



Stability and Climate Resilience Potential of Fodder Cowpea (*Vigna unguiculata*) Germplasm Across Diverse Environments

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ABSTRACT

Background: As global warming accelerates, developing climate-resilient crops is critical for agricultural sustainability. Amid increasing climatic disruptions, fodder cowpea, a drought-adapted legume, remains an essential nutritional security crop for livestock feed. Quantifying its phenotypic stability across heterogeneous environments would be fundamental for any breeding program capable of withstanding such intensifying climatic stresses.

Methods: This study evaluated twenty-three fodder cowpea germplasm lines and three popular varieties across three environments differing in temperature, moisture and soil fertility. The focus was on three major traits namely, green fodder yield per plant (GFY), crude fiber content (CFB) and crude protein content (CPR). We analyzed Genotype-by-Environment Interaction (GEI) using two models, Additive Main Effects and Multiplicative Interaction (AMMI) for individual trait evaluation and Multi-trait Stability Index (MTSI) for simultaneous evaluation of all the three traits.

Result: Significant GEI observation highlighted the need for environment-specific genotypes. Combined AMMI 1 and AMMI 2 biplot analyses found genotypes such as FD 1067 (G10), K-13-CP42 (G14) and CO (FC) 8 (G24) to be broadly stable performers for GFY, CPR and CFB across environments, while genotypes like GETC 40 (G21), GETC 41 (G22) and GETC 49 (G23) showed specific adaptation. The environments (E_1 - E_3) exhibited distinct discriminative capacities depending on the trait, highlighting the value of multi-environment trials for reliable genotype selection.

Key words: AMMI analysis, Climate-resilient breeding, Fodder cowpea germplasm, Genotype-by-environment interaction (GEI), Multi-trait stability index (MTSI).

INTRODUCTION

Fodder cowpea plays a critical role in smallholder farming systems, especially across tropical and semi-arid regions (Carvalho *et al.*, 2017; Boukar *et al.*, 2016; Singh *et al.*, 2003). Valued for its dual use for human consumption and animal feed, its importance is also growing on a global scale, with world production projected to increase from 9.8 million metric tons in 2020 to 12.3 million in 2030 and a market value expected to reach over USD 8 billion by 2025 (Faye *et al.*, 2024). Despite its resilience, increasing climate variability-with more frequent droughts and heat waves-poses significant challenges to stable fodder production and consequently to food and livestock security (Thornton *et al.*, 2014). As sustainable agriculture faces new threats from extreme environmental fluctuations, there is an urgent need for climate-resilient and stable varieties of fodder cowpea to maintain consistent productivity and support integrated crop-livestock systems (Munoz-Amatriain *et al.*, 2017; Sanginga *et al.*, 2003).

A major challenge in developing such resilient cultivars arises from genotype-by-environment interaction (GEI), which reflects the variable response of genotypes to different environmental conditions and complicates the identification of universally superior lines (Raza *et al.*, 2019; Yan and Tinker, 2006). GEI can obscure trait performance and lead to crossover effects-when genotype rankings shift across environments-making selection decisions less

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predictable. Researchers widely employ multi-environment trials (METs) for comprehensive evaluation of genotypes across diverse locations and seasons to address this, allowing breeders to dissect GEI and target both broad and specific adaptation strategies (Gauch, 2013).

To analyse GEI effectively, advanced statistical methods such as the Additive Main Effects and Multiplicative Interaction (AMMI) model and the Multi-Trait Stability Index (MTSI) have been widely adopted in crop research. The AMMI model combines analysis of variance with principal component analysis to distinguish genotype performance and interaction effects, thereby supporting the identification of nutrient-rich, high-yielding and stable genotypes (Gauch, 2013; Suvadra *et al.*, 2025). Meanwhile, the MTSI enables the simultaneous selection of genotypes with desirable mean performance and stability for multiple traits (Olivoto *et al.*, 2019). Although both methodologies have proven effective in crops like maize, wheat and pearl millet (Kang, 2020; Olivoto *et al.*, 2020), their application remains limited in fodder cowpea (Suvadra *et al.*, 2025; Cardona-Ayala *et al.*, 2021; Kindie *et al.*, 2022). Given the imperative for climate-resilient fodder options, this study focuses on fodder cowpea germplasm. The objective of this research is to assess comprehensively the stability and climate resilience potential of diverse fodder cowpea genotypes across varied environments, with particular attention to key agronomic traits such as green fodder yield (GFY), reduced crude fibre (CFB) and enhanced crude protein content (CPR). By employing AMMI and MTSI analyses, this study aims to identify stable and high-yielding fodder cowpea genotypes that can contribute to bridging the current forage supply deficit and enhance livestock sustainability under increasing climate variability.

MATERIALS AND METHODS

Plant materials and field experiments

The experimental material consists of two sets of fodder cowpea genotypes (Table 1). The first set comprised 23 germplasm lines, while the second set included three popular, released fodder cowpea varieties that are widely cultivated in the dry and semi-arid regions of Tamil Nadu. The germplasm in the first set was collected from various regions across India to evaluate its stability under the climatic conditions of Tamil Nadu.

The experiment was conducted over two cropping seasons, 2022-2023 and 2023-2024, at the Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The experimental station is located at a latitude of 11°00'58"N and a longitude of 76°58'31"E, within the Tamil Nadu uplands and the leeward flanks of the southern Sahyadris. This region falls under the hot, dry, semi-arid eco-subregion 8.1, as classified by the Indian Council of Agricultural Research (ICAR). The agroecological context of the experimental site is detailed in Table 2, which provides information on the region, eco-subregion, annual rainfall, seasonal rainfall distribution and predominant soil types.

The environmental conditions during the experiment are summarized in Table 3, which outlines the specific environmental setups (E1, E2 and E3) across the *Kharif* and *Rabi* seasons, including the corresponding periods

and details relevant to each environment. Fig 1 presents the monthly average temperature (°C) and total rainfall (mm) recorded across the three different environments during the experimental period, obtained from Meteostat (Meteostat, 2024).

Data recording and statistical analyses

A randomized complete block design (RCBD) with three replications was adopted during the two successive seasons. Each genotype in each replication was grown in two rows, each 4 meters long, with 0.30 m between rows and 0.10 m between plants, resulting in a net plot area of 2.4 m². The recommended package and practices for cowpea cultivation, including fertilization schedules, irrigation regimes and weed management protocols, were implemented to optimize yield. Guard plants were randomly selected from each replication at day to fifty percentage flowering for consistency and reliability, excluding the border plants. Green fodder yield per plant (GFY) was recorded for each genotype.

Nutritional content analysis was conducted in the laboratories of the Department of Forage Crops, TNAU, Coimbatore, India. Crude protein content was determined using the Kjeldahl method (AOAC, 2000). Crude fiber content (CFB) was analyzed through sequential detergent

Table 1: List of genotypes used in the study.

S.no.	Genotypes	Source
Set 1		
G1	CL 348	Pantnagar
G2	CL 321-1	Pantnagar
G3	N 311	Coimbatore
G4	IFC 9304	IGFRI, Jhansi
G5	IFC 9402	IGFRI, Jhansi
G6	CS 98	Hisar
G7	FD 711	TNAU, Coimbatore
G8	FD 719	TNAU, Coimbatore
G9	FD 1052	TNAU, Coimbatore
G10	FD 1067	TNAU, Coimbatore
G11	FD 1259	TNAU, Coimbatore
G12	EC 467380	NBPGR, New Delhi
G13	EC 240806	NBPGR, New Delhi
G14	K-13-CP42	TNAU, Coimbatore
G15	GETC 6	TNAU, Coimbatore
G16	GETC 10	TNAU, Coimbatore
G17	GETC 15	TNAU, Coimbatore
G18	GETC 18	TNAU, Coimbatore
G19	GETC 21	TNAU, Coimbatore
G20	GETC 23	TNAU, Coimbatore
G21	GETC 40	TNAU, Coimbatore
G22	GETC 41	TNAU, Coimbatore
G23	GETC 49	TNAU, Coimbatore
Set 2		
G24	CO (FC) 8	TNAU, Coimbatore
G25	CO 9	TNAU, Coimbatore
G26	TNFC 0926	TNAU, Coimbatore

methods (Van Soest *et al.*, 1991) using a Soxhlet extraction apparatus.

Statistical analyses were conducted using R version 4.4.1 (Team R.C. 2020). The Additive Main Effects and Multiplicative Interaction (AMMI) model was employed for stability analysis, integrating ANOVA with principal component analysis (PCA) techniques, as implemented in the metan package (Olivoto and Lucio, 2020). Additionally, the Multi-Trait Stability Index (MTSI) was calculated using the metan package to rank genotypes based on performance and stability across multiple traits.

RESULTS AND DISCUSSION

Genotypic variability and AMMI analysis of green fodder yield and quality traits in fodder cowpea

In a study aimed at addressing the impacts of climate change, 26 cowpea genotypes were evaluated over three

growing seasons. The results, as shown in Fig 2 and detailed in Table 4, revealed highly significant differences among the genotypes across various environmental conditions. Analysis across three environments revealed notable variability in green fodder yield per plant (GFY), crude fiber content (CFB) and crude protein content (CPR), underscoring the influence of environmental factors. In E1, GFY ranged from 192.67 g/plant for EC 467380 (G12) to 277.54 g/plant for GETC 23 (G20), with CFB peaking at 25.34% in GETC 15 (G17). CPR reached its highest at 22.14% for CO (FC)8 (G24). In E2, GFY achieved a high of 354.92 g/plant for GETC 40 (G21), while EC 467380 (G12) peaked in CPR at 23.56%, indicating favourable conditions for both yield and protein accumulation. E3 recorded a more balanced performance, with GFY up to 350.48 g/plant for EC 240806 (G13) and moderate fluctuations in CFB and CPR, reflecting consistent environmental conditions.

Table 2: Agro-ecological context of the experimental site.

Agro-ecological context	Details
Region	Tamil Nadu uplands and leeward flanks of South Sahyadris
Eco-subregion (ICAR)	Hot, dry semi-arid eco-subregion (8.1)
Annual rainfall (mm)	604
Seasonal rainfall distribution	Season Southwest Monsoon (June-Sep) Northeast Monsoon (Oct-Dec) Winter (Jan-Feb) Summer (Mar-May)
Soil types	Deep black soil and moderately deep black soils

Table 3: Description of environments.

Environment	Season	Period	Details
E ₁	Rabi (Rainfed)	November 2022-March 2023	Conducted at New Area Farm, TNAU, Coimbatore
E ₂	Rabi (Rainfed)	November 2023-March 2024	Similar conditions as E ₁
E ₃	Kharif (Rainfed)	June/July 2023-October 2023	Conducted at New Area Farm, TNAU, Coimbatore Focused on <i>Kharif</i> season variability.
Environmental data			Daily temperature and rainfall data are summarized in a bar chart (Fig 1) for each environment.

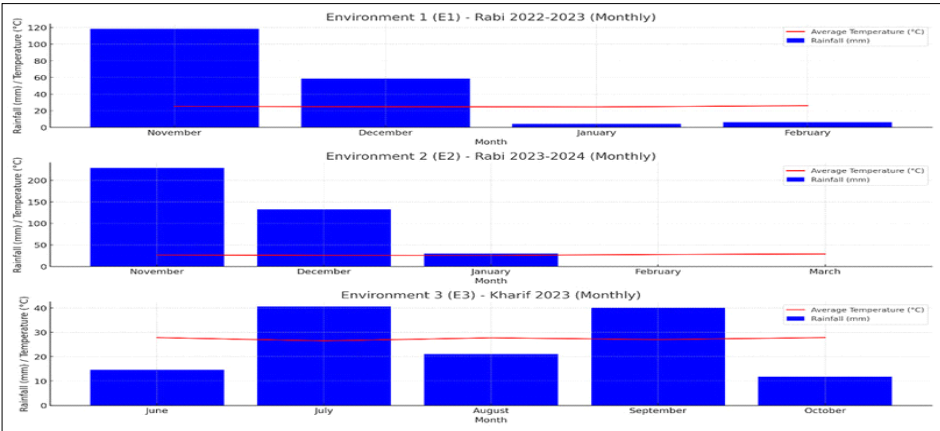


Fig 1: Monthly average temperature (°C) and total rainfall (mm) across three environments.

The AMMI analysis of variance for green fodder yield per plant (GFY) and quality traits-crude fibre content (CFB) and crude protein content (CPR)-revealed significant contributions ($p < 0.01$) from environmental factors (E), genotypic variation (G) and genotype-by-environment (GEI) interactions (Table 5). Environmental effects had the most substantial impact, with the highest variance observed in GFY (184,183), while the lowest variance was seen in residuals across all traits. Among the genotypes, GFY showed the greatest variability (4,902.25), indicating considerable genetic diversity, while CPR exhibited the least variability (3.23). The genotype-by-environment interaction was most prominent for GFY (3,734.23) and CFB also showed significant interaction variance (2.50), with CPR having the lowest (2.13). Principal components analysis highlighted that PC1 captured the most variance in GFY (6,324.63) and CFB (4.23). At the same time, PC2 contributed significantly to CPR (1.57), underscoring the substantial variability driven by environmental factors, genetic differences and their interactions.

Genotype performance analysis via AMMI biplots for GFY and quality traits

The pooled mean (Table 6) green fodder yield per plant (GFY) among genotypes ranged from 210.7 g/plant G5 to 298.4 g/plant G21. Among environments, E3 showed the highest mean GFY (296.2 g/plant), while E2 was lowest (199.2 g/plant), indicating substantial environmental influence. The AMMI 1 biplot (Fig 3) identified G10, G19 and G25 as being broadly adapted and stable, combining above-average yields with low PC1 scores. In contrast, G12, G14 and G22 showed high positive PC1 values, indicating specific adaptation to environments with strong positive interactions, such as E2. Genotypes G1, G3 and G8 had high negative PC1 scores, reflecting adaptation to

environments with negative interaction forces (E1 and E3). All environments exhibited large absolute PC1 values, confirming their highly discriminating nature for GEI in GFY.

The AMMI 2 biplot (PC1 vs. PC2; Fig 3) further clarified these interaction patterns. Genotypes near the origin (G10, G11, G15 and G17) were stable, while those distant from the origin, such as G21 (high positive PC1 and PC2) and G9 (high absolute PC2), exhibited pronounced, environment-specific responses. G21 was located far along the positive PC1 and PC2 axes, indicating strong adaptation to E2, which itself was positioned at the extreme positive PC1. On the negative side, G1, G3, G5 and G8 aligned with E1 and E3, each distinguished by negative PC1 values and differentiated further by their PC2 scores. Collectively, these results demonstrate that the AMMI 2 biplot effectively distinguishes both stable and specifically adapted genotypes and highlights each environment's unique discriminative power for green fodder yield.

The pooled mean (Table 6) for CFB ranged from G5 (21.2%) to G17 (23.5%), with E2 showing the highest mean environment value (23.7%) and E3 the lowest (20.6%). The AMMI 1 biplot (Fig 4) indicated that genotypes G1, G11 and G24 had PC1 values near zero, signifying broad adaptability and stable performance across environments; notably, G24 combined this stability with above-average CFB. In contrast, genotypes G23 and G14 exhibited high positive PC1 values, reflecting specific adaptation to E1 ($PC1 = 1.6$), while G26, G4 and G25 showed high negative PC1 values, indicating specific adaptation to E2 ($PC1 = -1.8$). Among environments, E1 and E2 had the largest absolute PC1 scores, marking them as highly discriminating, while E3, with a low PC1 (0.2) but a notable PC2 (-1.2), demonstrated discrimination based on secondary interaction effects.

The AMMI 2 biplot (PC1 vs. PC2; Fig 4) further differentiated genotype responses: G14, G12 and G23

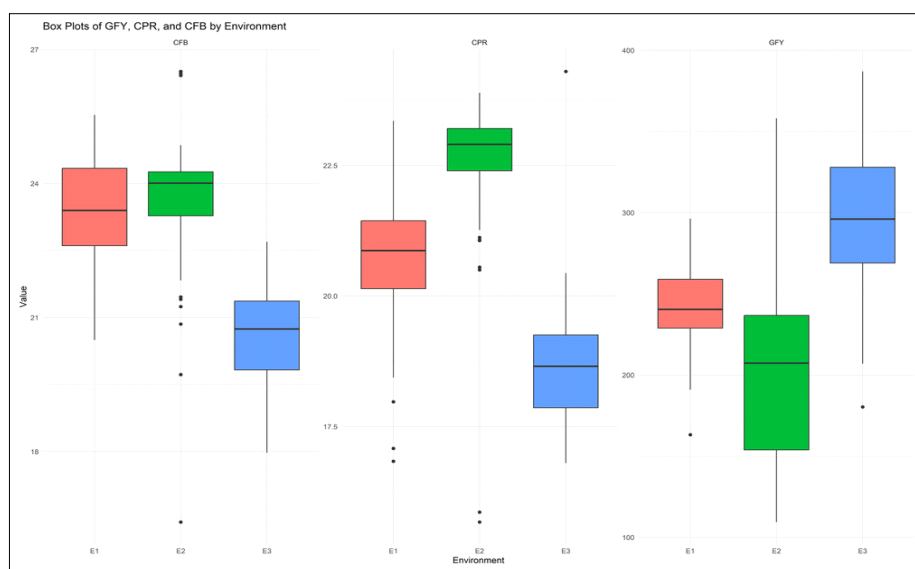


Fig 2: Genotypic performance across three different environments.

Table 4: Mean performance for green fodder yield per plant and nutritional traits of 26 fodder cowpea genotypes evaluated across three environments.

Genotypes	Green fodder yield (g/plant)			Crude fibre content (%)			Crude protein content (%)		
	E ₁	E ₂	E ₃	E ₁	E ₂	E ₃	E ₁	E ₂	E ₃
CL 348 (G1)	259.33	135.44	312.44	21.64	22.46	20.45	20.45	21.32	20.77
CL 321-1 (G2)	219.33	126.59	296.08	22.12	23.79	19.84	19.84	21.7	18.49
N 311 (G3)	238	117.58	310.2	21.76	24.07	19.65	19.65	21.07	18.46
IFC 9304 (G4)	237	120.65	275.93	21.13	24.22	19.63	19.63	20.83	18.49
IFC 9402 (G5)	237.67	115.85	278.46	20.53	23.46	19.57	19.57	20.89	18.3
CS 98 (G6)	267.67	190.66	273.14	21.07	23.51	19.39	19.39	22.46	18.65
FD 711 (G7)	240.67	167.21	300.57	23.21	24.06	19.91	19.91	22.88	18.43
FD 719 (G8)	255.67	111.05	279.5	22.64	24.08	20.15	20.15	23.12	18.42
FD 1052 (G9)	195	219.01	317.27	23.36	24.46	20.14	20.14	23.08	18.52
FD 1067 (G10)	254.67	227.75	307.38	22.93	24.42	20.26	20.26	22.94	18.75
FD 1259 (G11)	255.33	201.7	299.48	22.95	23.63	20.11	20.11	22.93	18.63
EC 467380 (G12)	192.67	245.02	273.28	23.73	23.17	20.8	20.8	23.56	18.6
EC 240806 (G13)	266	258.2	350.48	24.95	23.89	20.92	20.92	23.37	18.47
K-13-CP42 (G14)	242	252.88	301.21	24.91	22.89	21.34	21.34	22.88	18.81
GETC 6 (G15)	222	153.29	271.39	24.02	23.12	21.08	21.08	23.31	19
GETC 10 (G16)	216.48	206.49	303.65	24.87	23.67	21.39	21.39	22.87	19.12
GETC 15 (G17)	219.06	200.58	277.44	25.34	23.81	21.2	21.2	23.04	18.8
GETC 18 (G18)	267	166.08	305.25	24.38	23.3	21.73	21.73	22.68	19.1
GETC 21 (G19)	268.86	210.56	295.68	23.9	23.26	21.09	21.09	22.55	18.1
GETC 23 (G20)	277.54	224.07	291.8	23.88	22.98	21.6	21.6	23.06	18.35
GETC 40 (G21)	246.94	354.92	293.46	24.05	23.14	20.72	21.93	23.29	18.3
GETC 41 (G22)	246.78	248.77	294.97	24.45	23.37	20.93	22.03	23.28	18.24
GETC 49 (G23)	234.32	216.57	305.16	24.47	21.67	20.73	22.08	23.11	18.02
CO (FC) 8 (G24)	250.33	236.72	288.37	24.21	24.35	20.99	22.14	23.06	18.26
CO 9 (G25)	256.67	213.58	300.64	23.35	25.86	21.03	20.05	22.72	17.92
TNFC 0926 (G26)	250.67	258.37	299.2	22.47	25.29	21.54	20.67	18	18.22
Local mean	242.9	199.2	296.2	23.3	23.7	20.6	20.7	22.5	18.6

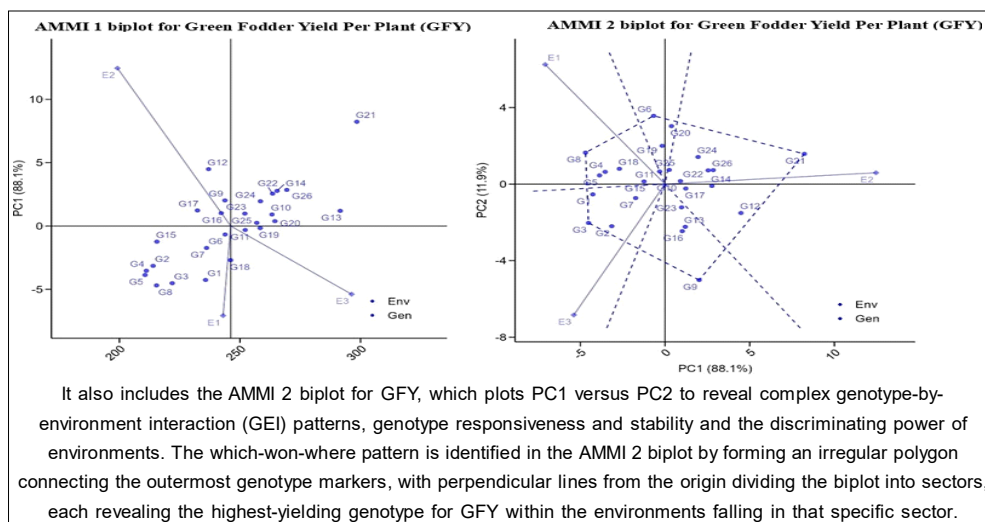


Fig 3: AMMI 1 biplot for green fodder yield per plant (GFY), which illustrates genotype stability, general adaptability and specific adaptation by plotting genotype and environment mean performance against the first principal component (PC1) for GFY.

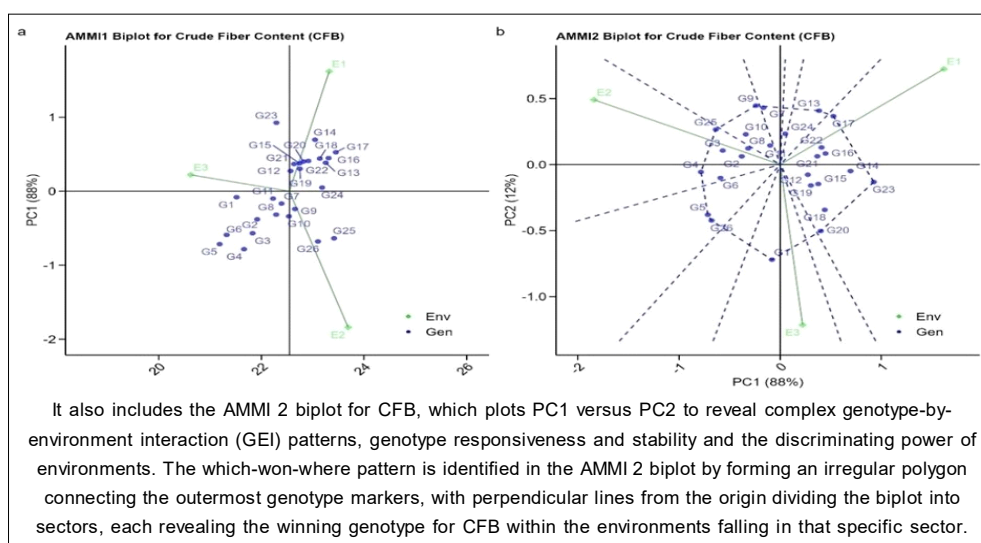


Fig 4: AMMI 1 biplot for crude fiber content (CFB), which illustrates genotype stability, general adaptability and specific adaptation by plotting genotype and environment mean performance against the first principal component (PC1) for CFB.

Table 5: AMMI analysis of variance for green fodder yield per plant (GFY) and nutritional traits of 26 fodder cowpea genotypes evaluated across three environments.

Source	Df	GFY	CPR	CFB
ENV (E)	2	184183**	294.16**	218.84**
REP (ENV)	6	5831.64**	3.27**	6.01**
GEN (G)	25	4902.25**	3.23**	3.83**
GEN: ENV (GEI)	50	3734.23**	2.13*	2.50**
PC1 (Proportion)	26	6324.63** (88.1)	2.64** (88)	4.23** (64.6)
PC2 (Proportion)	24	927.97** (11.9)	1.570** (12)	0.62** (35.4)
Residuals	150	537.076	1.069	0.82
Total	283	3462.53	3.75	3.334

*, **Significant at 5% ($p < 0.05$) and 1% ($p < 0.01$) probability levels, respectively.

Table 6: Pooled mean performance and AMMI IPCA scores (PC1, PC2) of 26 fodder cowpea genotypes across three environments.

Genotypes	GFY (g/plant)			CPR (%)			CFB (%)		
	Pooled mean	PC1	PC2	Pooled mean	PC1	PC2	Pooled mean	PC1	PC2
CL 348 (G1)	235.7	-4.3	-0.5	20.84	-0.99	0.59	21.5	-0.1	-0.7
CL 321-1 (G2)	214.0	-3.1	-2.2	20.01	-0.18	0.25	21.9	-0.4	0.1
N 311 (G3)	221.9	-4.5	-2.0	19.73	-0.38	0.23	21.8	-0.6	0.1
IFC 9304 (G4)	211.2	-3.5	0.6	19.65	-0.47	0.21	21.7	-0.8	-0.1
IFC 9402 (G5)	210.7	-3.9	0.5	19.59	-0.39	0.20	21.2	-0.7	-0.4
CS 98 (G6)	243.8	-0.7	3.6	20.17	0.08	0.59	21.3	-0.6	-0.1
FD 711 (G7)	236.1	-1.7	-0.7	20.41	0.25	0.37	22.4	-0.2	0.4
FD 719 (G8)	215.4	-4.7	1.6	20.56	0.32	0.30	22.3	-0.3	0.1
FD 1052 (G9)	243.8	2.0	-5.0	20.58	0.28	0.32	22.7	-0.2	0.4
FD 1067 (G10)	263.3	0.9	0.2	20.65	0.16	0.32	22.5	-0.3	0.2
FD 1259 (G11)	252.2	-0.3	0.7	20.56	0.20	0.35	22.2	-0.1	0.1
EC 467380 (G12)	237.0	4.5	-1.5	20.98	0.38	0.13	22.6	0.3	-0.1
EC 240806 (G13)	291.6	1.2	-2.2	20.92	0.34	0.02	23.3	0.4	0.4
K-13-CP42 (G14)	265.4	2.8	-0.1	21.01	0.04	-0.13	23.0	0.7	0.0
GETC 6 (G15)	215.6	-1.2	0.1	21.13	0.16	0.09	22.7	0.4	-0.1
GETC 10 (G16)	242.2	1.0	-2.5	21.13	-0.05	-0.07	23.3	0.4	0.1
GETC 15 (G17)	232.4	1.2	-0.2	21.01	0.11	-0.06	23.5	0.5	0.4
GETC 18 (G18)	246.1	-2.7	0.8	21.17	-0.14	-0.24	23.1	0.4	-0.3
GETC 21 (G19)	258.4	-0.2	2.0	20.58	0.14	-0.28	22.7	0.3	-0.2
GETC 23 (G20)	264.5	0.4	3.0	21.00	0.21	-0.35	22.8	0.4	-0.5
GETC 40 (G21)	298.4	8.2	1.6	21.17	0.29	-0.48	22.6	0.4	0.1
GETC 41 (G22)	263.5	2.6	0.7	21.18	0.29	-0.53	22.9	0.4	0.1
GETC 49 (G23)	252.0	1.0	-1.2	21.07	0.29	-0.64	22.3	0.9	-0.1
CO (FC) 8 (G24)	258.5	2.0	1.4	21.15	0.20	-0.61	23.2	0.0	0.2
CO 9 (G25)	257.0	0.2	0.7	20.23	0.33	0.14	23.4	-0.6	0.3
TNFC 0926 (G26)	269.4	2.8	0.7	18.96	-1.47	-0.70	23.1	-0.7	-0.4
E ₁	243.0	-7.1	6.2	20.74	-0.35	-1.51	23.3	1.6	0.7
E ₂	199.2	12.5	0.6	22.46	1.69	0.49	23.7	-1.8	0.5
E ₃	296.2	-5.4	-6.8	18.59	-1.34	1.01	20.6	0.2	-1.2

occupied positions near the origin, confirming their stability and moderate-to-high mean CFB, whereas G1 and G20, located further along the PC2 axis, reflected greater environmental sensitivity driven by secondary interaction components. Overall, environments were distinctly separated along the PC1 and PC2 axes, with E1 and E2 providing strong discrimination for identifying specific adaptations and E3 uniquely distinguishing genotypes according to secondary interaction patterns.

The pooled mean (Table 6) of crude protein content (CPR) values among genotypes ranged from G26 (18.96%) to G22 (21.18%) and G21 (21.17%), while environment means spanned from a high of 22.46% in E2 to a low of 18.59% in E3. The AMMI 1 biplot (Fig 5) identified G14, G16, G17 and G18 as genotypes with low PC1 values and above-average CPR, highlighting stable, broadly adapted performance. In contrast, G26 and G1 exhibited pronounced negative PC1 scores, indicating specific adaptation to environments with negative PC1 values (such as E3), while genotypes G12, G13, G21 and G22 showed positive PC1 values and thus specific adaptation to E2 (PC1 = 1.69), which exerts the strongest positive interactive force.

The AMMI 2 biplot (Fig 5) further distinguished genotype responses: G14, G16 and G17 were positioned near the origin, confirming exceptional stability across environments, while G26, G1 and G23 appeared much further from the origin, reflecting heightened sensitivity and stronger genotype-by-environment interaction effects. Regarding environments, E2 and E3 occupied positions with strong PC1 scores, thus acting as major discriminators among genotypes, whereas E1 was characterized by a large PC2 value, indicating that this environment primarily differentiated genotypes according to secondary, rather than primary, interaction effects.

Multi-trait stability index (MTSI)

In Fig 6, the MTSI radar chart distinctly marks genotypes G16, G7, G19 and G11 in red on the outermost circuit, highlighting their superior stability and adaptability across different environmental conditions. These genotypes exhibit the highest stability index values, making them particularly favourable for breeding programs focused on resilience and performance. Conversely, G26 is positioned near the centre, indicating the lowest stability, suggesting that its performance is less consistent across environments. This visualization effectively aids in identifying and prioritizing genotypes for further research and development.

The escalating threat of global warming necessitates the development of climate-resilient crops to ensure agricultural sustainability and food security (Muchero *et al.*, 2011; Samireddypalle *et al.*, 2017). Fodder cowpea, a drought-adapted legume, stands as a critical component of livestock feed, particularly in resource-limited regions (Mbeyagala *et al.*, 2021; Abiriga *et al.*, 2020). This study aimed to quantify the phenotypic stability of fodder cowpea germplasm across diverse environments, focusing on green fodder yield per plant (GFY), crude fiber content (CFB) and crude protein content (CPR), thereby identifying climate-resilient genotypes for sustainable fodder production.

The highly significant differences observed among genotypes, environments and their interaction (GEI) (Table 4, Table 6) confirm that fodder cowpea performance is a complex interplay of genetic potential and environmental influence. This aligns with extensive research on the critical role of GEI in crop breeding (Carvalho *et al.*, 2017; Raza *et al.*, 2019). The overwhelming contribution of the environment to performance variation, especially for GFY, underscores the profound impact that factors like moisture and

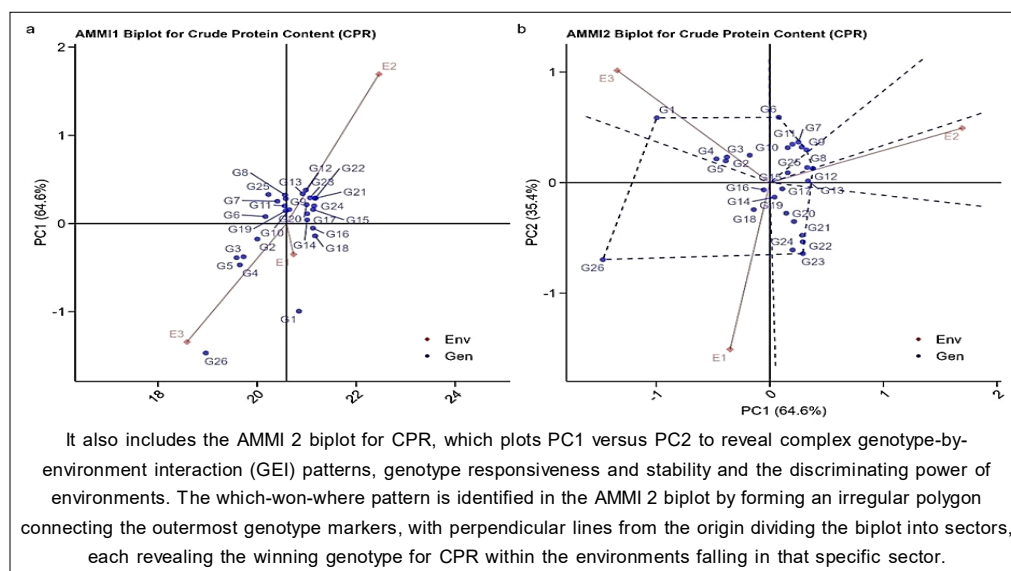


Fig 5: AMMI 1 biplot for crude protein content (CPR), which illustrates genotype stability, general adaptability and specific adaptation by plotting genotype and environment mean performance against the first principal component (PC1) for CPR.

temperature have on productivity and validates the necessity of the multi-environment trial approach used here (Slafer, 2003; Fageria *et al.*, 2011).

Our analysis revealed two distinct adaptation strategies among the genotypes: Specific adaptation and broad stability. For instance, the high yield of GETC 40 (G21) was realized exclusively under the favorable conditions of E2, suggesting it is a specialist genotype. This indicates that while its yield potential is high, it may lack the physiological plasticity to buffer against suboptimal conditions, possibly due to a less robust root system or higher moisture requirements (Iqbal *et al.*, 2024; Kebede *et al.*, 2023). In contrast, the consistent performance of genotypes like FD 1067 (G10) for yield and CO (FC) 8 (G24) for fiber content across all environment's points to broad stability. This suggests these genotypes possess superior homeostatic capabilities, likely conferred by robust physiological traits such as efficient water uptake or superior stomatal control, which are key markers for drought resilience (Kuruma *et al.*, 2019; Kindie *et al.*, 2022).

A crucial outcome of this study was the identification of genotypes that break the common trade-off between yield and quality under stress. The AMMI analysis identified K-13-CP42 (G14), G16 (GETC 10) and G17 (GETC 15) as exceptionally stable for high crude protein, making them invaluable genetic resources (Suvadra *et al.*, 2025; Cardona-Ayala *et al.*, 2021). By integrating these complex traits, the Multi-Trait Stability Index (MTSI) provided a holistic solution, conclusively identifying G16 (GETC 10), G7 (FD 711), G19 (GETC 21) and G11 (FD 1259) as the most superior genotypes overall. This approach is essential because selecting for yield alone can inadvertently lead to reduced nutritional value, thereby failing to address the regional fodder quality deficit (Omomowo and Babalola, 2021; Singh, 2023).

While studies like Popoola *et al.* (2024) have demonstrated significant GEI in cowpea across diverse continents, our research provides a high-resolution view

within the specific hot, semi-arid eco-region of Southern India. It confirms that substantial genotype re-ranking occurs even due to seasonal variations at a single location. The successful application of the AMMI model via the metan package (Olivoto and Lucio, 2020) reinforces the robustness of this contemporary analytical approach, aligning our work with numerous studies that have used it to identify superior genotypes (Mekonnen *et al.*, 2022).

The practical implications for regional breeding are significant. The stable, high-performing genotypes identified—such as G10 for green fodder yield per plant and G14, G16 and G17 for crude protein content—can be immediately integrated into breeding pipelines as elite parental material to develop new climate-resilient varieties (Fasahat *et al.*, 2015; Shekhawat *et al.*, 2024). Furthermore, the highly discriminative environments E1, E2 and E3 can be strategically used as testing laboratories to efficiently screen germplasm for specific strengths and weaknesses, accelerating the development of varieties tailored to distinct agro-ecological zones (Gauch *et al.*, 2008; Kang, 2020). Theoretically, this study reinforces that GEI analysis is a vital tool for making informed breeding decisions that can build more productive and sustainable agricultural systems in the face of climate change (Pour-Aboughadareh *et al.*, 2022).

However, certain limitations must be acknowledged. This study was conducted at a single location over two years, meaning its findings are most applicable to this specific agro-ecological zone (Pour-Aboughadareh *et al.*, 2022; Malosetti *et al.*, 2013). Broader validation across multiple locations is needed. Additionally, while we focused on key agronomic and quality traits, other factors critical for climate resilience, such as disease resistance and water use efficiency, were not assessed (Balapure *et al.*, 2016).

Future research should prioritize multi-location trials to confirm the stability of the elite genotypes identified. Molecular characterization of G10, G14, G16 and G17 could help identify the quantitative trait loci (QTLs) governing stability, paving the way for more efficient marker-assisted

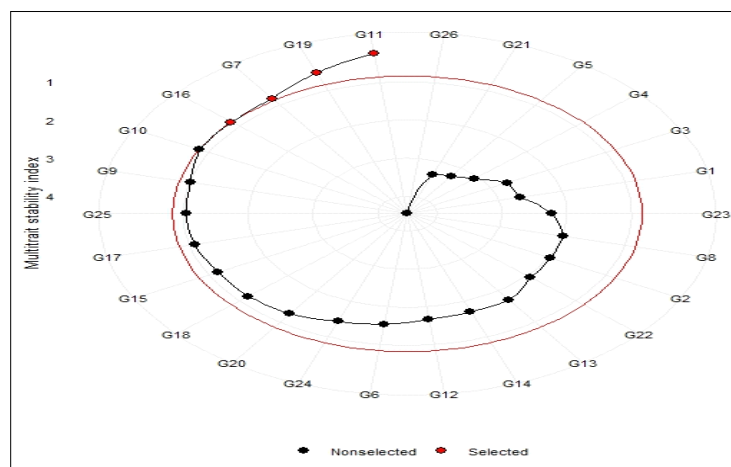


Fig 6: Ranking of twenty-six cowpea genotypes based on multi-traits stability index (MTSI).

breeding (Malosetti *et al.*, 2013). Finally, investigating the underlying physiological mechanisms of these stable genotypes will provide deeper insights into their resilience and help develop the next generation of climate-smart fodder crops.

CONCLUSION

This study successfully quantified the phenotypic stability of fodder cowpea germplasm, addressing the urgent need for climate-resilient crops. Our findings revealed highly significant differences among genotypes, environments and their interactions for key fodder traits, underscoring the complex interplay between genetic potential and environmental pressures. While AMMI analysis pinpointed broadly stable genotypes like G10 (FD 1067) for yield and G14 (K-13-CP42), G16 (GETC 10) and G17 (GETC 15) for protein content, the Multi-Trait Stability Index (MTSI) was crucial in identifying G16 (GETC 10), G7 (FD 711), G19 (GETC 21) and G11 (FD 1259) as exhibiting superior overall stability and adaptability. These elite genotypes represent valuable genetic resources for regional breeding programs, enabling their direct use as parental material and guiding the precise recommendation of climate-smart varieties. Although this research provides a critical foundation, its findings emphasize the necessity of future multi-location trials and molecular characterization to fully validate and accelerate the development of resilient fodder cowpea.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

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