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AMMI and GGE Biplot Analysis for Stability of Yield in Mid-early Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Genotypes

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ABSTRACT

Background: The genotype x environment interaction greatly influences the success of breeding and in multi-location trials complicates the identification of superior genotypes for a single location, due to magnitude of genotype by location interaction are often greater than genotype by year interaction. This necessitates genotype evaluation in multi environments trials in the advanced stages of selection.
Methods: Nine elite pigeonpea genotypes of mid-early duration were evaluated in six diverse locations in randomized complete block design with three replications during *kharif,* 2019 to ascertain the stable genotypes, environments discrimination and genotype by environment crossovers using AMMI and GGE biplot stability models.
Result: The results in the present investigation revealed that first two principal components explained 73.4% of variation interaction, while, 80.50% in GGE biplot. Both the models identified WRGE-126 (G6) as stable performer with high yield (1733 kg ha^{-1}) and among the locations Tandur (E1) measured as the ideal environment. Whereas, the environments, Adilabad (E3) and Warangal (E4) were observed representative with better discriminating ability.

Key words: AMMI model, GGE biplot analysis, Genotype x environment interaction, Mid-early pigeonpea.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], a multipurpose food legume and commonly known in India, as redgram or arhar or tur or thogari, occupies a prominent place in Indian rainfed agriculture. It is the second most important pulse crop next to chickpea, covering an area of around 4.42 m ha (occupying about 14.5% of area under pulses). India ranked first in area and production which accounts for 36% of the area and 23% of production, respectively of the worlds share. However, country's productivity at 853 kg ha^{-1} is far below the world average productivity of 1023 kg ha^{-1} and production of 2.86 MT (contributing to 16% of total pulse production). In Telangana state, pigeonpea is being cultivated in 3.22 lakh ha. area with productivity of 575 kg ha^{-1} (Anonymous, 2020).

The crop is sown during rainy season which flowers and matures in post-rainy season. The rainy months are hot and humid with diurnal temperature varying between 25 and 35°C (maximum) and 20 and 25°C (minimum) with an erratic rainfall. Occurrence of drought is frequent and at varying degrees which necessitates to match the duration of the soil moisture availability to that of the genotype duration for maximizing productivity in any given environment. Hence, there is a tremendous scope for the introduction of mid-early duration pigeonpea varieties (155-165 days) in black soils under rainfed condition where medium duration pigeonpea varieties suffer from terminal drought. Hence, in the present study, an attempt was made to evaluate the performance of the mid-early duration genotypes through multilocation testing.

There are two types of biplots that have been extensively used to visualize G × E interactions and these are the AMMI (Gauch 1988; Gauch and Zobel 1997) and GGE biplots; (Yan *et al.,* 2000). However, the application of the two biplots in research has been debated (Gauch *et al.,* 2008). Additive main effects and multiplicative interaction was found suitable

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to handle both the main effects and G × E interactions in multilocation yield trials more effectively and efficiently than any other statistical model. But the difference being the omission of E component in GGE biplot (Yan *et al.,* 2000; Gauch 2006; Yan *et al*., 2007; Gauch *et al.,* 2008). However, the comparison studies of GGE biplot with AMMI Models validate the equal efficiency of GGE biplot and AMMI models in understanding GEI (Dias *et al.,* 2003; Ma *et al.,* 2004).

The purpose of the study is to estimate the pattern of genotype × location interaction for few elite mid-early duration pigeonpea genotypes in order to take a decision on their potentiality as well as adaptability during rainy (*kharif*) season for different locations of Telangana State and also to do a comparative study of popular multivariate analysis models, *i.e.,* AMMI and GGE.

MATERIALS AND METHODS

The present experimental material comprised of 9 pigeonpea genotypes in which ICPIL-17133 and ICPIL-17142 were the derivatives of *C. platycarpus*, while, ICPIL-17103 is a derivative of ICPW 29 (*C. cajanifolius*) and Asha and developed through back cross method, WRGE-124, WRGE-126, WRGE-128 and WRGE-136 were developed through pedigree method of breeding and the entries TS-3R and PRG-176 were used as checks.

The experiments were conducted under rainfed conditions using Randomized Complete Block Design with three replications at six research stations of Professor Jayashankar Telangana State Agricultural University, Telangana State during *kharif*, 2019. The experimental plot size consists of four rows per each entry, having 4m row length with spacing of 120 cm between rows and 20 cm between the plants. Recommended package of practices were followed to raise the crop. Genotypes across the locations were sown during 1st week of July and harvested from each plot separately. Parentage details of pigeonpea genotypes along with environmental conditions were presented in (Table 1 and 2).

Statistical analysis

The performance of genotypes was tested over six locations using stability models *viz.* (1) Additive Main effects and Multiplicative Interaction (AMMI) (Gauch and Zobel 1996) and (2) GGE Biplot or Site Regression Model (Yan and Kang 2003). The AMMI model (Gauch 1988) was used in analyzing the stability and interaction for yield traits. The AMMI model is a combination of Analysis of Variance (ANOVA) and Principal Component Analysis (PCA). The G × E interaction was evaluated with the AMMI model by considering the first two principal components. ANOVA model was used to analyze the trait data with main effects of genotype and environment without the interaction, then, a principal component analysis was integrated using the standardized residuals. These residuals include the experimental error and the effect of the GEI. The analytical model can be written as

$$Y_{ij} = \mu + g_i + e_j + \Sigma\lambda k + \alpha ikyjk + R_{ij}$$

Where,

Y_{ij} is the yield of i^{th}-genotypes in j^{th}-environment

μ is the overall mean

g_i is the effect of the i^{th} genotype

e_j is the effect of the j^{th} environment

λk is the eigen value of the PCA for axis k

α_{ik} and y_{jk} are the genotype and environment principal components scores for axis k,

respectively

R_{ij} is the residual term. Environment and genotype PCA scores are expressed as unit vector times the square root of λk.

The GGE biplot graphically represents G and GEI effect present in the multi-location trial data using environment centered data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also sources of variation in GEI analysis of multilocation trial data (Yan *et al.* 2000;Yan 2001). GGE biplots were used to evaluate (1) Mega Environment Analysis (which-won-where pattern), where genotypes can be recommended to specific mega environments. (2) Genotype evaluation, where stable specific genotypes can be recommended across all locations and (3) location evaluation, explains discriminative power of target locations for genotypes under study. The data was subjected to IRRI P.B. tools 1.4 version to get AMMI and GGE Biplots.

Table 1: Parentage details of Pigeonpea genotypes.

Code	Genotype	Parentage
G1	ICPIL-17133	[(ICPL 85010 x (ICPL 85010 x (ICPL 85010 x (ICPL 85010 x (ICPW 68 x ICPL 85010)))))] -60-B-B-B-B-B-B-B-B-4-5
G2	WRGE-136	WGRE-97X ICPL-88039
G3	WRGE-124	ICPL-85063 X BDN-2004
G4	ICPIL-17103	[(ICPL 87119 x (ICPL 87119 x (ICPL 87119 x ICPW 12)))]-5-B-B-B-2-5
G5	PRG-176©	ICPL-88039 X ICPL-88034
G6	WRGE-126	JSA-59X UPAS-120
G7	WRGE-128	ASHAX CORG-7
G8	TS-3R©	TS-3 X ICP-8863
G9	ICPIL-17142	[(ICPL 85010 x (ICPL 85010 x (ICPL 85010 x (ICPL 85010 x (ICPW 68 x ICPL 85010)))))] -66-B-B-B-B-B-B-B-B-3-1

RESULTS AND DISCUSSION

Mean performance of the pigeonpea genotypes across the environments along with genotype by ranking presented in (Table 3). Combined analysis of variance for yield at six environments indicated that the effects of genotype, environment and genotype x environment interaction on yield were significant, with the proportion of the total treatment variation of 11.58% for genotype, 60.30% for the environment and 18.56% for interaction (Table 4).

A larger proportion of yield variation explained by environments, indicated that the environments were diverse, with large differences among environments causing the most of the variation for grain yield. The grain yield over environments ranged from 1112 kg ha^{-1} in Palem (E2) to 2343 kg ha^{-1} in Tornala (E6). The Genotypic grain yield ranged from1293 kg ha^{-1} G5 (PRG-176) to 1955 kg ha^{-1} G3 (WRGE-124) (Table 3). GE interaction was a crossover type with different yield ranking of genotypes across environments. The significant interaction in genotype and environment for yield validated the need to take more care while selecting the promising genotypes by considering stability and adaptability. Significant differences across years were also observed by Jogender Singh *et al.* (2018) in pigeonpea using AMMI model. With further putrefaction of GEI using AMMI analysis, two significant principal components were separated explaining 73.4% of variance interaction (PC1 44.7% and PC2 28.7%) (Table 4). Earlier reports confirmed that in most of the cases the maximum genotype and environment interaction could be explained through using the first two PCAs (Fikere *et al.,* 2014; Biswas *et al.,* 2019). Hemanth Kumar *et al.* (2018) had reported similar reports in Chickpea genotypes from AMMI analysis. Therefore, IPCA1 and IPCA2 were used for construction of AMMI1 and AMMI2 biplots. The results of AMMI analysis further enlightened the relative contribution of the first two IPCA axes to the interaction effects by plotting with genotype and environment means as presented in (Fig.1). In the biplot, environments are designated by the letter ‘E’ followed by numbers 1 to 6 as suffix (Table 2), while genotypes represented by numbers from 1 to 9 (Table 1). The quadrants in the graph represent: (QI and QII) higher mean, (QIII and QIV) lower mean, (QI and QIV) +ve IPCA1 and (QII and QIII) –ve IPCA1 scores (Fig 1). When a variety and environment have the same sign on PCA1 axis, their interaction is positive and if opposite, their interaction is negative. Thus, if a variety has a PCA1 score near to zero,

Table 2: Details of locations under study.

Code	Environments	Latitude	Longitude	MSL
E1	Tandur	17^{0} 15’N	77^{0} 35’E	553.18 m
E2	Palem	$16^{O}35^{1}$N	78^{0}10’E	642.00 m
E3	Adilabad	19^{0}39" N	78^{0}32’ E	268.80 m
E4	Warangal	18^{o} 03’N	79^{0} 22’E	270.00 m
E5	Jagtial	18^{0} 49’ N	78^{0} 56’ E	243.40 m
E6	Tornala	18^{0} 06’ N	78^{0} 44’ E	483.80 m

Table 3: Mean yield (kg ha^{-1}) of the pigeonpea genotypes across six environments.

Genotype	Genotype No.	Tandur (E1)	Palem (E2)	Adilabad (E3)	Warangal (E4)	Jagtial (E5)	Tornala (E6)	Genotype mean	Genotype by Ranking
ICPIL-17133	G1	1057	1177	1391	1157	2401	2201	**1564**	**6**
WRGE-136	G2	1170	934	2374	1201	2171	2536	**1731**	**5**
WRGE-124	G3	1634	1463	2298	1880	1885	2572	**1955**	**1**
ICPIL-17103	G4	1551	1037	1508	1925	2157	2269	**1741**	**3**
PRG-176©	G5	1201	847	1139	774	1433	2365	**1293**	**9**
WRGE-126	G6	1366	1025	2010	1568	2044	2388	**1733**	**4**
WRGE-128	G7	1244	1538	1408	1928	2252	2187	**1759**	**2**
TS-3R©	G8	929	1049	1083	1166	2290	2461	**1496**	**7**
ICPIL-17142	G9	1263	938	1267	943	2025	2105	**1423**	**8**
Environment mean		**1268**	**1112**	**1609**	**1393**	**2073**	**2343**	**1633**	

Table 4: AMMI Analysis of Variance for yield (kg ha^{-1}) of nine pigeonpea genotypesacross six environments.

Source of Variation	d.f	SS	MS	% Explained SS
Total	161	51925797	322520	
Genotypes (G)	8	6014466	751808	11.58
Environment (E)	5	31313746	6262749	60.30
Genotypes X Environment (G X E)	40	9640769	241019	18.56
IPCA 1	12	4312372	359364	44.7
IPCA 2	10	2764825	276482	28.7
IPCA 3	8	1626794	203349	16.9
IPCA 4	6	570936	95156	5.9
Error	108	4956814	45896	

it has small interaction effect and was considered as stable over wide environments. Conversely, varieties with high mean yield and large PCA scores were considered as explicitly adapted to specific environments (Abdi and Williams 2010; Askari *et al*., 2017; Mustapha and Bakari 2014; Rao, P.J.M. *et al*., 2020).

Accordingly, the pigeonpea genotype, G3 (WRGE-124) recorded maximum grain yield followed by G7 (WRGE-128), G4 (ICPIL-17103), G6 (WRGE-126) and G2 (WRGE-136), while, G3 (WRGE-124), G6 (WRGE-126) and G2 (WRGE-136) positive IPCA 1 score indicating positive Genotype X Environment interaction, G4 (ICPIL-17103) and G7 (WRGE-128) were high yielding genotypes with negative IPCA 1 scores indicating the negative interaction, where as the genotype G5 (PRG-176) recorded poor yield with IPCA 1 score near to zero and considered as stable with poor yield. From AMMI 2 biplot analysis (Fig 2), environments E1(Tandur) is the most "Ideal" environment for all the genotypes, Since it was positioned near to the origin, followed by E2 (Palem). Among the genotypes, G6 (WRGE-126) exhibited very less Genotype x environmental interaction showing broader adoptability with high yield, Where as G5 (PRG-176) recorded negative IPCA score and close to the origin implying the poor yield with wider adoptability.

In summary, analysis of the nine pigeonpea genotypes using AMMI model showed that higher proportion of variation explained by environment compared to GEI and genotypes. The genotype, G3 (WRGE-124) was found superior among all the genotypes as well as over the checks and across all the locations under study. However, it was highly interactive with environment. On the other hand, genotype G6 (WRGE-126) exhibited minimum interaction with the environments (IPCA 1 score near to zero) convincing the reliability of its performance of high yield. Among all the environments, E1 (Tandur) noticed as ideal environment.

Table 5: GGE analysis of variance for yield (kg ha^{-1}) of nine pigeonpea genotypes across six environments.

Source of Variation	d.f	SS	MS	% Explained SS
Total	161	51925797	322520	
Genotypes (G)	8	6014466	751808	11.58
Environment (E)	5	31313746	6262749	60.30
Genotypes X Environment (G X E)	40	9640769	241019	18.56
IPCA 1	12	8642424	720202	55.2
IPCA 2	10	3957737	395773	25.3
IPCA 3	8	1984455	248056	12.7
IPCA 4	6	612759	102126	3.9
Error	108	4956814	45896	

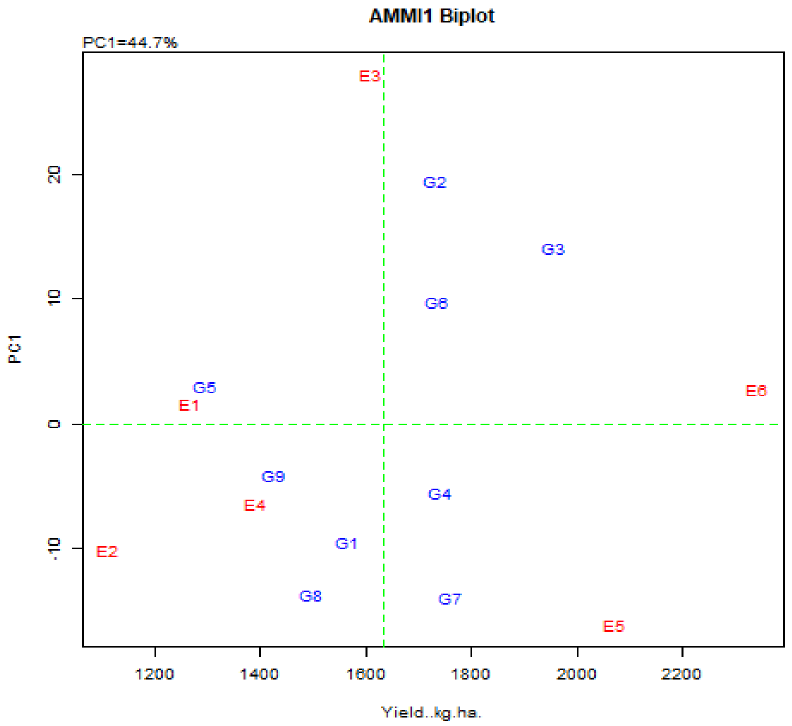

Fig 1: AMMI 1 Biplot for grain yield (kg ha^{-1}) of nine pigeonpea genotypes (G) and six environments (E) using genotypic and environmental scores.

GGE biplot analysis also enables visual assessment of adaptability and yield stability. GGE biplot is presented with two principal components explaining a total of 80.50% GGE variation (PC1 55.2%, PC2 25.3%) (Table 5). The first principal component is represented on the X axis and across its value is estimated yield, i.e., genotypes that have higher PC1 values are considered be more productive. The second principal component is represented on the Y axis and presents the stability of genotypes. Estimation of yield and stability of genotypes was done by using so-called AEC (average coordinates of the environment) method (Yan 2001; Yan and Hunt 2000). By projecting the genotypes on AEA axis, the genotypes are ranked by yield, where the yield increases in the direction of the arrow. In this study, G6 (WRGE-126) considered as high yield with stable performance, while, G5 (PRG-176) and G9 (ICPI-17142) observed as poor yielder with wider adoptability, similarly, G7 (WRGE-128) and G2 (WRGE-136) were performed high yield with low stability (Fig 3).

Genotypes having specific adaptive ability for specific environment or group of environments were identified using “What-Won-Where pattern analysis” and “ranking of genotypes in individual environments” using GGE Biplot tools. The studied environments were divided into three mega environments *i.e.,* E3, E4 and E6. In mega environment E3 (Adilabad), the winning genotype was G3 (WRGE-124), while the genotype G7 (WRGE-128) was the winner in mega environment E4 (Warangal), whereas, E2 (Palem) andE5 (Jagtial) were closely related and fall under the same mega environment E4 (Warangal). E6 (Tornala) is the mega environment with only one winning genotype *i.e.*, G2 (WRGE-136). The polygon view of the GGE bi-plot Fig 4 indicated the best genotype(s) in each environment. The vertex genotypes (G3, G2, G5, G8 and G7) have the longest vectors, in their respective direction, which is a measure of responsiveness to environments. The vertex genotypes for each sector are the ones that gave the highest yield for the environments that fall within that sector. The genotype with the high yield in E3 and E1 is G3 followed by G6, while in E4, E2 and E5, the best genotype is G7 followed by G4. In E6 the best genotype was G2. The other vertex genotypes G1, G8, G9 and G5 are the poorest in all environments because there is no environment in their sectors.

Discriminating and representativeness are the most important parameters of the GGE biplot when evaluating an environment. In Yan and Thinker (2006) model, a long environmental vector had high discriminating ability and a short one had low discrimination. Therefore, as shown in Fig.5, test locations E3 (Adilabad) and E4 (Warangal) were identified as the potential environments for discriminating ability and representativeness. Yan *et al.* (2000) also emphasized that the environments with long vectors and

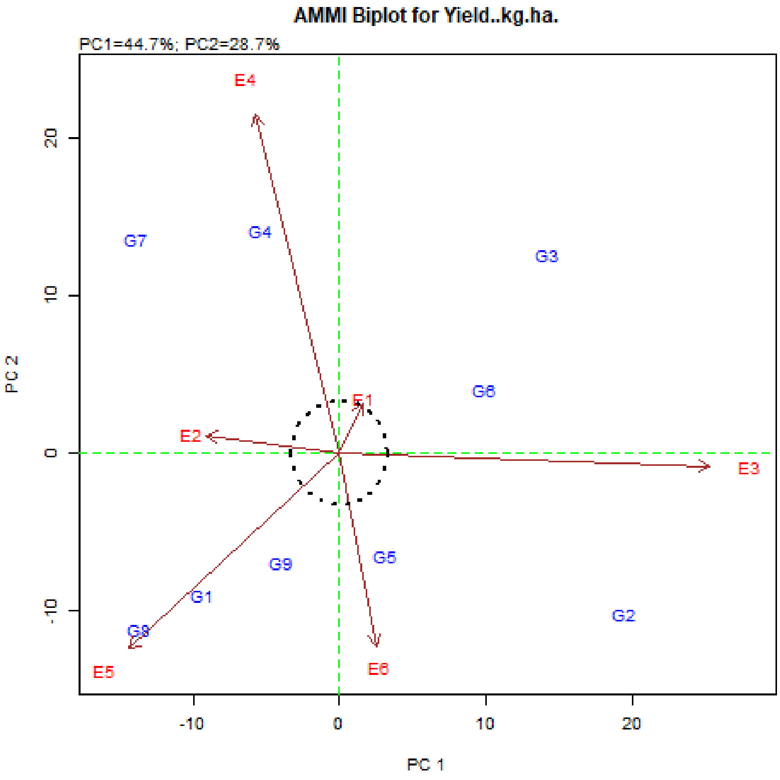

Fig 2: AMMI 2 Biplot for grain yield (kg ha^{-1}) showing the interaction of IPCA2 against IPCA1 scores of nine pigeonpea genotypes (G) in six environments (E).

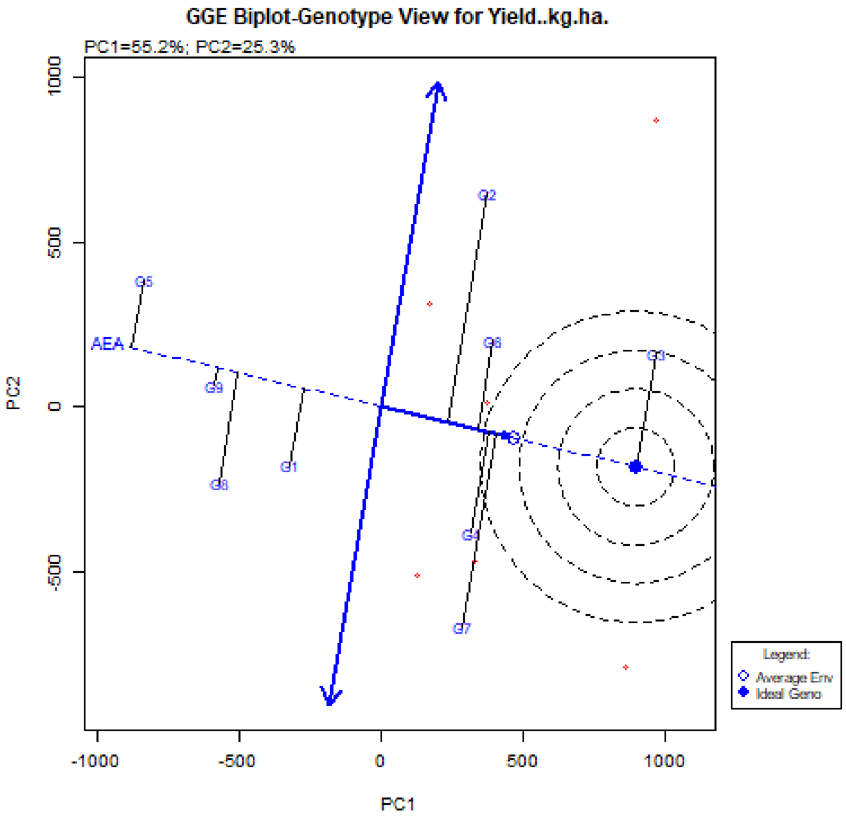

Fig 3: Biplot of stability and mean performance of genotypes across average Environments.

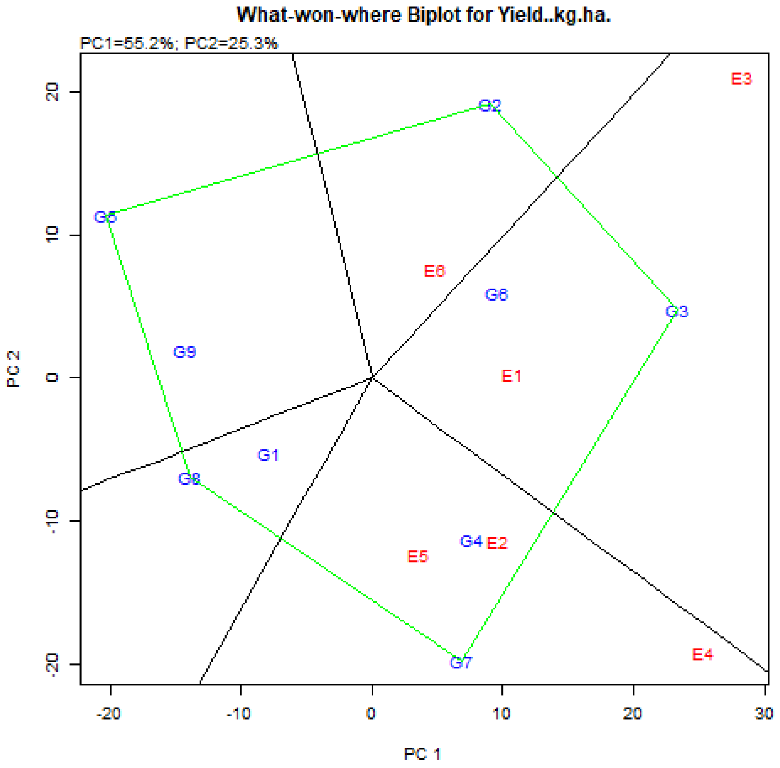

Fig 4: What-Won-Where GGE- Biplot for yield (kg ha^{-1}).

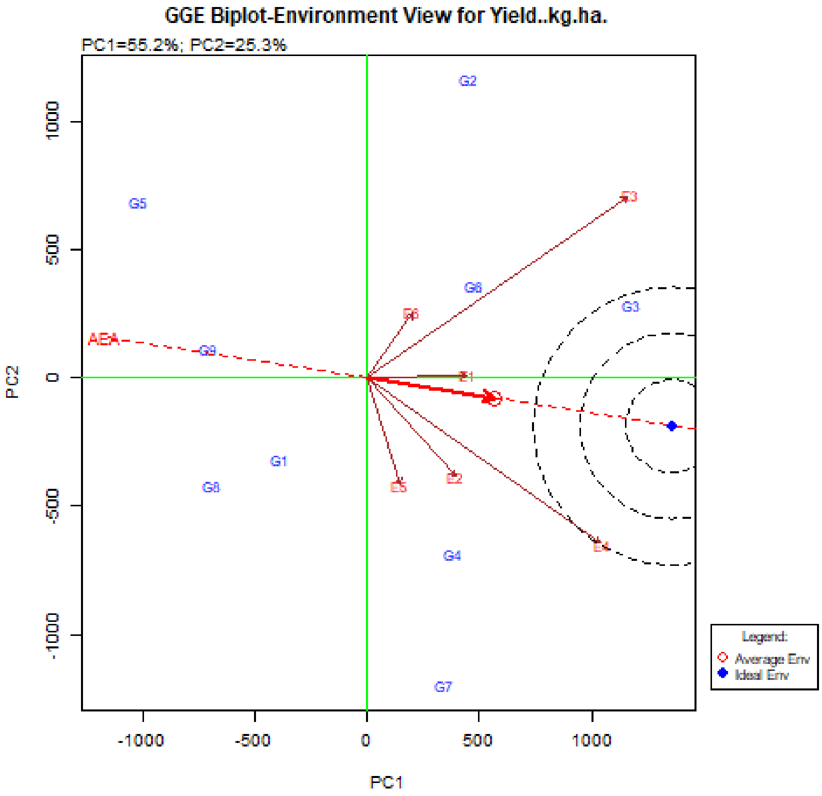

Fig 5: GGE biplot on environment focused for comparing environments with ideal

less cosines are more discriminating and representative for consideration in future studies.

The results of the both models were exposed that the genotype G6 (WRGE-126) was high yielder (1733kg ha^{-1}) with stable performance. AMMI biplot always explains less G+GE variation than the GGE biplot. In contrast, AMMI biplot can be simpler constructed and interpreted because its axes are used directly for selection of mega environments, AMMI2 biplot can also be used successfully by relating the first two principal components (PC1 and PC2).

According to both the analyses, WRGE-126 (G6) exhibited almost minimum interaction with the environments convincing the reliability of the stable performance, While, WRGE-124 (G3) recorded the highest yield (1955 kg ha^{-1}) among all the genotypes and found to be specific to Palem followed by another promising genotype *i.e.,* WRGE-128 (1759 kg ha^{-1}) found better and suited for environments Palem, Warangal and Jagtial. Among the test environments, Tandur (E1) considered as the ideal environment whereas, Adilabad (E3) and Warangal (E4) were observed representative with better discriminating ability. Multivariate mathematical models can be of great benefit in multi year or multi location testing for identification of stable genotypes.

Authors' contribution

Conceptualization of research (PJMR); Designing of the experiments (PJMR, NSK); Contribution of experimental materials (PJMR,NSK);Execution of field/lab experiments and data collection (PJMR, NSK, SS, GN, AS, PMR and DMD); Analysis of data and interpretation (NSK,N.L); Preparation of manuscript (NSK).

Declaration

The authors declare no conflict of interest.

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