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Evaluation of extra-early cowpea [*Vigna unguiculata* (L.) Walp.] genotypes for yield in multiple environments

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Abstract

Genotype and environment interaction (GEI) is a primary constraint in cowpea improvement, as differential genotypic responses to contrasting growing conditions complicate the identification of broadly adapted, high-yielding varieties. The objectives of the present study were: (i) to examine the effect of genotype, environment, and genotype $\times$ environment interaction (GEI) on grain yield and its determinant; and (ii) to identify superior genotypes that exhibit high performance using the genetic tools of genotype-by-environment interaction and genotype stability indices. Twenty-four extra-early cowpea genotypes were evaluated across six environments using an alpha-lattice incomplete block design with three replications. Analysis of variance revealed highly significant effects of environment, genotype, and their interaction for all six traits: days to first flower (DAF), days to 50% flowering (DAF50), days to 50% maturity (MAT50), pod yield (PY), grain yield (GY), and fodder yield (FY). Environment was the dominant source of variation for yield traits, while genotype effects were comparatively significant for phenological traits. Pearson correlations revealed significant positive associations among phenological traits ($r = 0.94\text{--}0.97$, $p < 0.001$) and between pod and grain yield ($r = 0.87$, $p < 0.001$). The GGE biplot which-won-where analysis identified two mega-environments, with Tara consistently isolated from the Mgr cluster. Finlay-Wilkinson regression classified eight genotypes as specifically adapted to favorable environments ($b > 1.2$), seven as broadly stable ($0.8 \leq b \leq 1.2$) and nine as adapted to poor environments ($b < 0.8$). Lin and Binns' superiority index (P_i) ranked G1 ($P_i = 195,790$), G5 (207,502), and G7 (216,876) as the three most superior genotypes, while Huehn's S1 rank stability identified G14 ($S1 = 5.9$, rank 5, $GY = 930.9 \text{ kg ha}^{-1}$) and G19 ($S1 = 5.6$, rank 4, $GY = 887.6 \text{ kg ha}^{-1}$) as the best combination of above-average yield with stable ranking across environments.

These findings provide an integrated scientific basis for the selection and release of extra-early cowpea varieties for the Sahelian production systems of Niger.

Keywords: *Vigna unguiculata*; GEI; GGE biplot; Finlay-Wilkinson regression; radar chart; stability; Sahel; Niger

1 Introduction

Cowpea (*Vigna unguiculata* [L.] Walp.) is one of the most important grain legumes of the Semi-Arid tropics, valued for its nutritional contents, drought tolerance, and capacity to fix atmospheric nitrogen [1]. It serves simultaneously as food, livestock feed, a cash crop and a soil-fertility-restoring component of smallholder farming systems across sub-Saharan Africa [2,3]. The global cowpea production stands at approximately 9.8 million tons at about 15 million hectares, with West Africa accounting for 87.2% of cultivated area and 86.0% of total production. Republic of Niger is the second largest cowpea producer, contributing 39.0% of the world's cultivated area and 27.5% of production [4]. Despite this, national average yields remain critically low at approximately 448 kg ha⁻¹, reflecting convergent biotic and abiotic constraints, including recurrent terminal drought, low soil fertility, high insect pest pressure, parasitic weeds (*Striga gesnerioides*), lack of improved varieties, and the predominantly short and erratic rainy season [5]. Extra-early maturing varieties reaching maturity within 55–65 days represent an important breeding target in this context, enabling escape from terminal drought, reduction of the hunger period, and minimization of exposure to *Striga* and late-season pests [6–9]. Genotype interactions with environmental factors, including location, cropping season, soil characteristics, and agricultural practices, represent a key consideration in plant breeding. The interaction between genotype and environment is generally non-additive, indicating that the relative performance of cultivars differs across environments. As a result, genotype rankings are often inconsistent across environments, leading to genotype × environment interaction (GEI), which complicates the identification of broadly adapted and stable genotypes [10–12]. While previous cowpea breeding efforts often relied on controlled or single-location research facilities, current climate variability demands a shift toward multi-location trials. The identification of superior genotypes requires evaluating advanced breeding lines across a diverse range of environmental conditions. Because environmental factors and varying biotic and abiotic stresses influence crop performance, breeding lines often exhibit considerable differences in their phenotypic expression when tested across multiple locations and seasons [13,14]. Consequently, multi-environment trials (METs) are essential for assessing the adaptability and stability of genotypes [15]. Understanding and quantifying GEI are therefore critical for identifying genotypes with broad or specific adaptation and for making informed selection decisions in plant breeding programs. Genotype × environment interaction (GEI) is a fundamental phenomenon in plant breeding that substantially influences the expression of quantitative traits [16]. It occurs when genotypes exhibit different relative performances across varying environmental conditions, causing changes in their ranking from one environment to

another [17]. To evaluate the productivity, adaptability, and stability of breeding materials, candidate cultivars are typically assessed across multiple locations and growing seasons through multi-environment trials (METs). These trials encompass diverse environmental conditions and often reveal varying types of GEI [18]. Several techniques have been developed to address genotype $\times$ environment interaction (GEI) in plant breeding. One technique is to disregard GEI and select genotypes based solely on their average performance across environments. Alternatively, GEI can be minimized by dividing the target population of environments into smaller, more homogeneous groups, thereby improving selection efficiency within each subgroup. A third technique is to exploit GEI by explicitly modeling genotype responses, enabling the identification of genotypes with either broad adaptation or specific adaptation to particular environmental conditions [16,19,20]. To achieve this, a wide range of statistical methods has been developed, including fixed-effect linear models, such as factorial regression; bilinear methods such as partial least squares; linear–bilinear models including the additive main effects and multiplicative interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) biplot models; linear mixed models for multi-environment data; and linear–bilinear mixed models based on factor analytic structures [21]. In addition to these modeling techniques, GEI can also be investigated through variance component partitioning and the delineation of mega-environments [19]; the Finlay-Wilkinson regression model [22]; Wricke ecovalence [23]; and the superiority index (Pi) [24]. Integrating multiple analytical methods provides a more comprehensive understanding of GEI within the target population of environments, thereby supporting breeders in selecting the most appropriate breeding tool and identifying superior cultivars with high productivity, adaptability, and stability.

The objectives of this study were to (i) evaluate the grain yield performance of advanced cowpea genotypes across multiple environments, (ii) investigate the magnitude and pattern of genotype $\times$ environment interaction (GEI), (iii) identify high-yielding and stable genotypes with broad or specific adaptation to support cowpea improvement and cultivation in Niger, and (iv) delineate mega-environments to enhance the efficiency of future germplasm evaluation and breeding programs. Beyond their breeding value, genotypes combining high yield with broad stability directly reduce production risk for resource-poor Sahelian farmers who lack irrigation or other means to buffer environmental variability, a risk that is central to household food security in a region where cowpea is a primary source of dietary protein and household income [25,26].

2 Materials and Methods

2.1 Experimental design, germplasm, and crop management

Trials were conducted from 2020 to 2022 across six environments in the major cowpea-producing regions of the Republic of Niger: Magaria (12°59'N, 6°56'E), Maradi (15°26'N, 8°33'E), and Tara (11°53'N, 3°20'E). Each year-by-location combination was treated as a distinct environment (Mgr1, Mgr2, Mgr3, Mgr4, Tara, and Mdi), yielding six environments in total. The panel comprised 24 genotypes: 21 newly developed INRAN extra-early lines derived from two cross combinations (N'Diambour × IT84S22-46-6 and IN15_150 × IT87D-1083) and three widely used checks—IT90K-372-1-2 (IITA), TN5-78 (INRAN), and UAM09_1055_6 (UAM) (Table 1). Trials were laid out in a 4×6 alpha-lattice design with three replications. Each plot comprised four rows of 4 m, 4 m, with 0.5 m intra- and inter-row spacing. The distance between blocks and replications was 2.5 m and 4 m, respectively (Figure 1). Two seeds were sown per hill and thinned to one plant three weeks after emergence. Weeds and insect pests were controlled as needed. Six traits were recorded: DAF, DAF50, MAT50, pod yield (PY, kg ha⁻¹), grain yield (GY, kg ha⁻¹) and fodder yield (FY, kg ha⁻¹). Phenological traits were scored as days from planting to the corresponding growth stage. Yield traits were adjusted to 10% moisture content.

Table 1. Description of the 24 cowpea genotypes used in the multi-environment trial.

Designation	Code	Pedigree	Seed colour	Seed size	Source	Status
IN17-260	G1	IN15_150 × IT87D-1083	Light brown	Medium	INRAN	New line
IN17-185	G2	N'Diambour × IT84S22-46-6	Brown	Medium	INRAN	New line
IN17-175	G3	N'Diambour × IT84S22-46-6	White	Medium	INRAN	New line
IN17-178	G4	N'Diambour × IT84S22-46-6	Brown	Small	INRAN	New line
IN17-243	G5	IN15_150 × IT87D-1083	Brown	Medium	INRAN	New line
IN17-181	G6	N'Diambour × IT84S22-46-6	Brown	Small	INRAN	New line
IN17-286	G7	N'Diambour × IT84S22-46-6	White	Medium	INRAN	New line
IN17-234	G8	N'Diambour × IT84S22-46-6	Brown	Medium	INRAN	New line
IN17-235	G9	N'Diambour × IT84S22-46-6	White	Small	INRAN	New line
IN17-151	G10	N'Diambour × IT84S22-46-6	Brown	Small	INRAN	New line
IN17-203	G11	N'Diambour × IT84S22-46-6	White	Medium	INRAN	New line
IT90K-372-1-2	G12	—	White	Medium	IITA	Check
IN17-169	G13	IN15_118 × IT87D-1083	White	Medium	INRAN	New line
IN17-171	G14	N'Diambour × IT84S22-46-6	Brown	Small	INRAN	New line
IN17-167	G15	N'Diambour × IT84S22-46-6	White	Medium	INRAN	New line

IN17-186	G16	N'Diambour × IT84S22-46-6	Brown	Medium	INRAN	New line
IN17-236	G17	N'Diambour × IT84S22-46-6	White	Small	INRAN	New line
IN17-238	G18	N'Diambour × IT84S22-46-6	White	Small	INRAN	New line
IN17-230	G19	N'Diambour × IT84S22-46-6	White	Small	INRAN	New line
IN17-199	G20	IN15_150 × IT87D-1083	Brown	Medium	INRAN	New line
IN17-182	G21	N'Diambour × IT84S22-46-6	White	Small	INRAN	New line
TN5-78	G22		Brown	Medium	INRAN	Check
IN17-215	G23	N'Diambour × IT84S22-46-6	Brown	Medium	INRAN	New line
UAM09_1055_6	G24	—	White	Medium	UAM	Check

INRAN = Institut National de la Recherche Agronomique du Niger ; IITA = International Institute of Tropical Agriculture ; UAM = University of Agriculture, Makurdi



Fig.1 Example of layout design at one location.

2.2 Statistical analysis

All statistical analyses were conducted in R statistical software. The analytical pipeline covered six sequential steps: variance estimation, descriptive statistics, correlation analysis, stability analysis, GGE biplot, and clustering. Variance estimation and BLUP. Genotypic performance across environments was evaluated through a multi-environment trial (MET) linear mixed model framework. Genotype effects and genotype-by-environment interaction (GEI) effects

were treated as random, and variance components were estimated by Restricted Maximum Likelihood (REML). Pearson correlation coefficients were computed among all pairs of traits and among environments to quantify linear associations and detect redundancy or complementarity between traits. The genotype main effect plus genotype-by-environment interaction (GGE) biplot [27] was used to simultaneously visualize genotypic performance and stability across environments. Two complementary views were generated: the polygon view (which-won-where pattern) to identify mega-environments and environment-specific winning genotypes and the Average Environment Coordinate (AEC) view (mean vs. stability pattern) to rank genotypes simultaneously by mean performance and stability. Genotype stability across environments was assessed using two complementary techniques. First, Finlay-Wilkinson (FW) regression [22,28] was applied to relate individual genotype grain yield to the environment mean yield, which was used as an index of environmental productivity. The regression slope (β) served as the stability parameter: genotypes with $\beta \approx 1$ were classified as broadly stable, those with $\beta > 1.2$ as specifically adapted to favorable environments, and those with $\beta < 0.8$ as specifically adapted to poor environments. The FW model assumes that the performance of the i -th genotype in the j -th environment follows the linear predictor:

$$y_{ij} = \alpha_i + \beta_i w_j + e_{ij} \quad \dots (1)$$

where y_{ij} is the observed mean grain yield (kg ha^{-1}) of genotype i in environment j ; α_i is the genotype-specific intercept, representing the overall mean performance of genotype i across all environments when the environmental index is mean-centered; and β_i is the genotype-specific regression slope, interpreted as a sensitivity parameter. Small absolute values of β_i indicate stable responses over changing environments; w_j is the environmental index, estimated as the arithmetic mean of all observed genotype yields in environment j [22]. This index serves as a surrogate for the overall productivity of the environment, integrating the combined effects of all environmental factors; e_{ij} is the residual error term, assumed to be independently and identically distributed. For balanced data, the environmental index w_j was estimated by the arithmetic mean grain yield across all genotypes in each environment, as originally proposed by Finlay and Wilkinson [22]. The regression coefficients α_i and β_i were estimated by ordinary least squares.

Wricke ecovalence (W_i) and yield stability index (YSi) were computed as previously described [23]. According to Lin and Binns [24], the superiority index (P_i) can be partitioned into two components: the first reflects genetic deviation among genotypes, while the second quantifies the contribution of genotype $\times$ environment interaction (GEI).

Superiority index (Pi) as:

$$P_i = (1 / (2E)) * \sum (Y_{ij} - M_j)^2$$

Where: P_i = superiority index of genotype i , Y_{ij} = yield of genotype i in environment j , M_j = maximum yield in environment j , and E = number of environments. P_i can be partitioned into two components: $P_i = P_i(\text{genetic}) + P_i(\text{G} \times \text{E interaction})$

The genetic component of the superiority index reflects the inherent yield potential of a genotype, whereas the genotype $\times$ environment interaction (GEI) component quantifies the extent to which environmental variation influences genotype performance across test environments. A larger genetic component indicates that genotype superiority is primarily attributable to genetic effects, while a greater GEI component suggests increased sensitivity to environmental fluctuations. To complement the parametric assessment of adaptability and stability. Three non-parametric stability statistics, namely S_1 , S_2 , and S_3 , which evaluate phenotypic stability based on the ranks of genotypes across multiple environments, were also used [29]. Because these statistics rely on genotype rankings rather than absolute yield values, they are robust to deviations from normality and effectively measure the consistency of genotype performance across diverse environments. Genotypes with lower S_1 , S_2 , and S_3 values are considered more stable, as they exhibit smaller changes in rank across environments

$$S_1 = (2 / (n-1)) * \sum |r_{ij} - r_{ij'}|, S_2 = \sum (r_{ij} - \bar{r}_i)^2 / (n - 1), S_3 = \sum |r_{ij} - \bar{r}_i| / \bar{r}_i.$$

where $S_i^{(1)}$ = mean of the absolute differences among the classifications of the i -th cultivar in the n environments, r_{ij} = classification of the i -th cultivar in the j -th environment, n = number of environments, $S_i^{(2)}$ = variance of the classifications of the i -th cultivar in the environments, $\bar{r}_i = \sum r_{ij} / n$ and $S_i^{(3)}$ = sum of absolute deviations in yield units of each classification relative to the mean classification.

Radar charts were constructed for the top 10 genotypes (by mean GY) using normalized (0–100) trait scores across all six traits to provide a holistic multi-trait comparison.

3 Results

3.1 Descriptive statistics

Considerable variation was observed across environments for all traits (S1Table; Figure 2). For DAF, it ranged from 32.0 days at Tara to 38.3 days at Mgr3. GY means ranged from 397.3 kg ha⁻¹ at Mgr3 to 1216.0 kg ha⁻¹ at Mgr2—a threefold difference highlighting the environmental heterogeneity. Coefficients of variation exceeded 60% at Mgr3 and Mgr4 for GY, indicating strong within-environment genotypic variation. The distributions for DAF, DAF50, and MAT50 are narrow and relatively symmetric across all six environments, indicating low inter-

environment variability for phenological traits. All environmental clusters are close to the grand mean (red dashed line), confirming that genotypic ranking for flowering and maturity is consistent regardless of environment (Figure 2). Mgr1 shows the widest distribution for DAF, indicating greater genotypic diversity in flowering time at that environment. Tara consistently shows the earliest and most compact distributions across all three phenological traits, confirming it as the earliest-maturing environment. Mgr3 and Mgr4 have shifted rightward to the grand mean for MAT50, indicating genotypes mature later at these environments. A significantly different pattern emerges for yield traits. Distributions are wide, significantly skewed, and highly variable across environments, a direct visual signature of significant GEI. Mgr1 consistently shows the most leftward distribution for PY and GY, with its median well below the grand mean, confirming it as the lowest-yielding environment for grain and pod production. Mgr2 and Mgr4 show the widest and most rightward-extended distributions for PY and GY, with long right tails indicating that a subset of genotypes performs exceptionally well in these environments. The grand mean line falls to the right of most environment medians for GY, pulled rightward by the high-yielding tail at Mgr2 and Mgr4. For FY, Mgr4 shows an exceptionally wide distribution extending beyond 6000 kg/ha, the widest of all environments, indicating significant fodder yield variability; that environment is the most discriminating against for fodder selection. Mgr3 has the most compact and leftward distribution for all yield traits, confirming it as the poorest-performing environment and the most stressful for cowpea production. Mdi shows a moderate, symmetric distribution for GY centered near the grand mean, making it a representative environment for average conditions (Figure 2).

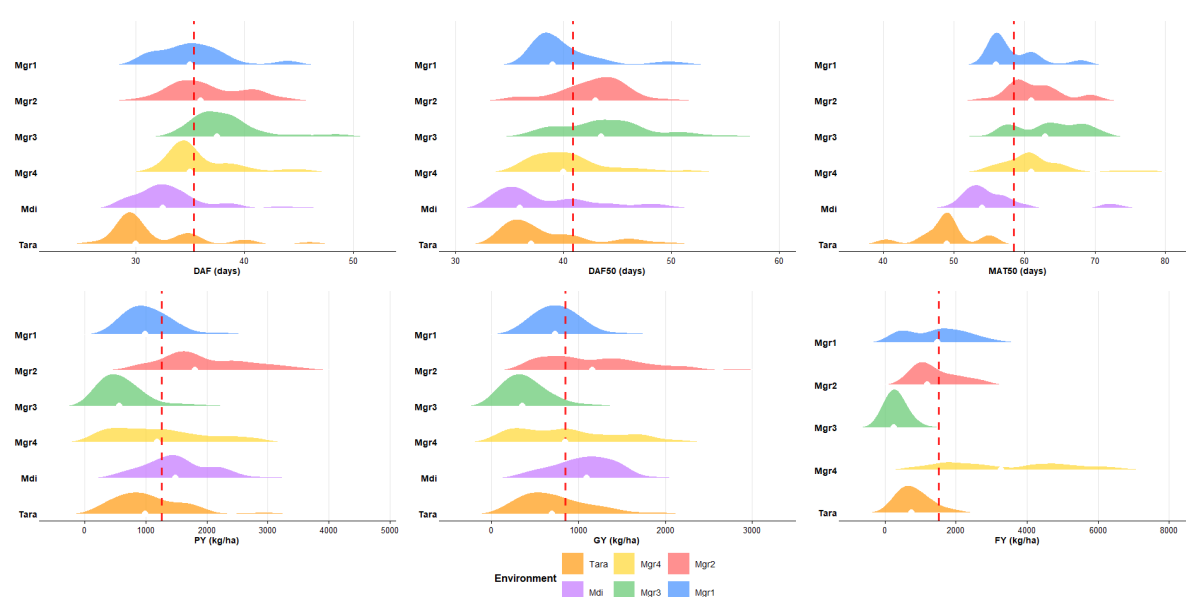


Fig.2 Density distribution of days to first flowering (DAF), days to 50% flowering (DAF50), days to 50% maturity (MAT50), pod yield (PY), grain yield (GY), and fodder yield (FY) of 24 cowpea genotypes across six environments (Tara, Mgr1, Mgr2, Mgr3, Mgr4, and Mdi) in Niger. Red dashed lines indicate the overall mean for each trait.

3.2 Combined analysis of variance

Environment, genotype, and GEI effects were highly significant ($p < 0.001$) for all traits (Table 2). Environment explained the largest proportion of variation for yield traits ($F = 59.23$ – 242.01), while genotype effects dominated for phenological traits ($F = 41.83$ – 51.19). The GEI was significant for all traits ($F = 3.15$ – 3.79), confirming differential genotype responses across environments and justifying the stability analyses that follow.

Table 2. Combined analysis of variance for six traits of 24 extra-early cowpea genotypes across six environments.

Trait	Source of Variation	SS	MS	F value	p-value	Sig.
DAF	ENV	1800.24	360.05	98.35	<0.001	***
	GEN	3522.42	153.15	41.83	<0.001	***
	GEN×ENV	1444.15	12.56	3.43	<0.001	***
	Residuals	812.75	3.66	—	—	
DAF50	ENV	1733.57	346.71	85.41	<0.001	***
	GEN	4114.16	178.88	44.07	<0.001	***
	GEN×ENV	1511.49	13.14	3.24	<0.001	***
	Residuals	901.18	4.06	—	—	
MAT50	ENV	10643.24	2128.65	410.18	<0.001	***
	GEN	6110.20	265.66	51.19	<0.001	***
	GEN×ENV	1930.03	16.78	3.23	<0.001	***
	Residuals	1152.08	5.19	—	—	
PY	ENV	959,995	991,999	80.64	<0.001	***
	GEN	168,910	485,605	2.45	<0.001	***
	GEN×ENV	806,074	624,401	3.15	<0.001	***
	Residuals	828,448	198,319	—	—	
GY	ENV	236,578	847,316	59.23	<0.001	***
	GEN	714,711	161,509	1.64	0.038	*
	GEN×ENV	592,068	335,583	3.40	<0.001	***
	Residuals	819,234	98,730	—	—	
FY	ENV	676,909	169,227	242.01	<0.001	***
	GEN	884,966	994,999	6.83	<0.001	***
	GEN×ENV	14,699	663,203	3.79	<0.001	***

	Residuals	160,701	438,706	—	—	
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231 *SS* = sum of squares; *MS* = mean squares; *** $p < 0.001$; * $p < 0.05$; — not applicable.

232 3.3 Genotype means performance across environments

233 Mean GY ranged from 552.9 kg ha⁻¹ (G24) to 1017.7 kg ha⁻¹ (G1), with a grand mean of 848
234 kg ha⁻¹ (Table 3). The top five genotypes were G1, G2, G5, G14 and G15. Eleven genotypes
235 exceeded the grand mean. Large rank changes across environments — notably G2 (305.3 kg
236 ha⁻¹ at Mgr3 vs. 1821.2 kg ha⁻¹ at Mgr4) and G9 (194.0 kg ha⁻¹ at Mgr3 vs. 1807.3 kg ha⁻¹ at
237 Mgr4) — confirm the crossover nature of GEI and the need for stability analysis.

238 **Table 3.** Mean grain yield (kg ha⁻¹) of 24 extra-early cowpea genotypes across six environments
239 (ordered by grand mean).

Genotype	MDI	Mgr1	Mgr2	Mgr3	Mgr4	Tara	Grand Mean
G1	1461.7	714.0	2290.0	269.3	949.7	421.7	1017.7
G2	1325.0	815.0	1045.0	305.3	1821.2	453.3	960.8
G5	488.3	1152.7	1598.3	407.3	1338.5	653.3	939.8
G14	1177.0	925.3	1270.0	637.3	645.8	930.0	930.9
G15	1399.3	1183.0	1001.7	471.7	468.8	1041.7	927.7
G22	1060.0	685.3	1375.0	772.7	258.7	1306.7	909.7
G3	923.0	757.3	1725.0	751.7	76.4	1210.0	907.2
G7	1060.0	998.3	1640.0	198.7	763.9	750.0	901.8
G19	1289.7	632.3	1055.0	457.3	1107.6	783.3	887.6
G4	835.0	982.0	1553.3	537.0	543.4	830.6	880.2
G18	1434.0	906.7	1303.3	398.3	692.7	470.0	867.5
G12	998.3	748.3	998.3	618.0	340.3	1478.3	863.6
G10	1470.0	854.0	1418.3	367.3	362.8	683.3	859.3
G13	553.3	658.0	856.7	493.3	1581.6	973.3	852.7
G9	1100.0	492.7	665.0	194.0	1807.3	691.7	825.1
G8	993.3	618.3	1216.7	326.7	1416.7	376.7	824.7
G21	1160.0	679.7	908.3	616.0	901.0	571.7	806.1

G6	690.7	943.0	1275.0	381.0	677.1	833.3	800.0
G16	1221.7	759.0	561.7	255.0	1331.6	598.3	787.9
G17	1238.0	680.0	916.7	303.3	838.5	720.0	782.8
G11	1040.0	562.7	1140.0	270.3	748.3	876.7	773.0
G20	865.0	737.7	1293.3	177.3	1159.7	380.0	768.8
G23	1059.7	498.0	986.7	138.0	1178.8	413.3	712.4
G24	795.0	360.7	1091.7	188.7	371.5	510.0	552.9

3.4 Pearson correlations among traits and environments

Strong positive correlations were detected within the phenological trait group: DAF–DAF50 ($r = 0.97$, $p < 0.001$), DAF–MAT50 ($r = 0.94$, $p < 0.001$) and DAF50–MAT50 ($r = 0.96$, $p < 0.001$), confirming tight genetic integration of flowering and maturity timing (Figure 3). PY and GY were significantly correlated ($r = 0.89$, $p < 0.001$), confirming that pod yield is a reliable proxy for grain yield. No significant correlations were detected between yield and phenological traits, indicating that high yield can be combined with extra-early maturity without penalty (Figure 3). Environment correlation network analysis for each trait separately revealed dense, positive networks for phenological traits ($r = 0.53$ – 0.96), indicating consistent genotype ranking across environments for maturity-related traits. In contrast, for PY and GY, networks were sparse with a notable negative correlation between Mgr4 and Tara ($r = -0.58$ and -0.55 respectively), confirming crossover GEI and identifying these as contrasting environments for yield selection (Figure 4).

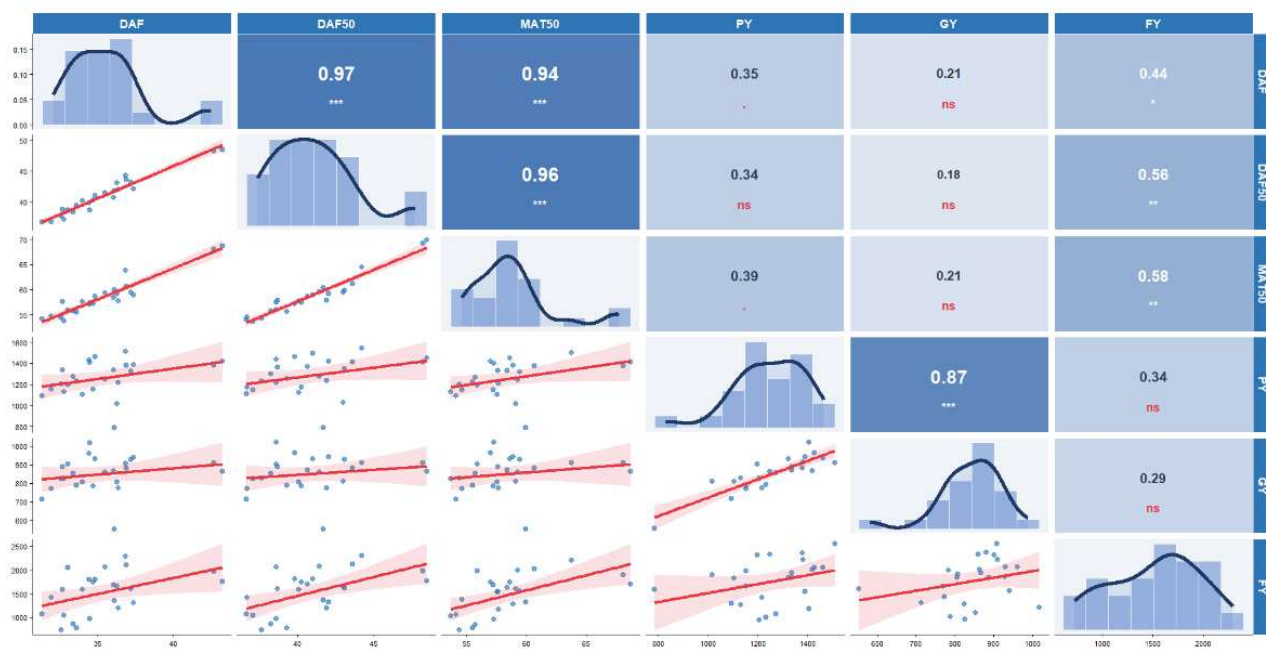
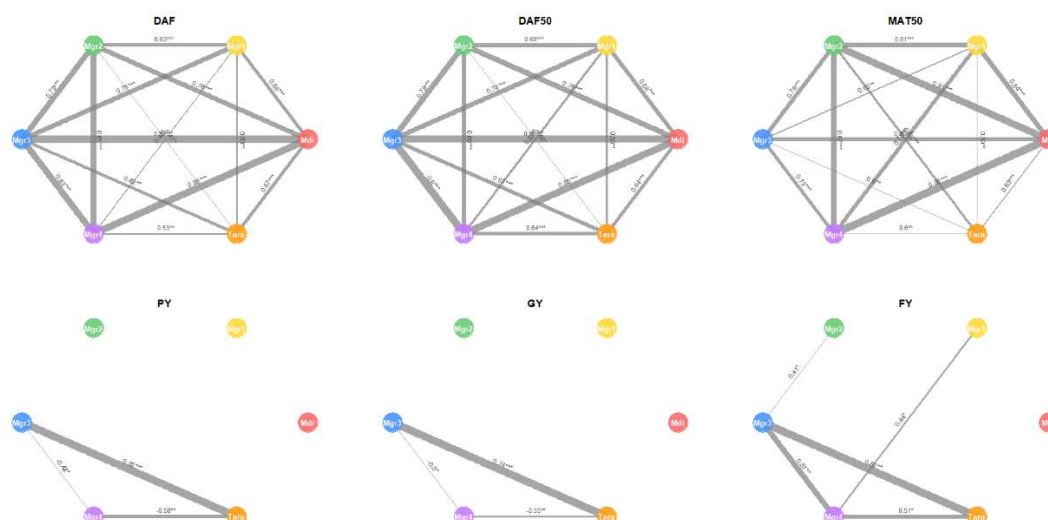


Fig.3 Pairwise Pearson correlation matrix among six agronomic traits (DAF, DAF50, MAT50, PY, GY, and FY) evaluated across 24 cowpea genotypes. The upper panel shows correlation coefficients with significance levels (ns: not significant; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$), the diagonal shows trait distributions, and the lower panel shows scatter plots with regression lines



262

263 **Fig.4** Network-based correlation analysis among six environments (Tara, Mgr1, Mgr2, Mgr3, Mgr4, and Mdi) for
 264 six agronomic traits (DAF, DAF50, MAT50, PY, GY, and FY). Edge thickness represents the magnitude of the
 265 Pearson correlation coefficient and only statistically significant correlations are displayed.

266

267 3.5 GGE biplot analysis

268 3.5.1 Which-won-where pattern

269 The which-won-where pattern of the GGE biplot polygon view based on 24 genotypes and six
 270 environments for four evaluated traits is shown in Figure 5. The first two principal components
 271 (PC1 and PC2) explained 88.71%, 67.28%, 72.23%, and 94.20% of the variation for days to
 272 50% flowering, pod yield, grain yield, and fodder yield respectively. The polygon view revealed
 273 which group of environments consistently shared the best set of genotypes. For days to 50%
 274 flowering (Figure 5a), the biplot was divided into distinct sectors, and the environment Tara
 275 was clearly isolated in a separate sector from the remaining environments (Mgr1, Mgr2, Mgr3,
 276 Mgr4, and Mdi), suggesting the existence of two mega-environments. The winning genotype
 277 in the Tara environment was G5, while genotypes such as G12 and G4 were the best performers
 278 in the Mgr cluster of environments. Genotype G23 was located at a vertex between sectors,
 279 indicating broad adaptation across both groups.

280 For pod yield (Figure 5b), the biplot revealed multiple sectors. Tara was again separated into
 281 its own sector, where G22 or G24 emerged as the top performing genotypes. In the
 282 environments grouping Mgr2 and Mgr4 (lower sector), G4 and G5 were the vertex genotypes.
 283 Environments MDI and Mgr3 appeared near the center of the biplot, suggesting these locations
 284 were less discriminating among genotypes.

285 For grain yield (Figure 5c), the biplot was divided into several sectors. Tara was again located
 286 in an isolated sector on the upper left, where G12 was the winning genotype. Mgr4, positioned
 287 far to the right along PC1, occupied a distinct sector where G2 or G9 was the best performer.
 288 Mgr2, located in the lower-left area, was associated with G1 and G10 as vertex genotypes. Mgr1
 289 and Mdi clustered near the center of the biplot, indicating limited discrimination between
 290 genotypes in those environments. The high PC1 variance explained (50.88%) indicates strong
 291 genotypic main effects driving grain yield variation across environments.

292 For fodder yield (Figure 5d), which showed the highest total variance explained (94.20%), the
 293 biplot identified a dominant PC1 axis, indicating limited genotype-by-environment interaction
 294 relative to genotypic main effects. Mgr4 was isolated far to the right, where G3 or G10 was the
 295 winning genotype. Tara and Mgr1 were positioned near the upper-center area, associated with
 296 G5 and G12 as top performers. G2, G7, and G23 appeared at vertices in other sectors. Overall,
 297 genotypes G12 and G5 showed consistent performance across multiple environments and traits,
 298 suggesting broad adaptation, while G1, G2, and G9 showed more specific adaptation to
 299 environments.

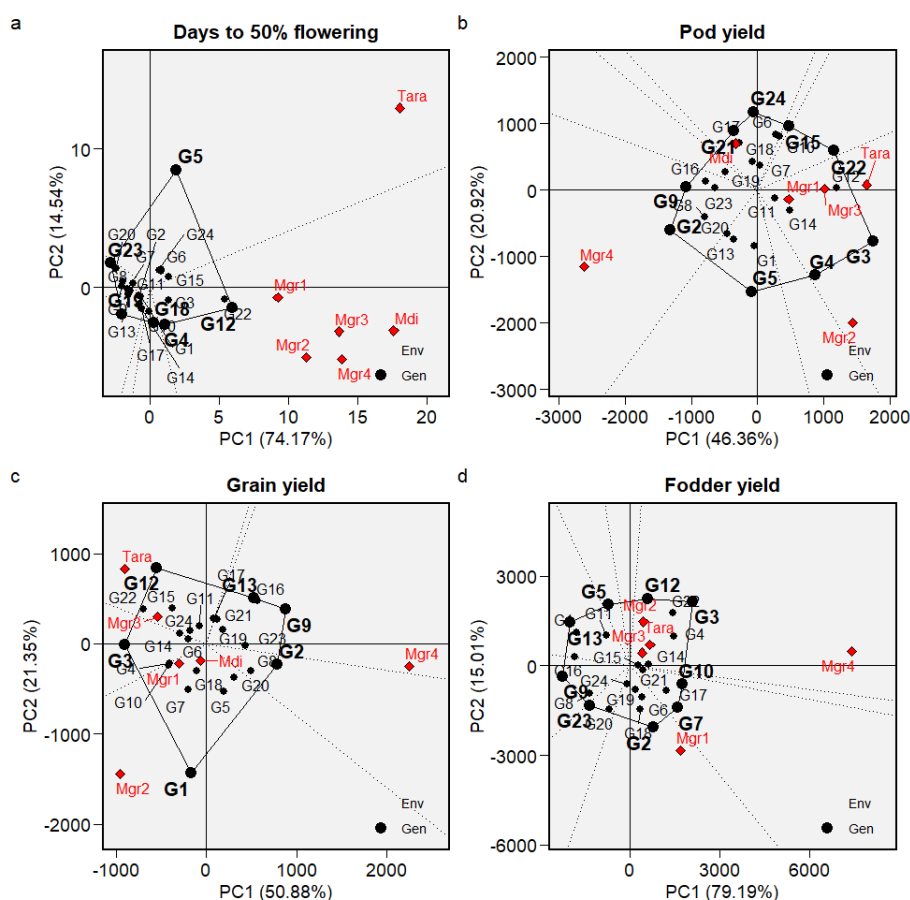


Fig.5 Which-won-where pattern of the GGE biplot polygon view based on 24 cowpea genotypes across six environments for days to 50% flowering (a), pod yield (b), grain yield (c), and fodder yield (d).

3.5.2 Mean vs. Stability Pattern

The mean vs. stability pattern was examined for each identified mega-environment using the Average Environment Coordinate (AEC) view of the GGE biplot. This view simplifies genotype assessment by simultaneously representing mean performance and stability within each mega-environment. In the AEC framework, the abscissa is defined as the line connecting the biplot origin to the average environment coordinate, with the arrow direction indicating increasing genotypic mean performance. The AEC ordinate, perpendicular to the abscissa and passing through the biplot origin, serves as the stability axis. Genotypes positioned close to the ordinate exhibit consistent performance across environments, while those positioned farther from it in either direction display greater sensitivity to environmental variation and are therefore considered less stable. The results obtained for the 'mean vs. stability' pattern of the GGE biplot revealed 88.71%, 67.28%, 72.23%, and 94.20% of $G + G \times E$ variation for days to 50% flowering, pod yield, grain yield, and fodder yield, respectively.

For days to 50% flowering (Figure 6a), the environment Tara was positioned far to the right along the AEC abscissa with a large deviation from the axis, indicating that it was the earliest-flowering and most discriminating environment. Genotypes grown at Tara reached 50% flowering earlier than at any other location, likely reflecting the hotter and more arid conditions that accelerate phenological development at this site. Despite its early-flowering character, Tara showed high instability (large deviation from the AEC abscissa), indicating that genotype rankings for DAF50 were inconsistent across seasons at this location. Environments Mgr3, Mdi, Mgr2, and Mgr4 are also ranked on the right side of the abscissa, reflecting relatively late-flowering conditions with moderate instability. Mgr1 was positioned near the center, suggesting intermediate flowering time and moderate stability as a test environment. Among genotypes, G12 and G22 were the latest-flowering accessions and showed relatively good stability due to their proximity to the AEC abscissa. Genotype G5, positioned high on the ordinate axis, was an early flowering but unstable genotype. Many accessions, including G23, G24, G3, G15, G19, and G14, clustered near the origin on the left side of the abscissa, indicating early and stable flowering behavior across environments.

For pod yield (Figure 6b), the environment Mgr4 was positioned far to the left along the AEC abscissa, indicating it was the lowest-yielding environment, while Mgr2 ranked to the right with high pod yield but some instability. Tara, Mgr1, and Mgr3 were located near the center of the

biplot, suggesting moderate discriminating ability for this trait. Among genotypes, G3 was the highest-yielding accession but showed low stability due to its distance from the AEC abscissa. Genotypes G24, G15, G22, and G10 combined high pod yield with moderate stability, making them desirable candidates. Genotypes G1 and G14, positioned close to the AEC abscissa near the origin, showed moderate yield with good stability across environments.

For grain yield (Figure 6c), among environments, Mgr4 was positioned far to the right along the AEC abscissa, indicating it was the highest-yielding location, while Mgr2 was the poorest-yielding environment. Tara was associated with low grain yield and high instability. Among genotypes, G9 emerged as the highest-yielding and relatively stable accession, followed by G2.

For fodder yield (Figure 6d), the very high PC1 variance explained (79.19%) indicates that genotypic main effects dominated over G×E interaction, reflecting strong repeatability of performance rankings across environments. Mgr4 was by far the highest-yielding environment for fodder, while Mgr1 was the least productive. Genotypes G3, G22, G12, and G5 showed the highest fodder yields, positioned to the upper-right area of the biplot. Genotypes G2, G7, and G10 were ranked lower for fodder yield. Tara was positioned near the center of the biplot, indicating moderate fodder yield and relatively stable behaviors. Genotypes G16, G13, and G11, close to the AEC abscissa, combined moderate fodder yield with good stability across the tested environments.

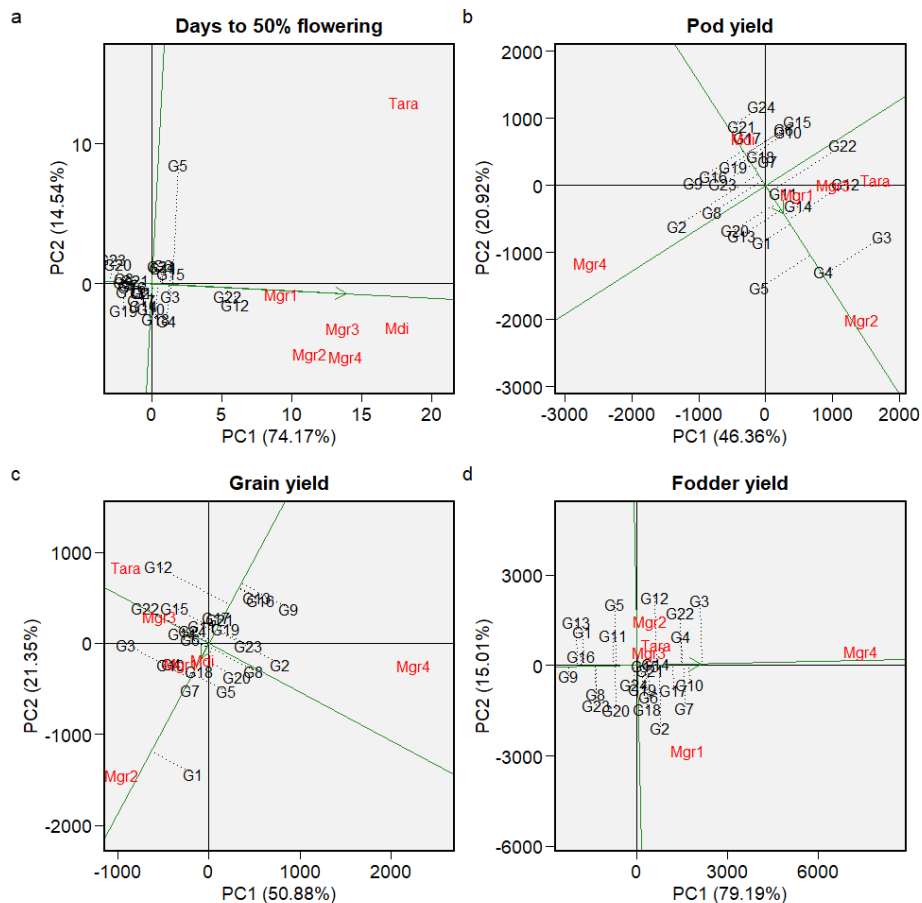


Fig.6 Mean vs. stability pattern of the GGE biplot (Average Environment Coordinate view) based on 24 cowpea genotypes across six environments for days to 50% flowering (a), pod yield (b), grain yield (c), and fodder yield (d).

3.6 Finlay-Wilkinson stability regression

Finlay-Wilkinson regression classified the 24 genotypes into three adaptation groups based on the regression slope (β) of individual genotype grain yield. Figure 7 shows plots of each genotype's grain yield against the environmental index. Genotypes adapted to favorable environments (red lines) showed the steepest positive slopes and the widest spread of predicted yields, reflecting strong responsiveness to increasing environmental productivity; the line for G1 diverged most sharply from the mean response, consistent with its extreme slope ($\beta = 2.43$) and the highest model fit among favorable-adapted genotypes ($R^2 = 0.85$). Genotypes adapted to poor environments (blue lines) showed comparatively flat slopes clustered below the mean response line, with G12 and G13 displaying the shallowest slopes ($\beta = 0.29$ and 0.33 , respectively) and correspondingly low coefficients of determination ($R^2 = 0.04$ and 0.05), indicating that their grain yield was largely unresponsive to, and poorly predicted by, the

environmental index. Broadly stable genotypes (green lines) tracked closely around the mean response line across the full range of environmental productivity, with G5 ($\beta = 1.01$) lying almost exactly on the population mean slope. Eight genotypes showed specific adaptation to favorable environments ($\beta > 1.2$): G1 ($\beta = 2.43$), G7 ($\beta = 1.54$), G10 ($\beta = 1.38$), G20 ($\beta = 1.33$), G18 ($\beta = 1.29$), G2 ($\beta = 1.25$), G23 ($\beta = 1.24$), and G8 ($\beta = 1.22$). Seven genotypes were classified as broadly stable ($0.8 \leq \beta \leq 1.2$): G24 ($\beta = 1.06$), G11 ($\beta = 1.05$), G5 ($\beta = 1.01$), G19 ($\beta = 0.95$), G17 ($\beta = 0.94$), G4 ($\beta = 0.92$), and G9 ($\beta = 0.91$). Nine genotypes showed specific adaptation to poor environments ($\beta < 0.8$): G12 ($\beta = 0.29$), G13 ($\beta = 0.33$), G22 ($\beta = 0.54$), G21 ($\beta = 0.59$), G15 ($\beta = 0.70$), G16 ($\beta = 0.73$), G14 ($\beta = 0.74$), G3 ($\beta = 0.79$), and G6 ($\beta = 0.79$).

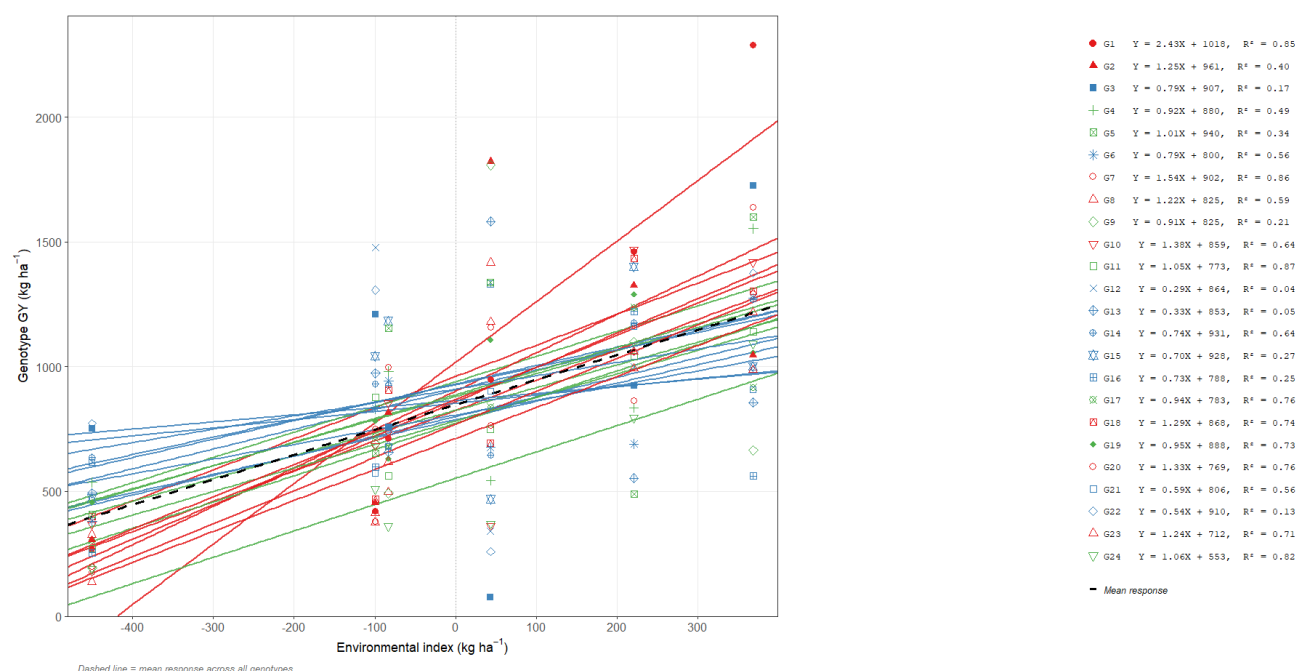


Fig.7 Finlay-Wilkinson regression of grain yield (GY) for 24 cowpea genotypes across six environments. Each line represents a genotype colored by adaptation type: broadly stable (green), specifically adapted to favorable environments (red), and specifically adapted to poor environments (blue). The dashed black line represents the average regression across all genotypes.

Mean grain yield did not differ markedly among the three adaptation groups (favorable = 864.1 kg ha⁻¹; broadly stable = 805.9 kg ha⁻¹; poor = 865.1 kg ha⁻¹), confirming that the FW slope captures environmental responsiveness independently of overall productivity rather than simply separating high- from low-yielding genotypes (Figure 8). However, the coefficient of determination declined systematically from the favorable group (mean $R^2 = 0.69$) to the broadly stable group (mean $R^2 = 0.60$) to the poor-environment group (mean $R^2 = 0.30$), indicating that

genotypes adapted to poor environments are also the least predictable in their response to the environmental gradient — a pattern with direct implications for selection confidence in stress-prone target environments. Among the broadly stable group, G5 and G4 combined regression slopes closest to unity (1.01 and 0.92, respectively) with above-average mean grain yield (939.8 and 880.2 kg ha⁻¹), distinguishing them as the most reliable candidates for wide adaptation within this classification.

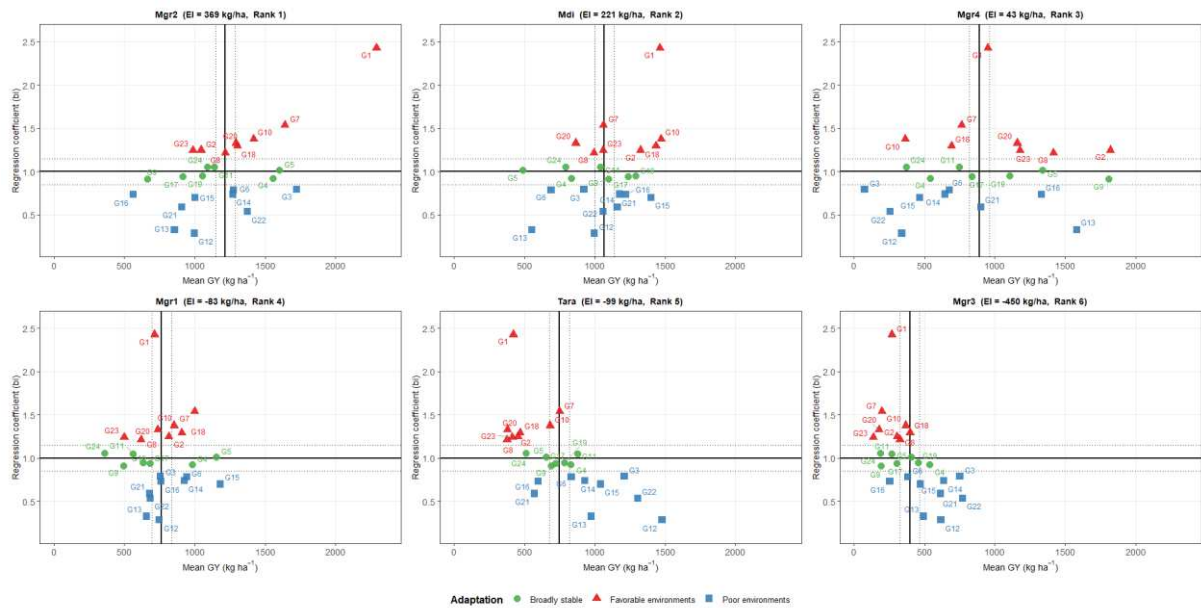


Fig.8 relationship between sensitivity (slope from the regression model prediction) and grain yield as a function of environmental index.

3.7 Lin and Binns' superiority index and Huehn's rank stability

The slope graphs (Figure 9) comparing mean yield (panel a), Pi (panel b), and S1 rank stability (panel c) between the three highest-yielding environments (Mgr2, Mdi, and Mgr4) and the three lowest-yielding environments (Mgr1, Tara, and Mgr3) reveal contrasting patterns of genotype response across environment quality groups. In panel (a), the majority of genotypes showed declining mean yields from high- to low- yielding environments, as expected, but the magnitude of decline differed substantially. G1 and G7 showed the steepest decline, consistent with their high FW slopes and specific adaptation to favorable conditions. G14 and G19 displayed comparatively shallow declines, maintaining competitive yields even in the low-productivity environment group. In panel (b), Pi values increased from high- to low-yielding environments for most genotypes, reflecting greater deviation from the environment maximum under stress conditions. G24 maintained the highest Pi (worst superiority) in both environmental groups, confirming its uniformly below-average performance regardless of productivity level. In panel

(c), S1 rank stability values changed between environment groups for several genotypes, with G1 and G7 showing the most pronounced rank instability in the low-yielding environment group, further evidence of their environment-specific adaptation. G14, G19, G5, and G4 maintained the most consistent ranks between the two environment groups, reinforcing their classification as broadly adapted genotypes. Overall, Figure 9 and Table 4 confirm that G5, G4, G14, and G19 represent the most desirable genotypes, combining above-average grain yield with consistent superiority and stable ranking across contrasting agro-ecological environments.

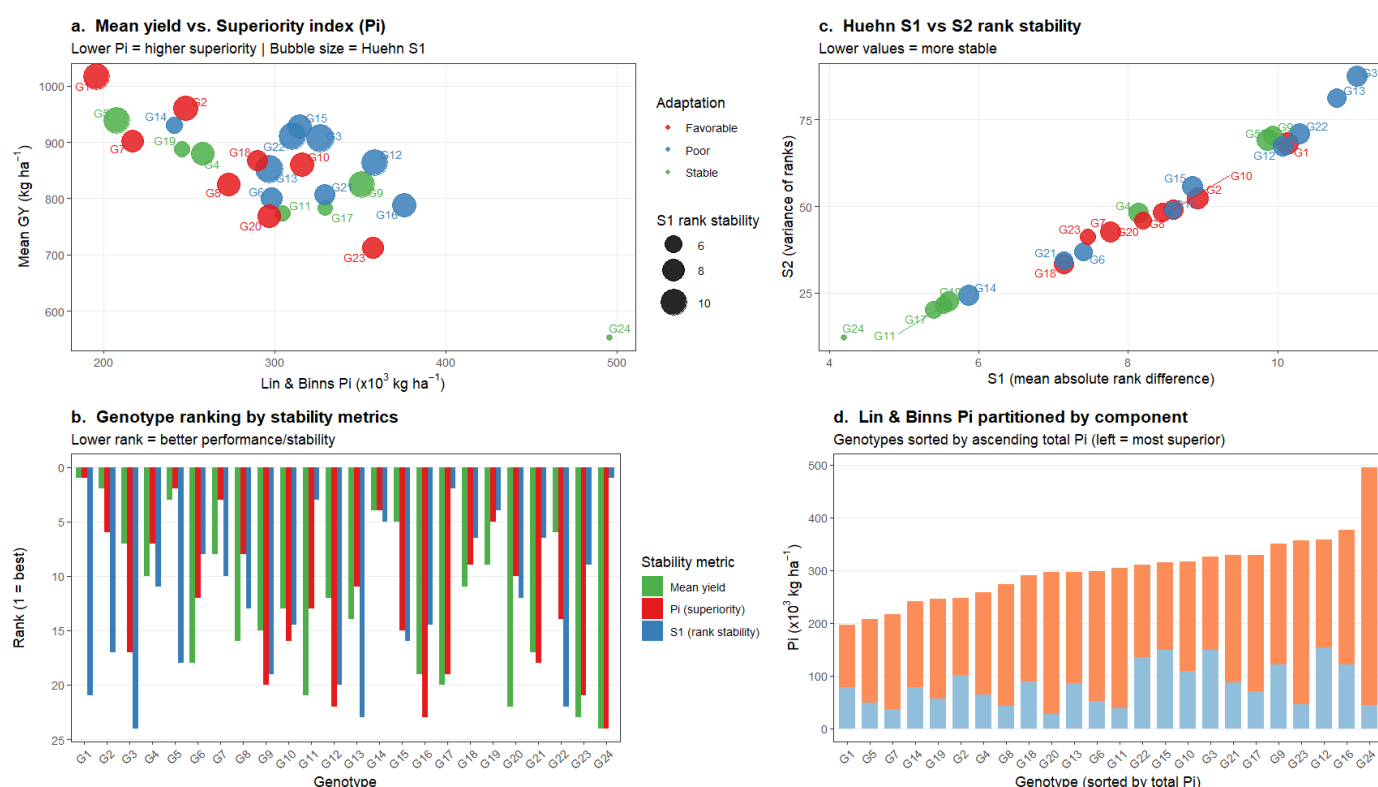


Fig.9 Integrated evaluation of cowpea genotype performance and stability across six environments using Lin and Binns' superiority index (Pi) and Huehn's non-parametric stability statistics. (a) Mean grain yield versus Pi (bubble size represents Huehn's S1); (b) genotype rankings based on mean grain yield, Pi, and S1; (c) relationship between Huehn's S1 and S2 stability parameters; and (d) partitioning of Lin and Binns' superiority index into genetic and genotype $\times$ environment interaction ($G \times E$) components. Lower Pi, S1, and S2 values indicate greater superiority and stability across environments.

The Lin and Binns superiority index (Pi) and Huehn's non-parametric rank stability parameters (S1, S2, S3) provided independent, distribution-free validation of the parametric stability classifications. Pi values ranged from 195,790 (kg ha^{-1})² for G1 (Pi rank 1, highest superiority) to 495,673 (kg ha^{-1})² for G24 (Pi rank 24, lowest superiority). The top five genotypes by Pi were G1 (195,790), G5 (207,502), G7 (216,876), G14 (241,089), and G19 (246,048), all of

which had mean grain yields above 880 kg ha⁻¹. The partitioning of Pi into genetic deviation and G×E interaction components revealed important biological differences among these top performers. G7 had the highest proportion of Pi attributable to the genetic component (83.2%), indicating that its superiority over the environment maximum was primarily driven by a consistently high genotypic yield potential rather than environment-specific responsiveness. Similarly, G5 (76.3%) and G19 (76.9%) showed predominantly genetic superiority with relatively low G×E interaction components (49,145 and 56,949 kg ha⁻¹)² respectively, indicating that their competitive performance was stable across contrasting environments. By contrast, G1, despite ranking first in total Pi, had only 60.0% of its Pi attributable to the genetic component, with 78,270 kg ha⁻² attributable to G×E interaction—the largest interaction component among the top five Pi genotypes. This confirms that G1's superiority is substantially environment-dependent, consistent with its extreme Finlay-Wilkinson slope ($b = 2.43$). G24, the lowest-ranking genotype in both mean yield (552.9 kg ha⁻¹) and Pi superiority, had 91.0% of its Pi attributable to the genetic component and only 44,795 (kg ha⁻¹)² to interaction, confirming that its poor performance relative to the environment maximum was consistent and repeatable across all environments rather than environment-specific; it was uniformly outperformed regardless of productivity level.

For S1, the five most rank-stable genotypes were G24 (S1 = 4.2, rank 1), G17 (S1 = 5.4, rank 2), G11 (S1 = 5.5, rank 3), G19 (S1 = 5.6, rank 4), and G14 (S1 = 5.9, rank 5). The S2 and S3 rankings were fully concordant: G24 (S2 rank 1, S3 rank 1), G17 (S2 rank 2, S3 rank 3), and G11 (S2 rank 3, S3 rank 2) again ranked as the most stable. However, G24 and G17 combined this high rank stability with below-average mean yields (552.9 and 782.8 kg ha⁻¹, respectively), meaning their stable ranking reflects consistently average or below-average performance rather than consistently competitive performance, a stability without agronomic value. Among the top-ranked S1 genotypes, only G19 (S1 = 5.6, rank 4, mean GY = 887.6 kg ha⁻¹) and G14 (S1 = 5.9, rank 5, mean GY = 930.9 kg ha⁻¹) combined low rank variability with above-average grain yield, making them the most agronomically valuable genotypes identified by the Huehn framework. G1, despite its highest mean yield (1017.7 kg ha⁻¹) and top Pi rank, ranked 21st for S1 (S1 = 10.1), confirming that its performance ranking fluctuates dramatically across environments entirely consistent with its favorable-environment classification. The five least rank-stable genotypes were G3 (S1 = 11.1, rank 24), G13 (S1 = 10.8, rank 23), G22 (S1 = 10.3, rank 22), G12 (S1 = 10.1, rank 20), and G1 (S1 = 10.1, rank 21), all showing strong but environment-dependent responses.

Table 4: Mean grain yield, Lin and Binns' superiority index (Pi), and Huehn's nonparametric stability statistics for 24 cowpea genotypes evaluated across six environments.

Geno	Mean_GY	Rank	Pi_total	Pi_genetic	Pi_interact	Pct_genetic	S1	Rank_S1	S2	Rank_S2	S3	Rank_S3
G1	1017.7	1.0	195790.0	117520.5	78269.5	60.0	10.1	21.0	68.0	19.0	3.6	19.0
G2	960.8	2.0	247958.3	146731.5	101226.8	59.2	8.9	17.0	52.4	16.0	3.3	17.0
G3	907.2	7.0	326364.0	177190.2	149173.8	54.3	11.1	24.0	87.6	24.0	4.6	24.0
G4	880.2	10.0	257839.5	193629.8	64209.7	75.1	8.1	11.0	48.3	13.0	3.4	18.0
G5	939.8	3.0	207502.2	158356.8	49145.4	76.3	9.9	18.0	69.2	20.0	3.8	21.0
G6	800.0	18.0	297797.6	246764.5	51033.1	82.9	7.4	8.0	37.0	8.0	2.2	9.0
G7	901.8	8.0	216876.1	180429.4	36446.7	83.2	7.8	10.0	42.6	10.0	2.8	14.0
G8	824.7	16.0	272860.1	229711.8	43148.3	84.2	8.5	13.0	48.2	12.0	2.0	6.0
G9	825.1	15.0	350664.8	229452.9	121211.9	65.4	9.9	19.0	70.3	21.0	2.6	13.0
G10	859.3	13.0	315925.0	206867.4	109057.6	65.5	8.6	14.5	49.1	15.0	3.1	15.0
G11	773.0	21.0	304808.8	266115.5	38693.2	87.3	5.5	3.0	21.5	3.0	1.3	2.0
G12	863.6	12.0	358066.8	204114.6	153952.2	57.0	10.1	20.0	67.4	18.0	3.2	16.0
G13	852.7	14.0	296733.3	211132.7	85600.6	71.2	10.8	23.0	81.2	23.0	3.7	20.0
G14	930.9	4.0	241088.9	163371.0	77717.9	67.8	5.9	5.0	24.3	5.0	2.5	11.0
G15	927.7	5.0	314595.3	165226.0	149369.3	52.5	8.9	16.0	55.8	17.0	4.2	23.0
G16	787.9	19.0	375887.7	255364.3	120523.4	67.9	8.6	14.5	49.0	14.0	2.5	10.0
G17	782.8	20.0	329483.3	259036.7	70446.6	78.6	5.4	2.0	20.2	2.0	1.5	3.0
G18	867.5	11.0	290123.2	201627.2	88496.0	69.5	7.1	6.5	33.5	6.0	2.6	12.0
G19	887.6	9.0	246048.4	189099.7	56948.7	76.9	5.6	4.0	22.7	4.0	2.0	5.0
G20	768.8	22.0	296331.4	269148.7	27182.7	90.8	8.2	12.0	45.8	11.0	2.2	8.0
G21	806.1	17.0	329307.6	242494.9	86812.8	73.6	7.1	6.5	34.3	7.0	2.1	7.0
G22	909.7	6.0	310322.7	175709.2	134613.5	56.6	10.3	22.0	70.8	22.0	4.0	22.0
G23	712.4	23.0	357160.9	312141.4	45019.5	87.4	7.5	9.0	41.2	9.0	1.7	4.0
G24	552.9	24.0	495673.2	450878.4	44794.8	91.0	4.2	1.0	12.2	1.0	0.8	1.0

3.8 Wricke ecovalence and yield stability index

Wricke ecovalence (Wi) ranked G5, G4, and G19 among the most stable genotypes (lowest Wi), while G1, G7, and G10, despite their high mean yields, showed the highest ecovalence values, reflecting their strong but inconsistent GEI contributions. The Yield Stability Index (YSi) bubble chart, which plots mean GY against Wi with bubble size proportional to YSi desirability, placed G5 and G4 in the ideal upper-left quadrant (high yield, high stability), confirming their priority status for wide release. G1 occupied the high-yield but low-stability quadrant, suitable for favorable-environment-only recommendation. G24 was consistently in the low-yield, low-stability quadrant (S2 Table).

3.9 Hierarchical cluster analysis

Hierarchical cluster analysis based on Ward's D² method grouped the 24 cowpea genotypes into four distinct clusters (Figure 10). The normalized trait profiles of each cluster are illustrated in

the accompanying bar chart (Figure 8, right panel). Cluster 1 was the largest group, comprising 11 genotypes (G1, G2, G3, G4, G5, G7, G10, G14, G15, G18, and G19). This cluster was characterized by intermediate days to first flower (mean DAF = 35.4 days), intermediate days to 50% flowering (DAF50 = 41.1 days) and maturity (MAT50 = 58.8 days), and the highest pod yield (PY = 1364.6 kg ha⁻¹) and grain yield (GY = 916.4 kg ha⁻¹) among all clusters. Fodder yield (FY) was also high (mean = 1751.8 kg ha⁻¹), with considerable variability within the cluster (964.2–2290.4 kg ha⁻¹). The normalized score bar chart confirmed the high scores of Cluster 1 for PY, GY, and FY relative to the other clusters. These genotypes represent broadly productive accessions combining good grain and fodder output with intermediate phenology.

Cluster 2 included five genotypes (G6, G11, G17, G21, and G24). This cluster showed similar phenological characteristics to Cluster 1 (DAF = 35.5 days, DAF50 = 41.4 days, MAT50 = 58.3 days) but was markedly inferior in yield components, with the lowest pod yield (PY = 1054.9 kg ha⁻¹) and the lowest grain yield (GY = 744.4 kg ha⁻¹) of all clusters. Notably, G24 had the lowest pod yield (785.1 kg ha⁻¹) and grain yield (552.9 kg ha⁻¹) of all 24 genotypes. Fodder yield was moderate (mean FY = 1499.9 kg ha⁻¹). The normalized bar chart reflected low scores for PY and GY in this cluster. Cluster 2 genotypes are therefore characterized by average phenology but below-average productivity.

Cluster 3 was the smallest group, consisting of only two genotypes: G12 and G22. This cluster was clearly distinguished from all others by its late phenology, recording the highest values for days to first flower (DAF = 43.0 days), days to 50% flowering (DAF50 = 48.3 days), and days to maturity (MAT50 = 68.4 days)—approximately 10 days later than the other clusters. Despite this late maturity, Cluster 3 genotypes maintained competitive pod yield (PY = 1399.7 kg ha⁻¹) and the highest fodder yield among all clusters (FY = 1856.0 kg ha⁻¹). The normalized score bar chart strikingly confirmed this pattern, with Cluster 3 scoring nearly 100 for DAF, DAF50, and MAT50 while also scoring highest for FY. These two genotypes may be of interest for environments where a longer growing cycle can be accommodated and high biomass production is a priority.

Cluster 4 comprises six genotypes (G8, G9, G13, G16, G20, and G23). This cluster was characterized by the earliest phenology of all groups, with the lowest mean values for DAF (32.6 days), DAF50 (37.6 days), and MAT50 (54.7 days). However, early maturity was associated with the lowest overall productivity: pod yield (PY = 1180.9 kg ha⁻¹), grain yield (GY = 795.3 kg ha⁻¹), and particularly fodder yield (FY = 979.8 kg ha⁻¹) was all lowest or near lowest among the four clusters. The normalized bar chart showed that Cluster 4 scored near zero for DAF, DAF50, and MAT50 while also recording the lowest scores for FY. These genotypes may nonetheless be relevant

for very short growing seasons or as parents in breeding programs targeting early maturity, if yield penalties can be mitigated through other traits.

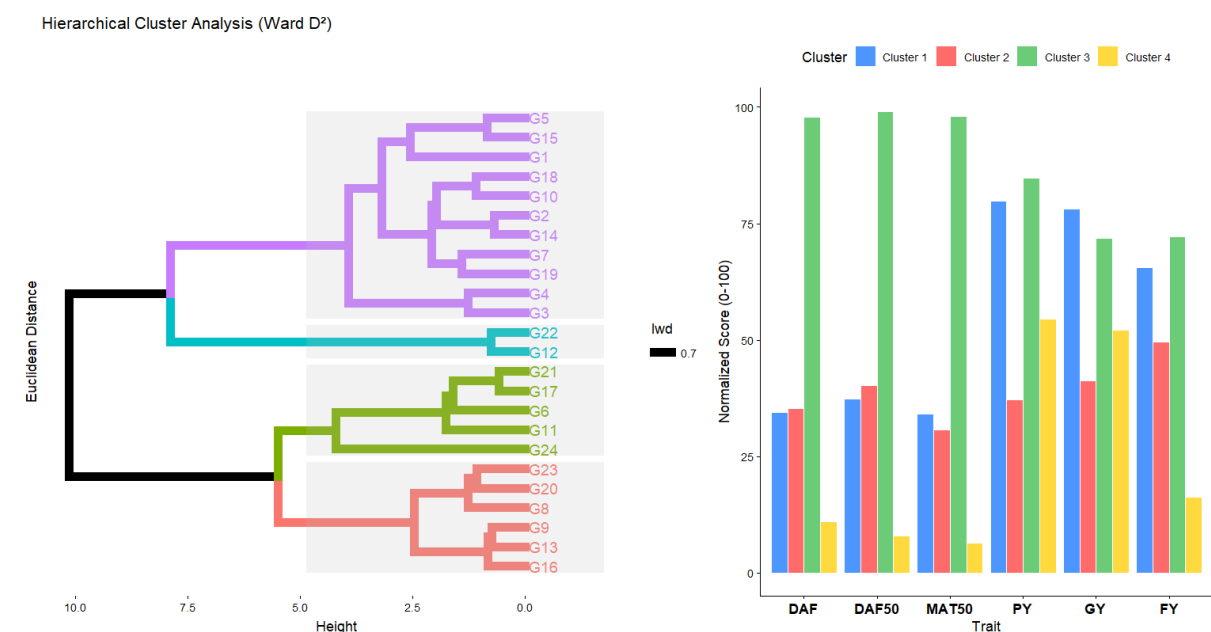


Fig.10 Hierarchical cluster analysis (Ward's D²) and normalized trait profiles of 24 cowpea genotypes based on six agronomic traits (DAF, DAF50, MAT50, pod yield, grain yield, and fodder yield).

3.10 Radar chart: multi-trait profiles of the top 10 genotypes

The radar chart (Figure 11) provides a holistic visual comparison of the top 10 genotypes by mean GY across all six traits simultaneously, with each trait normalized to a 0–100 scale to enable direct comparison across different units. G1, the highest-yielding genotype (1017.7 kg ha⁻¹), displays the largest overall polygon area in the radar chart, reflecting above-average performance across most traits. However, its phenological scores (DAF = 34.0, MAT50 = 57.7) are among the highest of the top 10, meaning it is relatively later maturing than the ideal extra-early type. Its FY is moderate. The large and asymmetric shape of G1's radar polygon reflects its unequal performance across traits — very strong on yield but less competitive on phenology. This profile is consistent with its Finlay-Wilkinson classification as a favorable-environment-adapted genotype. G5 (939.8 kg ha⁻¹) shows the most balanced radar polygon among the top performers—high normalized GY score, acceptable FY, early phenology (DAF = 33.5 days), and moderate DAF50 and MAT50 values. The near-circular shape of G5's radar profile is the hallmark of a broadly adapted, multi-trait stable genotype. This visual pattern directly confirms its Finlay-Wilkinson broad stability classification ($b = 1.014$) and its placement in the ideal

quadrant of the Wricke ecovalence bubble chart. G5 is the genotype whose radar polygon most closely resembles an ideotype for Sahelian production. G4 (880.2 kg ha⁻¹) shows a similarly balanced polygon to G5, with slightly lower GY but very early phenology (DAF = 31.9 days, MAT50 = 56.0 days) and good FY relative to its yield level. The compact, even shape of G4's radar profile reinforces its classification as broadly stable ($b = 0.919$) and confirms it as a priority candidate for wide release, particularly in environments where ultra-early maturity is essential for drought escape. G14 and G15 show radar profiles characterized by very early phenology (DAF = 30.1 and 30.8 days, respectively) combined with moderate yield scores. Their polygons are smaller in the yield sector but well-developed in the phenology sector, consistent with their FW classification as poor-environment-adapted genotypes ($b = 0.736$ and 0.696). G22, together with G12, belongs to the late-maturing group (DAF = 42.7 days, MAT50 = 68.1 days) with the second highest fodder yield in the panel (FY = 1,959.4 kg/ha). Its radar polygon is characterized by strong FY and PY axes but a comparatively narrow phenology axis, reflecting its later maturity relative to other top-yielding genotypes. G22 may be of specific interest for production systems where a longer growing cycle is agronomically feasible and high fodder biomass is a priority. G19 shows a well-balanced profile similar to G5 and G4, with moderate scores across all traits, supporting its inclusion in the broadly stable category.

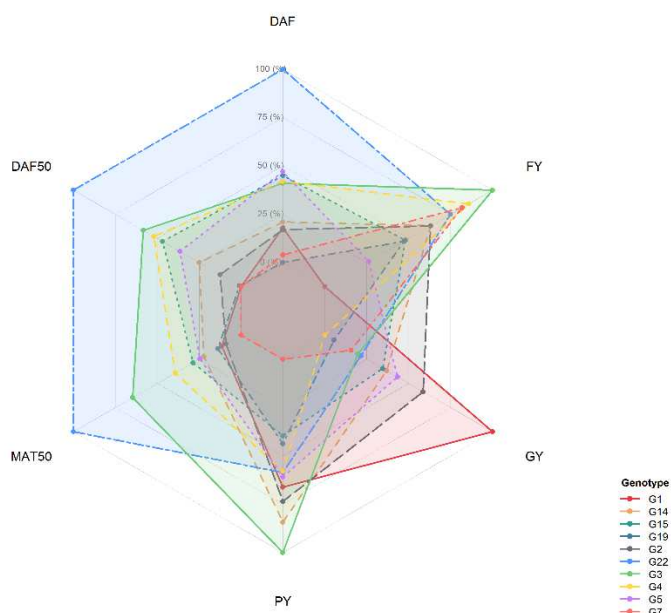


Fig.11 Radar chart comparing the normalized multi-trait performance (DAF, DAF50, MAT50, PY, GY, and FY) of ten selected cowpea genotypes across all six environments. Values are expressed as percentages of the maximum observed value for each trait.

4 Discussion

Multi-environment trials (METs) remain the cornerstone of cultivar evaluation because they provide reliable information on genotype performance, adaptability, and stability across contrasting agroecological zones [30]. This study shows that extra-early cowpea performance in Niger is shaped by environment, genotype, and genotype-by-environment interaction, with the environment exerting the largest influence on yield traits and genotype effects being more important for phenological traits. That pattern is typical of multi-environment trials in drought-prone systems, where rainfall distribution, soil conditions, and local management differences often dominate yield expression. The significant GEI for all traits means that genotype rankings cannot be assumed to remain constant from one location or season to another, which justifies the use of stability analyses rather than relying on a mean yield alone framework [23,27,28]. The wide variation in grain yield across environments also confirms the strong heterogeneity of the Sahelian production context. Some sites, especially the high-performing environments, allowed genotypes to express much higher yield potential, while others imposed enough stress to sharply reduce performance. The fact that phenological traits were much more consistent across environments than yield traits suggests that flowering and maturity are under stronger genetic control and less sensitive to external conditions than yield components. This is useful for breeding because it means earliness can be selected with greater confidence, even when yield remains unstable [19,31,32]. The significant positive correlations noted among phenological traits ($r = 0.94-0.97$, $p < 0.001$) indicate a pleiotropically integrated genetic architecture governing flowering time. The absence of significant correlations between yield and phenological traits confirms that extra-early maturity and high productivity are genetically independent in this genomic panel, validating simultaneous selection for both traits without inherent trade-off penalties. This genetic independence is not universal in cowpea germplasm: [33] noted that earliness can be associated with yield penalties in some populations, particularly in environments with terminal drought stress. The finding that this independence holds in INRAN's extra-early panel is therefore a notable result that validates the breeding strategy of targeting this maturity class specifically for Niger's short-season environments. The significant positive relationship between pod yield and grain yield correlation ($r = 0.87$, $p < 0.001$) is also agronomically important. Because pod yield tracked grain yield closely, pod yield can serve as a useful selection proxy when resources are limited or when grain yield measurement is expensive and time-consuming. For breeding programs, this offers a faster screening route, especially in large segregating populations. It also suggests that improvements in pod

production were translated efficiently into grain production in this set of genotypes. The inter-environment correlation network further revealed a strongly negative correlation between Mgr4 and Tara for grain yield ($r = -0.58$) and pod yield ($r = -0.55$). These negative correlations provide direct quantitative evidence of crossover GEI, a phenomenon where the relative performance of genotypes reverses between environments and are the biological and statistical basis for the mega-environment structure identified by the GGE biplot analysis [34]. Crossover GEI is particularly consequential for variety recommendation because it means that a genotype recommended on the basis of one environment may actively underperform in another [35]. The GGE biplot which-won-where analysis is one of the most informative tools for identifying mega-environments and environment-specific winning genotypes in plant breeding MET data [36]. In the present study, the analysis consistently isolated Tara as a distinct mega-environment from the Mgr cluster across all four traits evaluated. This mega-environment differentiation is analogous to findings reported by Goa et al. [32], who identified three mega-environments and concluded that environments with similar seasonal rainfall and temperature profiles cluster into recommendation domains that share the same winning genotypes. In the present study, the differentiation of Tara from the Mgr cluster likely reflects its markedly lower mean productivity (Tara contributed to the three lowest-yielding environments) and the associated crossover GEI noted in the correlation analysis. The consistent isolation of Tara across multiple traits is particularly informative because it suggests that the environmental factors driving this differentiation are trait-general rather than trait-specific, pointing to fundamental differences in growing conditions between Tara and the other environments rather than environment-by-trait interactions. The high PC1 variance explained for fodder yield (79.19%) further indicates that FY rankings are dominated by genotypic main effects rather than interaction, making this trait the most reliably selectable across environments in this genomic panel, an important advantage for dual-purpose variety development where breeders must simultaneously optimize grain and fodder production [37,38]. The absence of a single genotype that won in both mega-environments simultaneously for grain yield (with G12 leading in the Tara sector while G2 and G9 excelled in the Mgr cluster) confirms that a uniform national variety recommendation is statistically unjustified and would result in systematic underperformance in at least one of the two mega-environments. This finding aligns with the recommendation framework of previous studies that noted that mega-environment delineation should precede variety release decisions in any breeding program operating across diverse agro-ecological zones [32,39,40]. From a food-security policy perspective, the identification of two distinct mega-environments implies that a single national variety recommendation would systematically underserve one zone,

underscoring the need for zone-differentiated seed distribution strategies in Niger's national cowpea seed system rather than a uniform release policy. The Finlay-Wilkinson regression is among the most widely used parametric stability methods in plant breeding because it simultaneously provides an estimate of mean performance and a quantitative measure of environmental responsiveness, enabling genotypes to be classified into biologically meaningful adaptation categories [22,28,41]. The steep slope pattern combined with high R^2 observed in G1 is the hallmark of a genotype that responds strongly and consistently to environmental productivity, performing exceptionally under favorable conditions but dropping sharply under stress. A similar pattern was reported by Nafi et al. [42] for MN-Clearwater and TLI-C5 in intermediate wheatgrass, where the two highest-yielding populations had slopes significantly greater than 1, indicating above-average sensitivity to favorable conditions. The practical recommendation from both studies is identical: such genotypes should be targeted specifically to high-potential environments rather than recommended for wide release. A key finding requiring specific discussion is the reclassification of G14 ($\beta = 0.74$) and G15 ($\beta = 0.70$) as poor-environment genotypes despite their belonging to Ward Cluster 1, the highest-yielding hierarchical cluster. This apparent contradiction is resolved by recognizing that cluster analysis groups genotypes by their grand mean performance across all environments [43], while the FW slope captures how performance varies with environmental productivity [44]. G14 and G15 maintain competitive grand mean yields (930.9 and 927.7 kg ha⁻¹, ranking 4th and 5th overall) because they perform consistently at or above average across both good and poor environments; their low FW slopes confirm that this consistency is expressed precisely by not benefiting disproportionately from favorable conditions, a pattern of genuine stress buffering rather than high-input responsiveness. This distinction is directly analogous to the contrast between Rush ($\beta = 0.45$, low responsiveness, stable ranking) and MN-Clearwater ($\beta = 1.4$, high responsiveness, unstable ranking) described by Nafi et al. [42], and confirms that stability and productivity, while correlated in some germplasm, operate as semi-independent genetic dimensions in this cowpea panel. Breeders should therefore be cautious about using cluster membership as a proxy for stability classification without explicit regression-based validation. The broadly stable genotypes G5 ($\beta = 1.01$) and G4 ($\beta = 0.92$) combined slopes closest to unity with above-average mean grain yields (939.8 and 880.2 kg ha⁻¹, 3rd and 10th overall), identifying them as the genotypes that best satisfy the dual requirement of high productivity and broad adaptability. Wricke's ecovalence corroborated this classification: G5, G4 and G19 ranked among the lowest Wi contributors to the total GEI sum of squares, while G1, G7, and G10 ranked highest despite their superior mean yields. The corroboration of the FW regression

663 by Wricke's ecovalence of two parametric frameworks based on entirely different mathematical
664 principles, is particularly meaningful because it substantially reduces the risk of method-
665 specific artifacts in the stability classification. When two independent parametric stability
666 metrics converge on the same genotypes as broadly stable (G5 and G4) and the same genotypes
667 as environment-responsive specialists (G1, G7), this convergence itself constitutes evidence
668 that the classification reflects genuine biological differences in adaptation strategy rather than
669 statistical noise [45], consistent with reports that parametric and non-parametric stability
670 measures are strongly inter-correlated and can be used as mutual validation in multi-
671 environment trials [46]. The non-parametric [24,46] superiority index provided independent,
672 distribution-free validation of the parametric stability classifications. Non-parametric methods
673 are particularly valuable when data deviate from normality distributions, as commonly occurs
674 in MET data with highly variable environments [47,48]. Their concordance with the parametric
675 results in the present study therefore substantially strengthens confidence in the overall stability
676 classification. The five most superior genotypes by Pi were G1 (195,790), G5 (207,502), G7
677 (216,876), G14 (241,089), and G19 (246,048), all with mean grain yields above 880 kg ha⁻¹.
678 This confirms that these genotypes consistently approached the environment-specific yield
679 across the six test environments, a criterion that was identified as the most agronomically
680 relevant measure of genotype superiority [49]. The Pi partitioning revealed important biological
681 differences: G7 had the highest proportion of Pi attributable to the genetic deviation component
682 (83.2%), indicating that its competitive performance was primarily driven by stable genotypic
683 superiority rather than environment-specific responsiveness. G5 (76.3%) and G19 (76.9%)
684 showed similarly high genetic contributions with small GxE interaction components (49,145
685 and 56,949, respectively), confirming that their competitive performance was broadly
686 expressed across environments. By contrast, G1, despite ranking first in total Pi, had only 60.0%
687 genetic contribution with the largest GxE interaction component among the top five (78,270),
688 confirming environment-dependent superiority entirely consistent with its extreme FW slope
689 ($\beta = 2.43$) and paralleling the findings of Nafi et al. [42] for highly responsive wheatgrass
690 populations. G24 had 91.0% of its Pi attributable to the genetic deviation component and the
691 smallest interaction component (44,795), reflecting uniformly below-average performance
692 across all environments. This represents the agronomically worst scenario: a genotype that
693 consistently fails to approach the environmental maximum, regardless of environmental
694 productivity. G24 simultaneously high rank stability by S1 ($S1 = 4.2$, rank 1) further illustrates
695 a critical interpretive point that is often overlooked in stability analyses: rank stability measures
696 consistency of relative ranking, not quality of performance. For Huehn's S1, only G14 ($S1 =$

5.9, rank 5, mean GY = 930.9 kg ha⁻¹) and G19 (S1 = 5.6, rank 4, mean GY = 887.6 kg ha⁻¹) combined low rank variability with above-average grain yield. G1, despite its highest mean yield (1,017.7 kg ha⁻¹), ranked 21st for S1, confirming that its performance ranking fluctuates dramatically across environments. These S1 findings parallel the results of Goa et al. [32], who identified genotypes as stable and high-yielding cowpea genotypes using AMMI stability values and GGE biplots in Ethiopia—demonstrating that non-parametric rank stability consistently identifies a different and complementary class of desirable genotype compared to mean-yield ranking alone. The significant chi-square test for S2 ($p < 0.01$) but non-significant test for S1 ($p > 0.05$) in the present study indicates that while genotype mean ranks were similar across environments (S1), the variance of those ranks differed significantly among genotypes (S2), confirming meaningful heterogeneity in the stability of relative performance that is biologically real and agronomically relevant. Ward D2 hierarchical clustering identified four phenotypically coherent groups. The internal stability heterogeneity within Cluster 1—containing genotypes from all three FW adaptation categories—confirms that productivity and stability are statistically distinct dimensions requiring explicit multi-method stability analysis beyond simple cluster-based pre-selection. Cluster 3 (G12, G22) showed markedly late phenology (MAT50 = 68.4 days) combined with the highest fodder yield of all clusters (1,856 kg ha⁻¹), identifying a distinct niche for irrigated or long-season dual-purpose systems. Clusters 2 and 4 contained the consistently lowest-yielding genotypes and are not recommended for advancement. The radar chart confirmed G5 as the genotype with the most balanced multi-trait profile across all six traits, most closely approaching the dual-purpose Sahelian ideotype combining early maturity, competitive grain yield, and adequate fodder production.

5 Conclusion

Twenty-four extra-early cowpea genotypes were evaluated across six environments in Niger using an integrated seven-method analytical pipeline. Significant genotype-by-environment interaction was detected for all six traits ($p < 0.001$), with environment dominating yield variation ($F = 59.23\text{--}242.01$) and the GEI sum of squares exceeding the genotype main effect for grain yield. The GGE biplot which-won-where analysis identified two distinct mega-environments, with Tara consistently isolated from the Mgr cluster across all traits evaluated, confirming that a uniform national variety recommendation cannot adequately serve all of Niger's cowpea production zones. The five most superior genotypes by Lin and Binns Pi were G1 (195,790), G5 (207,502), G7 (216,876), G14 (241,089), and G19 (246,048). Among these, G14 and G19 uniquely combined high Pi superiority with the best Huehn S1 rank stability scores (ranks 5 and 4 respectively) and above-average mean yields (930.9 and 887.6 kg ha⁻¹),

making them the most agronomically valuable genotypes for stress-prone and low-input environments. G5 and G4, classified as broadly stable by Finlay-Wilkinson regression ($b = 1.01$ and 0.92) and confirmed by Wricke ecovalence and radar chart profiling, are proposed as promising candidates for broader multi-locational testing wide national release across Niger's diverse agro-ecological zones. G1 and G7, as favorable-environment genotypes with the highest mean yields ($1,017.7$ and 901.8 kg ha^{-1}) and steep response slopes ($b = 2.43$ and 1.54), are recommended specifically for high-potential irrigated or favorable environments. The convergence of seven independent analytical frameworks on a coherent tiered recommendation provides particularly robust scientific support not only for INRAN's variety-release decisions but also for zone-specific seed distribution policy aimed at strengthening cowpea-based food security across Niger's diverse production systems.

Declarations

Ethics approval and consent to participate

The collection, use, and evaluation of *Vigna unguiculata* (L.) Walp. plant material in this study complied with applicable local and national guidelines and regulations of the Republic of Niger. The cowpea genotypes were cultivated and evaluated under field conditions as part of the cowpea breeding program of the Institut National de la Recherche Agronomique du Niger (INRAN). The study did not involve the collection of wild plant material or protected species. No specific permits or licences were required for the cultivation and evaluation of the cowpea genotypes used in this study.

Consent for publication

Not applicable

Authors' contributions

S.A. Writing – review & editing; Supervision; Resources, Methodology, Investigation, Conceptualization. **A.M.I.S.** Writing – original draft, Software, Methodology, Formal analysis, Data curation, Conceptualization.

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Competing interests

The authors declare no competing interests.

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