Delineating G × E interactions by AMMI method for yield attributes in cowpea (*Vigna unguiculata*(L.) Walp.)

Manish Sharma[1] · M. P. Patel[1] · P. R. Patel[1] · P. J. Patel[2]

Abstract

Cowpea can tolerate a wide range of climate conditions. Despite this, crop yields are often low due to a lack of stable, drought-tolerant varieties. The additive main effects and multiplicative interactions (AMMI) model was used in the current study to examine how cowpea genotypes responded to environmental conditions based on variations in yield and its contributing factors. The experiment used a randomized complete block design with three replications over two consecutive years at six locations. Over multiple harvests, yield and its component traits such as the total number of pods per plant, pod length (cm), hundred seeds weight (g), and yield per hectare were evaluated in the rainy season in 2020 and 2021. Stability tests for multivariate stability parameters were performed based on analyses of variance. For all the traits, the pooled analysis of variance indicated highly significant (p < 0.01) variations between genotypes, environments, and genotypes by environment (GEI). Furthermore, the first, second, and third main component axes (IPCA1, IPCA2, and IPCA3) explained most of the GEI for these attributes. AMMI1 and AMMI2 biplot analyses showed differential stability of genotypes for yield and its component traits with few exceptions. The best genotype, according to the ideal genotype ranking, was genotype KGC 1. Genotypes KGC5 and KGC2, on the other hand, had high yields that were especially suited to the LAD environment during the 2021 growing season. Location-specific adaptation of genotypes indicates that location-specific breeding needs to be undertaken along with the focus on wider adaptability.

Keywords Cowpea · Stability · Environment · AMMI

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important warm-season and drought-tolerant legume that is mostly farmed by subsistence farmers in the semiarid tropics for human and animal use. Cultivated cowpea is a diploid (2n = 2x = 22), self-pollinated annual crop of the family Fabaceae, subfamily Faboideae, tribe Phaseoleae, subtribe Phaseolinae, and genus *Vigna* (Boukar et al. 2019). The crop and grain have several health advantages, qualities that promote soil fertility, opportunities to contribute to food and feed security, potential for improving livelihood and sustainability in income creation for resource-poor households

(Simion 2018). Cowpea genotypes may be impacted positively or negatively by the environment, the growing season, rainfall distribution and intensity. To gauge and comprehend the complexity of the genotype across environments, plant breeders analyze genotypes in many environments that represent both favorable and unfavorable growing conditions (Mekonnen et al. 2022). Therefore the primary goal of cowpea breeding, to create high-yielding cultivars must include an understanding of stability so that the variety can be grown in different environments. Cowpea genotypes, on the other hand, have been found to have significantly inconsistent performance across different environments (Ajayi et al. 2022), a phenomenon known as genotype-by-environment interaction (GEI). Before releasing new genotypes or varieties, their GEI must be assessed to identify those that exhibit both superior performance in terms of mean yield and exceptional stability across multiple environment trials (Pour-Aboughadareh et al. 2022). However, inconsistency in genotype performance as a result of GEI is restricting the creation of stable high-yielding cultivars. Each year, it

✉ Manish Sharma
  manisharmagpb@sdau.edu.in

1 Pulses Research Station, SDAU, Sardarkrushinagar, Palanpur, Gujarat, India

2 Seed Spices Research Station, SDAU, Jagudan, Mahesana, Gujarat, India

is crucial to perform multi-environment trials to examine GEI for choosing stable genotypes for yield and other essential attributes. Following these trials, compatible and stable genotypes can then be suggested to the farmers as cultivars (Ebdon and GauchJr 2022). Numerous multivariate strategies have already been used to evaluate the presence of yield stability and G×E in legume crops (Horn et al. 2018; Kumar et al. 2021; Azam et al. 2020; Sharma et al 2022a, b). The Additive Main Effect and Multiplicative Interaction (AMMI) model (Kempton 1984; Zobelet al.1988; Crossa et al.1990) which has proved superior and more effective in explaining the GEI has been developed to take over from the traditional stability analysis. In the past, AMMI analysis has been used to increase the likelihood of successful selection (Gauch and Furnas 1991). GauchJr (1992) AMMI model is a multivariate method that employs analysis of variance (ANOVA) and principal component analysis (PCA) to explain the GEI in more than one dimension. It is crucial to understand the extent of effects of the environment, genotype, and their interaction on yield and stability performance of cowpea genotypes across environments because these factors reduce the efficiency of the genetic gain through the development of high-yielding genotypes with desirable agronomic traits (Simion 2018). Therefore the objectives of this study were to evaluate advanced breeding lines of cowpea for their performance in grain yield and yield components for multiple years at different locations to identify genotypes that can be distributed to farmers to supplement current ones.

Material and methods

Material for the present study comprised of twelve cowpea genotypes/lines (Table 1) developed by hybridization followed by the pedigree method of selection at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India. The advanced purelines were chosen with consideration given to grain productivity, earliness, plant architecture, grain quality, and pest and disease resistance. The current experiment was conducted during the rainy season of 2020 and 2021, at six locations viz., Sardarkrushinagar (SKN), Bhiloda (BHI), Ladol (LAD), Radhanpur (RAD), Targadhiya (TAR) and Deesa (DEE) in the Banaskantha, Sabarkantha, Patan and Mehsana districts of Gujarat State that represented various agro-ecological zones (Table 2). Three replications of the experimental material were examined in each environment using a randomized complete block design. Eight rows of 4 m each with a 10 cm spacing between plant and a 45 cm between rows comprised the experimental units. The crops were planted in rainfed conditions with additional irrigation applied as and when necessary. To record the observations

Table 1 List of cowpea genotypes used in the study and their parentage

S.No	Code	Pedigree
1	KGC 1	GC 0012×PGCP 4
2	KGC 2	GC-2×PGCP-1 (I)
3	KGC 3	TC-2004×GC-4
4	KGC 4	GC 2×GC 0723
5	KGC 5	GC 0502×GC 0203
6	KGC 6	GC 502×GC 203
7	KGC 7	V-16 × Black eye 7–31
8	KGC 8	GC 5×PGCP 12
9	KGC 9	GC 2×GC 203
10	KGC 10	Dholar × GC 2
11	KGC 11	GC 5×GC 0706
12	KGC 12	GC 2 × GC 8963

on the number of pods per plant, the length of the pods, and the number of seeds per pod, five competitive plants from each replication were randomly chosen in each plot. The outer rows were not used for yield estimation and six middle rows (net plots) were harvested to estimate grain yield per plot, later converted to yield per hectare (t ha^{-1}) to control border effects and to minimize experimental error. In total, twelve experimental trials were considered as environments to analyze GEI. The GEI was studied as per the AMMI model (Zobel et al. 1988) and analyses were carried out using the software, PB tools (ver 2.0) developed by the International Rice Research Institute, Philippines.

Results and discussion

In literature, a large magnitude of G×E interactions has been observed in cowpea (El-Shaieny et al. 2015; Odeseye et al. 2018; Patel et al 2018; Singh et al. 2020; Sharma et al. 2022a). The statistical analysis of the data collected in each of the twelve environments indicated significant variations in seed yield and the variables that contribute to it across the genotypes of cowpea. Furthermore, a pooled analysis of variance for each attribute was performed on the data from all the locations (Table 3). The findings showed that there was a substantial GEI for seed yield, so it was appropriate to do a stability analysis on the data. The huge sum of squares and substantial effect for environments showed that the six locations where the trials were conducted had different agroclimatic conditions resulting in differences for environmental means causing variation in seed yield. This variation is useful when studying the impacts of GEI and evaluating genotype phenotypic stability (Patel et al. 2021 and Ajayi et al. 2022).

Table 2 Different environments used in the present study

Environment	Place	Altitude	Latitude	Longitude
E1 (SKN) 2020	Sardarkrushinagar	164 m	24.32347395	72.31582424
E2 (SKN) 2021				
E3 (DEE) 2020	Deesa	137 m	24.2594977	72.1803348
E4 (DEE) 2021				
E5 (RAD) 2020	Radhanpur	29 m	23.8315668	71.6103884
E6 (RAD) 2021				
E7 (LAD) 2020	Ladol	129 m	23.6220256	72.7333374
E8 (LAD) 2021				
E9 (TAR) 2020	Targhadiya	169 m	22.2769386	70.8919247
E10 (TAR) 2020				
E11 (BHI) 2020	Bhilloda	204 m	23.796667	73.308333
E12 (BHI) 2021				

Table 3 Pooled ANOVA for seed yield and its attributes in cowpea

Character	Genotype	Environment	GEI
	Mean sum of squares		
Degree of freedom	11	11	121
Pods per plant	1246.40**#	142.00**	23.68**
Pod length	27.13**	11.15**	1.92**
Seeds per pod	79.51**	7.58**	1.44**
Seed Yield (t/ha)	4.23**	0.23**	0.08**

#Significance codes: '**' = 0.01, '*' = 0.05

Plant breeders are extremely concerned about the GEI since it has the potential to diminish selection gains and make it challenging to identify superior cultivars. The AMMI model retrieves the part of the sum of squares that determines the GEI which is called the standard portion i.e. the genotype and environment effect and a residual portion that corresponds to unpredictable and uninterruptable model responses (Cornelius et al. 1996). The AMMI biplot analysis ANOVA revealed that genotype, environment, and GEI effects were all very significant ($p < 0.001$) for pods per plant (PP), Pod length (PL), Seeds per pod (SP) and seed yield (SY) revealing the presence of variability among genotypes as well as environments under which experiments were undertaken (Table 4). Further, the sum of squares due to GEI for PP, PL, SP and SY was mainly explained by the first, second and third interaction principal components (IPCA1, IPCA2 and IPCA3) with 32.50%, 22.55% and 18.35% for PP; 37.41%, 30.23% and 10.87% for PL; 30.20%, 27.32% and 14.30% for SP and 40.25%, 29.84% and 10.31% for SY. Therefore, AMMI, which has three components based on the interaction principle, was the best predictive model in the current investigation. Kumar et al. (2021); Omilabu et al. (2020) and Gumede et al. (2022) have also reported environment and interactions as a predominant source of variation for seed yield in cowpea.

Table 4 AMMI analysis of variance for 12 cowpea genotypes

Sources of variation	Degree of freedom	Sum of squares	Mean sum of squares	% explained
Pods per plant				
Genotypes	11	315.11	28.65**#	
Environments	11	4570.14	415.47**	
G*E Interaction	121	1019.84	8.43**	
IPCA I	21	331.47	15.78**	32.50%
IPCA II	19	230.00	12.11**	22.55%
IPCA III	17	187.15	11.01**	18.35%
Pod length				
Genotypes	11	52.41	4.76**	
Environments	11	99.49	9.04**	
G*E Interaction	121	83.28	0.69**	
IPCA I	21	31.15	1.48**	37.41%
IPCA II	19	25.17	1.32**	30.23%
IPCA III	17	9.06	0.53**	10.87%
Seeds per pod				
Genotypes	11	22.63	2.06**	
Environments	11	291.52	26.50**	
G*E Interaction	121	69.28	0.57**	
IPCA I	21	20.92	0.99**	30.20%
IPCA II	19	18.93	0.99**	27.32%
IPCA III	17	9.90	0.58**	14.30%
Seed Yield (t/ha)				
Genotypes	11	0.63	0.06*	
Environments	11	15.50	1.41**	
G*E Interaction	121	3.17	0.03**	
IPCA I	21	1.27	0.06**	40.25%
IPCA II	19	0.94	0.05**	29.84%
IPCA III	17	0.33	0.02**	10.31%

#Significance codes: '**' = 0.01, '*' = 0.05

One significant breeding endeavor is the creation of novel genotypes with high yield and acceptable levels of stability. The genotypic mean, stability index and relative rankings

of genotypes based on yields are presented in Table 5. The mean seed yield of 12 genotypes evaluated across the environments during the rainy seasons of 2020 and 2021 ranged from 0.66 t/ha to 0.92 t/ha. Genotype KGC 6 recorded the highest mean grain yield of 0.92 t/ha followed by KGC 4 (0.88 t/ha) and KGC1 (0.87 t/ha). KGC11 recorded the lowest yield of 0.66 t/ha. On the expected lines the highest yielding genotype KGC6 also has the highest number of pods per plant. The high yield of KGC4 can be attributed to the high number of seeds per pod while the lowest yielder KGC11 has a very less number of pods per plant as well as seeds per pod. Similar findings about yield and variables that affect yield in cowpea were also observed by Ndenkyanti et al. (2022).

It is crucial to compare several genotypes over multiple environments and/or years in order to find high-yielding cultivars as well as sites that most accurately reflect the target environment. In AMMI 1 biplot, Yan et al. (2007) demonstrated that genotypes that appear almost on a perpendicular line have similar means and those that fall almost on a horizontal line have a similar interaction pattern. Further genotypes with large IPCA 1 scores in both positive and negative directions have high interactions, whereas genotypes with IPCA 1 scores near zero have small interactions. Therefore AMMI 1 biplot (Fig. 1a), depicted that for PP, environments RAD had below-average main effects and was very poor while environments LAD and DEE had the highest main effects and were favorable to the performance of most of the genotypes for this trait. Considering the genotypes, KGC7, KGC8 and KGC 9 recorded high mean and IPCA values near zero were considered stable for this trait. From similar analysis, genotypes KGC8, KGC4 and KGC10 were most stable for PL (Fig. 1b) and SP, genotypes KGC8, KGC9 and KGC4 were high yielder and most stable (Fig. 1c).

Accordingly, for SY, AMMI1 analysis depicted that five of the twelve environments had below-average main effects and were poor. Environments LAD and SKN had the highest main effects and were favorable to the performance of most of the genotypes in both years. Genotypes KGC8 and KGC6 were the most stable, as indicated by values near the origin of the IPCA1 axis, which is indicative of a smaller contribution to the G×E interaction. A similar grouping of genotypes as desirable, stable and unstable, have been reported by Gerrano et al. (2019) and Omilabu et al. (2020).

According to AMMI2 analysis, stable environments and genotypes with low scores for the two axes (IPCA1 and IPCA2) of the interaction are found close to the origin. Genotypes KGC2 and environment SKN and RAD in both years for PP (Fig. 2a), genotype KGC8 and environment DEE and SKN in the year 2021 for PL (Fig. 2b), genotypes KGC9 and environment SKN in 2020 and TAR in 2021for SP (Fig. 2c), were the most desirable genotypes as they possessed high stability and above average mean value for concerned traits. Developing high-yielding cultivars suitable for cultivation in varied environments is the basic target in plant breeding. For SY, AMMI2 analysis revealed that environments SKN and TAR in 2020 and DEE, RAD and LAD in 2021 exerted strong interaction forces while the rest of the environments did less. Genotypes, KGC7, KGC3, KGC9 and KGC 5 were more responsive since they were away from the origin whereas genotypes KGC11, KGC1, KGC8, KGC6 and KGC12 were close to the origin and hence they were less sensitive to environmental forces. Genotypes KGC5 and KGC2 were high-yielding specifically adapted for the LAD environment during 2021 season. In general, KGC1 exhibited very less Genotype x environmental interaction showing high stability with good yield. daCruz et al. (2020) and Mekonnen et al. (2022) also classified genotypes and environments accordingly and obtained similar results in cowpea.

Table 5 Mean (μ), Stability index (SI) and ranking (R) of genotypes for Yield and its attributes

Genotype	Pods per plant			Pod length (cm)			Seeds per pod			Seed yield (t/ha)		
	μ	SI	R	μ	SI	R	μ	SI	R	μ	SI	R
KGC 1	16.92	0.58	5	11.58	−0.19	6	11.92	0.2	5	0.87	0.07	3
KGC 2	17.8	1.47	3	11.25	−0.52	12	11.59	−0.13	8	0.79	-0.02	8
KGC 3	16.38	0.05	6	11.69	−0.07	5	11.55	−0.17	9	0.82	0.01	6
KGC 4	17.39	1.05	4	11.43	−0.34	10	11.98	0.26	2	0.88	0.07	2
KGC 5	17.89	1.55	2	11.90	0.13	3	11.93	0.21	3	0.83	0.02	5
KGC 6	18.75	2.41	1	11.52	−0.25	8	11.93	0.21	3	0.92	0.11	1
KGC 7	13.74	−2.60	12	13.64	1.87	1	12.56	0.84	1	0.73	−0.07	11
KGC 8	15.79	−0.55	9	11.44	−0.33	9	11.69	−0.03	7	0.82	0.02	6
KGC 9	16.15	−0.19	8	11.55	−0.22	7	11.92	0.2	5	0.84	0.03	4
KGC 10	15.09	−1.25	10	11.89	0.12	4	11.19	−0.53	11	0.76	−0.05	10
KGC 11	13.93	−2.41	11	11.97	0.2	2	11.34	−0.38	10	0.66	−0.14	12
KGC 12	16.22	−0.12	7	11.38	−0.39	11	11.03	−0.69	12	0.77	−0.04	9

Fig. 1 AMMI biplot showing AMMI1 for **a**. Pods per plant, **b**. Pod length **c**. Seeds per pod and **d**.Seed yield
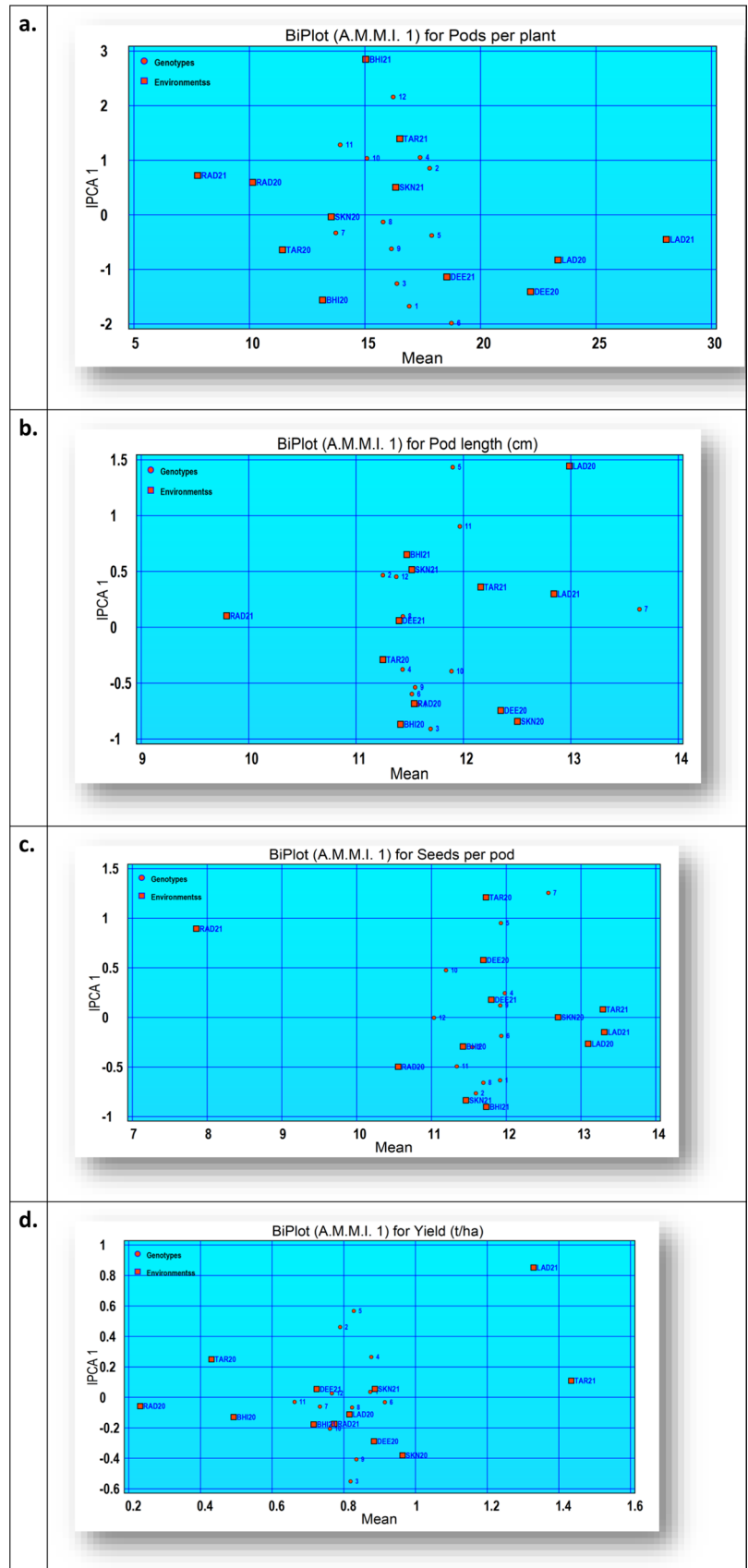
Fig. 2 AMMI biplot showing AMMI2 for **a**. Pods per plant, **b**. Pod length **c**.S per pod and **d**. Seed yield
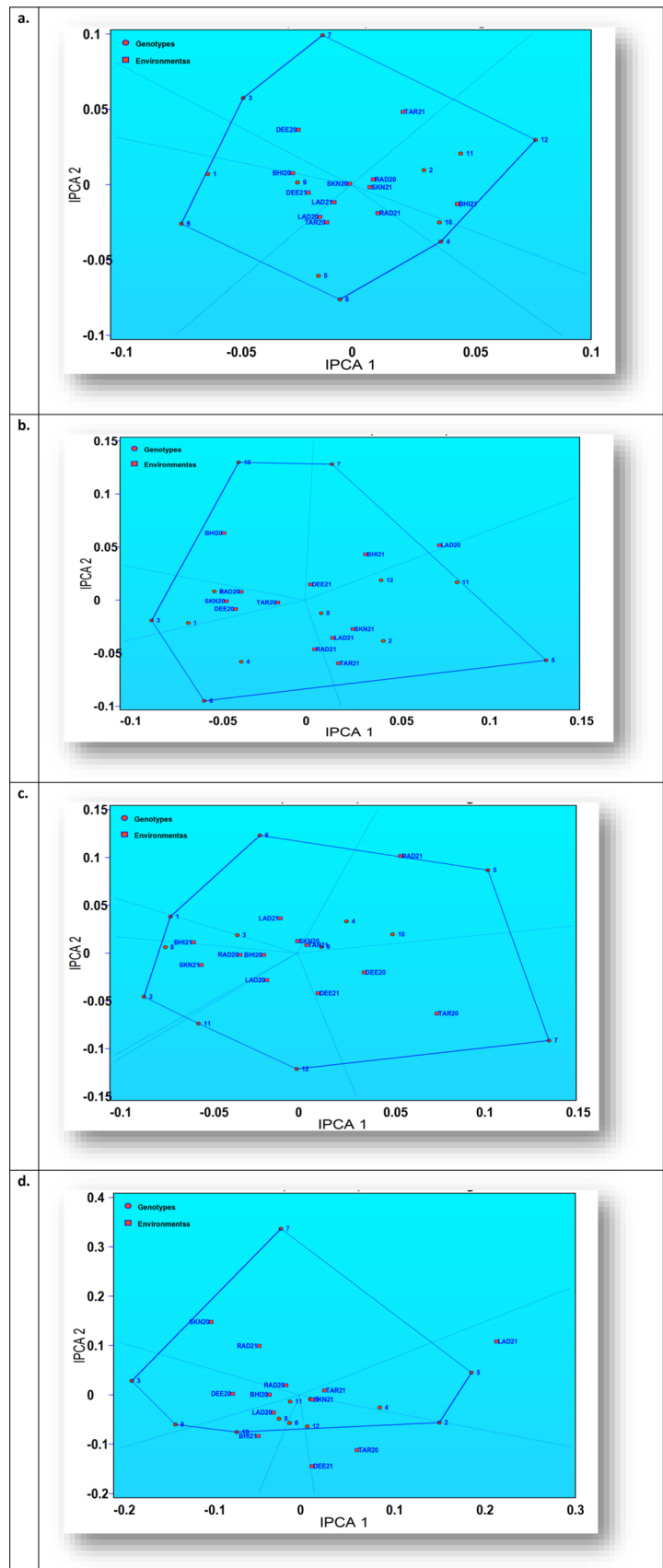
Conclusion

The main objective of the current multi-environmental investigation is to evaluate cowpea genotypes based on mean performance under a wide range of environments to identify superior genotypes. The genotype x environment interaction (GEI) has long been a concern for plant breeders involved in performance testing. The GEI diminishes the link between phenotypic and genotypic values, resulting in a bias in estimations of gene effects and combining ability for various environmental-sensitive features. The AMMI model is useful in this scenario since it contributes to a bigger share of the GEI sum of squares and separates the main and interaction effects. The current study found that environment and GEI had a significant impact on yield attributes, indicating that the traits are controlled by different sets of genes and that the cumulative expression of these genes will vary significantly depending on the environment, which is observed as variation in stability of genotypes for pods per plant, pod length, seeds per pod and ultimately yield. Further, through AMMI biplots, environments were categorized into favorable and unfavorable for yield and the attributes that contribute to it. As revealed by the present study, the genotype KGC 1 identified as the most adapted line and stable performer with negligible GEI and high yield, could be a potential candidate to be used as a variety which can improve cowpea productivity as this crop is mainly grown in varied and harsh environments. Genotype like KGC5 which was a high yielder and specifically adapted to the LAD environment can be promoted for that particular location. Furthermore, the current varietal release system only considers a genotype's average across years and places and its superiority over checks, ignoring the stability of genotypes. The presence of considerable cross-over interactions indicates that the current system does not accurately reflect the current situation logically. Instead, genotypes with broad adaptability and strong yield might be prioritized across environments, whereas genotypes with high yield but lacks stability could be suggested for a specific environment.

Declarations

Conflict of interest Authors declare there is no conflict of interest to disclose.

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