



Stability analysis for yield in early duration pigeonpea based on AMMI, GGE and multi trait stability index

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Abstract

Pigeonpea (*Cajanus cajan* (L.) Millsp.) productivity is significantly influenced by genotype $\times$ environment interaction (GEI), necessitating the identification of stable and widely adapted genotypes. The present study evaluated seventeen early duration pigeonpea genotypes across three cropping seasons (E1: *Kharif* (June) 2022, E2: *Kharif* (July) 2023 and E3: *Rabi* (September) 2023-24) at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore, using a randomized block design with three replications. Twelve yield and yield-related traits were recorded and analysed using pooled ANOVA, Additive Main Effects and Multiplicative Interaction (AMMI), Genotype plus Genotype $\times$ Environment Interaction (GGE) biplot and Multi-Trait Stability Index (MTSI). Pooled ANOVA and AMMI ANOVA revealed significant genotype, environment and GEI effects for most of the traits. For single plant yield, AMMI analysis indicated that the first interaction principal component axis (IPCA1) explained 93.70 % of the GEI variation. Based on AMMI analysis, CORG7, ICPL19038 and ICPL19010 were identified as high-yielding genotypes, whereas ICPL19010 combined high yield with stability. Likewise, GGE biplot also identified ICPL19010 as the ideal genotype with high yield and stability, whereas CORG7 exhibited higher productivity with specific adaptation to Environment 1. Environment 1 was identified as the most representative and discriminating testing environment. MTSI analysis further identified ICPL19008, ICPL19010 and ICPL19017 as superior genotypes based on simultaneous evaluation of all twelve traits. Overall, ICPL19010 consistently combined high yield, stability and broad adaptation across environments, making it a promising genotype for pigeonpea breeding and varietal improvement.

Keywords: AMMI Model, GGE, MTSI, pigeonpea, Yield stability

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.], commonly known as redgram, arhar or tur, is one of the most important grain legume crops cultivated in tropical and subtropical regions, particularly under rainfed agricultural conditions. The crop belongs to the family Fabaceae with diploid chromosome number of $2n = 22$. Owing to its deep root system, drought tolerance, wide adaptability and compatibility with diverse cropping systems, pigeonpea occupies a significant place in sustainable agriculture. It can be successfully cultivated under a broad range of climatic conditions and intercropped with several crops without exhibiting allelopathic effects (Bhaskaran and Muthiah, 2005). Besides serving as a major source of dietary protein, pigeonpea contributes substantially to soil fertility through biological nitrogen fixation.

India is the largest producer, consumer and cultivator of pigeonpea in the world, accounting for nearly 72 % of the global area under cultivation and approximately 85 % of global production and consumption (Danekar *et al.*, 2014; Arulselvi *et al.*, 2025). Pigeonpea is the second most important pulse crop in the country after chickpea. It occupies an area of 43.36 lakh hectares with a production of 36.24 lakh tonnes and an average productivity of 836 kg ha⁻¹ (Indiastat, 2025). Among the pigeonpea growing states, Maharashtra is the leading producer, cultivating the crop over 12.27 lakh hectares and producing 14.23 lakh tonnes with a productivity of 1160 kg ha⁻¹ (Indiastat, 2025). Karnataka ranks second with a production of 9.98 lakh tonnes.

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Despite its economic and nutritional importance, pigeonpea productivity remains highly variable due to fluctuations in environmental conditions. The phenotypic performance of a genotype is determined by the combined effects of genotype, environment and their interaction. Differential responses of genotypes to temporal environmental variations result in genotype $\times$ environment interactions (GEI), leading to inconsistent performance across years and challenging the identification of superior cultivars. Therefore, understanding the magnitude and pattern of GEI is essential for the development of stable and high-yielding pigeonpea varieties. Evaluation of genotypes across multiple seasons provides valuable information

on GEI and facilitates the identification of high yielding genotypes with stable performance and wider adaptation under varying climatic conditions, thereby supporting effective breeding and varietal improvement programmes (De Leon *et al.*, 2016; Ranjani *et al.*, 2021).

Several statistical approaches have been developed to analyse GEI and assess phenotypic stability. These methods are broadly classified into univariate and multivariate techniques. Among the multivariate approaches, the Additive Main Effects and Multiplicative Interaction (AMMI) model effectively partitions the additive effects of genotypes and environments from the multiplicative GEI component, thereby improving the interpretation of genotype responses across environments (Zobel *et al.*, 1988). In addition, Genotype plus Genotype $\times$ Environment Interaction (GGE) biplot complements the AMMI model by graphically displaying genotype performance together with GEI, enabling the identification of superior genotypes, ideal testing environments and “which-won-where” patterns (Yan and Tinker, 2006). GGE biplot has become one of the most widely adopted methods in multi-environment trials because it simultaneously evaluates mean performance, stability, discriminating ability and representativeness of environments. Nevertheless, both AMMI and GGE biplot primarily focus on individual traits, whereas genotype selection in breeding programmes generally depends on the simultaneous improvement of several agronomic traits. To overcome this limitation, the Multi-Trait Stability Index (MTSI) proposed by Olivoto *et al.* (2019) integrates mean performance and stability of multiple traits into a single selection criterion based on factor analysis, allowing the identification of genotypes that combine superior agronomic performance with stability across environments.

Therefore, the present investigation was undertaken to evaluate the genotype $\times$ environment interaction of seventeen early duration pigeonpea genotypes across three cropping seasons using AMMI and GGE biplot analyses and to identify stable, high-yielding and broadly adapted genotypes. In addition, the MTSI was employed to facilitate simultaneous selection based on multiple yield and yield-related traits, thereby facilitating the identification of high-yielding and stable genotypes for use in breeding programmes and varietal development.

MATERIALS AND METHODS

Seventeen early duration and photo-insensitive pigeonpea genotypes were evaluated in a Randomized Block Design (RBD) with three replications across three cropping seasons, viz., Kharif 2022 (E1 – June sowing), Kharif 2023 (E2 – July sowing) and Rabi 2023-24 (E3 – September sowing). The experiment was conducted at the Department of Pulses, Centre for Plant Breeding & Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (11°N latitude, 77°E longitude and 427 m above mean sea level). Each genotype was raised in 5

m long row with a spacing of 60 x 30 cm. Recommended agronomic practices and plant protection measures were followed uniformly throughout the crop growth period to ensure optimal crop establishment and development. Observations were recorded on twelve biometrical traits, viz., days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, pod-bearing length (cm), number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, shelling percentage, hundred-seed weight (g) and single plant yield (g). Days to 50 per cent flowering and days to maturity were recorded on a plot basis, whereas observations on the other traits were recorded from five random plants.

Statistical analysis

Pooled ANOVA was performed to evaluate genotype (G), environment (E) and genotype $\times$ environment interaction (GEI). AMMI analysis was used to partition GEI, while GGE biplot analysis was used to identify superior genotypes, mega-environments and ideal testing environments for single plant yield.

The Multi-Trait Stability Index (MTSI) proposed by Olivoto *et al.* (2019) was employed to simultaneously evaluate mean performance and stability across all twelve traits. An ideotype was defined by assigning lower values for days to 50 per cent flowering and days to maturity, and higher values for the remaining traits. MTSI values were calculated as the euclidean distance of each genotype from the ideotype in the factor-analytic space, with lower values indicating greater proximity to the ideotype and, consequently, superior overall performance and stability. A selection intensity of 20 % was applied to identify the most desirable genotypes. All statistical analyses were performed using the metan package in R software version 4.5.2.

RESULTS AND DISCUSSION

Genotype $\times$ Environment interaction

The pooled analysis of variance across environments revealed highly significant ($P < 0.01$) differences among genotypes for all the twelve evaluated traits, indicating the presence of substantial genetic variability. The environmental effect was also highly significant for all traits except for number of clusters per plant. Genotype $\times$ Environment interaction (GEI) was highly significant for the majority of the traits viz., days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, pod-bearing length, number of pods per plant, hundred-seed weight and single plant yield, demonstrating differential genotypic responses across test environments (Table 1).

The presence of significant GEI indicates that genotype performance was inconsistent across environments, emphasizing the importance of evaluating genotypes under multiple season/environments. Similar observations on the importance of GEI in determining

Table 1. Pooled analysis of variance (ANOVA) for 12 yield and yield related traits in pigeonpea genotypes across three seasons

Source	df	DFF	DM	PH	NBPP	PBL	CPP	PPP	PL	SPP	SP	HSW	SPY	
Replication	1	0.04	0.48	3.00	0.08	13.60	34.70	79.00	0.00	0.03	72.80	0.00	3.40	
Genotypes	16	51.09**	78.08**	1579.90**	7.03**	325.10**	1271.60**	6957.00**	0.44**	0.27**	110.20**	4.14**	508.90**	
Environment	2	391.80**	495.91**	15549.70**	24.35**	27929.20**	14450.70	97943.00**	1.22**	1.05**	3370.50**	7.16**	10882.10**	
G x E	32	23.43**	45.52**	542.30**	3.42**	229.10**	651.00	3122.00**	0.09	0.09	73.50	0.76**	413.10**	
Residuals	50	1.14	1.40	88.80	1.43	56.10	110.30	306.00	0.07	0.06	53.30	0.22	115.80	
Mean		69.96	118.38	138.78	8.71	78.41	83.61	150.33	5.71	3.89	60.49	10.20	42.11	69.96

DFF-Days to 50 per cent flowering, DM-Days to maturity, PH-Plant height, NBPP-Number of branches per plant, PBL-Pod bearing length, CPP-Number of clusters per plant, PPP- Number of pods per plant, PL-Pod length, SPP-Number of seeds per pod, SP-Shelling percentage, HSW-Hundred seed weight and SPY-Single plant yield, ** Significant at 1% level

Table 2. AMMI analysis for single plant yield of pigeonpea genotypes

Sources	df	Mean square	Proportion (%)
Environment	2	10882.09**	-
Genotype	16	508.88**	-
G x E	32	413.09**	-
PC1	17	728.43	93.70
PC2	15	55.70	6.30
Residuals	48	117.75	

PC1 and PC2 represented the first two principal components, df- degrees of freedom, ** Significant at 1% level.

yield performance have been reported in pigeonpea by Reddy *et al.* (2011), Kumara *et al.* (2016) and Singh *et al.* (2018). The significant GEI observed in the present study justified the use of AMMI, GGE biplot and Multi-Trait Stability Index (MTSI) analyses to identify stable and widely adapted pigeonpea genotypes.

The environmental influence on maturity and yield-related traits is further illustrated through the box plots (**Fig. 1**). Days to maturity, hundred-seed weight and single plant yield varied across the environments, indicating significant environmental effects on these traits. The higher mean days to maturity observed in Environment 1 (E1) along with increased hundred-seed weight and single plant yield, suggesting that the environmental conditions in E1 were conducive for growth and enhanced yield. Single plant yield varied among genotypes across the three test environments. In Environment 1 (E1), it ranged from 78.33 g (ICPL19021) to 166.17 g (CORG 7). The high yielding genotypes were CORG 7 (166.17 g), followed by ICPL19038 (160.83 g) and ICPL19010 (136.17 g). In Environment 2 (E2), single plant yield ranged from 69.75 g (ICPL19047) to 96.18 g (ICPL19021). ICPL19021 recorded the maximum yield (96.18 g), followed by ICPL19029 (87.82 g) and CORG 7 (87.38 g). In Environment 3 (E3), single plant yield ranged from

76.17 g (ICPL19022) to 97.50 g (ICPL19010). The high yield was recorded by ICPL19010 (97.50 g), followed by ICPL19009 (92.67 g) and CORG 7 (90.00 g).

AMMI analysis for single plant yield

The AMMI analysis of variance revealed that the main effects of genotype, environment (E) and GEI were highly significant ($p < 0.001$) (**Table 2**). The significant GEI indicates that genotypes respond differently to varying environments, emphasizing the need to consider both genetic and environmental factors when selecting high yielding stable pigeonpea genotypes. Similar findings of significant genotype, environment and GEI interaction for single plant yield in pigeonpea have been reported by Singh *et al.* (2018) and Bomma *et al.* (2024).

The interaction principal component axis (IPCA 1) accounted for the majority of the GEI variation for single plant yield (93.70 %) which was followed by IPCA 2 (6.30 %). The predominance of IPCA 1 indicates that most of the interaction pattern was captured by the first principal component, thereby facilitating reliable interpretation of genotype stability. The dominance of IPCA 1 in the interaction is consistent with the study of Markos *et al.* (2025), confirming its vital role in selecting high-yielding and stable genotypes.

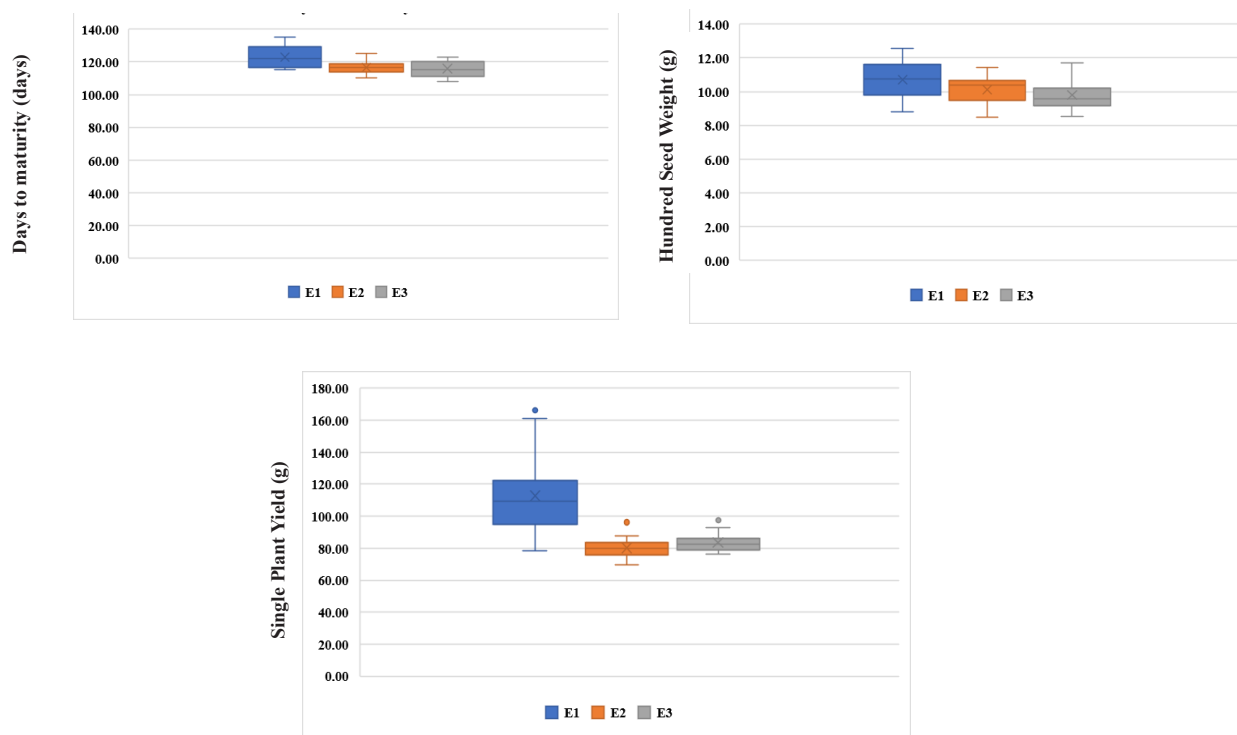


Fig. 1. Box plot depicting the mean performance of days to maturity, hundred seed weight and single plant yield across three seasons

The AMMI 1 biplot distinguished high and low-yielding genotypes based on their position along the abscissa, while stability was inferred from their proximity to the IPCA1 axis. Genotypes positioned close to the horizontal axis exhibited greater stability due to lower interaction effects, whereas those located farther from the axis showed greater environmental sensitivity (Yan and Tinker, 2006). CORG 7, ICPL19038 and ICPL19010 were identified as high-yielding genotypes, whereas ICPL19025, ICPL19024, ICPL19022, ICPL19021, ICPL19012 and ICPL19013 exhibited comparatively lower mean single plant yield (**Fig. 2 a**). Among the environments, E1 was positioned on the positive side of the abscissa, indicating its favorable conditions for higher yield, whereas E2 and E3 were comparatively less productive (**Fig. 2 a**).

The AMMI 2 biplot (**Fig. 2 b**) further illustrated genotype stability based on the distance from the origin. Genotypes located near the origin exhibited lower GEI effects and wider adaptation, whereas those positioned farther away were more responsive to environmental changes (Purchase, 1997). Genotypes viz., CORG 7, ICPL19038, ICPL19021 and ICPL19009 had relatively longer vector lengths, indicating stronger interaction with environment and comparatively less stable. Conversely the genotypes viz., ICPL19017, ICPL19022, ICPL19030, ICPL19011 and ICPL19013 positioned close to the origin were highly stable across environments.

GGE biplot analysis for single plant yield

The GGE biplot explained 96.50 % of the G + GE variation, with PC1 and PC2 accounting for 90.45 % and 6.05 % of the variation, respectively. The “which-won-where” pattern, as described by Yan and Tinker (2006), is evident in the bi-plot. Genotypes at the vertices are the winners in their respective environments. The “which-won-where” biplot (‘WWW’ biplot) identified two mega-environments, with CORG 7 winning in E1 and E3 and ICPL19021 in E2, indicating specific adaptation of these genotypes (**Fig. 3 a**). The mean versus stability GGE biplot indicated that CORG 7, ICPL19038 and ICPL19010 were high-yielding genotypes, as they were positioned in the direction of the average environment coordination (AEC). Among these, ICPL19010 exhibited stability owing to its shorter projection onto the AEC ordinate, whereas CORG 7 and ICPL19038 were comparatively less stable (**Fig. 3 b**).

An ideal genotype is one that has both high mean yield and high stability. The center of the concentric circles represents the position of an ideal genotype in GGE ranking biplot. A genotype is more desirable if it is closer to the ideal genotype. The genotype ranking biplot identified ICPL19010 as closest to the ideal genotype followed by CORG 7 and ICPL 19038 (**Fig. 4 a**). Likewise, the environment ranking biplot identified E1 as the ideal testing environment because of its high discriminating

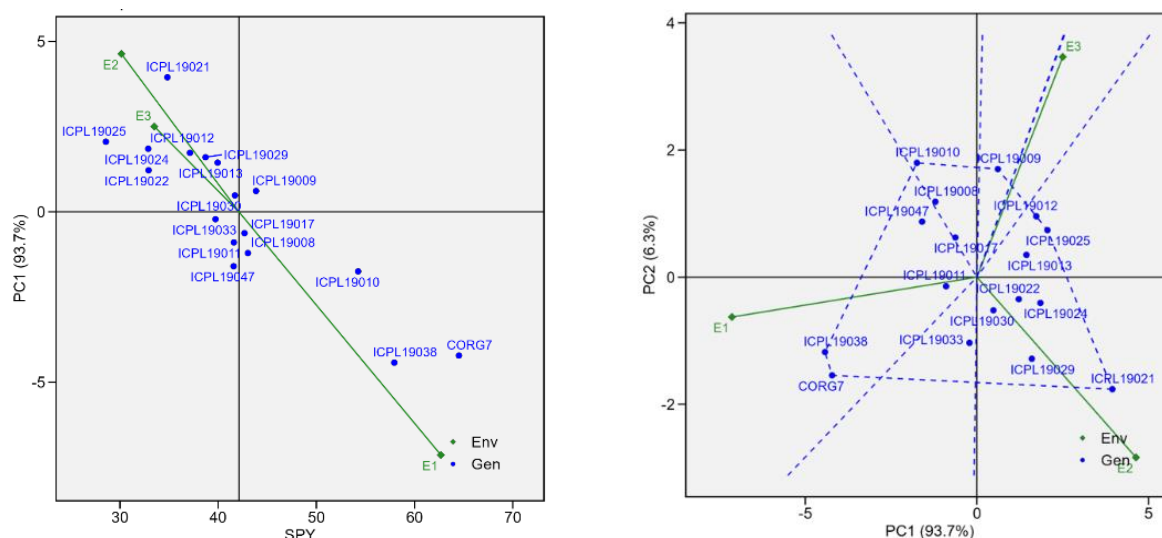


Fig. 2. AMMI1 and AMMI2 biplots showing the distribution of pigeonpea genotypes and test environments in relation to mean single plant yield, IPCA 1 and IPCA 2

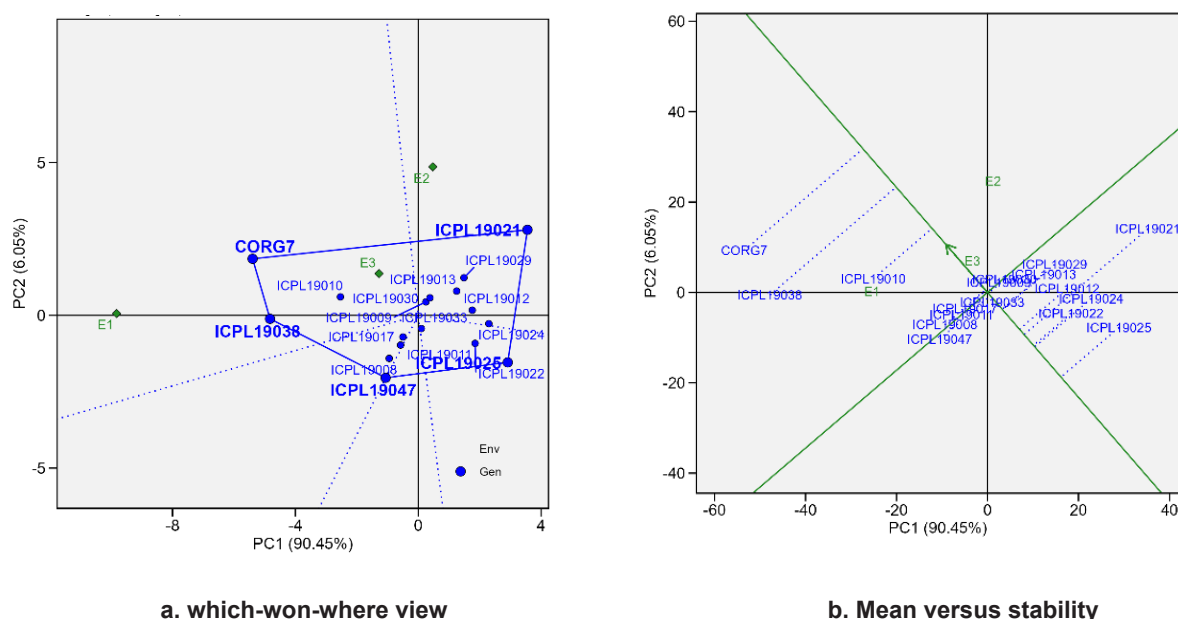


Fig. 3. Genotype plus genotype-by-environment (GGE) bi-plot for single plant yield of the pigeonpea genotypes which-won-where view (a) and mean versus stability (b)

ability and representativeness, making it the most suitable environment for evaluating pigeonpea genotypes (Fig. 4 b).

Multi-Trait Stability Index (MTSI)

The Multi-Trait Stability Index (MTSI) proposed by Olivoto *et al.* (2019) was employed to simultaneously evaluate mean performance and stability across the twelve yield and yield-related traits, thereby providing a comprehensive criterion for genotype selection. Unlike AMMI and GGE biplot analyses, which primarily assess stability based on a single trait, MTSI considers mean

performance and stability across multiple yield and yield-related traits into a single index through factor analysis. Similar approaches of using MTSI have been successfully adopted for identifying superior and stable genotypes in lentil (Sellami *et al.*, 2021), lablab (Markos *et al.*, (2025) and grass pea (Maleki *et al.*, 2024).

The MTSI represents the Euclidean distance of each genotype from the ideotype in the factor-analytic space, where lower values indicate closer proximity to the ideal genotype possessing superior mean performance and stability across all evaluated traits

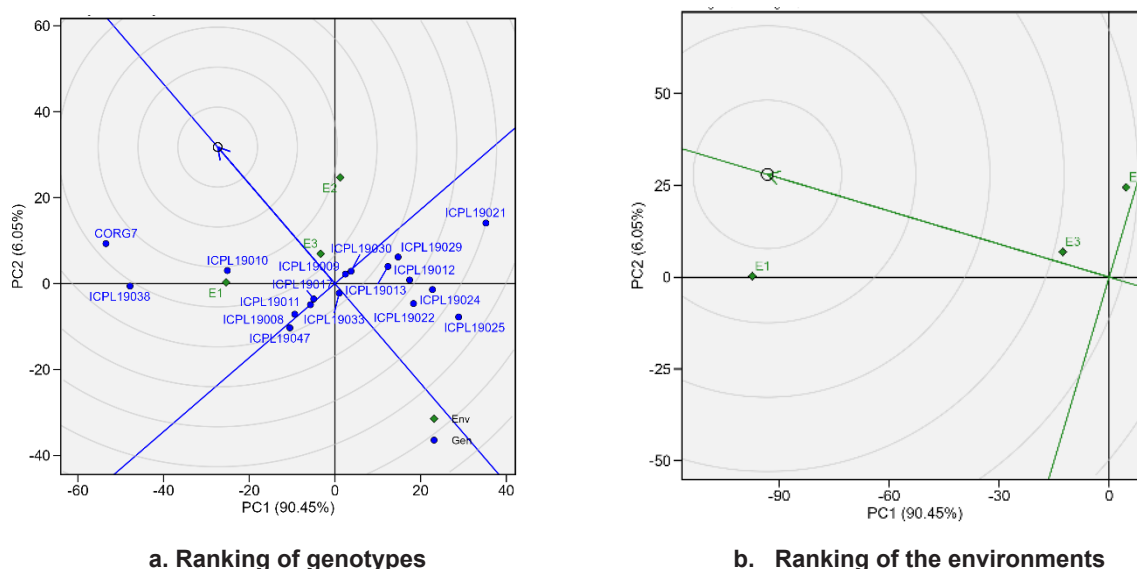


Fig. 4. Genotype plus genotype-by-environment (GGE) bi-plot for single plant yield of the pigeonpea genotypes, ranking of genotypes (a) and ranking of the environments (b)

(Olivoto *et al.*, 2019). With a selection intensity of 20 %, MTSI analysis identified ICPL19008, ICPL19010 and ICPL19017 as the superior genotypes. These genotypes combined desirable mean performance with high stability across environments and therefore exhibited the closest resemblance to the ideotype. In contrast, the highest MTSI values were recorded by ICPL19021, followed by ICPL19011 and ICPL19025, indicating that these genotypes were undesirable for simultaneous selection of mean performance and stability.

The superiority of ICPL19010 and ICPL19017 identified through MTSI was largely consistent with the results obtained from AMMI and GGE biplot analyses. Both

genotypes exhibited low genotype $\times$ environment interaction effects and occupied relatively stable positions in the AMMI2 biplot, while ICPL19010 was also positioned close to the ideal genotype in the GGE genotype-ranking biplot. Likewise, the superior ranking of ICPL19008 by MTSI suggests that although it was not among the highest-yielding genotypes for single plant yield alone, its balanced performance across all yield and yield-related traits resulted in excellent overall adaptability. The concordance between the multi-trait index and the stability analyses based on AMMI and GGE biplots enhances the reliability of genotype selection and agrees with earlier reports in pigeonpea (Rao *et al.*, 2022) and greengram (Aruna *et al.*, 2024).

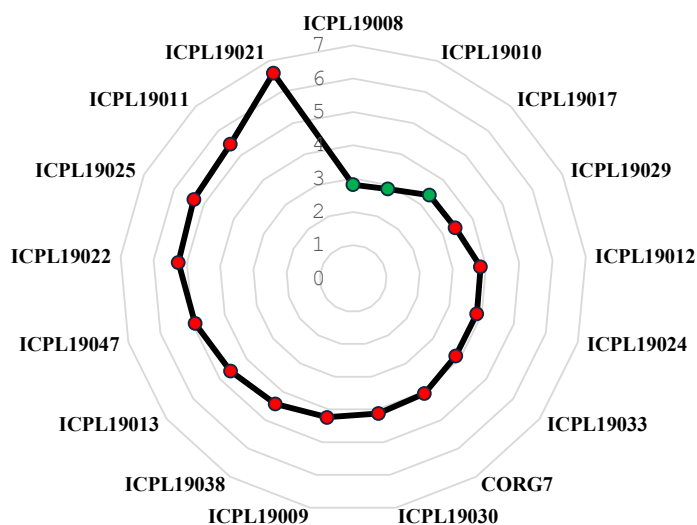


Fig. 5. Selection of pigeonpea genotypes based on multi-trait stability index (MTSI) using 12 yield contributing and yield parameters (Selected genotypes - Green; Non selected - Red)

Overall, the combined analyses of mean performance, AMMI, GGE biplot and MTSI provided complementary insights into the adaptation and stability of pigeonpea genotypes across environments. Based on single plant yield, CORG 7, ICPL19038 and ICPL19010 were identified as the highest-yielding genotypes. Among them, ICPL19010 exhibited superior yield coupled with greater stability across environments, whereas CORG 7 showed high productivity but stronger genotype $\times$ environment interaction, indicating specific adaptation, particularly to Environment 1. The GGE biplot further identified E1 as the most representative and discriminating environment for evaluating pigeonpea genotypes.

However, selection based solely on single plant yield may overlook genotypes possessing desirable performance for other agronomic traits. The MTSI analysis, which integrates mean performance and stability across all twelve yield and yield-related traits, identified ICPL19008, ICPL19010 and ICPL19017 as the most desirable genotypes under a 20 % selection intensity. Notably, ICPL19010 was consistently identified by AMMI, GGE biplot and MTSI analyses, demonstrating superior productivity, stability and overall agronomic performance across environments. Therefore, ICPL19010 can be considered the most promising genotype for broad adaptation, while ICPL19008 and ICPL19017 may serve as valuable genetic resources for developing stable, high-performing pigeonpea cultivars in multi-environment breeding programmes.

The combined analyses of mean performance, AMMI, GGE biplot and MTSI effectively identified stable and high-performing pigeonpea genotypes across diverse environments. Among the evaluated genotypes, ICPL19010 consistently exhibited superior yield, stability and broad adaptation, making it the most promising genotype for multi-environment cultivation. The MTSI further identified ICPL19008 and ICPL19017 as desirable genotypes with superior overall multi-trait performance. These genotypes represent valuable genetic resources for pigeonpea breeding programmes aimed at developing stable, high-yielding cultivars with wide adaptation.

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