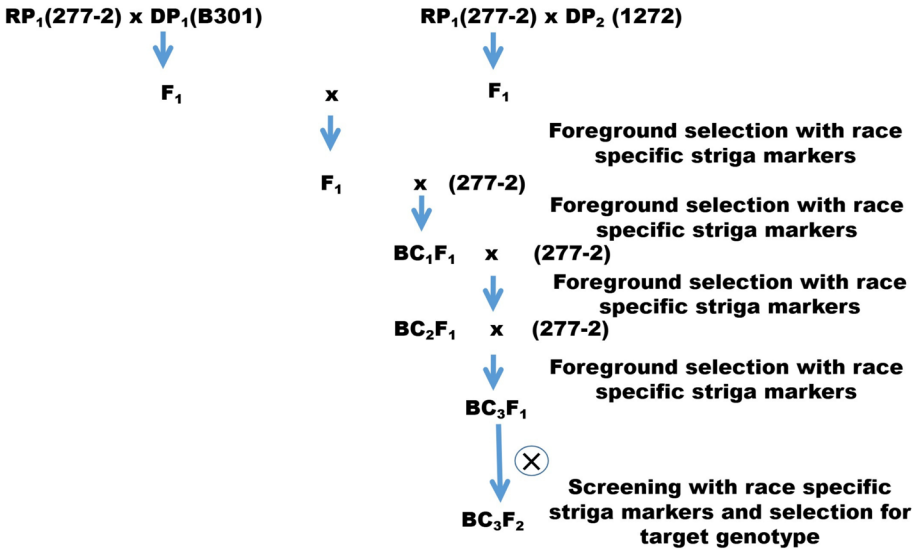

Fig. 1 Generation of population 1 for the study. Gene pyramiding of *Striga* resistance from different sources using marker-assisted backcrossing

A similar procedure was followed for Population 2, where IT90K-277-2 was crossed separately with TVu-16,514 and TVu-1272, followed by intercrossing of the F_1s and successive backcrossing to the recurrent parent up to the BC_3F_1 generation, with marker-assisted foreground selection at each stage.

The BC_3F_1 plants from both populations were selfed to generate the BC_3F_2 populations used for phenotypic evaluation. The breeding schemes for Population 1 and Population 2 are illustrated in Figs. 1 and 2, respectively.

2.3 Molecular marker used for foreground selection

Foreground selection for Striga resistance was performed using the SSR1 marker, previously reported to be associated with resistance to S. gesnerioides in cowpea [21]. Primer sequences and associated traits are provided in Table 2.

2.4 Source and preparation of striga inoculum

Striga gesnerioides seeds were collected from three major cowpea-producing and Striga-endemic locations in Nigeria: Migibri in Kano State (12.0022° N, 8.5920° E), Malammadori in Borno State (12.3333° N, 10.4167° E), and Sule Tankarka in Jigawa State (11.7574° N, 9.3377° E). These locations represent diverse Striga populations commonly encountered in Nigerian cowpea production systems.

To simulate broad parasite pressure under controlled conditions, seeds from the three locations were weighed, mixed thoroughly in equal proportions, and used as a composite inoculum. Seed density was estimated following the method described by Ugbaa

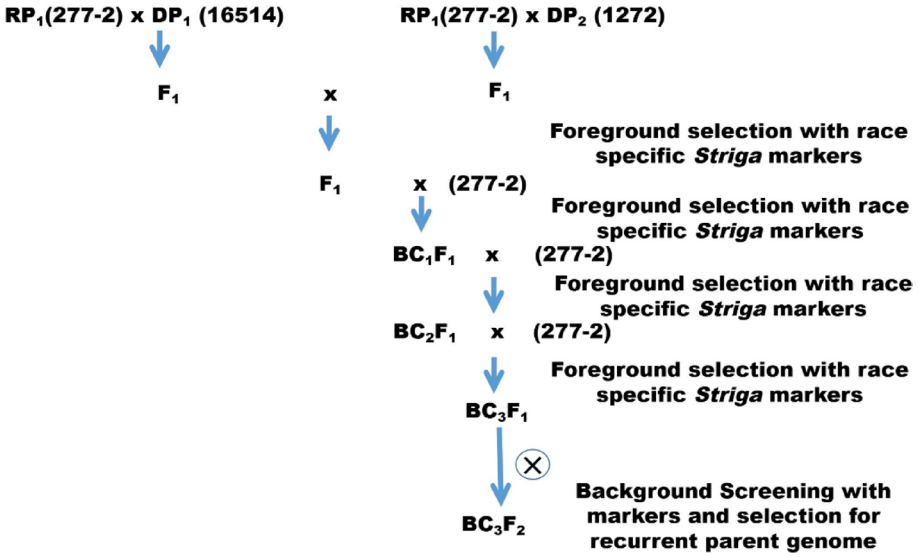

Fig. 2 Generation of population 2 for the study. Gene pyramiding of Striga resistance from different sources using marker-assisted backcrossing

et al., [29]. One thousand seeds were counted under a compound microscope (Brunel Microscope 0723219; ×400 magnification) and weighed using a digital sensitive balance (Denver Instruments TP-3002). Based on the measured weight of 0.125 g per 1,000 seeds, 5,000 seeds corresponded to 0.625 g of inoculum.

2.5 Evaluation of BC_3F_2 lines under pot culture conditions

Phenotypic screening was conducted using a pot culture technique as described by Omoigui et al., [21]. Pots were filled with a 2:1 mixture of topsoil and sand and inoculated with 5,000 Striga seeds per pot using the mixed inoculum. Inoculated pots were preconditioned for seven days to enhance Striga seed germination prior to planting.

The experiment was laid out in a Completely Randomised Design with three replicates. A total of 140 BC_3F_2 lines, along with parental checks, were evaluated.

2.6 Data collection

Observations were recorded on Striga resistance parameters, including days to first Striga emergence, Striga counts at 42, 49, and 56 days after planting (DAP), number of Striga attachments, number of haustorial attachments, Striga height at 56 DAP (cm), and Striga dry weight (g).

After harvest, cowpea roots were carefully washed by submerging pots in water for five minutes, followed by gentle removal of adhering soil. Roots were examined for haustorial attachment. Plants exhibiting Striga attachment and shoot emergence were classified as susceptible, while plants with no attachment or infection were classified as resistant.

Agronomic traits recorded included days to first flowering, plant height at three weeks after planting (cm), shoot dry weight (g), root dry weight (g), number of pods per plant, and 100-seed weight (g). Data were collected from all BC_3F_2 individuals and their parental genotypes.

2.7 Data analysis

The phenotypic data of cowpea plant and Striga parameters of the BC_3F_2 were Phenotypic data were subjected to analysis of variance (ANOVA) using GenStat software (17th Edition; VSN International Ltd.). Mean separation was performed using Duncan's Multiple Range Test (DMRT) at the appropriate significance level.

Multivariate analysis was conducted using hierarchical clustering and heatmap visualisation implemented in the ClustVis web tool [17]. Euclidean distance and Ward's linkage method were used to explore relationships among genotypes and traits.

Chi-square (χ^2) tests were performed to assess the goodness-of-fit of observed segregation patterns for Striga resistance to the expected 1:1:1:1 ratio for a two-gene backcross population.

$X^2 = \sum \frac{(O-E)^2}{E}$

The test statistic was calculated using the standard formula, where χ^2 represents the chi-square value, O the observed frequency, and E the expected frequency. The analysis assumed independent assortment of two unlinked dominant resistance genes (Table 3).

3 Results and discussion

3.1 Phenotypic screening of striga resistance pyramided BC_3F_2 lines

Analysis of variance revealed highly significant ($p < 0.0001$) effects of genotype, population, and genotype × population interaction for all cowpea agronomic traits and Striga-related parameters evaluated (Table 4). These results indicate substantial phenotypic variation among BC_3F_2 lines derived from the two pyramided populations and confirm the presence of exploitable genetic diversity for both resistance and yield-related traits.

The significant genotype effect reflects inherent genetic differences among the BC_3F_2 lines, while the population effect indicates that the two breeding populations differed in overall performance. The significant genotype × population interaction demonstrates that individual genotypes responded differently across the two populations, suggesting that resistance alleles from different donor combinations were expressed with varying effectiveness. This interaction highlights the importance of evaluating pyramided lines across distinct genetic backgrounds when combining resistance genes.

Broad-sense heritability (h^2) estimates ranged from 0.61 to 0.80 across all traits (Table 4), indicating moderate to high genetic control. High heritability values for key yield components such as 100-seed weight (h^2 = 0.80), pod weight (h^2 = 0.80), and seed weight per plant (h^2 = 0.72) suggest that these traits are amenable to effective selection in early

Table 3 Gene Action Based on Graph form, Skewness and Kurtosis

Normality test	Graph form	Gene action/number of genes
Skewness = 0	Normal distribution	Additive gene action
Skewness < 0	Abnormal distribution	Additive gene action with the effect of duplicate epistasis
Skewness > 0	Abnormal distribution	Additive gene action with the effect of complementary epistasis
Kurtosis = 3	Mesokurtic	
Kurtosis < 3	Platykurtic	Many genes (polygenic)
Kurtosis > 3	Leptokurtic	Few genes

Source: Dasriani et al. [11]

Table 4 Mean square estimate, P values and Heritability for Striga and Plant Parameter from Reaction of BC_3F_2 segregating population 1 and 2 to Striga infestation

Parameter	Genotype	Population	Genotype x Population	Genotype	Population	Genotype x population	Heritability
	Mean square estimates			*P* value			
Days to first flower	8444.47	1089.2	12293.47	< 0.0001	< 0.0001	< 0.0001	0.66
Plant height @ 3 weeks DAP	33.55	262.01	30.86	< 0.0001	< 0.0001	< 0.0001	0.77
Days to first Striga emergency	538.55	1537.33	344.96	< 0.0001	< 0.0001	< 0.0001	0.76
Striga count @ 42 DAP	0.36	0.04	0.37	< 0.0001	< 0.0001	< 0.0001	0.61
Striga count @ 49 DAP	5.98	1.81	5.79	< 0.0001	< 0.0001	< 0.0001	0.69
Striga count @ 66 DAP	16.63	49.32	12.43	< 0.0001	< 0.0001	< 0.0001	0.76
Number of Striga attached	15.77	50.97	12.35	< 0.0001	< 0.0001	< 0.0001	0.75
Striga haustorium attached	2.42	7.89	2.08	< 0.0001	< 0.0001	< 0.0001	0.73
Striga height @ 56 DAP	15.03	5.84	10.81	< 0.0001	< 0.0001	< 0.0001	0.69
Striga dry weight	1.18	4.58	1.21	< 0.0001	< 0.0001	< 0.0001	0.71
Plant shoots dry weight (g)	24.59	438.43	22.29	< 0.0001	< 0.0001	< 0.0001	0.77
Plant root dry weight (g)	11.98	58.5	11.92	< 0.0001	< 0.0001	< 0.0001	0.75
Pods per plant	1.79	16.3	1.71	< 0.0001	< 0.0001	< 0.0001	0.76
Pod weights (g)	7.75	33.23	5.94	< 0.0001	< 0.0001	< 0.0001	0.80
Seed weight per plant	1.32	15.84	1.52	< 0.0001	< 0.0001	< 0.0001	0.72
100 seed weight (g)	102.24	639.42	78.78	< 0.0001	< 0.0001	< 0.0001	0.80
Number of seeds per plant	95.62	1436.25	119.22	< 0.0001	< 0.0001	< 0.0001	0.71
Number of seeds per pod	25.63	451.02	34.56	< 0.0001	< 0.0001	< 0.0001	0.69

generations. Similar heritability ranges have been reported for cowpea agronomic traits by Boukar et al., [7], reinforcing the robustness of these findings.

Plant architecture and biomass traits, including early plant height, shoot dry weight, and root dry weight, also exhibited high heritability (0.75–0.77), consistent with previous reports by Aliyu and Makinde [1]. These traits are particularly relevant under Striga pressure, as early vigour and biomass accumulation may enhance host tolerance.

Striga resistance traits, including days to first Striga emergence, number of attachments, and haustorial attachment, showed high heritability values (0.73–0.76),

indicating strong genetic control of resistance mechanisms. Notably, heritability for Striga counts increased with plant age, from 0.61 at 42 days after planting (DAP) to 0.76 at 56 DAP. This trend suggests that resistance responses become more pronounced as plants mature, potentially reflecting delayed attachment or post-attachment resistance mechanisms. Similar observations have been reported for resistant cowpea genotypes that suppress Striga development over time [8, 14].

Overall, the phenotypic variation observed among the BC_3F_2 lines confirms the successful combination of resistance alleles from multiple donor parents and demonstrates the potential to select lines that combine effective Striga resistance with favourable agronomic performance.

3.2 Clustering of BC_3F_2 genotypes and character associations

Hierarchical clustering and heatmap analysis based on 19 cowpea and *Striga* parameters grouped the combined BC_3F_2 populations and parental genotypes into three distinct phenotypic clusters (Fig. 3). This clustering reflects underlying genetic differentiation among the lines with respect to resistance and productivity traits.

Cluster I comprised BC_3F_2 lines characterised by low *Striga* infestation indicators, including reduced *Striga* counts, minimal haustorial attachment, and low *Striga* dry weight, alongside superior performance for yield-related traits such as pod weight and seed weight. These genotypes represent desirable combinations of resistance and productivity, indicating that pyramiding resistance genes did not impose yield penalties in these lines. The identification of such lines supports the feasibility of developing

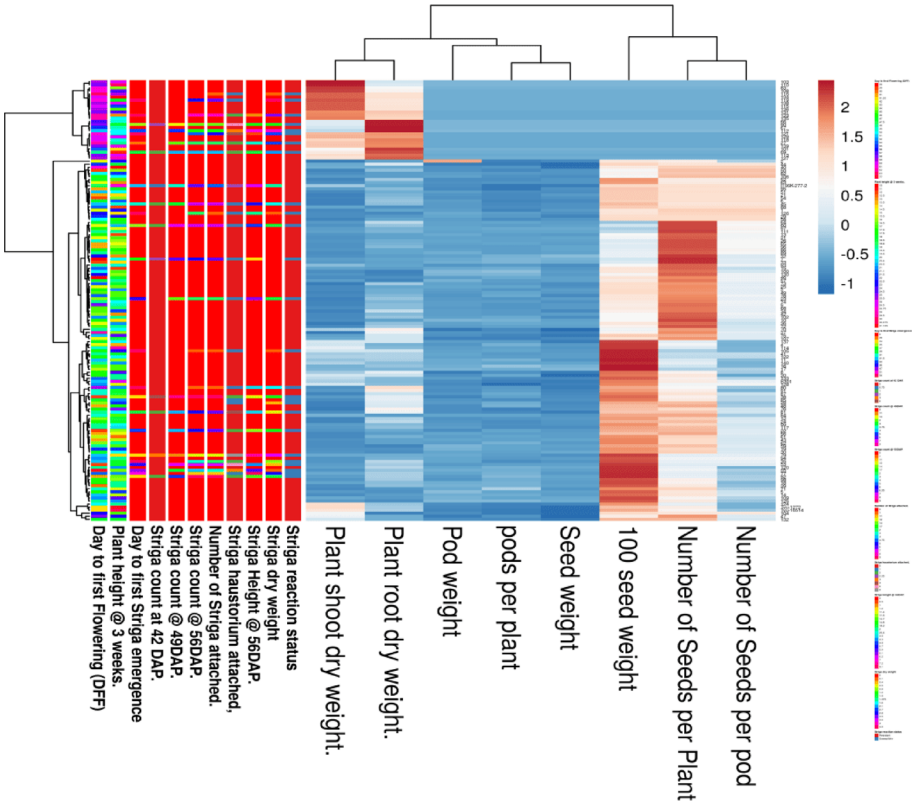

Fig. 3 Hierarchical Cluster Dendograms of BC_3F_2 Genotypes, Striga and Cowpea plant Parameters, and Heat map of Associations between Parameters

high-yielding cowpea cultivars with durable *Striga* resistance, as also reported by Attamah et al., [4].

Cluster III consisted predominantly of susceptible BC_3F_2 lines with high *Striga* infestation levels and poor agronomic performance, illustrating the severe negative impact of *Striga* parasitism on host growth and yield. This pattern is consistent with earlier studies showing substantial yield reductions in susceptible cowpea genotypes under *Striga* infestation.

Cluster II represented an intermediate and heterogeneous group, containing lines with mixed resistance and yield responses. The presence of this group reflects the segregating nature of the BC_3F_2 populations and suggests quantitative variation in resistance expression, which is typical of populations derived from marker-assisted back-crossing [5].

Trait-based clustering further revealed that *Striga* infestation parameters, including *Striga* counts at 42, 49, and 56 DAP, number of attachments, haustorial attachment, *Striga* height, and dry weight, clustered tightly together. The correlation matrix (Fig. 4) confirmed strong positive correlations among these traits ($r = 0.4–0.8$), indicating that they collectively represent the intensity of *Striga* parasitism. This finding suggests that a reduced subset of these traits, such as *Striga* count at 42 DAP, could serve as reliable proxies for resistance screening, thereby improving phenotyping efficiency in breeding programmes.

Yield-related traits, including pod weight, seed weight, number of seeds per pod, and 100-seed weight, also formed a distinct cluster with strong positive correlations. These relationships are consistent with previous reports in cowpea [2, 7] and indicate that selection for one yield component is likely to result in correlated gains in others.

Notably, root and shoot dry weights were positively associated with yield traits and negatively associated with *Striga* infestation parameters. This underscores the importance of root system vigour in mitigating the effects of *Striga* parasitism. Since *Striga gesnerioides* attaches to host roots and diverts water and nutrients, a more robust root

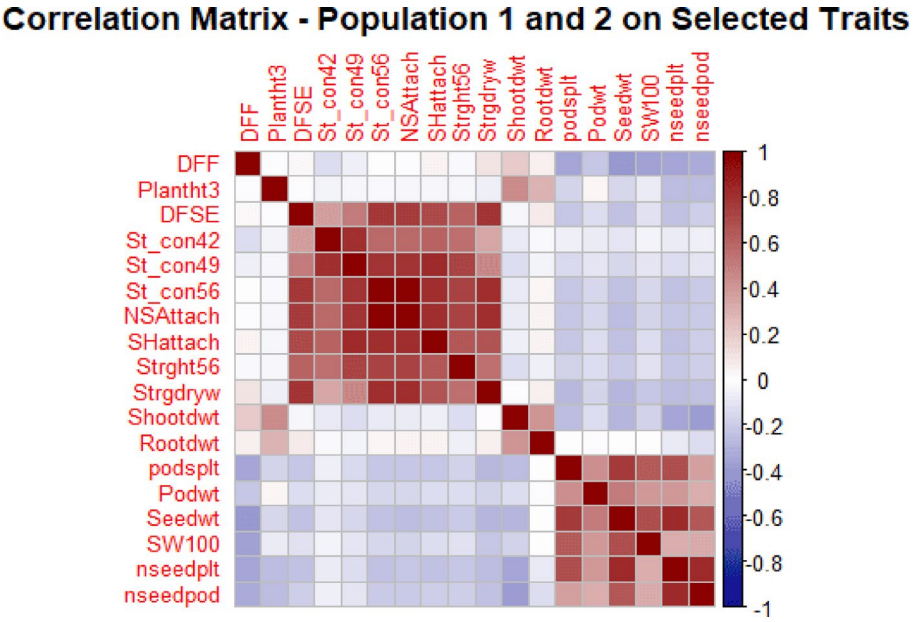

Fig. 4 Heat Map of Correlation Matrix for Association Striga Parameters and Cowpea Plant Parameters in BC_3F_2 Population of Cowpea

system may enhance tolerance by sustaining host growth despite parasitic pressure [16, 24].

A strong negative association was observed between *Striga* infestation traits and yield components ($r < -0.8$), confirming the detrimental impact of *Striga* on cowpea productivity. While some studies have reported trade-offs between resistance and yield [13, 28], the presence of high-yielding, resistant lines in this study demonstrates that such trade-offs are not inevitable and can be overcome through targeted pyramiding strategies.

3.3 Genetic architecture and inheritance of striga resistance

Chi-square analysis of segregation patterns in both BC_3F_2 populations showed no significant deviation from the expected 1:1:1:1 ratio for a two-gene backcross population (Table 5). The calculated χ^2 value of 2.34 for both populations was well below the critical value of 7.815 at the 5% significance level, indicating a good fit to the expected ratio.

These results suggest that resistance to Striga gesnerioides in the BC_3F_2 populations is controlled by two independently assorting genes, consistent with the pyramiding of dominant resistance alleles from the donor parents. This finding aligns with earlier reports of dominant gene action for Striga resistance in cowpea [3, 26].

The successful recovery of expected segregation ratios, combined with phenotypic evidence of strong resistance, underscores the effectiveness of marker-assisted pyramiding in combining multiple resistance sources. Such an approach enhances the likelihood of achieving durable resistance and provides a solid foundation for advancing elite cowpea lines suited to Striga-prone environments in Nigeria.

4 Conclusion

The phenotypic evaluation of BC_3F_2 cowpea lines pyramided for Striga gesnerioides resistance revealed substantial genetic variation for both Striga resistance traits and agronomic performance under controlled infestation conditions. The significant effects of genotype, population, and genotype × population interaction confirm the successful introgression and segregation of resistance alleles from multiple donor parents and demonstrate differential expression of resistance and yield-related traits within the breeding populations.

Moderate to high broad-sense heritability estimates for Striga resistance parameters and yield components indicate strong genetic control of these traits and support their suitability for effective selection at early generations of breeding. The clustering and heatmap analyses further identified a subset of BC_3F_2 lines that combined low Striga infestation with favourable agronomic performance, indicating that resistance can be incorporated without necessarily incurring yield penalties. The strong negative association between Striga infestation parameters and yield components highlights the severe impact of Striga parasitism on susceptible genotypes and reinforces the importance of resistance as a primary breeding objective.

Segregation analysis based on chi-square tests was consistent with a two-gene model of resistance segregating independently in both BC_3F_2 populations, supporting the involvement of major dominant resistance genes derived from the donor parents. This genetic architecture validates the effectiveness of the marker-assisted pyramiding strategy employed in this study.

Table 5 Chi-square Goodness-of-Fit to Expected Genetic ratio for Backcross with two Genes

Generation	*N*	Observed				Expected				Genetic ratio	Calculated χ2 value	Critical χ2 value
		R			S	*R*			S			
		RrSs	Rrss	rrSs	rrss	RrSs	Rrss	rrSs	Rrss			
Pop1 (BC3F2)	70	20	19	19	12	17.5	17.5	17.5	17.5	1:1:1:1	2.34*	7.815
Pop-2 (BC3F2)	70	19	20	19	12	17.5	17.5	17.5	17.5	1:1:1:1	2.34*	7.815

*= significant calculated χ2 value, indicating "goodness-of-fit" to Genetic ratio at 95% level of significance; N= Number of lines evaluated; R= Number resistant; S= Number susceptible; Resistant genotypes= RrSs, Rrss, rrSs, Susceptible genotypes= rrss

Overall, the BC_3F_2 lines developed in this study represent valuable genetic material for advancing cowpea breeding for Striga gesnerioides resistance. The identification of lines combining strong resistance with stable agronomic performance provides a foundation for subsequent field validation and varietal development, particularly for Striga-endemic cowpea-producing regions of northern Nigeria.

5 Methods

5.1 Experimental sites

Field experiments were conducted during the 2024 cropping season. Trials were established at Makurdi, Benue state (southern Guinea Savanna; 7.7307° N, 8.5361° E). This site was selected to capture ecological diversity in cowpea production areas and to evaluate varietal performance under natural *Striga gesnerioides* infestation pressure.

5.2 Plant materials and sources

The cowpea genotypes (IT90K-277-2, Tvu-16514, Tvu-1272 and B301) evaluated included gene-pyramided breeding lines carrying resistance genes against *Striga gesnerioides*, obtained from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. Local cowpea varieties used as checks were collected from farmers' fields in Benue state, representing widely grown farmer-preferred cultivars.

5.3 Permissions for plant materials

All plant materials were obtained with appropriate permissions. Seed materials from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, were accessed under institutional guidelines for research use. No special permits were required for the use of cultivated cowpea, as it is not classified as an endangered or protected species.

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Author contributions
Isaiah A. Gabriel: Conceptualisation (lead); Writing—original draft (lead); Formal analysis (lead); Writing—review and editing (equal); Methodology (lead); Visualisation (lead). Lucky O. Omoigui: Supervision (lead); Validation (lead); Writing—review and editing (equal)

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Data availability
The datasets generated and/or analysed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate
Not applicable. This article does not contain any studies with human participants or animals performed by any of the authors.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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