

Research Article

MULTI-TRAIT SELECTION FOR YIELD, EARLINESS, AND SEED SIZE IN A COWPEA (*VIGNA UNGUICULATA*) MAGIC POPULATION: AMMI, WAASB, AND MTSI ANALYSES ACROSS SIX ENVIRONMENTS IN BURKINA FASO

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ABSTRACT

Cowpea is widely cultivated legume in Burkina Faso. However, rainfall fluctuation and soil poverty are major constraints to its production. This study aimed to identify superior cowpea genotypes combining favorable agronomic traits and earliness. To achieve this, 52 MAGIC genotypes and two checks were planted using an alpha lattice design with two replications at Kamboinsé, Farako-Bâ, and Saria during the 2019 and 2022 rainy seasons. The likelihood ratio test applied to the restricted maximum likelihood model showed a significant genotype $\times$ environment interaction for grain yield, hundred-seed weight, and days to 95% maturity. Heritability on genotype-mean basis (h^2_{mg}), reflecting genotypic efficiency in multi-environment trials, was low for grain yield (0.28) and high for maturity (0.67) and hundred-seed weight (0.77). AMMI analysis revealed significant mean squares for the first four interaction principal components, with the first two axes explaining 71.8% of the variance for maturity, 69.9% for yield, and 63.7% for HSW. A combined statistical analysis of stability revealed stable yield performance in G46, G29, G16, and G53 stable earliness in G12, and stable seed size in G20, G22, and G65. Based on a multi-trait selection index, genotypes G16, G58, G65, G46, G33, and G12 emerged as stable ideotypes combining high grain yield and early maturity, G56 and G29 excelled for seed size. Overall, G16 (MAGIC061) and G46 (MAGIC228) were confirmed as the most promising candidates.

Keywords: Agronomic performance, Genotype, Cowpea production, Multi-Environment Trials, Trait stability.

INTRODUCTION

Cowpea (*Vigna unguiculata* L. Walp) is grown for both dry seeds and fodder. It provides a substantial amount of protein, carbohydrates, minerals, and vitamins (Sombie *et al.*, 2018; Affrifah *et al.*, 2022) to millions of humans and domestic animals, contributing to nutritional security and well-being (Jayathilake *et al.*, 2018). Furthermore, the crop provides income to farmers (Dabat *et al.*, 2012). Beyond its nutritional value, the crop plays a significant role in soil fertility restoration through atmospheric nitrogen fixation, making it an excellent crop for rotation systems (Sánchez-Navarro *et al.*, 2019). Consequently, maximizing cowpea production is essential to ensure food security, quantity, and quality. However, production is severely constrained

by the impacts of climate change, including poor soil fertility, rainfall variability, and drought, as well as diseases and insect attacks. Indeed, cowpea is produced under marginal conditions within farming systems. In Burkina Faso, the estimated average yield of cowpea on farmers' fields is approximately 735 kg ha⁻¹ (DGESS/MARAH, 2024), whereas the potential of released varieties ranges between 1.5 and 2.5 t ha⁻¹ in West Africa (Boukar *et al.*, 2018). The yield gap between experimental cultivar trials and actual yields in farmers' fields has been estimated at more than 40% (reference required). This differential agronomic performance among genotypes is highly influenced by genotype-by-environment interaction (Batiéno *et al.*, 2025). Stability in yields of the genotypes is

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regarded as the ultimate goal in cowpea improvement (Kuruma *et al.*, 2019). However, improving cowpea productivity is often limited by its narrow genetic base (Batieno *et al.*, 2018). Then, multi-parental crosses coupled with the use of single nucleotide polymorphism (SNP) markers led to the development of Multi-parent Advanced Generation Inter-Cross (MAGIC) populations. Characterizing the response of these MAGIC genotypes across diverse environments is essential to select high-yielding and stable genotypes, minimizing genotype-environment interactions (GEI) and helping smallholder farmers to increase productivity across the target areas. To the best of our knowledge, no study in Burkina Faso has evaluated the multi-character stability of a MAGIC population of cowpea under Sudanian conditions, nor has compared AMMI, WAASB, and MTSI on this material. Multi-environment trials (METs), mostly employed to identify more stable and higher-yielding genotypes, can be analyzed using the Additive Main Effects and Multiplicative Interaction (AMMI) model (Mbeyagala *et al.*, 2021; Goa *et al.*, 2022). To complement this, the Weighted Average of Absolute Scores (WAASB) index and the WAASBY index offer a robust quantitative measure of genotypic stability that accounts for all significant IPCAs (Olivoto *et al.*, 2019). The multi-trait stability index (MTSI) has proven highly efficient for the

simultaneous selection of multiple traits (Abdou *et al.*, 2026; PS *et al.*, 2026). Therefore, this study aimed to identify superior cowpea MAGIC genotypes combining high grain yield, earliness, and medium seed size using AMMI, WAASB, and MTSI analyses across environments.

MATERIAL AND METHODS

Experimental Materials

The plant material comprised 54 cowpea genotypes, namely 52 lines drawn from a Multi-parent Advanced Generation Inter-Cross (MAGIC) population and two released checks (Komcallé and Niizwé), developed at INERA. The MAGIC population was derived from the intercrossing of 12 founder parents. The selection for seed size, yield, and resistance to insects and diseases was assisted with single nucleotide polymorphism (SNP) molecular markers in collaboration with the University of California, Riverside, and some other West African Research partners such as SARI-Ghana, ISRA-Senegal, and IITA Nigeria. Some individuals (G7, G8, G13, G14.) were excluded due to an insufficient germination rate observed during the multiplication stages. This is why the G codes are discontinuous.

Table S1. Plant material used: MAGIC lines and the checks (Komcallé and Niizwé).

Code	Genotypes	Statut	Code	Genotypes	Statut	Code	Genotypes	Statut
G1	Komcallé	Check	G23	MAGIC089	New	G46	MAGIC228	New
G2	MAGIC003	New	G25	MAGIC096	New	G47	MAGIC229	New
G3	MAGIC006	New	G26	MAGIC114	New	G48	MAGIC230	New
G4	MAGIC013	New	G27	MAGIC116	New	G49	MAGIC232	New
G5	MAGIC015	New	G28	MAGIC129	New	G51	MAGIC243	New
G6	MAGIC016	New	G29	MAGIC130	New	G52	MAGIC245	New
G9	MAGIC034	New	G31	MAGIC139	New	G53	MAGIC246	New
G10	MAGIC036	New	G32	MAGIC142	New	G55	MAGIC257	New
G11	MAGIC044	New	G33	MAGIC143	New	G56	MAGIC258	New
G12	MAGIC047	New	G34	MAGIC148	New	G57	MAGIC262	New
G15	MAGIC060	New	G35	MAGIC166	New	G58	MAGIC263	New
G16	MAGIC061	New	G36	MAGIC169	New	G59	MAGIC268	New
G17	MAGIC065	New	G37	MAGIC180	New	G61	MAGIC282	New
G18	MAGIC066	New	G38	MAGIC187	New	G62	MAGIC286	New
G19	MAGIC077	New	G39	MAGIC200	New	G63	MAGIC293	New
G20	MAGIC082	New	G40	MAGIC205	New	G64	MAGIC297	New
G21	MAGIC083	New	G43	MAGIC217	New	G65	MAGIC298	New
G22	MAGIC088	New	G45	MAGIC220	New	G66	Niizwé	Check

Experimental site and methods

Field experiments were conducted over 2 years (2019 and 2022) across three (3) research stations (Kamboinsé (E1), Saria (E2) and Farako-Bâ (E3)) (Table S1). Each year × location combination was considered as one environment, giving six environments (E1_2019, E2_2019, E3_2019,

E1_2022, E2_2022 and E3_2022). Kamboinsé (12°26' N, 1°33' W), Saria (12° 16' 0" N, 2° 9' 0" W) and Farako-Bâ (11° 04' 54" N, 4° 20' 29" W) are located in the Centre, Nando and Guiriko regions, respectively. The soils of Kamboinsé and Saria are classified as leached tropical ferruginous soils, whereas the soil of Farako-Bâ is a eutrophic tropical brown soil (Gnankambary, 2015). The

three locations received variable rainfall from July to September; Farako-Bâ recorded the highest cumulative rainfall, and rainfall was higher in 2022 than in 2019 (insert the cumulative rainfall and mean temperature values in Table S1). Planting was carried out on 16 July 2019 and 14 July 2022 at Kamboinsé; 17 July 2019 and 15 July 2022 at Saria; and 18 July 2019 and 15 July 2022 at Farako-Bâ. The trials were laid out in an alpha lattice design with two replications, incomplete blocks of six (6) blocks x 9 plots per replication. Each plot measured 3.2 m x 4 m and consisted of four 4-m-long rows, with a spacing of 0.80 m between rows and 0.40 m between plants. The distance between adjacent plots and replications was maintained at 0.8 m and 1.5 m, respectively. Two weeks after planting, NPK fertilizer (14-23-14) was applied at the rate recommended for cowpea production in Burkina Faso (100 kg ha⁻¹). Insect pests were controlled with two insecticide applications (Deltacal (deltamethrin) and K-Optimal 35 EC (Acetamiprid + Lambda-cyhalothrin) and the first at flower bud initiation and the second at pod setting. Additionally, two rounds of hand weeding were performed during the crop growing period.

Data collection

Data were collected for three quantitative traits, namely the number of days to 95% maturity (MAT), grain yield (Yield), and the hundred seed weight (HSW), recorded on the two middle rows, with the two outer rows being considered as borders. Days to 95% maturity were - as the number of days from sowing until 95% of the pods on a plot had reached physiological maturity. Grain yield was obtained by weighing the sun-dried threshed grain of the two middle rows, adjusted to 12 % moisture content and converted to kg ha⁻¹. Hundred-seed weight was measured on a random sample of 100 sound seeds per plot. These three traits are of major economic importance, match end-user preferences, and are known to be sensitive to environmental variation.

Data analysis

The collected data were subjected to a linear mixed model analysis using the restricted maximum likelihood (REML) method to estimate variance components and the best linear unbiased prediction (BLUP) method to predict genetic effects. The genotype (GEN) and the genotype-by-environment interaction (GEN: ENV) were modelled as random effects, whereas the environment, the replication within environment and the incomplete block within replication were modelled as fixed effects. The significance of the random effects was tested with a likelihood ratio test (LRT). Genotypic mean performance across environments was estimated using the BLUPs derived from the mixed model.

The model is expressed as:

$$Y_{ijk} = \mu + E_i + B_{k(i)} + G_j + GE_{ij} + \varepsilon_{ijk}$$

where: Y_{ijk} = observed phenotypic value of the i th genotype in the j th environment and the k th replication; μ = overall mean; E_j = fixed effect of the j th environment; $B_{k(j)}$ = effect

of the k th Block nested within the j th environment, G_j = effect of the i th genotype, GE_{ij} = genotype x environment interaction effect, ε_{ijk} = residual error associated with the observation.

Additive Main Effects and Multiplicative Interaction (AMMI) analysis was performed to extract significant principal component interactions (IPCA). To assess stability of yield and yield components, AMMI biplots were constructed, and the weighted average of absolute scores of the BLUP-based IPCAs (WAASB) was computed from all significant IPCAs (Olivoto *et al.*, 2019a). Genotypes with a lower WAASB value were considered stable, whereas those with a higher WAASB value were generally unstable. It was calculated using the following equation:

$$WAASBi = \frac{\sum_{k=1}^n (IPCA_{ik} \times EP_k)}{\sum_{k=1}^n EP_k}$$

Where EP_k is the portion of variation explained by the k th interaction principal component axis (IPCA) and $(IPCA_{ik})$ is the score of the i th genotype (or environment) in the k th IPCA

The WAASBY superiority index was computed using a 50/50 performance/stability weighting (Olivoto *et al.*, 2019a). It was calculated using the following equation

$$WAASBYi = \frac{(rGi \times \theta_y) + (rWi \times \theta_s)}{\theta_y + \theta_s}$$

Where θ_y and θ_s are the weights for the response variable and stability (WAASB).

Furthermore, a multi-trait stability index (MTSI) was computed using a selection intensity of approximately 15% to identify superior genotypes combining high performance and stability across all studied traits (Olivoto *et al.*, 2019b). The lower MTSI values indicate genotypes closer to the desired ideotype. All statistical analyses were performed with the metan package (Olivoto & Lúcio, 2020) in R version 4.5.0 (R Core Team, 2022).

RESULTS AND DISCUSSION

The descriptive statistics for grain yield, days to 95% maturity, and hundred-seed weight are presented in Table 2. In 2019, the number of days from sowing to physiological maturity significantly varied across locations, with Kamboinsé, Saria, and Farako-Bâ recording 66.92, 63.51, and 56.86 days after sowing (DAS), respectively. Physiological maturity averaged 63 DAS across all locations in 2022. The earliest 95% maturity was observed in Farako-Bâ in 2019 (56.86 DAS), while the latest was recorded at Kamboinsé during the same year (66.92 DAS). Grain yield varied across locations and years. The highest grain yield was achieved in Saria in 2019, whereas the lowest was recorded at Farako-Bâ in 2022 (Table 2). The highest hundred seed weight (16.79 g) was obtained at Kamboinsé in 2019, and the lowest (13.68 g) in Farako-Bâ in 2022. These results demonstrate that grain yield, seed weight, and maturity are highly influenced by both location and year, warranting further analysis to evaluate the

specific impact of these environmental components on trait expression.

Table S2. Descriptive statistics of yield and yield components.

Trait	2019			2022		
	Location	Kamboinsin	Saria	Kamboinsin	Saria	Farako-Bâ
95% Maturity	Means					
	±SE	66.92±0.43	63.51±0.32	56.86±0.23	63.24±0.17	63.19±0.23
	Min	58	55	51	60	61
	Max	75	70	60	67	66
	SD	4.51	3.29	2.43	1.80	0.83
Grain yield	Means					
	±SE	1261.35±80.03	1844.71±111.69	1417.38±53.09	1591.96±130.43	1591.21±98.16
	Min	19.06	64.31	376.88	44.08	56.25
	Max	3491.25	6344.38	2962.50	7250.00	5363.94
	SD	831.66	1160.69	551.69	1355.50	1020.08
HSW	Means					
	±SE	16.79±0.35	15.97±0.36	15.86±0.29	14.94±0.30	15.14±0.32
	Min	8.30	10.08	10.30	8.80	8.00
	Max	26.0	25.3	26.8	23.2	23.0
	SD	3.60	3.74	3.03	3.08	3.29

Variance components and genetic parameters for Yield, 95% maturity, and hundred seed weight of cowpea genotypes across six environments are presented in Table 3. The likelihood ratio test (LRT) showed a significant genotype × environment interaction (GEI) for the three traits ($P < 0.001$ for grain yield and hundred-seed weight; $P < 0.05$ for 95% maturity). The genotype main effect was highly significant for 95% maturity and hundred-seed weight ($P < 0.001$) but was not significant for grain yield ($P = 0.10$). The significant genotype effect for maturity and seed weight indicates substantial genetic differentiation among the MAGIC genotypes for these two traits and a real potential for selection, whereas the non-significant genotype effect for grain yield is consistent with the low heritability reported below. These results reveal that the genetic variance heavily drives the phenotypic expression of maturity and seed weight across all environments. In contrast, grain yield variance is predominantly governed by environmental factors and severe crossover-type interactions, which mask the standalone genotypic main effect. Notably, the genotypic coefficient of variance (CV_g) was low for maturity (1.78%), suggesting limited genetic variability for day of maturity. Because MAGIC populations are generated by intercrossing a limited number of founder parents, the narrow variation in crop cycle duration may be explained by a shared genetic background for maturity among these founders. Conversely, the CV_g was high for grain yield (13.9%) and HSW (10.7%), indicating that the MAGIC population maintains genetic variability for these traits. This makes HSW a reliable and promising trait for improving yield components. However, direct selection for yield across all environments is difficult because of the strong crossover interactions. The significant effects of GEI indicate that genotypic performance was influenced by environmental conditions. This differential response of cowpea genotypes

across environments in Burkina Faso aligns with recent findings by Batieno *et al.* (2025). Indeed, the climate in Burkina Faso is highly contrasted, characterized by micro-regions with varying temperatures, soil properties, and rainfall (Sieza *et al.*, 2019; Waongo *et al.*, 2024). Similar significant effects of environment, genotype, and GEI on cowpea agronomic parameters have been widely documented (Oluwaseye & Ogwuche, 2026; Abdou *et al.*, 2026). The genotype-by-environment coefficient of determination (R^2_{ge}) was low for 95% maturity (0.12) but higher for HSW (0.20) and grain yield (0.23), implying that maturity was less sensitive to environments, whereas grain yield and HSW were more sensitive to environmental variations. Furthermore, the low genotypic correlation among environments (r_{ge}) was observed for grain yield (0.24) and HSW (0.28), suggesting that grain yield and hundred seed weight were influenced by specific environmental conditions. For maturity, the very low genotypic correlation among environments combined with the narrow genetic variance reported above suggests that minor environmental fluctuations easily altered the ranking of the largely homogeneous lines. The effectiveness of selection depends fundamentally on the heritability of the traits. Compared to plot-based heritability, heritability on a genotype mean basis (h^2_{mg}) provides a more accurate and realistic estimate of the selection response in several environments. In this study, h^2_{mg} ranged from low to high, with values of 0.28 for grain yield, 0.67 for maturity, and 0.77 for HSW. This indicates that 28%, 67%, and 77% of the variance of the genotype means for yield, maturity, and seed size, respectively, were of genetic origin. These results predict a high genetic gain from selection for seed size and for 95% maturity. The low heritability of grain yield limited the effectiveness of direct selection. Similar results were reported in cowpea by Abdou *et al.*, 2026. Selective accuracy was moderate for yield (0.53) and high for 95%

maturity (0.82) and HSW (0.88). Similar selection accuracies were obtained by Abdou *et al* (2026), confirming the robustness of BLUP-based predictions. It is necessary to adopt indirect selection via correlated and more heritable secondary traits or to carry out a multi-trait selection in order to maximize genetic progress. Ensuring the stability of yield and its components remains critical for the effective cultivation of cowpea across diverse environments.

Table S3. Likelihood Ratio Test for genotype, genotype x environment interaction effect and genetic parameters for grain yield, maturity and hundred seed weight

Source of variation	Grain yield	95% maturity	Hundred seed weight
GEN	1.03e-01	6.79e-09	1.75e-15
GEN: ENV	2.23e-05	1.22e-02	1.47e-06
Genetic parameters			
Phenotypic	899883.	7.74	10.2
Heritability	0.0395	0.161	0.263
GEI _r 2	0.234	0.122	0.203
h ₂ mg	0.284	0.668	0.771
Accuracy	0.533	0.818	0.878
rge	0.244	0.146	0.275
CV _g	13.9	1.78	10.7
CV _r	59.6	3.74	15.2
CV ratio	0.233	0.475	0.702

Phenotypic: phenotypic variance; Heritability: broad-sense heritability on a plot basis; R₂ge the coefficient of determination of the interaction effects; h₂mg the heritability on the mean basis; Accuracy the selective accuracy; rge the genotype-environment correlation ; CV_g the genotypic coefficient of variation ; CV_r the residual coefficient of variation ; CV ratio the ratio between genotypic and residual coefficient of variation ; the values of the first two lines are LRT p-values.

The Additive main effects and multiplicative interaction (AMMI) analysis confirm that yield and yield components of 54 cowpea genotypes were significantly affected by environment, genotype and genotype by environment interaction (GEI), with a p-value less than 0.001 (Table S2). The analysis revealed that the first four interaction principal components (PC1-PC4) contributed significantly to the GEI ($P < 0.05$ to $P < 0.001$) and cumulatively explained 95.6%, 94.2%, and 93.3% of the interaction variance for maturity, yield, and HSW, respectively (Table 4). The first two interaction principal component axes (IPCA1 and IPCA2) explained more than 50% of the overall variance. According to Gauch and Zobel (1996), the first two axes would be precise in identifying stable genotypes. In the AMMI1 biplot, the distribution of genotypes and environments based on trait means and IPCA1 values was shown in Figure 1. The X-axis represents the trait’s mean across environments, whereas the Y-axis displays the IPCA1 score. A genotype or environment with a PC score near zero indicates minimal interaction. For yield, days to 95 % maturity (MAT), and hundred seed weight (HSW), the first component explained the maximum interactive variance of 45.6%, 49.4%, and 41.7%, respectively (Figure 1a, 1b, 1c). Environments E3_2019, E2_2019, E1_2022, and E2_2022, placed on the right side of the mean yield, were favourable environments for high seed yield. E1_2019 and E2_2019 were more favourable for large seed size. Among them, environment E3_2019 was positioned close to the origin for yield, and E2_2019 for HSW, indicating minimal interaction (Ghazy *et al.*, 2025). Genotypes located to the right of the overall

mean demonstrated superior performance for both grain yield and HSW. Within this group, genotypes G29, G46, G16, G53, G59, G61, and G56 exhibited high stability for yield, and genotypes G1, G20, G22, and G65 presented high stability for HSW, suggesting low sensitivity to GXE interaction. For days to 95% maturity, environments E2_2019 and E2_2022 were positioned close to the origin, indicating minimal interaction and high stability across environments. Conversely, E3_2019, placed on the left side of the mean, demonstrated high interaction and strong suitability for early maturity. The genotype located on the left of the mean of 95% maturity promoted early maturity. Those with IPCA1 values near zero included genotypes G56, G1, G12, and G16 and had similar maturity across the environments. Based on the AMMI1 biplot analysis, genotypes G16 and G56 were simultaneously selected for their yield stability and early maturity, while genotype G1 was identified for its combination of large seed size and early maturity.

AMMI2 biplot provided information on the genotype-environment interaction and specific genotype adaptability based on the first two principal components (IPCA1 and IPCA2) (Figure 2). IPCA1 and IPCA2 together explained 71.8% of the variation for 95% maturity, 69.9% for yield, and 62.6% for HSW. Based on their proximity to the biplot origin, the genotypes G29, G49, and G45 for yield, and G20, G9, G22, G56, G47, and G65 for HSW were considered more stable. For 95% maturity, genotypes G12, G62, G46, G56, G48, G20, G47, G5, and G43 were located near the origin, indicating their low sensitivity to environmental variations. For grain yield, the AMMI2

biplot illustrated that the environments E2_2019, E2_2022, and E1_2022 were the most discriminant, and the genotypes G55, G61, and G23 had specific adaptability to E1_2022, E2_2019, and E2_2022, respectively. For maturity, E1_2019 and E2_2019 were the most discriminant, and the genotypes G51 and G40 had specific

adaptability to E1_2019, and G27 was specifically adapted to E2_2019. For HSW, environments E3_2022 and E3_2019 were the most discriminant, and genotypes G61 and G35 have specific adaptability to E3_2022 and E3_2019, respectively.

Table 4. Multiplicative effects analysis and principal component interactions (IPCA's).

Source of variation	df	Sum of Squares	Mean of Squares	Relative variance	Cumulative variance
95% maturity (MAT)					
PC1	57	1947.7	34.17***	49.4	49.4
PC2	55	881.2	16.02***	22.4	71.8
PC3	53	508.3	9.59**	12.9	84.7
PC4	51	432.3	8.48*	11.0	95.6
PC5	49	172.2	3.51	4.4	100.0
Grain yield (Yield)					
PC1	57	2.60e+08	4556112***	45.6	45.6
PC2	55	1.38e+08	2516138***	24.3	69.9
PC3	53	7.87e+07	1484770***	13.8	83.7
PC4	51	6.02e+07	1180210*	10.6	94.2
PC5	49	3.28e+07	669443	5.8	100.0
Hundred Seed Weight (HSW)					
PC1	57	983.2	17.25***	39.8	39.8
PC2	55	561.4	10.21***	22.7	62.6
PC3	53	473.4	8.39**	19.2	81.8
PC4	51	279.0	5.47*	11.3	93.1
PC5	49	170.8	3.49	6.9	100.0

*** significant at the 0.1% level; ** significant at the 1% level; * significant at the 5% level; df: degrees of freedom; Sum of Squares: sum of squares; Relative variance: percentage of the interaction sum of squares explained by each component

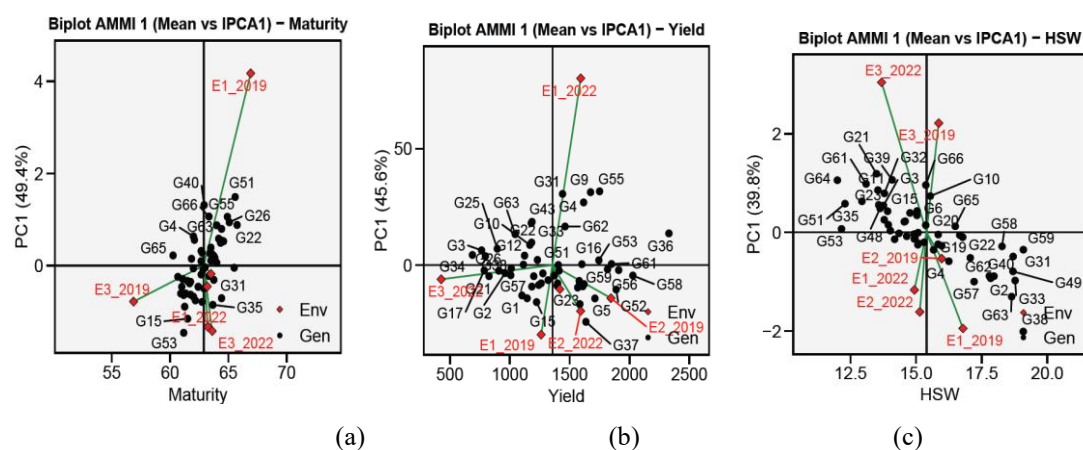


Figure S1. AMMI1 biplots of 54 cowpea genotypes evaluated in six environments for (a) days to 95% maturity (MAT), (b) grain yield, and (c) hundred-seed weight (HSW). The x-axis shows the trait mean, and the y-axis shows the IPCA1 score. E1 = Kamboinsé, E2 = Saria, E3 = Farako-Bâ; 2019 and 2022 refer to the cropping season.

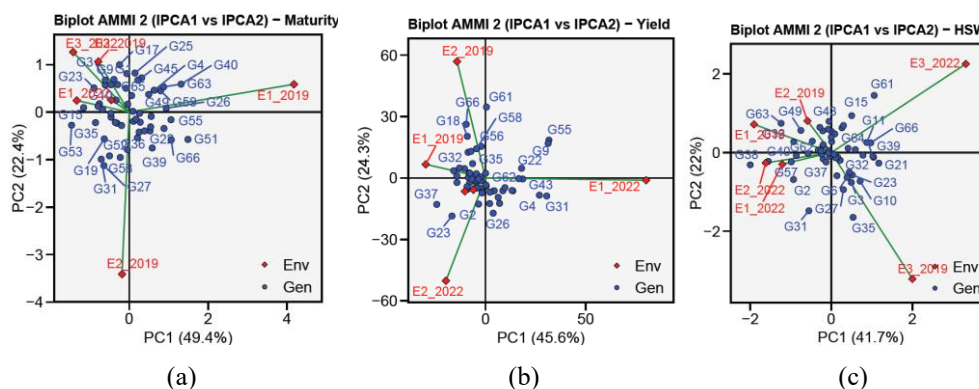


Figure 2. AMMI2 biplots (IPCA1 $\times$ IP2A2) of 54 cowpea genotypes evaluated in six environments for (a) days to 95% maturity (MAT), (b) grain yield and (c) hundred-seed weight (HSW).

The BLUP, the WAASB and the WAASBY values of tested genotypes are presented in supplementary Table S3. BLUP value for 95% maturity ranged from 61.1 days after sowing (DAS) for G22 to 64.8 DAS for G65. The MAGIC genotypes were therefore as early as the checks Komcallé and Niizwé, which reached maturity at 62.03 and 63.2 DAS, respectively. Regarding the predicted genotypic values, the genotype G36 recorded high grain yield (1632 kg/ha), while G34 obtained the lowest (1166 kg/ha). The check Niizwé and Komcallé produced 1567 kg/ha and 1296 kg/ha, respectively. HSW ranged from 12.8 g (G64) to 18.2 g (G38), compared with 15.7 g for Komcallé and 15.4 g for Niizwé. High-yielding, large-seeded genotypes are of commercial interest, but their stability across environments must also be established. The WAASB plot segregated the environments and genotypes into four quadrants (Figure 3). High WAASB values indicate low stability, and low WAASB values indicate high stability. In quadrant I, the genotypes had lower productivity than the grand mean and high WAASB values. In quadrant II, the genotypes had higher performance and high WAASB values. Quadrant III had low performance and low WAASB values. Quadrant IV contained genotypes with higher performance and lower WAASB values. Genotypes within Quadrants IV (for grain yield and HSW, for which higher values are desired) and III (for MAT, for which lower values are better) are assumed to be desirable. For maturity, 20 genotypes located in the third quadrant of the plot, including G12, G48, and G56,

had a lower WAASB value and a shorter or equal number of days from sowing to 95% maturity compared to the overall mean. No environment presented high stability for this trait. For yield, quadrant IV contained 16 genotypes, among which G29, G46, G53, and G16 exhibited high yield performance combined with high stability (low WAASB value). Environment E3_2019 provided high performance and stability for this trait. For HSW, quadrant IV contained 13 genotypes, including the stable genotypes G46, G20, G22, and G65, which produced seed weight higher than the grand mean. No environments showed low discrimination ability for this trait. To enhance selection efficiency, the WAASB analysis was complemented by the WAASBY index. The performance of 54 cowpea genotypes was ranked based on estimated WAASBY values (Figure S1, Table S3). Genotypes with the highest WAASBY values combine the highest mean performance with the greatest stability. The top-performing genotype for yield was G53, followed by G56, G29, G46, G58, and G16. For physiologic maturity, G36, G46, G21, and G12 recorded high WAASBY values, indicating their stability. Genotypes G59, G20, G58, G22, and G65 were ranked for their high seed size and stability. However, classifying genotypes based solely on individual WAASBY values of each trait limits selection objectives under field conditions. To overcome this limitation and enable a concurrent selection for all three traits, the Multi-Trait Stability Index (MTSI) was applied.

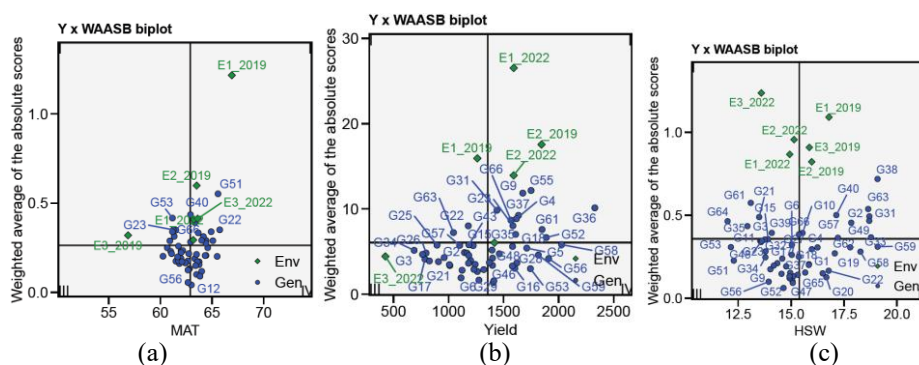


Figure 3. WAASB $\times$ mean performance biplots for (a) days to 95% maturity, (b) grain yield and (c) hundred-seed weight of 54 cowpea genotypes evaluated in six environments. The vertical and horizontal dashed lines represent the grand mean and the mean WAASB value, respectively.

In the present study, genotypes were selected for high yield, seed size, and early maturity using the Multi-Trait Stability Index (MTSI), with a selection intensity controlled at 15% for both mean performance and stability (Olivoto *et al.*, 2019). Based on MTSI scores, the superior genotypes identified were G56, G16, G58, G65, G46, G33, G12, and G29 (Figure 4a). The factor analysis for the 3 traits of cowpea genotypes is described in Table 5. Two factors were retained: FA1, with an eigenvalue of 1.09, and FA2, with an eigenvalue of 1.08 (Shrestha, 2021), together explaining 69.6% of the total variance. Factor 1 (FA1) was strongly associated with grain yield and 95% maturity, whereas F2 (FA 2) was associated with HSW (Table 5). Both traits loaded negatively on FA1, indicating a positive association between grain yield and cycle length, in agreement with the findings of Asrat *et al.* (2021). Conversely, hundred seed weight was independent of these traits. Communalities were high, ranging from 0.54 for grain yield to 0.99 for HSW. Uniqueness values were low, ranging between 0.009 and 0.46 across all traits (MAT, yield, and HSW). Grain yield and HSW showed positive selection differentials, whereas 95% maturity showed a negative one (Table 6). The highest genetic gain was predicted for grain yield (37.4 kg ha⁻¹, i.e. 2.76%), and by hundred-seed weight (0.48 g, i.e. 3.14%), whereas the gain for 95% maturity was negative (-0.28 day, i.e. -0.44%), indicating a slight shift towards earliness. These gains remain modest for the cycle length, which is expected given the positive association between yield and maturity on FA1. Nevertheless, these results demonstrate that the MTSI managed to identify elite genotypes that successfully break this unfavorable correlation by combining higher yield with a maintained, slightly shorter cycle. Regarding

the strengths and weaknesses of the cowpea genotypes, FA1 showed low contributions to genotypes G16, G58, G65, G46, G33, and G12, (Figure 4b) indicating their proximity to the ideotype for combined yield performance, early maturity, and stability. FA2 exhibited low contributions to genotypes G56 and G29, recording hundred seed weight stability. On average, the selected genotypes required 62.5 DAS to reach physiological maturity, compared to the overall mean of 62.9 DAS, confirming their early maturity (Dorvlo *et al.*, 2022). Early-maturing cowpea varieties are highly preferred by local populations (Ishikawa *et al.*, 2020). Furthermore, the selected genotypes recorded an average HSW of 16 g, compared to 15.4 g for the overall mean. Cowpea genotypes classified as medium-seeded genotypes (15-20 g/100 seeds) are preferred by the majority of farmers in the north of Burkina Faso (Ishikawa *et al.*, 2020). The mean predicted grain yield of the selected genotypes was 1459 kg/ha, above the overall mean of 1356 kg ha⁻¹ and above that of the check Komcallé (1296 kg ha⁻¹). Specifically, the genotypes G16 (MAGIC061), G58 (MAGIC263), G65 (MAGIC298), G46 (MAGIC228), G33 (MAGIC143), and G12 (MAGIC047) exhibited high values for grain yield and early maturity along with strong stability across environments. These MAGIC genotypes represent ideal plants to ensure high agricultural production, even in the face of increasingly short rainy seasons. Consequently, these MAGIC genotypes represent elite candidates to enhance cowpea production in Burkina Faso and West Africa under changing climate conditions and limited rainfall. Concurrently, the genotypes G56 (MAGIC258) and G29 (MAGIC130) stood out as stable ideotypes for the 100-seed weight factor across environments.

Table 5. Eigenvalues, Factorial loadings, communalities, and uniqueness for selected genotypes.

Traits	Factor1 IPCA1	Factor 2 IPCA2	Communality	Uniquenesses
Yield	-0.745	-0.0659	0.538	0.462
MAT	-0.61	0.0729	0.559	0.441
HSW	-0.0167	0.995	0.991	0.00878
Eigenvalues	1.09	1.08		
Variance (%)`	36.4	33.2		
Accumulated (%)	36.4	69.6		

Table 6. Selection differential using MTSI index.

VAR	Factor	Xo	Xs	SD	SDperc	h2	SG	SGperc	sense	goal
<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>	<dbl>
MAT	FA 1	62.9	62.5	-0.37	-0.58	0.76	-0.28	-0.44	decrease	100
Yield	FA 1	1356.	1459.	103.	7.60	0.36	37.4	2.76	increase	100
HSW	FA 2	15.4	16.0	0.59	3.81	0.82	0.48	3.14	increase	100

Xo: overall mean of the predicted genotypic values; Xs: mean of the selected genotypes; SD: selection differential; SDperc : selection differential expressed in percentage; FA: factor on which the trait loaded; ^H: heritability on a genotype-mean basis; SG: selection gain; SGperc: selection gain in percentage; sense: direction of the desired change; goal: weight given to the trait; yield (kg ha⁻¹), HSW = hundred-seed weight (g), MAT= Days to 95% maturity.

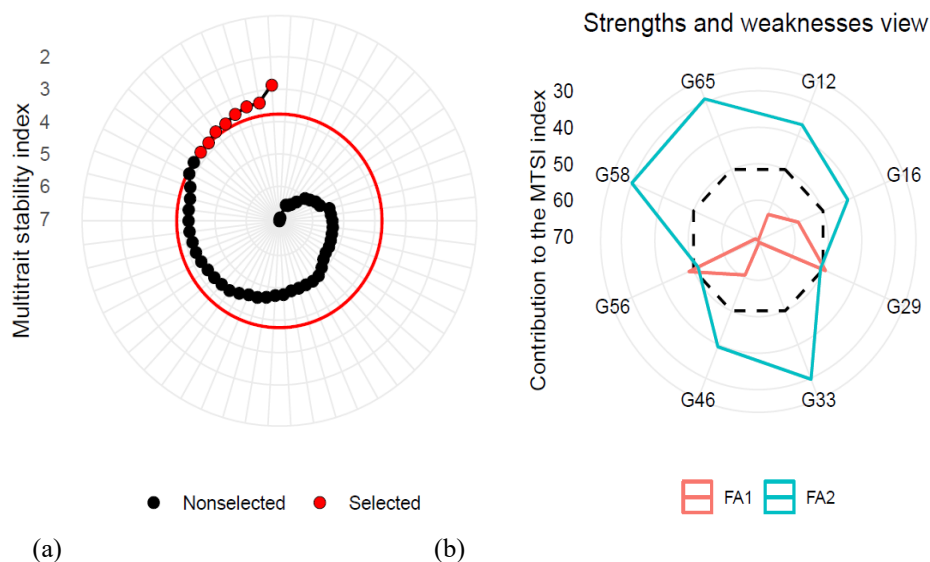


Figure 4. (a) Genotype ranking based on the multi-trait stability index (MTSI) at a selection intensity of 15%; the red circle delimits the selected genotypes. (b) Strengths and weaknesses of the selected genotypes; a small contribution of a factor indicates that the genotype is close to the ideotype for the traits loading on that factor.

CONCLUSION

The present study showed that the environment and the genotype-by-environment interaction had significant effects on the three traits studied, whereas the genotype main effect was significant for maturity and seed size only. Complementary statistical analyses, including AMMI, WAASB, WAASBY, and MTSI models, provided valuable insights into genotype performance and stability for yield and its components. A cross-model comparison of AMMI1, WAASB, and WAASBY revealed that genotypes G46, G29, G16, and G53 were consistently selected, combining high yield performance with environmental stability; G12 was identified for its earliness and stability, and G20, G22, and G65 were selected for high seed size stability. Based on the MTSI index, the genotypes G16 (MAGIC061), G58 (MAGIC263), G65 (MAGIC298), G46 (MAGIC228), G33 (MAGIC143), and G12 (MAGIC047) offered an attractive combination of grain yield and early maturity stability; G56 (MAGIC258) and G29 (MAGIC130) stood out as stable ideotypes for the 100-seed weight. Ultimately, the high grain yield stability of G46 and G16 was robustly confirmed across the AMMI, WAASB, WAASBY, and MTSI, making them excellent candidates. Studies conducted in more than 6 environments could be conducted in Burkina Faso to confirm these results.

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CONFLICT OF INTERESTS

The authors declare no conflict of interest

ETHICS APPROVAL

Not applicable

FUNDING

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AI TOOL DECLARATION

The authors declare that no AI and related tools are used to write the scientific content of this manuscript.

DATA AVAILABILITY

Data will be available on request

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