

Multi-Traits Selection Index for Selection of Cowpea [*Vigna unguiculata* (L.) Walp.] Genotypes For Resistance to *Striga gesneroides*

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Abstract

Original Research Article

Cowpea is the most widely cultivated legume in West Africa as staple food and income source. However, parasitic weed (*Striga gesneroides*) remains a major constraint on farmers' fields leading to significant seasonal losses. Identifying superior genotypes that combine high levels of resistance to *Striga* with improved agronomic attributes is crucial for commercialization. The objective of this study was to assess a panel of cowpea germplasm and identify superior cowpea genotypes that combines improved agronomic attributes with adequate *Striga* resistance for recommendation to SSA farmers. One hundred and eighty-eight cowpea accessions assembled from five west African gene banks were evaluated for three seasons using an augmented experimental design. Significant variation was observed ($p < 0.01$) in the performance of the cowpea accessions for all the traits measured. Moderate to high broad-sense heritability was observed for all traits except for pod weight and number of seeds per pod. *Striga* adaptive traits showed negative correlations with yield related traits. Using the multi-trait genotype-ideotype distance index (MGIDI), 28 superior potential genotypes were identified with improved *Striga* resistance and agronomic attributes among which 11 have not been realized. These promising genotypes could be explored as progenitors in cowpea improvement programs targeting *Striga* resistance improvement to develop cowpea genotype with improved levels of resistance to *Striga* for commercialization in the Sahelian and Savanna regions of Africa.

Keywords: Agronomic quality traits, Cowpea, multi-trait genotype-ideotype distance index, *Striga gesneroides* resistance, Strength and Weakness plot.

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1. INTRODUCTION

Native to Africa, cowpea [*Vigna unguiculata* (L.) Walp.] holds significant economic importance as a grain legume. Rich in protein, it serves as a key source of food for both humans and animals, and plays a vital role in regional trade within sub-Saharan Africa (SSA) (Langyintuo *et al.*, 2003). Due to the relatively high protein content, cowpea serves as an essential dietary supplement for various African populations whose staple foods are high in fiber and carbohydrates but deficient in protein (Abebe & Alemayehu, 2022). Packed with plant protein and essential minerals, like iron and zinc, cowpea offers an affordable way to address the problem of malnutrition in rural communities (Okonya & Maass, 2014). In addition to dietary importance, cowpea

contribute to soil fertility by providing adequate cover to the soil, which limit erosion, and by fixing atmospheric nitrogen. This is particularly crucial in smallholder farming systems where farming is characterized by limited or no fertilizers (Kyei-Boahen *et al.*, 2017). Cowpea stands out among staple food crops for its exceptional tolerance to the frequent droughts that plague the Sahelian and Savannah regions. This remarkable characteristic makes it a highly suitable choice for cultivation in countries with limited annual rainfall (Agbicodo *et al.*, 2009). The area dedicated to cowpea cultivation worldwide has seen a substantial growth over the past five decades, increasing from 2.5 to 14 million hectares that yielded more than 8 million tons annually (FAOSTAT, 2022). Nigeria is the major

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cowpea grower contributing about 40 % to 50 % of the global production, with an annual production of more than 3 million tons on 5 million hectares. Niger republic is ranked second with more than 2 million tons on similar hectareage of land (FAOSTAT, 2022).

In major cowpea growing areas such as Niger, cowpea production is far below the crop's potential (3 tons/ha) due to several limiting factors (Omomowo & Babalola, 2021). On farmers' fields in the Sahelian and Savannah regions of SSA, realizable yield is between 0.3 and 0.5 tons/ha. Of the constraints to the productivity, parasitic weed *Striga gesnerioides*, an obligate root-parasitic flowering plant has been reported as a major problem on several farmers' fields. *Striga* threat in sub-Saharan is intensified by its exquisite adaptation to the semi-arid tropics' climatic conditions, high reproductive capacity, and the longevity of seed reserves in tropical soils (Ejeta & Butler, 2015).

Among parasitic flowering plant, *Striga* species like *S. gesnerioides* (targeting legumes), *S. hermonthica* (Del.) Benth and *S. asiatica* (L.) Kuntze (targeting cereals) poses a great threat to sustainable food production in tropical and subtropical regions. These parasitic plants infest an estimated 100 million hectares of African savannas annually causing significant damage (Ejeta & Butler, 2015). *Striga* threat has gained a major attention since early 1970's as more and more people need food and farmers start using the land more intensively (Sadda *et al.*, 2021). *Striga* population has increased with monocropping, abandonment or reduction of fallows, soil fertility degradation and the introduction of exogenous germplasm that had not evolved under *Striga* pressure (Dubé & Olivier, 2011). Yield losses between 30 and 59 % in cowpea cultivars have been reported in Burkina Faso and Northern Ghana (Leandre *et al.*, 2018). Severe *Striga* infestations can lead to total crop failure. Considering the ongoing production challenges, there is a need to evaluate cowpea germplasm to select best performing genotypes with resistance to this parasitic weed and improved agronomic and quality attributes (Abdou Razakou *et al.*, 2017).

Thus, the objective of the study was to assess a panel of cowpea germplasm for selection of desirable genotypes/ideotypes combining resistance to *S. gesnerioides* with improved grain yield and related traits and identify stable cowpea genotypes that could be recommended for cultivation in Sahelian and Savanna regions of Africa.

2. MATERIALS AND METHODS

2.1. Germplasm, site description, and experimental design

One hundred and eighty-eight cowpea accessions collected from five different West African gene banks (Niger, Nigeria, Ghana, Senegal and Burkina Faso) were assessed under natural *Striga* infested field at Manga, research station. The research field area falls within latitudes 10° and 11° North and longitudes 0° and 1° west, with an altitude of 224 m above the sea level, near Bawku, Upper East, Ghana. The germplasm collection consists of landraces and breeding cowpea materials from Burkina Faso (9), Ghana (42), Niger (25), Nigeria (26), Senegal (71), Uganda (9), India (4), and USA (2). Seeds from each genotype were sown in rows of 2.2 meters with a 1-meter alley and 0.2 m within rows. Seeds were sown at 2 seeds per hole giving a total of 25 seeds per plot. The experiment followed a row/column design with one replication and augmented representation of four checks (WangKae, Kirkhouse, IT90K-372-2-1 and Apagbaala). The experiment was conducted for three seasons from 2021 to 2023. In addition to experiment conduct in Manga research station, in 2022, the cowpea germplasm was also evaluated at Kalapate Ngounga, Dosso (13°12'0" N, 2°57'0" E), and at Ndounga, Kollo, Tillaberi (13° 20' 30" N, 2° 19' 00" E), Niger republic in 2023. All the three trials were conducted under rainfed conditions. Lists of evaluated germplasm are provided in Appendix 1.

2.2 Data Collection

During the evaluation, data were collected on yield, related parameters, and *Striga* indicator traits as detailed in Table 1.

Table 1: List of data collected on yield, related traits, and *Striga* indicator traits

Trait	Trait type	Collection Period	Collection Method
Days to first flowering (DFFA)	QTT	From 30 days after planting	Visual observation, early in the morning
<i>Striga</i> resistance status (SRS)	QLT	From 30 days after planting	Presence or absence of <i>Striga</i> on the plot
number of <i>Striga</i> per plot (NSPlot),	QTT	Nine weeks after planting	Counting the number of <i>Striga</i> per plot
Plant Aspect (PASP)	QLT	Nine weeks after planting	1 means bad and 5 means good
Number of peduncles per plant	QTT	ten weeks after planting	10 plants are chosen per plot
Number of pod per peduncles (NPedPod)	QTT	ten weeks after planting	10 plants are chosen per plot
Pod length (PL)	QTT	At harvest 90 days after planting	Measured using a ruler
Number seed per pod	QTT	At harvest 90 days after planting	Counting the number of seed on ten pod per plot
Pod weight (PW)	QTT	At harvest 90 days after planting	Measured using weighing balance
Seed weight (SW)	QTT	At harvest 90 days after planting	Total seed harvested after threshing
fodder weight (FW)	QTT	At harvest	Weighing the total dry matter after pod harvested

QTT : Quantitative trait ; QLT : Qualitative trait

2.3. DATA ANALYSIS

Analysis of variance (ANOVA) was conducted using the augmented RCBD package (Aravind *et al.*, 2015) in R (R Core, 2020). Variance components, genetic and phenotypic coefficient of variation (GCV & PCV) respectively, Broad-sense heritability estimates (H^2), and the Best Linear Unbiased Estimates (BLUE) for each trait were also extracted from the final analysis. The H^2 was classified as low (<30 %), medium (30 – 60 %), and high (> 60%) (Johnson *et al.*, 1955). The PCV and GCV values greater than 20% were rated as high, between 10 and 20 % as medium, and lower than 10% as low (Deshmukh *et al.*, 1986). Pearson correlation coefficient was determined among traits using Corrplot R package (R Core, 2020) to identify the pattern and magnitude of traits relationship. To pinpoint the traits that contribute most to the observed genetic variation, the principal component analysis (PCA) was conducted using FactoMineR package in R (R Core, 2020). To identify cowpea ideotypes that combine *Striga* resistance with improved agronomic traits, The Multi-Traits Genotype-ideotype Distance Index (MGIDI) suggested by (Olivoto & Nardino, 2021) was used. MGIDI is based on four principles starting from rescaling the traits so that they all have a 0-100 range, factor analysis to account for the correlation structure and data dimensionality reduction, planning of ideotype based known/desired trait values, and computing the distance between each genotype and planned ideotype. Traits rescaling was done using the formula below.

$$rX_{ij} = \frac{\eta_{nj} - \varphi_{nj}}{\eta_{oj} - \varphi_{oj}} * (\theta_{ij} - \eta_{nj}) + \eta_{nj}$$

Where: η_{nj} and φ_{nj} are the new maximum and minimum values for the trait j after rescaling, respectively; φ_{oj} and η_{oj} are the original maximum and minimum values for the trait j , respectively, and θ_{ij} is the original value for the j th trait of the i th genotype/treatment.

The values for η_{nj} and φ_{nj} were chosen as follows. For the traits in which negative gains are desired $\eta_{nj} = 0$ and $\varphi_{nj} = 100$ was used. For the traits in which positive gains are desired then, $\eta_{nj} = 100$ and $\varphi_{nj} = 0$ was used (Olivoto & Nardino, 2021); (Olivoto & Lúcio, 2020). In the rescaled two-way table (rX_{ij}), each column has a 0–100 range that considers the desired sense of selection (increase or decrease) and maintains the correlation structure of the original set of variables.

The factorial scores of each genotype was estimated using the rescaled values after which factor analysis was computed to group correlated traits into factors as follows:

$$X = \mu + Lf + \mathcal{E}$$

Where X is a $p \times 1$ vector of rescaled observations; μ is a $p \times 1$ vector of standardized means; L is a $p \times f$ matrix of factorial loadings; f is a $p \times 1$ vector of common factors; and \mathcal{E} is a $p \times 1$ vector of residuals. Furthermore, the initial loadings were obtained by the traits having

more than one eigenvalue that is acquired from the correlation matrix of rX_{ij} .

Then, final loadings were estimated by using the varimax rotation criterion [13] below

$$F = Z(A^T R^{-1})^T$$

Where: F is a $g \times f$ matrix with the factorial scores; Z is a $g \times p$ matrix with the standardized means (rescaled); A is a $p \times f$ matrix of canonical loadings; and R is a $p \times p$ correlation matrix between the traits. g , f , and p denote the number of test genotypes, factors retained (FA), and traits analyzed, respectively.

Ideotype planning

Ideotype design (ID) assumed that the selected genotype has the highest rescaled value (i.e., 100) across the traits analyzed. Hence, the ID can be defined by $1 \times p$ vector ID such that $ID = [100, 100, \dots, 100]$. Additionally, ID final scores were calculated according to equation Z.

The MGIDI

The Multi-Trait Genotype-Ideotype Distance Index (MGIDI) facilitates the ranking of genotypes based on their performance across multiple traits. This index effectively addresses multicollinearity among traits by transforming them into uncorrelated principal components, thus preventing redundant weighting of correlated information. The MGIDI was calculated using the mgidi function within the metan package in R (Olivoto & Lúcio, 2020).

$$MGIDI_i = \left[\sum_{j=1}^f (\gamma_{ij} - \gamma_j)^2 \right]^{0.5}$$

Where γ_{ij} is the score of the i th genotype in the j th factor ($i = 1, 2, \dots, g$; $j = 1, 2, \dots, f$) and γ_j is the j th score of the ideotype. The genotypes with the lowest MGIDI values, i.e., genotypes closer to the ID, exhibited the desired values for all the traits under study.

The proportion of the MGIDI index of the i th genotype explained by the j th factor (ω_{ij}) explained the strengths and weaknesses of each genotype as shown below:

$\omega_{ij} =$

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=i}^f \sqrt{D_{ij}^2}}$$

Where D_{ij} is the distance between the i th genotype and the ideotype for the j th factor. Low contributions of a factor specify that the traits within that factor are similar to the ideotype designed.

The fmsb package (Rocha *et al.*, 2018) implemented in R was used to construct the radar chart.

The predicted genetic gain SG (%) was computed from the MGIDI index for each trait considering $\alpha\%$ selection intensity as follows:

$$SG (\%) = \frac{(\bar{X}_s - \bar{X}_o)h^2}{\bar{X}_o}$$

Where: \bar{X}_s is the mean of the selected genotypes, \bar{X}_o is the mean of the original population, and h^2 is the heritability.

3. RESULTS

3.1 Variability in agronomic traits

The Analysis of variance (ANOVA) revealed significant differences ($p < 0.001$) among cowpea genotypes for the assessed agronomic traits (Table 2). The Block effect was significant for all traits except for number of peduncles per plant (NPed). However, the interaction between treatment vs checks was significant ($p < 0.001$) for days to first flowering (DFFA), *Striga* resistance status (SRS), Number of pods per peduncle, and pod length (PL).

The average pod weight per plot, was 192.14 g/plot (873 kg/ha), ranging from 20.59 g/plot to 361.39 (50 to 2 840 kg/ha), while the average number of *Striga* plant per plot was 11 (range: 0 – 70). The average number of days to first flowering was 40, starting for 33 to 55 days and the fodder weight per plot showed an average of 0.54 kg/plot (2.47 t/ha), ranging from 0.08 kg/plot to 2.14 kg/plot (0.4 to 11.54 t/ha). For plant aspect at 9 weeks after planting, the average score observed was 2.56, ranging from 1.33 for the worst looking plot and 4 for the best-looking plot. For the number of peduncles bearing pod per plant the average was 4.20 (range: 1 - 11.46). The average number of pods per peduncles counted was 10.5 (range: 3.46 - 22.06). For pod length, the average was 14.23 (range: 9.75 - 18.60). For the number of seeds per pods, the average was 11 (range: 6.5 to 15.5). The coefficient of variation varied from 10.32% for the number of days to first flowering to 122.40 % for the number of *Striga* plant per plot indicating a high level of diversity among genotypes (Table 1).

Table 2: Mean squares and mean performance of agronomic traits of 188 cowpea accession evaluated under *Striga*-infested research conditions

Source of variation	Df	DFFA	NSPlot	Nped	NPodPed	NSPod	PW	SW	FW
Block (ignoring Treatments)	36	215.34***	3338.37***	17.55ns	105.38**	44.43***	240488***	96195***	1.43**
Treatment (eliminating Blocks)	187	51.57***	476.05ns	7.03ns	37.54**	7.58ns	12347.92ns	6374.96ns	0.24ns
Treatment: Check	3	206.5***	262.39ns	19.79ns	371.58***	7.64ns	20925.61ns	15281.82ns	0.19ns
Treatment: Test and Test vs. Check	184	49.05***	479.53ns	6.82ns	32.09ns	7.58ns	12208.07ns	6229.74ns	0.24ns
Residuals	409	10.99	459.05	18.03	26.56	6.71	16947.51	8566.96	0.35
Mean		40.32	10.75	4.2	10.50	10.96	192.14	119.82	0.54
Min		33	0	1	3.46	6.46	20.59	12.45	0.08
Max		54.66	70	11.46	22.06	15.53	361.39	248.52	2.14
CV		10.31	122.39	35.81	31.41	14.86	37.54	41.83	54.22

*, **, *** significant at $p < 0.05$, $p < 0.01$, and $p < 0.001$ respectively. DFFA: days to first flowering; NSPlot: number of *Striga* per plot; Nped: number of peduncles per plant; NPodPed: number of pods per peduncle; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight.

3.2. Genetic variability and broad-sense heritability of agronomic traits

Genotypic and phenotypic variance components, genotypic and phenotypic coefficients of variations (GCA and PCV), and broad-sense heritability of evaluated traits were presented in Table 3. The GCV ranged from low to high. The lowest observable GCV (10.52) was for number of seeds per pod and the highest (94.23) was for *Striga* resistance status. The H^2 estimates ranged from 13 % for number of *Striga* per plot to 79 % for days to first flowering. Other than DFFA, low to moderate H^2 were obtained for the other traits (Table 3).

3.3. Dimensional reduction analysis

The principal component analysis revealed that the first four PC with Eigen values higher than unity accounted for 73.5% of the total phenotypic variance. Of this total variance, the first PC explained 32% and the variation was associated with PASP, Nped, NPodPed, PW, and SW. The second PC accounted for 16% of the

total variability and it is associated with PL, NSPod, and FW. The third PC accounted for 14% of the total variation and it is associated with DFFA only. The fourth PC explained 11% of the observed variability and was associated with NSPlot and *Striga*_S (Table 4).

The variable contribution plot (Figure 1) of PC1 and PC2 which accounted for 49% of the total variability revealed that PW, SW, and NSPod that form the yield-related traits had strong contributions to the observed variability for these PCs. In addition, FW, PL, PASP, Nped, and NPodPed had intermediate level of contribution while DFFA, NSPlot, and *Striga*_S had minimum levels of contribution to these PCs.

3.4. Relationships among studied traits

The Pearson's correlation coefficients presented in Figure 2 revealed a significant positive correlation between PASP with PL ($p < 0.001$, $r = 0.41$) and PW ($p < 0.001$, $r = 0.57$) but negatively correlated

with NSPlot ($p < 0.001$, $r = -0.25$) and DFFA ($p < 0.001$, $r = -0.40$). In addition, *Striga*_S has a negative significant correlation with NSPod ($p < 0.001$, $r = -0.19$) and NsPlot ($p < 0.001$, $r = -0.48$). The yield-related traits FW, NSPod, SW, NPodPed, NPed, and PW all have positive

and significant correlations. Positive correlations suggest a similar direction in trait expression while negative correlations suggest the opposite direction in trait expression.

Table 2: Genotypic coefficients, phenotypic coefficients, and broad sense heritability of agronomic traits

.	δ^2P	δ^2G	GCV.	PCV	H ²
DFFA	52.02	41.03	15.89	17.89	78.88
NSPlot	528.15	69.1	76.23	95.74	13.08
<i>Striga</i> _S	0.31	0.18	94.23	96.94	56.27
PASP	0.67	0.12	13.38	31.8	17.7
NPed	6.83	2.85	22.03	14.11	41.04
NPodPed	31.55	4.99	21.27	53.46	15.83
PL	8	4.7	15.23	19.87	58.77
NSPod	8.04	1.33	10.52	25.86	16.54
PW	15791.12	NA	NA	65.4	NA
SW	7586.78	NA	NA	72.69	NA
FW	0.27	NA	NA	94.79	NA

δ^2P : phenotypic variance; δ^2G : genotypic variance; GCV: genotypic coefficient of variance; PCV: phenotypic coefficient of variation; H²: heritability; DFFA: days to first flowering; NSPlot: number of *Striga* per plot; *Striga*_S: *Striga* Resistance Status, PASP: plant

aspect; NPed: number of peduncles per plant; NPodPed: number of pods per peduncle; PL: pod length; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight.

Table 3: Principal Component Analysis of the Studied Traits

Trait	Dim1	Dim2	Dim3	Dim4	Dim5
DFFA	-0.22	0.33	0.64	0.44	0.25
NSPlot	-0.49	0.13	0.37	-0.52	0.19
<i>Striga</i> _S	0.41	-0.27	-0.37	0.59	0.27
PASP	0.70	0.09	-0.43	-0.26	0.13
NPed	0.59	-0.37	0.49	-0.05	0.32
NPodPed	0.71	-0.34	0.47	-0.07	0.16
PL	0.25	0.53	-0.37	-0.26	0.60
NSPod	0.19	0.78	0.20	-0.11	-0.13
PW	0.91	0.16	0.08	-0.09	-0.26
SW	0.90	0.14	0.14	-0.06	-0.27
FW	0.16	0.63	0.04	0.49	-0.02
Eigen	3.55	1.79	1.53	1.21	0.83
Variance (%)	32.27	16.25	13.93	11.01	7.50
Cumulative (%)	32.27	48.53	62.45	73.47	80.97

Dim: Dimension; DFFA: days to first flowering; NSPlot: number of *Striga* per plot; *Striga*_S: *Striga* Resistance Status, PASP: plant aspect; NPed: number of peduncles per plant; NPodPed: number of pods per peduncle; PL: pod length; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight.

3.5. Selection of cowpea genotypes combining *Striga* resistance with improved agronomic potential based on multi-trait genotype-ideotype distance index (MGIDI)

The best-performing cowpea genotypes combining *Striga* resistance with improved agronomic attributes were identified using the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), following a factor analysis (FA) for partitioning the studied traits and cowpea genotypes (Table 5 and Supplementary

Table S1). Based on the MGIDI analysis, traits were grouped into four factors.

Factor 1 (FA1) was primarily associated with Number of Peduncles (NPed) (loading: 0.83), Number of Pods per Peduncle (NPodPed) (loading: 0.91), Pod Weight (PW) (loading: 0.72), and Seed Weight (SW) (loading: 0.75). The predicted genetic gains for these traits were 19.70%, 22.55%, 51.27%, and 56.34%, respectively. All these traits had a 'desired increase' sense, aligning perfectly with the breeding goal of 100%.

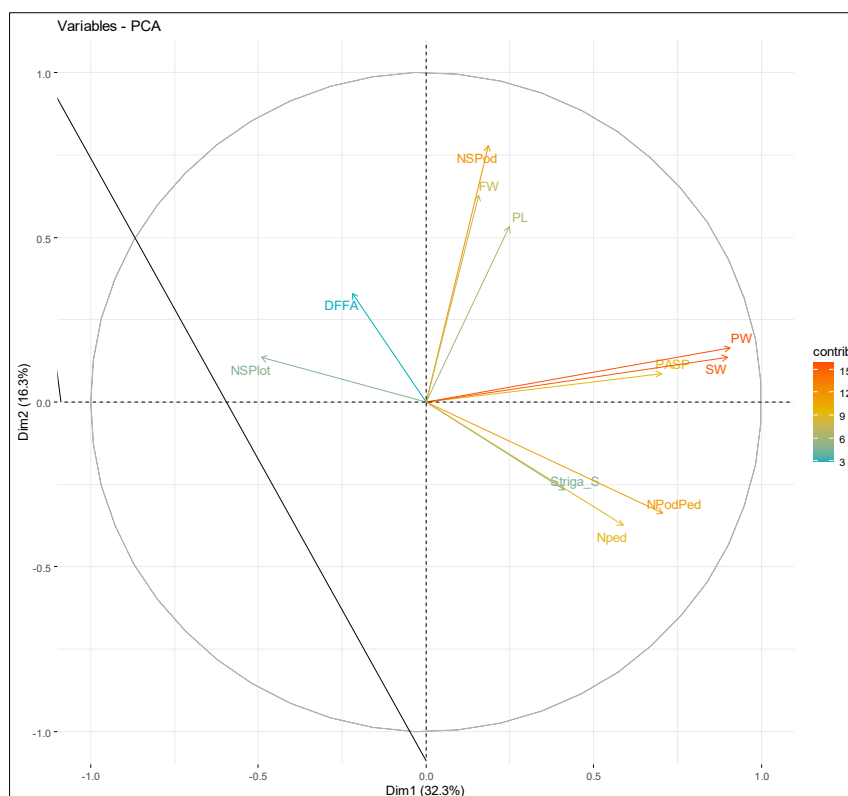


Figure 1: Variable contribution biplot view of the studied traits. DFFA: days to first flowering; NSPlot: number of Striga per plot; Striga_S: Striga Resistance Status, PASP: plant aspect; NPed: number of peduncles per plant; NPodPed: number of pods per peduncle; PL: pod length; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight

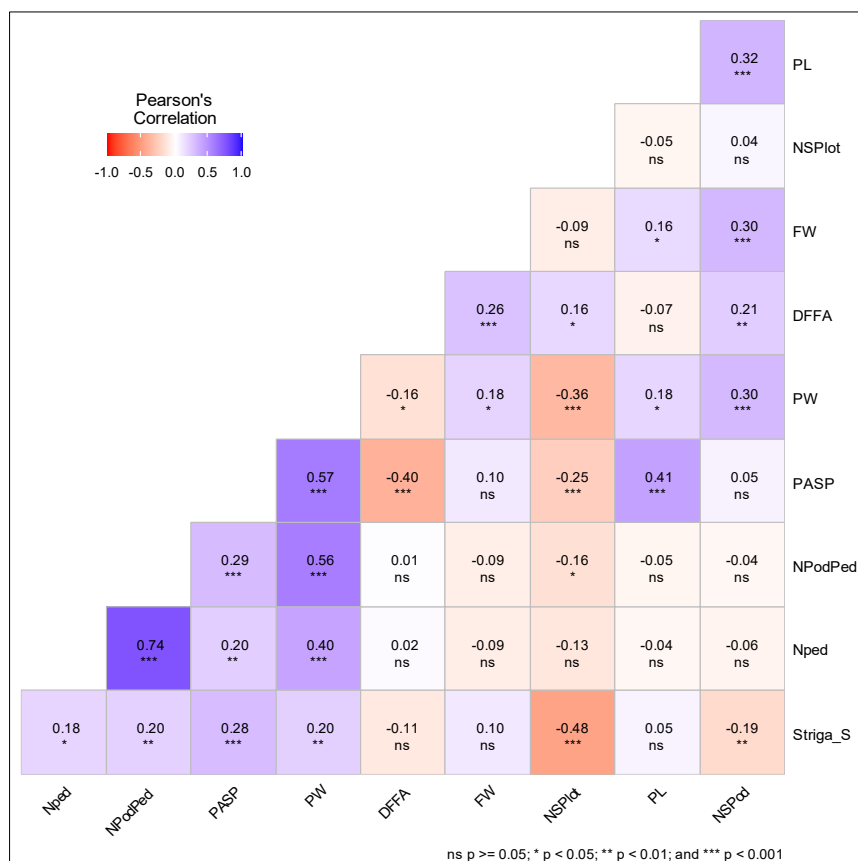


Figure 2: Correlation coefficients among studied traits. DFFA: days to first flowering; NSPlot: number of Striga per plot; Striga_S: Striga Resistance Status, PASP: plant aspect; NPed: number of peduncles per plant; NPodPed: number of pods per peduncle; PL: pod length; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight

Factor 2 (FA2) showed strong associations with Fresh Weight (FW) (loading: 0.77) and Number of Seeds per Pod (NSPod) (loading: 0.70), along with a negative loading for Days to First Flower Appearance (DFFA) (loading: -0.64). The predicted genetic gains for FW and NSPod were 26.89% and 14.83%, respectively, both with a 'desired increase' sense, achieving a 100% goal. Conversely, DFFA, despite a predicted genetic gain of 1.21%, had a 'desired decrease' sense, resulting in a 0% goal for this trait.

Factor 3 (FA3) was predominantly associated with Plant Aspect (PASP) (loading: 0.76) and Plant Length (PL) (loading: 0.68). The predicted genetic gains were 15.85% for PASP and 6.36% for PL. Both traits had

a 'desired increase' sense, perfectly aligning with the breeding goal of 100%.

Factor 4 (FA4) was primarily associated with Number of Striga Plants per Plot (NSPlot) (loading: 0.78) and Striga Syndrome (Striga_S) (loading: -0.85). The predicted genetic gains for these traits were -38.67% and -19.64%, respectively. While NSPlot had a 'desired decrease' sense, leading to a 100% goal, Striga_S, despite its negative predicted gain, also had a 'desired decrease' sense, resulting in a 100% goal.

The MGIDI analysis ultimately identified 28 superior cowpea genotypes (Figure 3.3) that successfully combined improved Striga resistance with enhanced agronomic attributes.

Table 4: Factorial loadings, population mean, selected genotypes mean, predicted genetic gain, trait sense, and goal from multi-traits genotype-ideotype distance index

VAR	FA1	FA2	FA3	FA4	Xo	Xs	GG%	Sense	Goal
DFFA	-0.05	-0.64	0.58	0.14	40.32	40.81	1.21	decrease	0
FW	-0.08	0.77	0.06	0.25	0.54	0.69	26.89	increase	100
Nped	0.83	-0.12	-0.13	0.05	4.20	5.03	19.70	increase	100
NPodPed	0.91	-0.09	-0.04	0.08	10.51	12.88	22.55	increase	100
NSPlot	0.14	0.05	0.15	0.78	10.75	6.60	-38.67	decrease	100
NSPod	0.08	0.70	0.33	-0.30	10.96	12.59	14.83	increase	100
PASP	0.31	-0.09	0.76	0.26	2.57	2.98	15.85	increase	100
PL	-0.12	0.26	0.68	-0.05	14.23	15.13	6.36	increase	100
PW	0.72	0.23	0.50	0.20	192.15	290.65	51.27	increase	100
Striga S	-0.11	0.04	-0.02	-0.85	0.27	0.21	-19.64	decrease	100
SW	0.75	0.24	0.44	0.20	119.82	187.33	56.34	increase	100

FA: factor analysis; DFFA: days to first flowering; NSPlot: number of *Striga* per plot; *Striga_S*: *Striga* Resistance Status, PASP: plant aspect; Nped: number of peduncles per plant; NPodPed: number of pods per peduncle; PL: pod length; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight.

Table 5: Factorial loadings, communality, uniqueness, predicted genetic gain, trait sense, and goal from multi-traits genotype-ideotype distance index

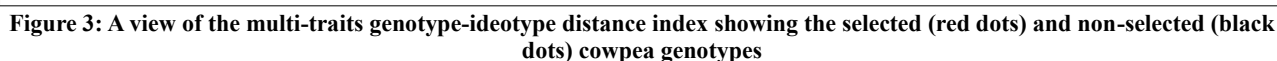
VAR	FA1	FA2	FA3	FA4	Communality	Uniquenesses	GG%	Sense	Goal
DFFA	-0.01	0.79	0.13	-0.36	0.78	0.22	-5.05	decrease	100
FW	-0.08	-0.04	-0.81	-0.24	0.73	0.27	24.21	Increase	100
Nped	-0.09	-0.34	0.04	0.77	0.72	0.28	0.17	Increase	100
NPodPed	0.23	-0.20	0.01	0.83	0.77	0.23	8.19	Increase	100
NSPlot	-0.05	0.09	0.29	0.52	0.36	0.64	-50.68	decrease	100
NSPod	-0.69	0.22	0.31	-0.32	0.72	0.28	-1.06	Increase	0
PASP	0.18	0.65	-0.59	0.07	0.81	0.19	11.98	Increase	100
PL	-0.79	0.23	-0.21	0.11	0.73	0.27	8.62	Increase	100
PW	0.84	0.35	-0.05	0.14	0.86	0.14	2.54	Increase	100
Striga S	-0.27	-0.01	-0.04	-0.83	0.76	0.24	55.43	decrease	0
SW	0.89	0.19	0.00	0.12	0.84	0.16	-6.36	Increase	0

DFFA: days to first flowering; NSPlot: number of *Striga* per plot; *Striga_S*: *Striga* Resistance Status, PASP: plant aspect; Nped: number of peduncles per plant; NPodPed: number of pods per peduncle; PL: pod length; NSPod: number of seeds per pod; PW: pod weight; SW: seed weight, FW: fodder weight.

3.6. Strength and Weakness of Selected Cowpea Genotypes

Following selection of the ideotypes, the final factorial loadings of the studied traits revealed that FA1 correlates with four yield-related traits (NSPod, PL, PW, and SW) while FA2 correlates with flowering (DFFA)

and *Striga* damage (PASP). The FA3 correlates with FW while the FA4 correlates with Nped, NPodPed, NSPlot, and *Striga_S* (Table 6). The strength and weakness view (fig. 4) of the selected 28 genotypes revealed that L73, L79, L9, L13, L14, L18, L20, L21, L26, L31, L38, and L42 had strength for FA1 associated traits i.e. they



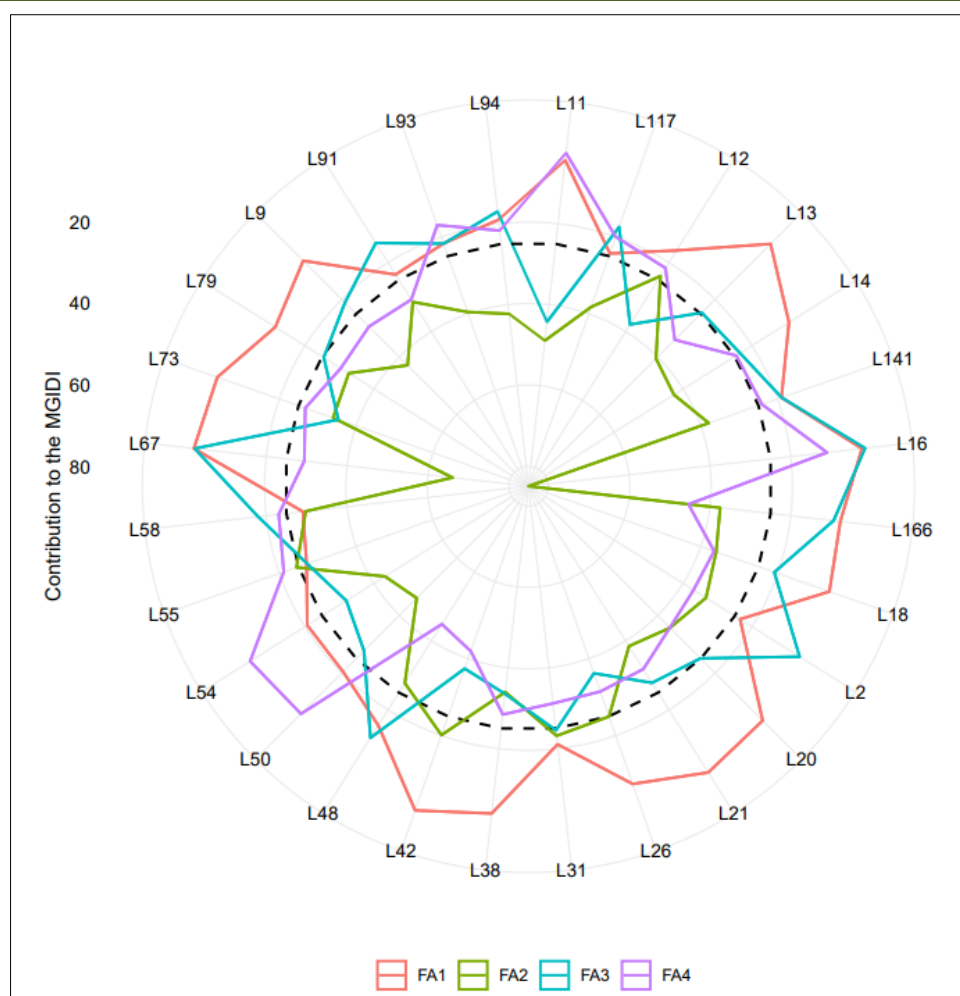


Figure 4: Strengths and weaknesses of the selected genotypes in each family based on MGIDI analysis. The black dashed line at the centre displays the theoretical value if all the factors contributed equally

4. DISCUSSION

This study comprehensively assessed the performance of 188 cowpea varieties across eleven key phenotypic traits. In plant breeding, a fundamental objective is to develop or identify ideal genotypes (ideotypes) that integrate multiple desirable attributes, thereby enhancing overall performance. Achieving this complex goal, particularly when considering numerous traits simultaneously, necessitates sophisticated selection methodologies. While selection has traditionally been practiced based on single traits, the need for efficient multi-trait selection has led to the development of various advanced models (Ribaut & Hoisington, 1998).

Plant breeding process often involves two stages: first, creating the genetic variability by crossing diverse parents, and then selecting the most desirable plants from the resulting offspring (segregating populations) (Ribaut & Betrán, 1999). In the present experiment, several multi-variate analyses were used to dissect the variability within the population of cowpea varieties assessed using eleven traits comprising *Striga* adaptive, yield, and related traits before the best performing genotypes were selected. The ANOVA revealed significant variations among genotypes across

the observed traits indicating high level of variability among genotypes, which could permit gains from selection. Similar observation was reported in a panel of cowpea accession evaluated for yield and yield components by Araújo *et al.*, (2021), Sanogo *et al.*, (2023), and Torres *et al.*, (2016).

Moderate to high broad-sense heritability estimates observed for pod length, number of peduncles, *Striga* status, flowering information indicated that these traits are mainly under genetic control with minimal environmental influence. Thus, there is possibility to observe faster response to selection. Conversely, for traits exhibiting lower heritability estimates, including number of *Striga* plants per plot, plant aspect, number of pods per peduncle, and number of seeds per pod, achieving genetic improvement may benefit from strategies such as increasing selection intensity, evaluating larger populations, improving phenotyping accuracy, or employing marker-assisted selection (MAS) to enhance selection efficiency.

Understanding the correlation between different traits is very valuable in a breeding program (Krstić *et al.*, 2022) as it provides information on traits relationship

that could be exploited by breeders for indirect selection. For *Striga* resistance breeding, a major concern is the variation in the *Striga* strains and recombination that occurs in the resistant lines. Indirect selection for correlated traits provides great opportunity in identifying cowpea genotypes that possess *Striga* resistance in the absence of *Striga* strains or hotspot for adequate evaluation. In the present study, Pearson correlation analysis revealed the possibility of indirect selection for traits that showed positive correlation, such as yield and its related traits (pod weight, number of seeds per pod, number of peduncles per plant, and number of pods per peduncles) with resistance to *Striga* adaptive traits. Positive correlation between high yield and yield related traits such as drought tolerance, *Striga* resistance, number of leaves per plant have been found by several cowpea breeders (Sanogo *et al.*, 2023); (Nwofia *et al.*, 2012); (Owusu *et al.*, 2021). Negative correlation was also observed between fodder weight and number of *Striga* per plot and susceptibility to *Striga*. Such correlation demonstrates the reality observed on farmer's field. This relationship suggests that fodder weight decreases with increasing susceptibility of the genotype and *Striga* count. Improving *Striga* resistance in cowpea is an ongoing battle for researchers and cowpea breeders, these findings are similar to that of Tchiagam *et al.*, (2010).

Identifying genotypes that effectively combine multiple desirable traits (ideotype) is a major challenge in crop improvement (Yadav *et al.*, 2023). Several methodologies including but not limited to the use of base-index and clustering techniques have been developed and used to facilitate the identification and selection of crop ideotype. However, none of these methods has proven to be very effective without a drawback. A practical example is the several fashions of base-index stemming from the popular Smith-Hazel index (Jahufer & Casler, 2015). The weakness of base-index is often the difficulty in handling multicollinearity which often arise from perfectly correlated traits (Olivoto & Nardino, 2021). The MGIDI is a unique selection method that offers a more efficient technique in identification and selection of crop ideotype while considering multicollinearity among traits. In addition, it provides information about the strength and weakness of each ideotype, which is a valuable information to the breeders. In this study, MGIDI was used to identify 28 superior genotypes from the 188 cowpea accessions assembled evaluated. These selected genotypes notably combine enhanced *Striga* resistance with improved agronomic attributes. The utility of the MGIDI for similar multi-trait selection purposes has also been demonstrated in other crops, such as *Dioscorea* species (Adewumi *et al.*, 2023 ; Norman *et al.*, 2022). The graphical depiction of the strengths and weakness of the chosen genotypes from the MGIDI index is an important tool that indicates the proportional contribution of each factor towards selection of best performing genotypes. The availability of such information on the weaknesses

and strengths of genotypes assists breeders in selecting putative parents in their breeding programs.

5. CONCLUSION

This study comprehensively assessed 188 diverse cowpea accessions based on eleven phenotypic traits, comprising eight agronomic and three *Striga* indicator attributes. Significant genetic variation existed within the 188-cowpea germplasm, a critical prerequisite for effective breeding. Moderate to high broad-sense heritability estimates were observed for the majority of the evaluated traits, indicating their strong genetic control and responsiveness to selection. Furthermore, correlation analysis identified specific trait relationships useful for indirect selection in cowpea improvement. Notably, positive correlations were observed between *Striga* adaptive traits and key yield components such as pod weight, number of seeds per pod, and number of peduncles per plant. This suggests a promising avenue for simultaneously improving both yield and *Striga* resistance. Utilizing MGIDI, as a robust selection method, 28 superior cowpea accessions were successfully identified among them 11 (L31, L11, L38, L9, L48, L5, L50, L53, L54, L117, L18) have not been released. These genotypes represent an optimal combination of enhanced *Striga* resistance and improved agronomic attributes. These promising genotypes are valuable progenitors for future cowpea improvement programs, providing a strong genetic foundation to develop new, high-yielding varieties with superior *Striga* resistance for the benefit of farmers in *Striga*-endemic regions. Strategic inter-crossing among these identified superior lines will be crucial to exploit heterosis and combine complementary desirable traits, thereby accelerating the development of more resilient and productive cowpea varieties.

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Availability of data and materials

The data used in this study can be obtained upon request from the corresponding author available on aliabkoura@gmail.com

Declarations Ethics approval and consent to participate

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review & editing, Bassirou Sani Boubacar Gaoh: Writing – review & editing. Ousmane Boukar: Supervision, review & editing. Harouna Issa Amadou; Writing, review & editing. Richard Abromah: Supervision, Writing, review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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