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Grain Yield Stability of Pigeonpea Genotypes (*Cajanus cajan* L.) Across Environments

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ABSTRACT

Background: Pigeonpea is a protein-rich vegetarian food crop predominantly cultivated in tropical and subtropical regions worldwide. It stands as the second-largest grain legume in India. Developing adaptable pigeonpea cultivars with stable yields throughout various environmental circumstances has been the primary goal of crop development efforts because of seasonal fluctuations and unpredictable rainfall patterns.

Methods: To ascertain the grain yield performance of thirty pigeonpea genotypes, research was executed across three consecutive summer seasons in 2019, 2020 and 2021 at the Agricultural College and Research Institute, Tamil Nadu Agricultural University, located in Thanjavur, Tamil Nadu, India. The experimental setup employed a randomized block design replicated twice to estimate pigeonpea genotype's yield stability, utilizing AMMI and GGE models.

Result: The AMMI (Additive Main effects and Multiplicative Interactions) analysis showed genotype and environmental interactions had been primary factors influencing pigeonpea genotype's grain yield performance. The initial 2 principal component axes (IPCA I and IPCA II) exhibited statistical significance, collectively explaining the total degrees of freedom associated with the interaction component. Genotype G30 was the best performer in the E3 environment, while G25, G6 and G22 were top performing pigeonpea genotypes in E1 environment. The environments E1 and E2 were closely related. Among the pigeonpea genotypes tested in this investigation, G25 and G6 were higher yielders with greater yield stability and can be recommended for cultivation in all three seasons. In contrast, G30 and G22 yielded higher but had unstable yield performance. Genotypes G16, G17, G12 and G15 showed greater stability but were poor yielders.

Key words: AMMI, Breeding, Pigeonpea, Pulses, Yield stability.

INTRODUCTION

Pigeonpea (*Cajanus cajan* L.), frequently referred to as tur, arhar, or red gram in various regions of India, holds significant importance in the country's agricultural landscape. It ranks as India's 2nd most essential pulse crop, following chickpea, both in terms of production and consumption. India dominates the global landscape for pigeonpea cultivation, accounting for approximately 72% of the overall area devoted to this crop worldwide (Fatokimi *et al*., 2021) and contributing up to 65% of the global production. The country produces 4.3 million tonnes of pigeonpea over an area of 5.00 million hectares, achieving the rate of productivity of 861.2 kilograms per hectare (FAOSTAT, 2022). Primary pigeonpea usage includes dehulled split peas, while its green seeds and pods are also consumed fresh or as green vegetables. In India, pigeonpea cultivation is particularly concentrated in certain states, with Maharashtra, Karnataka and Uttar Pradesh being the major contributors. Maharashtra leads the production, accounting for 31.49% of the total production, followed by Karnataka and Uttar Pradesh. Other states such as Madhya Pradesh, Gujarat, Jharkhand, Telengana and Odisha also contribute to its cultivation (Agricultural Statistics at a Glance, 2022). According to agricultural statistics, Maharashtra is the leading state in pigeonpea production, with an output of 1.37 million tons from 1.34 million hectares area, achieving 1.02 tons/hectare productivity (Agricultural Statistics at a Glance, 2022). Pigeonpea, belonging to the family Fabaceae, is a crop having diploid chromosomal number of 2n=22 that is frequently cross pollinated. Its hardiness, wide adaptability and drought tolerance make it suitable for cultivation across diverse environmental conditions and cropping systems. These characteristics contribute to its popularity among farmers in India and its significant role in the country's agricultural economy.

Agricultural yield is subject to significant fluctuations due to varying environmental conditions, both within and

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between years and locations. The phenotype of a plant, which refers to its observable characteristics, is influenced by both its genetic makeup (genotype) and environment in which it grows. However, the impact of genotype and environment are not always straightforwardly additive because of GEI (genotype-environment interaction). The term 'GEI' describes a genotype's uneven performance in various settings. Since genotype-environment interactions affect the stability and performance of crops under various situations, it is essential to comprehend and manage them in plant breeding (Egea-Gilabert *et al*., 2021). Breeders aim to improve yield stability, ensuring consistent performance in a variety of settings, which is vital for sustainable agricultural production. However, achieving yield stability can sometimes lead to trade-offs. For example, selecting for stability may result in lower average yields, while selecting for higher mean yields may compromise stability. Studies have shown contrasting outcomes when balancing yield stability and mean yield. Some research, like that of Holland *et al*. (2002), has demonstrated that selecting for broad adaptation to diverse surroundings can lead to both increased mean grain yield and improved stability in populations. This suggests that it's possible to achieve both higher average yields and greater stability through careful breeding and selection processes. Overall, managing genotype-environment interactions is a complex yet essential aspect of plant breeding (De Leon *et al*., 2016). Balancing the trade-offs between mean yield and stability requires careful consideration and may vary depending on the specific crop, environment and breeding objectives.

Multi-environment trials are pivotal in selecting optimal cultivars for future use across various locations and evaluating their stability across diverse environments before commercial release. When comparing a cultivar's yield performance across environments, multiple attributes are taken into account, with grain yield being particularly crucial (Vargas *et al*., 1999 and Vargas and Crossa, 2000). Numerous analytical methods have been devised to assess stability and forecast cultivar performance in multi-environment trials. AMMI model is unique among them since it combines principal component analysis with standard analysis of variance (Zobel *et al*., 1988). AMMI model is widely utilized for statistical analysis in multi-environment varietal trials (Crossa *et al*., 1990; Gauch and Zobel, 1997; Hossain *et al*., 2018). AMMI analysis's outcomes can be effectively visualized using biplots (Gabriel, 1971; Dias *et al*., 2003; Ma *et al*., 2004; Koutis *et al*., 2012), which offer a graphical representation facilitating the interpretation of genotype and environment interactions. Biplots provide a clear and intuitive means of understanding complex relationships between cultivars and environments, aiding breeders and researchers in making informed decisions regarding cultivar selection and deployment across diverse agricultural settings.

To evaluate genotype-by-year interaction patterns throughout the summer months in the New Cauvery Delta Zone, we examined pigeonpea in the present research. We evaluated 30 early-duration genotypes utilizing the AMMI analysis technique. This investigation aimed to gain insights into how different pigeonpea genotypes respond to variations in environmental conditions across different years, specifically focusing on the summer season in the New Cauvery Delta Zone. We aimed to determine which genotypes are more sensitive to changes in environmental conditions and which perform consistently over time utilizing AMMI analysis. The outcome of this investigation will enhance better comprehension of genotype-by-year interactions in pigeonpea cultivation, enabling breeders and researchers to make more informed decisions regarding genotype selection and breeding strategies tailored to the specific conditions of the New Cauvery Delta Zone during the summer season.

MATERIALS AND METHODS

This research was executed at the Agricultural College and Research Institute, Tamil Nadu Agricultural University, located in Thanjavur, Tamil Nadu, India, for three consecutive summer seasons: 2019, 2020 and 2021. The experimental materials consisted of thirty pigeonpea genotypes, including two standard checks, CO (Rg) 7 and VBN 3, obtained from the Ramiah Gene Bank, Department of Plant Genetic Resources, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. The trials were set up following a Randomized Blocks Design and replicated twice. Each pigeonpea genotype was planted in five rows, each measuring four meters long, with spacing of 60×20 cm among plants. Standard agronomic practices and crop protection measures, as outlined in the Crop Production Manual (TNAU, 2012), were closely adhered to guarantee optimal crop growth as well as development. At full maturity, the crop was harvested and the grains were dried until they reached a moisture content of 10 per cent. Grain yield data had been recorded on a plot basis and then scaled to kilograms per hectare for subsequent statistical analysis. The goal of this meticulous experimental design and data gathering procedure was to offer thorough insights into the performance of the pigeonpea genotypes throughout several years, facilitating informed decision-making for future breeding and cultivation practices.

Statistical analysis

In our research, we examined the stable yield performance of thirty pigeonpea genotypes across three consecutive years using the AMMI model. This statistical analysis had been conducted utilizing IRRI P.B. tools 1.4 version software package. In accordance with Zobel *et al*. (1988), AMMI model is a hybrid statistical technique that combines PCA (Principal Components Analysis) and ANOVA (Analysis of

Variance). By employing this model, we aimed to unravel the complex interactions between genotype and environment, thereby identifying genotypes that show stable as well as consistent performance across different years. This analytical approach allowed us to achieve substantial data on the pigeonpea genotypes' stability and potential yield, enabling us to make informed decisions regarding their suitability for cultivation across varying environmental conditions. The utilization of the AMMI model represents a robust methodology for assessing genotype-by-year interactions and holds significant implications for pigeonpea breeding and crop improvement programs.

In this investigation, we utilized a comprehensive approach to evaluate genotype-by-environment (G×E) interaction patterns, incorporating usual ANOVA trials to differentiate between additive and multiplicative variances. Subsequently, principal components analysis (PCA) was integrated into the analysis to extract patterns from G×E component identified in ANOVA. When combined with graphical representations through the utilization of Biplot analysis, the results of the least squares analysis made it easier to directly identify the causes of GxE interaction. Plotting corresponding PCA axis eigenvalues on Y-axis and the genotype as well as environment means on X-axis produced AMMI Biplot, essential outcome of this investigation. This approach allowed us to visually discern the relationships between genotypes and environments, identifying genotypes that exhibited stable performance across different environments and those showing specific adaptability patterns. By combining statistical analysis with graphical representation, we gained valuable insights into the complex interaction between genotypes and environments, assistance in selecting best pigeonpea genotypes for growing in a variety of environmental conditions.

The hybrid model's mathematical statement can be written as:

$$Y_{ge} = \mu + \sigma g + \sigma e + \sum_{N=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + E_{ger}$$

Here,

g = Genotypes.

e = Environments.

μ = Grand mean.

Y_{ge} = Yield of genotypes g in environment e.

σ_g = Genotype mean deviations.

σ_e = Environment mean deviations.

The number of IPCAs (Interaction Principal Component Axis) that are kept in model is N.

λ_n = singular value for IPCA axis ' n'.

γ_{gn} = genotype eigen values for IPCA axis 'n'.

δ_{en} = environmental eigen vector values for IPCA axis 'n'.

ρ_{ge} = residuals.

E_{ger} = random error.

Utilizing environment-centered data, the GGE biplot visually depicts the genotype (G) as well as genotype-environment interaction effects found in multi-environment trial data. The GEI analysis of multi-environment trial data utilizes a biplot to illustrate the components (G and GE) that are essential to genotype valuation along with as source of variation (Yan *et al*., 2000; Yan, 2001). GGE biplots are utilized for (i) Mega Environment Analysis (Which-Won-Where Pattern): Identifying and recommending genotypes suitable for particular mega environments (ii) Genotype Evaluation: Recommending stable genotypes that perform consistently across all environments and (iii) Location Evaluation: describing how target environments can discriminate against the genotypes under investigation.

Results and Discussion

In the realm of plant breeding, genotype-by-environment interactions often present challenges as cultivars are evaluated across various environmental conditions. The extent of these interactions can significantly influence varietal rankings, leading to notable differences in performance across environments. To assess these interactions and delineate the main impact systematically, a combinational analysis of variance is employed. In our current investigation, we employed the AMMI model to scrutinize genotype through environment interactions among thirty pigeonpea genotypes raised during the summer season across three consecutive years (2019, 2020 and 2021) at Agricultural College and Research Institute, Thanjavur, Tamil Nadu, India. This statistical model not only quantifies the interactions but also elucidates the main effects, providing a comprehensive understanding of how genotypes respond to various environmental conditions. By utilizing the AMMI model, we aimed to uncover the complex interplay between genotype and environment, shedding light on the genotypes of pigeonpeas' performance stability along with adaptability across diverse environmental settings. This approach facilitates informed decision-making for cultivar selection and breeding strategies, ultimately contributing to the advancement of pigeonpea cultivation and productivity.

ANOVA revealed that the genotypes, testing conditions and their interactions had a substantial impact on grain yield (Table 1). Notably, genotype × environment interactions ($p<0.01$) were of particular importance, permitting further detailed analysis. Estimates of stability parameters for grain production of thirty genotypes of pigeonpea in 3 distinct settings are displayed in Table 2. AMMI analysis of variance for grain yield data indicated that genotypic effects comprised 90.27 per cent of overall sum of squares, environmental impacts constituted 2.82 per cent and genotype × environment interaction impacts represented 2.64 per cent (Table 1).

AMMI biplot analysis is considered an efficient method for visually assessing genotype × environment interaction patterns (Olivoto *et al*., 2019). The additive component is distinguished from interaction by analysis of variance. Principal components analysis, which employs a multiplicative model, is utilized to examine the interaction

effect derived from the additive analysis of the variance model. The biplot depiction of principal component analysis outcomes facilitate visual examination as well as analysis of the genotype x environment interaction components.

The AMMI analysis outcomes revealed that 1st principal component axis (IPCA I) accounted for 75.88 per cent of the interaction sum of squares, whereas 2nd principal component axis (IPCA II) accounted for an additional 24.12 per cent of genotype × environment interaction sum of squares. The 2 axes (IPCA I and IPCA II) accounted for 100 per cent of genotype × environment interaction sum of squares, employing all available levels of freedom in interaction. This demonstrates that AMMI model with 2 major component axes is the most effective predictive model. This aligned with the conclusions of prior researchers (Fikere *et al*., 2014; Biswas *et al*., 2019 and Rao *et al*., 2022). This method facilitates the creation of a biplot and assessment of genotype and environmental influences (Gauch and Zobel, 1996; Singh *et al*., 2018 and Kona *et al*., 2024). Significant variation among the genotypes is suggested by the genotypes' considerable sum of squares, leading to considerable variation in grain yield.

In Fig 1 to 7, pigeonpea genotypes are denoted by the letter 'G' subsequent to numbers from 1-30 as suffixes and letter 'E' is employed to represent environments and subsequent to numbers 1-3. The AMMI biplot 1 (Fig 1) shows the major impact on abscissa and IPCA 1 values on ordinates. Quadrants Q1 and Q2 represent higher grain yield, while Q3 and Q4 represent lower grain yield. Additionally, Q1 and Q4 indicate positive IPCA 1 scores, whereas Q2 and Q3 indicate negative IPCA 1 scores. Genotypes (or habitats) positioned almost on a perpendicular axis exhibit comparable mean values, whereas those aligned along a horizontal axis display analogous interaction patterns. Genotypes (or environments) with substantial IPCA 1 scores, whether positive or else negative, demonstrate pronounced interactions, while those with IPCA 1 values near zero display negligible interactions, deemed stable across contexts.

Zobel *et al*. (1988) indicate that the anticipated yield for every genotype-environment combination in the AMMI model may be obtained from biplot 1 (Fig 1). Combinations of genotype as well as environment that have IPCA I scores of the same sign provide positive interaction impacts, whereas combinations that have IPCA I values of opposing signs produce particular interactions that are negative. Environment, E1 (514.4 kg/ha) had positive main effects whereas environments E2 (449.8 kg/ha) and E3 (403.4 kg/ha) had negative main effects (Table 2).

The G2, G4, G12, G15, G16, G17, G19 and G25 pigeonpea genotypes showed only changes in their major (additive) impacts and exhibited little interaction with the environments, suggesting that they are stable yielders in a variety of environments. Furthermore, the genotypes G25, G30, G6, G10, G22, G26, G11, G29, G27 and G13 showed differences only in their interaction effects but had a higher grain yield than the check varieties. Of these, G25 was the highest yielder with very low interaction with the environments and it is recommended for cultivation in all environments. In contrast, G6, G22, G11, G27 and G13 had a high grain yield with positive interaction effects, suggesting precise adaptation to favourable environments. Based solely on the IPCA 1 scores, these genotypes appeared more unstable but were high yielders well adapted to favourable environments. On the other hand, the genotypes G30, G10, G26 and G29 recorded high grain yields with negative interaction effects with the environments indicating specific adaptation and instability and suggesting they have less ability to respond to favourable environments (Table 2). These results aligned with the outcome of Kishore *et al*. (2022) and Rao *et al*., (2022).

In accordance with Vargas and Crossa (2000), a biplot (Fig 2) was made utilizing the environmental and genotype scores of the two AMMI components. The biplot is divided into 4 segments based on genotype signs and environmental scores. In accordance with the AMMI 2 biplot investigation, genotypes that exhibit little interaction on both axes are found close to the origin, while those with more interaction are farther from the origin. Therefore, genotypes that are closer to their place of origin tend to exhibit greater stability compared to others. The genotypes positioned farther from their place of origin are labelled as highly interacting with the environments. The AMMI 2 biplot analysis (Fig 2) shows none of the environments is ideal for cultivating all pigeonpea genotypes, as none of the

Table 1: Additive main effects and multiplicative Interaction (AMMI) analysis of variance for grain yield (kg/ha) of thirty pigeonpea genotypes across three environments.

Sources	df	Sum of squares	Mean squares	Explained (%)
Genotypes (G)	29	11940321.67	411735.23**	90.27
Environments (E)	2	373071.63	186535.82**	2.82
G × E interaction	58	348694.70	6011.98**	2.64
AMMI component 1	30	264583.73	8819.46**	75.88
AMMI component 2	28	84110.97	3003.96	24.12
Error	87	213424.63	2453.16	
Total	237	13227241.70	55811.15	

**Significant at 1% level of probability.

Table 2: Means and estimates of stability parameters (AMMI) for grain yield in pigeonpea genotypes.

Name of pigeonpea genotypes	Code used	Summer, 2019 (E1) Grain yield (kg/ha)	Summer, 2020 (E2) Grain yield (kg/ha)	Summer, 2021 (E3) Grain yield (kg/ha)	Grain yield over environments (kg/ha) Mean	Rank	IPCA I	IPCA II
VBN 3	G1	515.7	452.3	452.9	473.7	11	-1.86	-3.67
CO(RG)7	G2	495.8	448.0	352.6	432.2	12	0.82	4.02
CRG 2016-02	G3	419.5	305.1	262.8	329.2	17	3.46	-0.59
RKPV 413-02	G4	349.2	299.0	243.8	297.3	20	-0.60	0.82
AL 1922	G5	423.1	332.9	240.0	332.0	16	3.74	3.57
PA 477	G6	989.5	914.4	829.5	911.2	3	2.35	3.02
RKPV 492-01	G7	412.3	297.2	273.0	327.5	18	2.80	-2.01
AH 14-01	G8	349.4	318.0	264.1	310.5	19	-1.99	0.84
PUSA 2017-1	G9	288.8	201.0	248.2	246.0	24	-1.97	-7.49
AL 1992	G10	872.0	850.9	781.6	834.8	4	-2.11	2.12
UPAS 120	G11	757.4	689.4	605.2	684.0	7	1.82	3.02
CORG 9701	G12	265.4	206.8	167.2	213.2	26	-0.62	-0.46
AL 1932	G13	594.9	497.5	427.1	506.5	10	3.36	1.75
ICPL 12336	G14	445.9	346.1	312.0	368.0	15	2.10	-1.14
ICPL 88034	G15	277.9	193.7	164.4	212.0	27	0.80	-1.42
ICPL 12337	G16	240.8	147.4	134.2	174.2	30	0.82	-2.76
ICPL 20325	G17	247.1	169.5	141.4	186.0	29	0.28	-1.48
ICPL 11084	G18	346.1	264.4	208.9	273.2	21	1.66	0.66
ICPL 11023	G19	325.1	252.6	209.8	262.5	22	0.50	-0.28
ICPL 87091	G20	247.8	207.7	173.0	209.5	28	-2.13	-0.73
ICPL 91018	G21	358.9	219.8	178.8	252.5	23	5.17	-0.83
ICPL 149	G22	868.1	733.6	720.7	774.2	5	3.73	-3.03
ICP 2387	G23	370.1	472.8	423.6	422.2	13	-11.73	1.28
DPP3-244	G24	412.9	442.1	370.5	408.5	14	-5.60	2.61
ICPL 88036-1	G25	1128.4	1052.0	1025.1	1068.5	1	0.15	-1.57
AL 1733	G26	796.1	759.4	701.5	752.3	6	-1.45	1.12
AF 284/2/1	G27	622.6	548.4	466.5	545.8	9	2.17	2.79
ICP 245541	G28	305.2	185.1	166.2	218.8	25	2.94	-2.47
ICPL 85010	G29	654.6	639.5	540.8	611.7	8	-1.37	4.48
ICPL 87	G30	1028.6	1047.6	1035.3	1037.2	2	-7.23	-2.15
Environments								
Summer, 2019	E1	514.4	-	-	514.4	-	15.54	-0.75
Summer, 2020	E2	-	449.8	-	449.8	-	-6.91	10.48
Summer, 2021	E3	-	-	403.4	403.4	-	-8.63	-9.73

Environmental mean: 455.9 kg/ha.

environments is positioned near the origin. Among the pigeonpea genotypes, G23, G9, G30, G24, G29, G5, G21, G22, G1, G2 and G6 are more environmentally responsive since they are farther from origin. In contrast, genotypes G19, G12, G4, G18, G25, G26, G8, G20, G14, G15 and G17 are near to origin and are thus less susceptible to environmental influences, indicating they are stable across environments (Gaur *et al*., 2020; Khan *et al*., 2021; Esan *et al*., 2023; Kona *et al*., 2024 and Bomma *et al*., 2024). Among these stable pigeonpea genotypes, G25 and G26 displayed very low genotype × environment interaction, displaying broader adaptability and greater grain yield.

GGE Bi-plot analysis

GGE Bi-plot of environment view for grain yield

As illustrated in Fig 3, the environment vectors in an environment-centered GGE biplot are created to link test environments to biplot origin. To determine the level of correlation between two settings, the angle between them is utilized. The analysis clarified 99.4 per cent of the variance with first 2 principal components, where PC1 clarified 97.3 per cent and PC2 clarified 2.1 per cent (Fig 3). The most discriminating cultivar had been Environment E2, which had the longest vectors from origin. In contrast, environments E1 and E3 were moderately discriminating among the tested environments. Since the angles between all the environments were smaller than 90° (an acute angle), all the environments were positively correlated. Similar outcomes have been published by Bomma *et al*. (2024) and Kumar *et al*. (2021).

GGE Bi-plot of genotype view for grain yield

In a genotype-focused Scaling GGE Biplot, the vectors measure the dissimilarity in discriminating genotypes. Genotypes with the longest vectors from the origin, such as G25, G30, G6, G10 and G22, were the most discriminating of the environments. In contrast, genotypes G1, G2, G24, G13, G23 and G24 were less discriminating, while the rest were moderately discriminating of the environments (Fig 4). With angles smaller than 90°, genotypes G25, G30, G6, G10, G22, G26, G11, G20 and G27 were grouped together, indicating similar discrimination patterns. Another group included genotypes G2, G3, G4, G5, G7, G8, G9, G12, G14, G15, G16, G17, G18, G19, G21, G28 and G29. Genotypes G1, G13, G23 and G24 did not fall into either of these groups. The results demonstrated by Kishore *et al*. (2022) and Rao *et al*. (2022) are in line with these findings.

GGE Biplot on environment for comparing environments with an ideal environment

The testing environments' capacity to discriminate and their representativeness are key factors to consider in the GGE biplot analysis. According to Fig 5, Environment E2 was more discriminating than the other two environments.

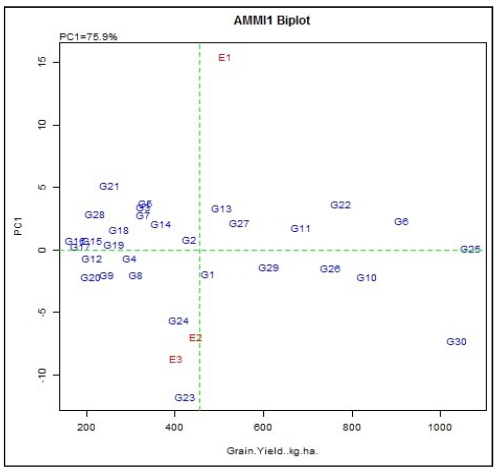


Fig 1: AMMI I biplot for grain yield mean (kg/ha) and G × E interaction of thirty pigeonpea genotypes in three environments.

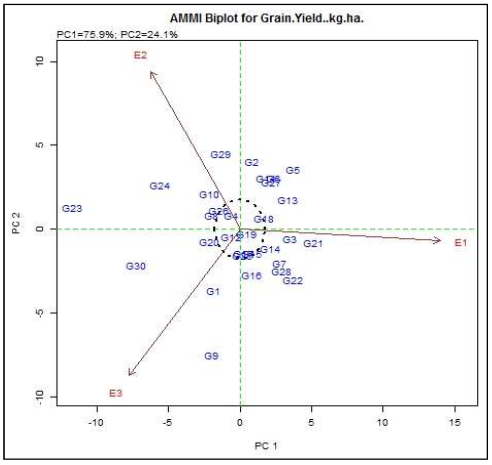


Fig 2: AMMI II interaction biplot of thirty pigeonpea genotypes in three environments for grain yield using genotypic and environmental scores.

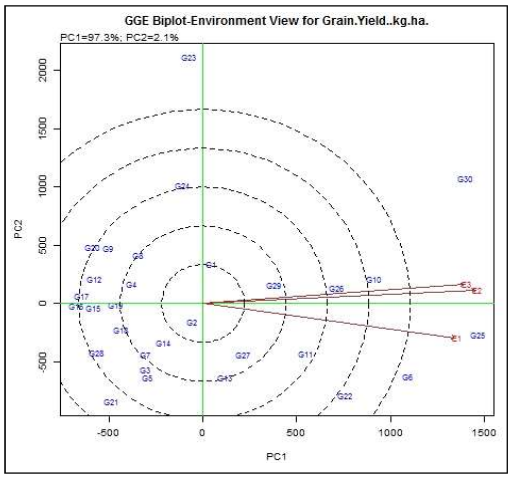


Fig 3: Vector view of GGE biplot of environment-focused scaling.

The line that crosses the biplot origin as well as the average environment is referred to as the AEA (Average Environment Axis). It is believed that test environment that produces a lesser angle with AEA is more indicative of other test environments (Yan and Rajcan, 2002). Based on this criterion, environments E2 and E3 had a better representation than environment, E1. Discriminatory yet non-representative test conditions are essential for choosing adaptable genotypes. Specifically, a discriminating and non-representative test environment, such as E1 is beneficial for this purpose.

Biplots of stability and mean performance of genotypes across average environments

In GGE biplot, 1st principal component (PC1) is denoted on X-axis, indicating the estimated yield. Genotypes exhibiting greater PC1 levels are considered more prolific (Fig 6). The 2nd main component (PC2) is depicted on Y-axis, indicating the stability of pigeonpea genotypes. The AEA is line originating from biplot's origin and representing average environment with a singular arrow. Genotype marker projections onto the AEA illustrate the average grain yield of pigeonpea genotypes, with genotypes sorted along the ordinate axis. A higher projection on the AEA ordinate, irrespective of direction, signifies enhanced instability of genotype. Based on this analysis, genotype G25 was the best yielder, followed by G30, G6, G10 and G22, whereas G16 was the lowest yielder, followed by G17, G20, G15 and G12. Among these, G25 and G6 were higher yielders with greater yield stability, while G30 and G22 were higher yielders with unstable yield performance. Genotypes G16, G17, G12 and G15 showed greater stability but were poor yielders. Comparable findings had been attained by Kumar *et al*. (2021) and Kishore *et al*. (2022).

"What-Won-Where" pattern analysis

Genotypes exhibiting distinct adaptive capabilities for certain contexts or clusters of environments were identified utilizing "What-Won-Where pattern analysis" and "ranking of genotypes in suitable environments" *via* GGE Biplot tools. The polygon representation of the GGE biplot depicted in Fig 7 emphasizes the highest performing genotypes for each environment. The study categorized environments into 2 mega-environments, E3 and E1. In mega-environment E3, genotype G30 emerged as top performer, while in mega-environment E1, the best performers were G25, G6 and G22. There was a close relationship between environments E2 and E3 and fell within the same mega-environment. The vertex genotypes (G30, G23, G20, G17, G16, G28, G21, G22, G6 and G25) had the longest vectors in their respective directions, indicating their responsiveness to environments. Each sector's vertex genotypes are those that yielded the most in the sector's settings. Specifically, genotypes with high yields in E1 were G25, G6 and G22, while in E2 and E3, the best genotype was G30. The remaining vertex genotypes (G23, G20, G12, G17, G16, G28 and G21) performed the worst in all the environments

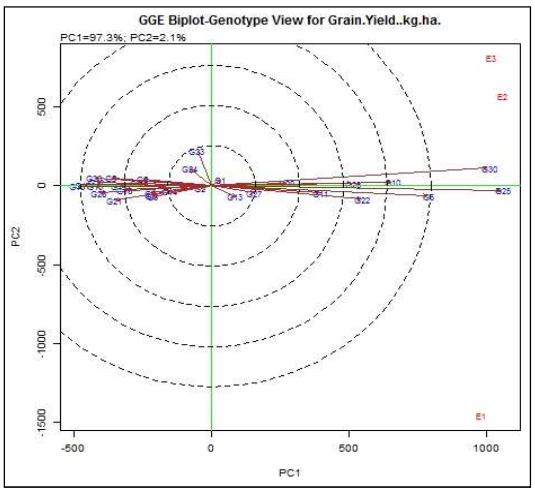


Fig 4: Vector view of GGE biplot of genotype-focused scaling.

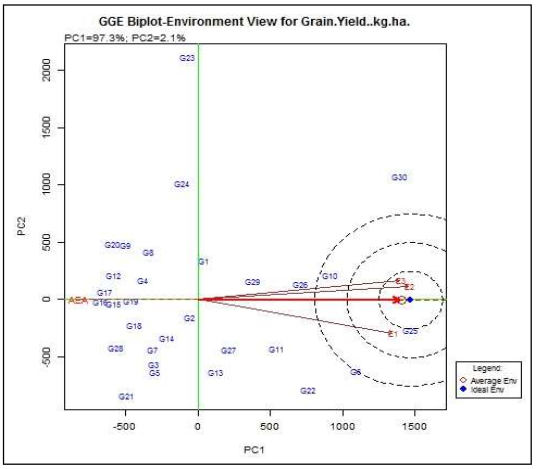


Fig 5: GGE biplot on environment focused Vector view of GGE biplot of environment-focused scaling.

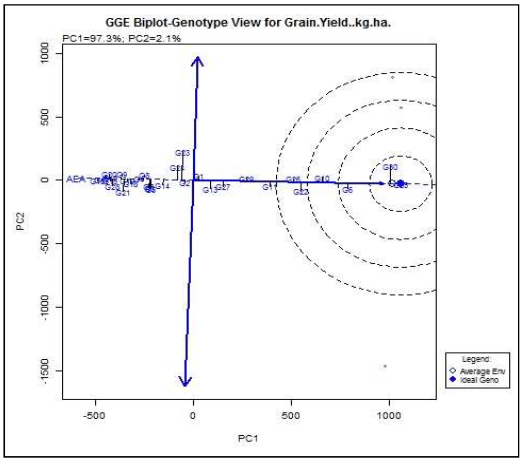


Fig 6: Biplot of stability and mean performance of genotypes across average.

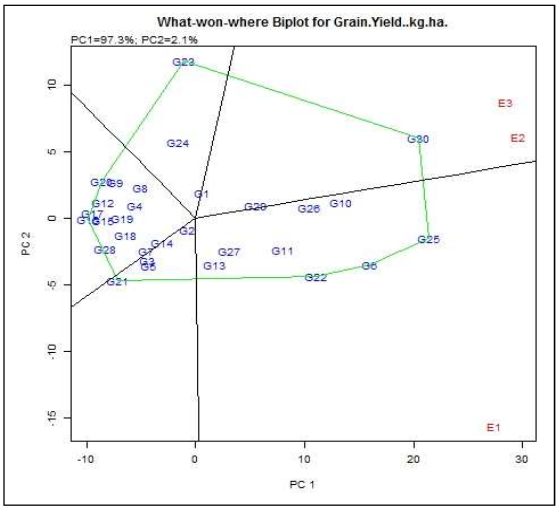


Fig 7: What-Won-Where GGE-Biplot for Grain yield (kg/ha).

as there were no environments within their respective sectors.

CONCLUSION

Both AMMI, as well as GGE biplot techniques, were employed in this investigation to find stable and high-yielding pigeonpea genotypes. The findings revealed that genotypes G25 and G6 consistently performed well across the years. Genotype G30 had been identified as top performer specifically in E3 environment, while G25, G6 and G22 were the best performers in the E1 environment. Additionally, environments E1 and E2 had been observed to be closely related. Despite their high yields, genotypes G30 and G22 exhibited instability in their yield performance. However, genotypes G16, G12, G15 and G17 had been noted for their stability, though they were lower yielders. Based on these results, genotypes G25 and G6 are recommended for large-scale adoption in the New Cauvery Delta Region to boost pigeonpea productivity and enhance food security for smallholder farmers.

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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.

Informed consent

NA.

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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