

GENETIC VARIABILITY, GENOTYPE $\times$ ENVIRONMENT INTERACTION AND YIELD STABILITY IN COWPEA GERMPLASM: IMPLICATIONS FOR BREEDING

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ABSTRACT

A total of 147 cowpea [*Vigna unguiculata* (L.) Walp.] germplasm accessions and two checks (C-152 and KBC-9) were evaluated at Bengaluru, Mandya and Pavagada during summer 2022 to assess genetic variability, genotype $\times$ environment interaction (GEI) and yield stability. The experiment was conducted using an α -lattice design with two replications per location. Pooled ANOVA revealed highly significant effects of genotypes, environments and GEI for grain yield and associated traits, indicating differential environmental responses. High heritability coupled with high genetic advance was observed for plant height, primary branches, pods per plant, pod length, seeds per pod and grain yield, suggesting additive gene action. K-means clustering grouped genotypes into 12 clusters, with maximum divergence between clusters VI and VII. AMMI and GGE biplot analyses identified KBC-2, IC-237422 and EC-170574 as high-yielding and stable genotypes. Specific adaptation was observed for IC-402159, CB-1024, IC-458492, NBC-51 and EC-472252. Stable genotypes identified through AMMI and stability indices can be utilized in breeding programmes.

KEYWORDS: AMMI, cowpea, genotype $\times$ environment interaction, GGE biplot, yield stability

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most important food legumes cultivated in tropical and subtropical regions of the world. It belongs to the family Fabaceae and is valued for its adaptability to diverse agro-climatic conditions, drought tolerance, and ability to improve soil fertility through biological nitrogen fixation. Cowpea serves multiple purposes as a grain, vegetable, fodder, and green manure crop, making it an integral component of sustainable farming systems, particularly in rainfed and resource-poor agricultural regions. The crop is rich in protein (20–25%), carbohydrates, vitamins, and essential minerals, thereby contributing significantly to food and nutritional security, especially among economically disadvantaged populations.

Globally, cowpea is cultivated on approximately 14 million hectares, with the majority of production concentrated in sub-Saharan Africa. In India, cowpea is grown across several states including Karnataka, Maharashtra, Gujarat, Rajasthan, Tamil Nadu, and Andhra Pradesh. Despite its importance, the productivity of cowpea remains relatively low compared to its genetic potential. This yield gap is attributed to several factors, including the cultivation of traditional low-yielding varieties, susceptibility to biotic and abiotic stresses, poor harvest index, asynchronous flowering, indeterminate growth habit, and inadequate adaptation to diverse production environments.

The success of any crop improvement programme largely depends on the availability and effective utilization of genetically diverse germplasm. Germplasm collections represent a valuable reservoir of useful genes governing yield, adaptation, resistance to pests and diseases, and tolerance to environmental stresses. Evaluation and characterization of germplasm facilitate the identification of superior genotypes and provide opportunities for broadening the genetic base of breeding populations. Moreover, knowledge of the extent of genetic variability present in breeding materials is essential for designing efficient selection strategies aimed at genetic improvement. Grain yield in cowpea is a complex quantitative trait influenced by several component characters and their interactions with environmental factors. Therefore, assessment of genetic variability, heritability, and genetic advance provides valuable information regarding the nature and magnitude of genetic control governing important agronomic traits. High heritability coupled with substantial genetic advance indicates the predominance of additive gene action and the possibility of achieving genetic improvement through direct selection. Such information enables breeders to identify traits that can effectively contribute to yield enhancement.

In addition to genetic variability, the performance of a genotype is greatly influenced by environmental conditions. The differential response of genotypes across locations and seasons results in genotype $\times$ environment interaction (GEI), which complicates the identification of superior genotypes. Significant GEI reduces the correlation

between phenotypic performance and genetic potential, thereby affecting the efficiency of selection. Consequently, evaluation of genotypes across multiple environments becomes essential to identify cultivars with broad adaptation and stable performance or those specifically adapted to particular environments.

Several statistical approaches have been developed to study GEI and genotype stability. Among them, the Additive Main Effects and Multiplicative Interaction (AMMI) model is widely used because it combines analysis of variance for additive effects with principal component analysis for interaction effects, thereby providing a comprehensive understanding of genotype responses across environments. Similarly, Genotype plus Genotype $\times$ Environment (GGE) biplot analysis offers a graphical representation of genotype performance, stability, and adaptation patterns, facilitating the identification of ideal genotypes and mega-environments. These analytical tools have proven highly effective in dissecting complex GEI patterns and supporting decision-making in plant breeding programs.

Genetic divergence analysis is another important component of germplasm characterization. Multivariate statistical techniques such as K-means clustering enable the classification of genotypes into distinct groups based on multiple traits simultaneously. Information on genetic divergence assists breeders in selecting genetically diverse parents for hybridization, thereby maximizing the probability of obtaining superior recombinants and transgressive segregants in subsequent generations.

Considering the importance of cowpea as a multipurpose legume crop and the need for developing high-yielding, stable, and widely adapted cultivars, the present investigation was undertaken to evaluate a diverse set of cowpea germplasm across multiple environments. The objectives of the study were to assess genetic variability for yield and its associated traits, investigate genotype $\times$ environment interaction and yield stability, analyze genetic divergence among genotypes, and identify superior germplasm accessions that can be utilized in future cowpea breeding programs aimed at enhancing productivity and stability under diverse agro-climatic conditions.

MATERIALS AND METHODS

Experimental Materials

The experimental material consisted of 147 cowpea [*Vigna unguiculata* (L.) Walp.] germplasm accessions collected and maintained under the All India Network Project (AINP) on Arid Legumes, Zonal Agricultural Research Station (ZARS), GKVK, Bengaluru. Two widely cultivated cowpea varieties, C-152 and KBC-9, were included as standard checks for comparison. The germplasm represented a broad spectrum of genetic diversity and was evaluated for yield and yield-attributing traits across multiple environments.

Experimental Sites and Environmental Conditions

The study was conducted during Summer 2022 at three geographically distinct locations in Karnataka, India, namely Bengaluru, Mandya, and Pavagada. These locations represent diverse agro-climatic conditions with variations in temperature, rainfall pattern, soil type, and moisture availability. The use of multiple locations facilitated the assessment of genotype $\times$ environment interaction (GEI) and identification of stable and high-yielding genotypes across environments.

Experimental Design and Crop Management

The experiment was laid out in an alpha-lattice (α -lattice) design with two replications at each location. Each genotype was grown in a single-row plot. Recommended agronomic practices for cowpea cultivation, including land preparation, sowing, nutrient management, irrigation, weed control, and plant protection measures, were uniformly followed at all locations to ensure optimum crop growth and development. Standard spacing was maintained between rows and plants throughout the experiment.

Recording of Observations

Observations were recorded on ten quantitative traits, namely days to 50 per cent flowering, plant height (cm), number of primary branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, pod length (cm), number of seeds per pod, hundred-seed weight (g), and grain yield per plant (g). Data for all traits were recorded from five randomly selected competitive plants in each genotype from each replication, except for days to 50 per cent flowering, which was recorded on a plot basis. The mean values obtained were subjected to statistical analysis for assessing genetic variability, genotype $\times$ environment interaction, and yield stability among the cowpea germplasm accessions. The mean values of the selected plants were used for statistical analysis.

Analysis of Variance

Analysis of variance (ANOVA) was performed separately for each environment and subsequently pooled across environments to determine the significance of genotypic, environmental, and genotype $\times$ environment interaction effects. The statistical significance of variation among genotypes was tested using appropriate F-tests under the α -lattice design.

Estimation of Genetic Parameters

Genetic variability among the germplasm accessions was assessed by estimating phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) following standard biometrical procedures. Broad-sense heritability (H^2) was estimated as the ratio of genotypic variance to phenotypic variance and expressed as a percentage. Genetic advance (GA) and genetic advance as percent of mean (GAM) were calculated to assess the effectiveness of selection and the nature of gene action governing the traits.

Genetic Divergence Analysis

Genetic divergence among the germplasm accessions was assessed using K-means clustering analysis based on the quantitative traits studied. Genotypes were grouped into distinct clusters according to their similarity and divergence patterns. Intra-cluster and inter-cluster distances were computed to identify genetically diverse groups suitable for hybridization and breeding programmes aimed at generating superior segregants and transgressive recombinants.

AMMI Analysis

Genotype $\times$ environment interaction for grain yield per plant was analyzed using the Additive Main Effects and Multiplicative Interaction (AMMI) model. The AMMI model combines analysis of variance for additive main effects of genotypes and environments with principal component analysis (PCA) of the interaction component. Interaction Principal Component Axes (IPCA) scores were estimated and used to interpret the response of genotypes across environments. Genotypes with IPCA scores closer to zero were considered more stable across environments.

Stability Parameters

The stability of genotypes was assessed using AMMI Stability Value (ASV) and Stability Index (SI). ASV was calculated based on the contribution of IPCA I and IPCA II scores to genotype $\times$ environment interaction. Lower ASV values indicated greater stability. Stability Index was computed by integrating both grain yield performance and stability parameters, enabling simultaneous identification of high-yielding and stable genotypes across environments.

GGE Biplot Analysis

Genotype plus genotype $\times$ environment (GGE) biplot analysis was performed to visualize genotype performance, stability, and specific adaptation across environments. The GGE biplot was used to identify ideal genotypes, evaluate test environments, and determine the "which-won-where" pattern for delineation of mega-environments. This graphical approach facilitated identification of both widely adapted and location-specific cowpea genotypes.

Statistical Software

All statistical analysis, including estimation of variability parameters, cluster analysis, AMMI analysis, and GGE biplot analysis, were performed using appropriate statistical software packages. The results obtained were used to identify genetically diverse, high-yielding, and stable cowpea genotypes for utilization in future breeding programs.

RESULTS AND DISCUSSION

The pooled analysis of variance across three environments (Bengaluru, Mandya and Pavagada) revealed highly significant differences among genotypes for grain yield per plant and all yield-related traits studied, indicating the presence of substantial genetic variability in the experimental material. The environment effect was also highly significant for most traits, reflecting the influence of varying agro-climatic conditions on trait expression. Further, genotype $\times$ environment interaction (GEI) was significant for grain yield per plant and key yield-contributing traits, suggesting differential response of genotypes across environments and the necessity of multi-location testing for reliable selection of superior genotypes.

The significant GEI observed for grain yield emphasizes that genotypes did not perform consistently across environments, thereby justifying the use of stability analysis tools such as AMMI and GGE biplot for identifying widely and specifically adapted genotypes.

Genetic Variability, Heritability and Genetic Advance

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) indicated moderate to high variability for most of the traits studied. In general, PCV values were slightly higher than corresponding GCV values, indicating a limited influence of environment on trait expression and the predominance of genetic factors.

High heritability coupled with high genetic advance as per cent of mean (GAM) was recorded for plant height, number of primary branches per plant, pods per plant, pod length, seeds per pod and grain yield per plant. This combination suggests the predominance of additive gene action for these traits and indicates that direct selection would be effective in improving yield. These findings are consistent with studies by Vishwa Nath *et al.* (2009) and Vir and Singh (2014), who also reported that additive gene effects play a major role in the inheritance of these yield-related characters in cowpea.

Traits such as days to 50% flowering and 100-seed weight exhibited moderate heritability and genetic advance, suggesting the involvement of both additive and non-additive gene effects, and hence may require selection in later generations (Poornima, 2023; Naga, 2024). (Table 1)

Genetic Divergence and Cluster Analysis

K-means clustering analysis grouped the 147 cowpea genotypes into twelve distinct clusters, indicating the presence of considerable genetic diversity among the germplasm evaluated. The distribution of genotypes across clusters was non-random, suggesting that genotypes from different geographical origins were grouped together, which may be attributed to exchange of breeding material and selection for similar agronomic traits. This observation aligns with the diversity patterns reported by Kanavi *et al.* (2020) in other *Vigna* species. Cluster VIII was the largest, containing the maximum number of genotypes, whereas cluster VII was the smallest, indicating the uniqueness of genotypes grouped within it. Maximum inter-cluster distance was observed between clusters VI

and VII, followed by clusters V and XI, indicating wide genetic divergence among these clusters. Genotypes belonging to such divergent clusters are expected to produce superior segregants and transgressive recombinants when used as parents in hybridization programmes. (Table 2, Fig. 1)

The minimum inter-cluster distance observed between certain clusters indicated genetic similarity, and hybridization between such clusters may not yield substantial variability.

Genotype $\times$ Environment Interaction and AMMI Analysis

AMMI analysis revealed that both genotype main effects and GEI effects were significant for grain yield per plant. The first two interaction principal component axes (IPCA I and IPCA II) together explained a major proportion of the total GEI variation, indicating their adequacy in explaining genotype response across environments. This indicates that the AMMI model was highly adequate in capturing the complex response of genotypes across environments, a finding that mirrors the results of Ngalamu (2019) in cowpea and Olanrewaju (2021) in other legume species.

According to the stability criteria established by Purchase (1997) genotypes with IPCA scores close to zero exhibited minimal interaction with environments and hence were considered stable. Genotypes such as KBC-2, IC-237422 and EC-170574-6 recorded high mean grain yield coupled with low IPCA scores, indicating their wide adaptability and yield stability across environments. These genotypes can be recommended for cultivation across diverse agro-climatic conditions.

On the other hand, genotypes with high IPCA scores showed specific adaptation to particular environments, indicating their suitability for location-specific cultivation rather than broad adaptation.

AMMI Stability Value and Stability Index

AMMI stability value (ASV), which combines IPCA I and IPCA II scores, was used to quantify yield stability of genotypes. Lower ASV values indicate higher stability. Genotypes EC-458483, EC-394708 and NBC-18 exhibited the lowest ASV values, indicating superior stability across environments.

While ASV identifies stability, it does not necessarily account for mean yield performance. Therefore, the Stability Index (SI) was utilized to identify genotypes that combine both high yield and stability, following the "simultaneous selection" approach suggested by Rao and Prabhakaran (2005). Genotypes IC-198355(45), EC-472271 and EC-394708 recorded high mean yield along with low SI values, indicating their consistent performance across environments and suitability for recommendation in breeding programmes targeting stable yield. Similar integrated selection indices have been successfully applied by Meena (2017) to identify superior cowpea germplasm in diverse Indian environments (Table 3 & 4).

GGE Biplot Analysis

GGE biplot analysis provided a graphical representation of genotype performance and stability across environments. The "mean vs. stability" view of the biplot identified genotypes KBC-2, IC-237422 and EC-170574-6 as ideal genotypes, as they exhibited high mean yield and greater stability. (Fig. 2)

The "which-won-where" pattern revealed a clear delineation of mega-environments among the test locations. Following the polygon-view methodology established by Yan et al. (2000) genotypes IC-402159 and CB-1024 were identified as winning genotypes in Bengaluru and Pavagada environments, indicating their specific adaptation to these locations. In contrast, IC-458492, NBC-51 and EC-472252 performed better in Mandya environment, suggesting their suitability for cultivation under the agro-climatic conditions prevailing at Mandya. (Fig. 3)

This delineation of environments into mega-environments is crucial for targeted varietal deployment. As noted by Olanrewaju (2021) and Rao and Prabhakaran (2005), identifying whether a genotype is widely adapted or location-specific allows breeders to maximize genetic gain in specific niche environments while maintaining reliable production in broader regions

The present investigation revealed the existence of substantial genetic variability among the evaluated cowpea germplasm for grain yield and its associated traits across three diverse environments. Significant differences among genotypes, environments and their interactions emphasized the influence of environmental factors on yield expression and highlighted the necessity of multi-location evaluation for reliable selection of superior genotypes. High heritability coupled with high genetic advance as per cent of mean for key yield-contributing traits such as plant height, number of primary branches per plant, pods per plant, pod length, seeds per pod and grain yield per plant indicated the predominance of additive gene action. This suggests that improvement in these traits can be effectively achieved through direct selection in early generations. The observed variability provides ample scope for genetic enhancement of cowpea productivity.

Multivariate analysis using K-means clustering grouped the genotypes into distinct clusters with wide inter-cluster distances, particularly between clusters VI and VII, indicating substantial genetic divergence. Genotypes from such divergent clusters can be effectively utilized as parents in hybridization programmes to generate broad variability and transgressive segregants for yield improvement.

The presence of significant genotype $\times$ environment interaction for grain yield necessitated stability analysis. AMMI and GGE biplot analyses proved effective in identifying both widely adapted and location-specific genotypes. Genotypes such as KBC-2, IC-237422 and EC-170574-6 consistently exhibited high mean yield with greater stability across environments and can be considered as potential candidates for wide adaptation. In contrast, genotypes IC-402159 and CB-1024 were specifically adapted to Bengaluru and Pavagada environments,

while IC-458492, NBC-51 and EC-472252 showed superior performance under Mandya conditions, indicating their suitability for location-specific deployment.

Further, stability parameters such as AMMI stability value (ASV) and stability index (SI) enabled identification of genotypes combining yield stability with consistent performance. Genotypes EC-458483, EC-394708 and NBC-18 were identified as highly stable, while IC-198355(45), EC-472271 and EC-394708 showed desirable stability index values, making them promising genetic resources for breeding programmes aimed at yield stability. Overall, the integration of genetic variability assessment, divergence analysis and stability analysis provided a comprehensive understanding of yield performance of cowpea germplasm. The superior and stable genotypes identified in this study can be directly utilized in varietal development or as parental lines in breeding programmes for enhancing productivity and stability of cowpea under diverse agro-climatic conditions.

Authorship Contribution Statement

Mubarak A. Sali: Planned and conducted the experiments, collected and analyzed the data, and prepared the initial draft of the manuscript.

Krishna T. V: Conceptualized the study, supervised the research work, guided data interpretation, and critically revised the manuscript.

Madhusudhan M R: Assisted in statistical analysis, interpretation of results, and manuscript editing.

Lohithaswa H C: Contributed to experimental planning, technical guidance, and manuscript review

Mahadevu P : Supported multi-location field experimentation and data collection.

Papireddy M : Assisted in germplasm evaluation, result interpretation, and manuscript refinement.

Palanna K B: Provided technical support and manuscript review.

Syed Mazar Ali: Assisted in field trials, data recording, and compilation of results.

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Table 1. Variability statistics of ten traits

Characters	Bengaluru				Pavagada				Mandya	
	PCV (%)	GCV (%)	h^2 (bs)	GAM (%)	PCV (%)	GCV (%)	h^2 (bs)	GAM (%)	PCV (%)	GCV (%)
Days to 50% flowering	8.47	8.20	93.32	16.36	8.38	8.07	90.69	13.29	9.10	7.69
Plant height (cm)	30.25	30.10	90.45	61.70	28.35	27.21	83.56	57.60	31.08	24.56
Primary branches plant ⁻¹	53.31	48.16	81.36	69.65	51.32	48.48	89.55	59.44	49.12	45.24
Clusters plant ⁻¹	35.99	33.34	21.44	47.51	32.42	28.11	17.36	42.65	44.30	43.32
Pods cluster ⁻¹	48.61	45.56	45.36	30.56	43.36	41.56	42.56	27.86	41.58	40.31
Pods plant ⁻¹	52.89	49.09	67.65	60.36	47.49	43.19	61.54	53.70	52.31	50.91
Average pod length (cm)	23.05	20.91	62.45	32.95	21.90	18.92	58.36	18.22	19.31	18.31
Average seeds pod ⁻¹	19.87	18.79	80.35	32.79	28.45	23.56	75.24	40.20	19.17	17.07
Average Grain yield plant ⁻¹ (g)	60.25	55.12	52.02	70.17	51.18	47.61	54.55	56.95	51.23	46.69
100 seed weight (g)	49.87	47.23	43.32	60.21	50.12	47.89	41.22	57.82	52.36	49.23

PCV (%) – phenotypic coefficient of variance; GCV (%) – genotypic coefficient of variance; h^2 (bs) – heritability; GAM (%) – genetic advance *per cent* of mean

Table 2. Grouping of genotypes in 12 clusters obtained using k-means clustering

Clusters	No. of genotypes	Genotypes
1	17	VCP-17-019, EC-458511, IC-402106, IC-402098, 27749(20), 201095(32), NBC-38, NBC-27 SUPER-30, NBC-43, GWHOPECB-10, C-33, NBC-25, CP-98, SKUA-WCP-49 and NBC-24
2	11	NBC-8, IC-202867(99), IC-603187, IC-462099, IC-58905, IC-237422, EC-458470, EC-472257, NBC-40, CPD-340 and NBC-44
3	13	IC-249141, IC-4506, IC-402125, IC-202325, IC-202792(72), IC-402175, EC-271040, EC-458489, EC-402159, V-589, EC-394708, EC-458438 and 202804(83)
4	8	IC-402048, IC-402114, EC-458485, EC-458473, EC-075180, EC-458483, EC-458411 and EC-458425
5	8	IC-402104, VCP-18-032, EC-458490, PMCP-1131, KBC-2, KM-5, GC-1602 and IC-402090
6	13	IC-253251, GC-3, IC-249593, 198355(45), IC-25105, IC-402101, V-604-7-29-3, EC-492292, EC-472250, TPTC-29, GC-1801, IC-2591054 and EC-458418
7	4	V-578, V-585, VC-458492 and NBC-51
8	22	IC-402172, IC-458430, IC-330996, IC-45061, IC-402135, IC-10171, 2574422(7), IC-402161, IC-107120, 202521(93), 202854(97), EC-458469, EC-458505, EC-170574-6, EC-170584-1.1, V-240, V-16, EC-394839, NBC-6, NBC-33, CPD-15 and NBC-7
9	11	IC-422174, IC-198326-38, IC-1070, IC-402164, EC-472252, IC-402166, EC-390287, NBC-23, NBC-36, NBC-4716, and IT-9715499-38

10	15	IC-402159, IC-249588, IC-202781, IC-202777, IC-402162, IC-202711(58), IC-202290, 202329-89, EC-394838, EC-458442, NBC-29, NBC-19, PMCP-1016, GC-1805 and C-24-1
11	7	EC-458440, EC-472271, CB-1024, EC-170604, NBC-30, NBC-18 and EC-458480
12	18	IC-1071, IC-219489, IC-206240, EC-47226, NBC-391, NBC-32, NBC-98, NBC-68, TOME-774, PCP-0306-1, NBC-14, NBC-016, CPD-331, PCD-1124-1, NBC-41, C-457, C-157 and EC-394779

Table 3. Top five stable cowpea genotypes across three locations identified based on ASV and SI for different traits.

Characters	Based on SI	Based on ASV
Days to 50% flowering	NBC-29, V-16, EC-458473, IC-58905, IC-202781	NBC-29, NBC-27, TOME-774, NBC-4716, NBC-44
Plant height (cm)	CP-98, IC-45061, IC-402161, IC-25105, IC-402098	IC-402161, 202804(83), CP-98, IC-402098, IC-458430
Primary branches plant⁻¹	EC-458480, 202804(83), KBC-2(c), EC-458485, IC-402048	EC-458485, EC-472250, PCD-1124-1, IC-402048, NBC-25
Clusters plant⁻¹	198355(45), IC-402159, V-589, NBC-14, IC-25105	IT-9715499-38, V-240, IC-202711(58), EC-394708, IC-402159
Pods cluster⁻¹	IC-10171, IC-4506, V-604-7-29-3, C-24-1, IT-9715499-38	IC-58905, IC-202781, IC-402106, EC-458483, IC-4506
Pods plant⁻¹	IC-198355, C-33, IC-202290, GC-1805, IC-402159	IC-202792(72), NBC-23, IC-402090, EC-458490, EC-472271
Average pod length (cm)	IC-402162, KBC-2(C), NBC-25, IC-402175, IC-603187	EC-472250, IC-402162, C-152 (c), IC-249593, NBC-25
Average seeds pod⁻¹	GC-1801, IC-402161, EC-170574-6, IC-462099, C-152(C)	NBC-23, EC-472250, KBC-9 (c), SKUA-WCP-49, IC-422174
Average Grain yield plant⁻¹ (g)	IC-198355, EC-170584-1.1, IC-402166, NBC-36, EC-458425	EC-458490, IC-402166, NBC-33, NBC-30, IC-402098
100 seed weight (g)	NBC-4716, TPTC-29, NBC-7, CB-10, IC-402106	IC-198326-38, Genotype-36, GC-1801, NBC-27, IC-202521

Table 4. Stable cowpea genotypes across three different locations identified based on SI for multiple traits.

Stable genotypes based on SI	Multiple traits for which genotypes found stable
IC-402161	Plant height (cm) and average pod length (cm)

IC-25105	Plant height (cm) and clusters plant ⁻¹
IC- 198355	Clusters plant ⁻¹ , pods plant ⁻¹ and average grain yield plant ⁻¹ (g)
IC-402159	clusters plant ⁻¹ and pods plant ⁻¹

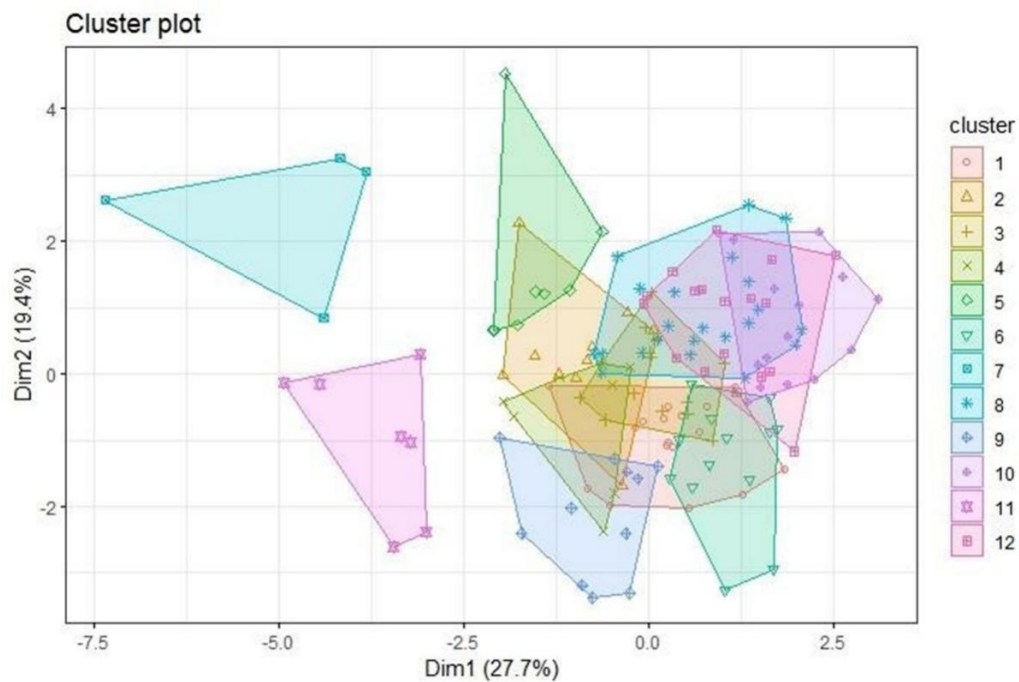


Fig. 1. Cluster plot representing twelve clusters derived using *k means* clustering of cowpea genotypes for yield and yield attributing traits

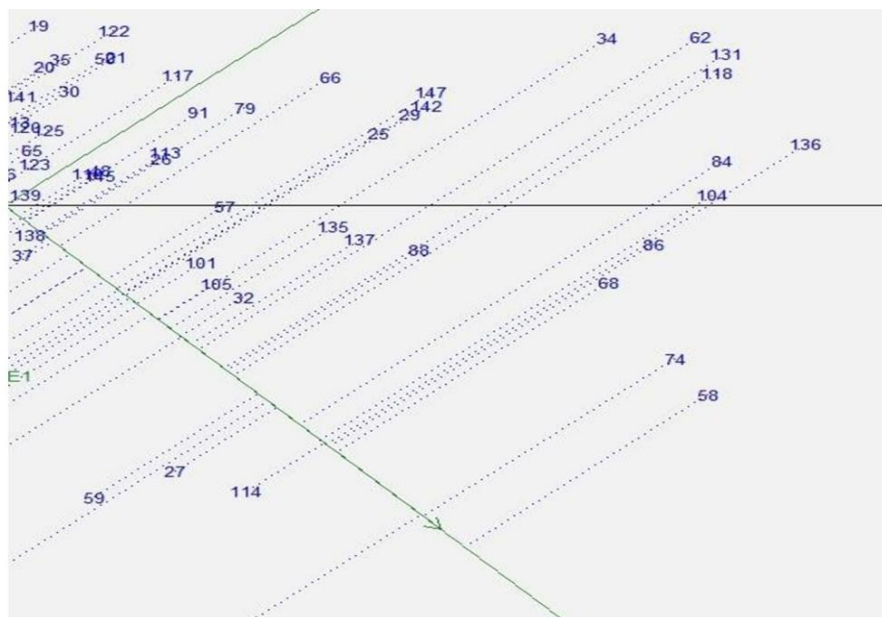


Fig. 2. Average environment coordination view of GGE-based on location environment focused scaling for the mean performance vs. stability for average yield plant⁻¹

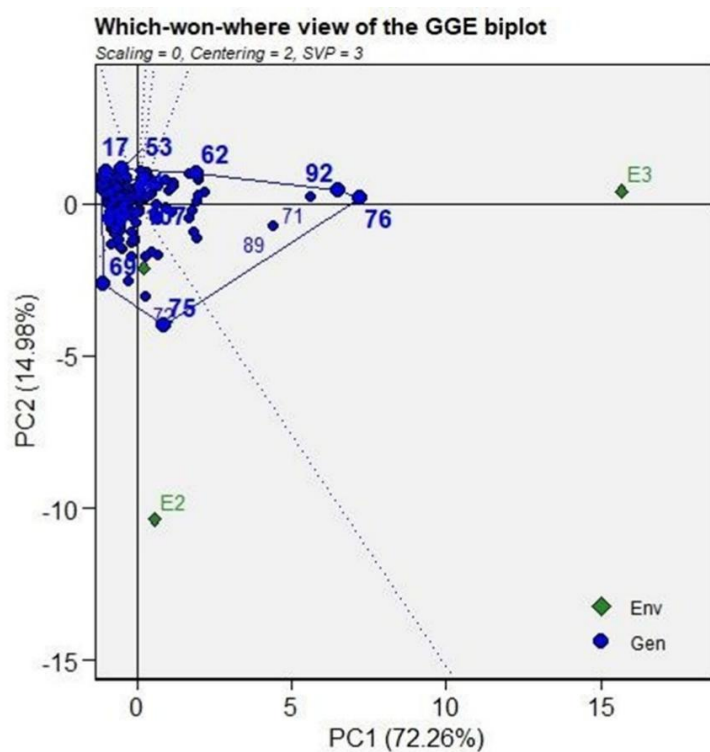


Fig. 3. Polygon view of GGE-biplot based on the symmetrical scaling for “which won- where” pattern of genotypes and location environments for average grain yield plant-1