International Journal of Bio-resource and Stress Management https://pphouse.org/ijbsm.php

IJBSM May 2022, 13(5):454-462 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR2870

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2022.2870

Stability Analysis for Assessment of Yield Performance and Adaptability of Selected Mango (*Mangifera indica* L.) Genotypes under Multi Location Trials in India

Sai Krishna K., Ram Kumar Chaudhary and Mahesh Kumar

Dept. of Basic Sciences and Languages, Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar (848 125), India

Open Access

Corresponding saikrishna.kancharla124@gmail.com

0000-0002-2890-1279

ABSTRACT

A study was conducted in April 2020 based on the data collected from the All-India Coordinated Research Project on Sub-Tropical Fruits (AICRP-STF) and Central Institute for Subtropical Horticulture (CISH), Lucknow, India. The objective was to identify the high yielding and stable genotypes of mango using Additive main effects and multiplicative interaction (AMMI) and Genotype plus Genotype×Environment interaction (GGE) biplot analyses. Data on sixteen genotypes of mango tested across four locations, viz., Rewa, Sabour, Sangareddy, and Vengurla, over nine years was considered for the study. Combined analysis of variance showed highly significant differences ($p<0.01$) for genotype, environmental main effects and genotype×environment interaction (GEI) effects. The significant GEI contributes about 42.81% of the total sum of squares. AMMI analysis partitioned the GEI into fifteen interaction principal component axes and a residual term. The first two interaction principal component axes (IPCA1, IPCA2) collectively accounted for 40.80% of GEI sum of squares. AMMI analysis recommended Zardalu, Mankurad and GGE biplot analysis recommended Totapari, Mankurad as superior mango genotypes for cultivation in all the test locations. GGE biplot analysis classified the test locations into two mega environments. The first mega environment includes Rewa and Sangareddy with Neelum as the best suitable genotype; the second includes Vengurla and Sabour with Suvarnarekha as the best suitable genotype. The present study also concluded that GGE biplot analysis was the best analytical tool for identifying location-specific genotypes of mango, and AMMI analysis was the best for identifying superior genotypes having high yield with stability across all the test locations.

KEYWORDS: Adaptability, AMMI, biplot, environment, GEI, GGE, mango, stability

Citation* (VANCOUVER)*: Krishna et al., Stability Analysis for Assessment of Yield Performance and Adaptability of Selected Mango (*Mangifera indica* L.) Genotypes under Multi Location Trials in India. *International Journal of Bio-resource and Stress Management,* 2022; 13(5), 454-462. HTTPS://DOI.ORG/10.23910/1.2022.2870.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 31st January 2022 RECEIVED in revised form on 08th May 2022 ACCEPTED in final form on 25th May 2022 PUBLISHED on 31st May 2022

1. INTRODUCTION

Mango is one of the most important commercially grown fruit crops in India. Major mango producing countries in the world are India, China, Thailand, Indonesia, Mexico, Pakistan, Brazil, Philippines, Nigeria, and Sudan (Anonymous, 2020a). Mango is cultivated in a vast area of 2,578 t ha^{-1}. The production is around 24.75 mt, accounting for about 45.13% of total world mango production 46.68% of world mango cultivated area (Anonymous, 2020a). The increasing population raises demand for agricultural produce, which is expected to enhance agricultural production. In a view of sustaining hunger, it is required to increase agricultural production per unit area. To encounter this requirement, various crop improvement programs have been initiated all over the world (Anonymous, 2019). In any crop improvement program, the performance of promising genotypes has been tested over different locations each year to identify the genotypes having both high yield qualities and wider adaptability over different environmental conditions (Kumar et al., 2021, Reddy et al., 2022). In Multi-location trials (MLT), most frequently, it is noticed that the genotypes respond differently to the diverse environmental conditions; this differential response of genotypes over diverse environments is known as Genotype environment interaction (GEI) (Pham et al., 1988, Farias et al., 2016, Pagi et al., 2017). Yet there is no single method developed so far that equally satisfies breeders for the study of GEI. There are many different statistical analyses in use today, including parametric and non-parametric methods to study the nature of interactions of genotypes with environments (Kaya et al., 2006, Jeberson et al., 2017, Oladosu et al., 2017, Rao et al., 2022).

Among various statistical techniques, Genotype plus Genotype×Environment Interaction (GGE) biplot and Additive Main Effects and Multiplicative Interaction (AMMI) models are being used predominantly for evaluating GEI and identifying superior genotypes (Purchase et al., 2000, Gauch Jr., 2006, Oliveira et al., 2010, Zali et al., 2012, Giridhar et al., 2016, Khan et al., 2021). AMMI model was introduced in 1988, and basically, the AMMI model is a combination of Analysis of Variance (ANOVA), which explains the main effects (Reddy et al., 2022), and Principal Component Analysis (PCA) which describes interaction effects (Gauch and Zobel, 1988, Singh et al., 2019). GGE biplot model concurrently depicts mean performance and stability and gives a comprehensive assessment of genotypes by creating a biplot. It can efficiently display the "which-won-where" patterns of MLT data (Singh et al 2019, Siddi et al., 2022). An important characteristic of this GGE biplot is that it removes the environment main effect and retains and combines genotype main effect and GEI. Thus, the biplot generated from the MLT data contains only G and GEI (Kang, 2002, Kumar et al., 2021, Sharma et al., 2016). GGE biplot and AMMI analyses has been carried out in understanding GEI in many crop species including pigeon pea (Rao et al., 2022, Reddy et al., 2022, Kumar et al., 2021, Sharma et al., 2016); wheat (Verma et al., 2021, Singh et al., 2019, Jeberson et al., 2017); ground nut (Khan et al., 2021); maize (Bozovic et al., 2020, Oliveira et al., 2010); rice (Chandra Mohan et al., 2021).

Genotype environment interaction is a major problem in selecting and recommending superior genotypes to cultivate crops. When dealing with perennial crops like Mango, Guava, etc., this problem gets intensified because choosing unstable cultivars puts the farmers in a risky income situation for many years. To avoid such circumstances and facilitate growth in farmers' income by recommending superior genotypes, the present study has been taken up.

2. MATERIALS AND METHODS

2.1. Source and description of data

Mango multi location trials were conducted at four locations namely Rewa (Madhya Pradesh), Vengurla (Maharashtra), Sangareddy (Telangana), and Sabour (Bihar) over different years. These trials were carried out in a randomized complete block design with three replications in each location. The present investigation has been carried out in April, 2020 based on the data collected from the All-India Co-Ordinated Research Project on Sub-Tropical Fruits (AICRP-STF) and Central Institute for Subtropical Horticulture (CISH), Lucknow, India. All the four locations contain common data for 16 genotypes of mango tested over nine years from 1997–2005 with three replications, and the same data were taken for the study. For the present investigation, the yield variable, i.e., the number of fruits per tree has been considered for the evaluation of MLT data of Mango. A combination of years and locations were considered as environments. As mango genotypes were grown in 4 different locations over nine different years, it gives 36 environments. Codes of selected mango genotypes, and environments used in the present study are shown in Table 1.

2.2. AMMI analysis

AMMI analysis is a mixture of additive and multiplicative effect analysis. At first, it calculates additive main effects by using ANOVA; briefly ANOVA partitions the total variance into 3 different components like deviations of genotypes, environments, and GEI from the grand mean. The second part, i.e., multiplicative part, divides the deviations of GEI into various IPCAs, these IPCA are tested for significance through ANOVA (Gauch Jr, 1992). Generally, AMMI uses PCA for analysing the multiplicative part of GEI. The AMMI model for T genotypes and S environments is given

Table 1: List of mango genotypes, test environments, and their codes

Genotype	Code	Environment	Code	Environment	Code
Banganpalli	G1	Rewa 1997	E1	Sangareddy 1997	E19
Suvarnarekha	G2	Rewa 1998	E2	Sangareddy 1998	E20
Neelum	G3	Rewa 1999	E3	Sangareddy 1999	E21
Totapari	G4	Rewa 2000	E4	Sangareddy 2000	E22
Fazli	G5	Rewa 2001	E5	Sangareddy 2001	E23
Chousa	G6	Rewa 2002	E6	Sangareddy 2002	E24
Mallika	G7	Rewa 2003	E7	Sangareddy 2003	E25
Zardalu	G8	Rewa 2004	E8	Sangareddy 2004	E26
Bombai	G9	Rewa 2005	E9	Sangareddy 2005	E27
Bombay Green	G10	Sabour 1997	E10	Vengurla 1997	E28
Himsagar	G11	Sabour 1998	E11	Vengurla 1998	E29
Kishan Bogh	G12	Sabour 1999	E12	Vengurla 1999	E30
Alphanso	G13	Sabour 2000	E13	Vengurla 2000	E31
Kesar	G14	Sabour 2001	E14	Vengurla 2001	E32
Mankurad	G15	Sabour 2002	E15	Vengurla 2002	E33
Vanraj	G16	Sabour 2003	E16	Vengurla 2003	E34
		Sabour 2004	E17	Vengurla 2004	E35
		Sabour 2005	E18	Vengurla 2005	E36

below,

$$Yij = \mu + g_i + e_j + \sum^{n'}_{(n=1)} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij} \text{.........} (1)$$

$\theta_{ij} \sim N(0, \sigma^2)$; i = (1, 2, 3, 4.........T); j = (1,2, 3....... S), Y_{ij} = Average yield of i^{th} genotype in j^{th} environment; μ= Grand Man; g_i = i^{th} genotypic main effect; e_j= j^{th} environmental main effect; λ_n= Eigen value of nth IPCA; α_{in} and γ_{jn} = ith genotype and jth environment PCA scores for the axis n; θ_{ij}= Residual; n'= Number of PCA axes retained in the model.

2.3. Stability parameters

2.3.1. AMMI stability value (ASV)

This measure utilizes only the first 2 IPCAs. The higher value of the ASV score indicates that the genotype is specially adapted to certain environments and lower the scores of ASV, the more will be the genotypic stability across different environments (Purchase et al., 2000). It can be calculated by the following formula.

$$ASV = \sqrt{[(IPCA1\ score)\ (IPCA1sum\ of\ squares)/(IPCA2sum\ of\ squares)]^2 + [IPCA2\ score]^2\ )} \text{..........} (2)$$

2.3.2. AMMI based stability measure (ASTAB$_i$)

ASTAB$_i$ incorporates all the significant principal components required for explaining the GEI. Genotypes having a lower value of ASTAB$_i$ are considered stable genotypes (Rao and Prabhakaran, 2005). This measure can be computed by the formula.

$$ASTAB_i = \sum^{N'}_{n=1} \lambda_n\ \gamma^2_{in} \quad \text{.........} (3)$$

= Number of significant IPCAs retained; = Singular value of nth IPCA; = i^{th} genotype eigenvector value

2.3.3. Yield stability index (YSI)

This measure combines mean yield and stability of a genotype in a single criterion. YSI can be computed by the addition of rank of stability measure (R_S) and rank of mean yield (R_Y) of a genotype. The lower the value of YSI, the higher will be the mean yield and stability of genotype across environments.

$$YSI = R_S + R_Y \text{............................} (4)$$

$$YSI_1 = Index\ 1 = R_{ASV} + R_Y \text{...............} (5)$$

$$YSI_2 = Index\ 2 = R_{ASTAB} + R_Y \text{.............} (6)$$

2.4. GGE biplot analysis

The concept of biplot was introduced by Gabriel in 1971. The prefix 'Bi' in the word biplot denotes the dual (genotypes and environment) exposing on the same graph. Biplot is a 2D visualization matrix that has two axes, first data was centered afterward sectionalizing the singular value (SV) into GE scores for individual principal components viz. PC1 and PC2 followed by intrigue the PC1 scores contrary to the PC2 scores to create a biplot (Gabriel, 1971). The greater PC1 value indicates greater yielding ability whereas the lower PC2 value signifies stability (Jeberson et al., 2017, Oladosu et al., 2017, Reddy et al., 2022). Genotypes, environments, and their interactions were portrayed on the biplot. The genotypes which were positioned near to the origin of the biplot origin are considered stable genotypes. However, the genotypes which are positioned far away from the origin of the biplot are considered unstable genotypes.

For better understanding and easy interpretation, various biplots have been derived from the basic GGE biplots. In the present study, 2 types of biplots namely: "Which-won-where" view and "Ranking genotypes" view of the GGE biplot have been utilized. "Which-won-where" biplot has been used for identifying mega environments and this identification of mega environments helps in classifying similar behaving environments as one group and accordingly genotypes have been recommended for each of the mega environments. "Ranking genotypes" biplot has been used to identify superior genotypes.

2.5. Statistical analysis

To explain the GEI, the multivariate stability analysis was performed graphically based on GGE biplot (Which-won-where view and ranking genotypes view) and AMMI using R studio (a simplified version of R statistical software) developed by the R Core Team. The Metan package of R studio was used for GGE biplots (Anonymous, 2020b), while the Agricolae package was used for AMMI (Mendiburu, 2020).

2.6. Data Transformation

To attain normality and homogeneity of error variances across environments, data was transformed using appropriate data transformation techniques. Yield variable data was transformed to normal using the "Ordered quantile normalization technique". R-package "best Normalize" has been employed for data transformation (Peterson and Cavanaugh, 2019).

3. RESULTS AND DISCUSSION

3.1. AMMI analysis

One of the vital objectives of the crop improvement program is to identify superior varieties with high yield and stability across diverse locations. A combined analysis of variance has been performed to describe the main effects and quantify the interactions among and within the sources of variation. Due to the significant combined analysis of variance, yield stability of genotypes was studied, and genotypes with specific adaptability to each environment and genotypes with general adaptability to all environments were measured (Reddy et al., 2022).

The mean squares of genotypes, environments and their interactions (i.e., GEI) showed significant differences ($p<0.01$) for the yield variable. Genotypes, environments, and GEI effect accounted for 6.95%, 37.78%, and 42.81% of the total sum of squares, respectively. As ANOVA confirmed the presence of significant GEI, additional statistical techniques such as AMMI and GGE biplot analyses were more helpful in unfolding and understanding the GEI (Khan et al., 2021). Application of the AMMI model for the apportioning of GEI revealed 12 significant interaction principal component axes (IPCA). IPCA1 and IPCA2 collectively accounted for 40.80% of GEI. The combined analysis of variance and AMMI analysis results were presented in Table 2. Sabaghnia et al. (2008) also observed about 40% of GEI contribution in total variation in the lentil genotypes. Reddy et al. (2022) reported similar findings that stated that the GEI effect contributed 36.49% of the variation for Sterility mosaic disease. Chandra Mohan et al. (2021) observed a highly significant difference in grain yield in rice hybrids by genotype (7.5%), environment (65.47%) and their interaction (21.19%). Further, Giridhar et al. (2016), Kumar et al. (2020), and Rao et al. (2022) also reported highly significant genotype-environment interactions.

Table 2: AMMI analysis of variance over 36 environments

Source of variation	df	SS	MSS	F-value
ENVI	35	651.77	18.62	69.10**
REP(ENVI)	72	19.40	0.27	1.41**
GEN	15	120.03	8.00	41.90**
ENVI: GEN	525	727.72	1.39	7.26**
IPCA1	49	188.00	3.84	20.09**
IPCA2	47	108.65	2.31	12.10**
IPCA3	45	99.56	2.21	11.58**
IPCA4	43	88.67	2.06	10.80**
IPCA5	41	59.36	1.45	7.58**
IPCA6	39	47.30	1.21	6.35**
IPCA7	37	32.93	0.89	4.66**
IPCA8	35	31.80	0.91	4.76**
IPCA9	33	18.26	0.55	2.90**
IPCA10	31	16.61	0.54	2.81**
IPCA11	29	12.23	0.42	2.21**
IPCA12	27	10.69	0.40	2.07**
IPCA13	25	6.65	0.27	1.39NS
IPCA14	23	5.26	0.23	1.20NS
IPCA15	21	1.74	0.08	0.43NS
Residuals	1080	206.27	0.19	

ENVI: environment; GEN: genotype; REP: replication; df: degrees of freedom, MSS mean sum of squares, TSS total sum of squares; **: Significant at $p\leq 0.01$, NS: Non significant at $p\leq 0.05$

3.2. Stability parameters of AMMI

Mango genotypes were ranked based on stability measures as well as simultaneous selection indices for yield and stability (SSIYS) using the interaction principal component axes (IPCA) scores obtained through AMMI analysis.

Values and ranks of the stability parameters are presented in Table 3 and Table 4, respectively. The genotype G4 exhibited the highest mean yield, followed by G2, G8, and G15. Genotypes with lower scores of ASV and $ASTAB_i$ are known as stable genotypes (Purchase et al., 2000, Rao and Prabhakaran, 2005). ASV scores were smaller for the genotypes G10, G8 and G7, while the $ASTAB_i$ scores were minimum for the genotypes G7, G5 and G15; hence these

Table 3: Mean yields and stability parameter estimates for 16 genotypes of mango tested in 36 environments

Genotypes	Code	Mean yield*	ASV	$ASTAB_i$	Index 1	Index 2
Banganpalli	G1	210.18 (-0.40)	1.55	4.00	29	30
Suvarnarekha	G2	328.79 (0.43)	1.23	2.63	12	7
Neelum	G3	280.53 (0.22)	2.22	4.23	21	21
Totapuri	G4	311.90 (0.44)	1.11	3.10	9	12
Fazli	G5	183.36 (-0.25)	1.50	2.32	25	15
Chousa	G6	166.01 (-0.28)	1.41	2.84	26	23
Mallika	G7	223.37 (0.04)	0.82	2.04	11	9
Zardalu	G8	297.93 (0.34)	0.51	2.82	5	10
Bombay	G9	187.13 (-0.10)	1.09	2.46	16	13
Bombay Green	G10	172.74 (-0.27)	0.40	3.57	15	26
Himsagar	G11	224.19 (0.05)	1.08	4.05	13	22
Kishan Bogh	G12	169.19 (-0.23)	1.04	3.06	17	22
Alphanso	G13	194.30 (-0.13)	2.03	2.81	24	16
Kesar	G14	258.89 (0.15)	1.20	2.93	15	15
Mankurad	G15	274.42 (0.22)	1.01	2.33	8	7
Vanraj	G16	200.26 (-0.21)	2.07	3.66	26	24

*Numerical in the parenthesis are transformed value of yield variable

Table 4: Ranks of mango genotypes according to their mean yields and stability parameters

Genotypes	Code	Mean yield*	ASV	$ASTAB_i$	Index 1	Index 2
Banganpalli	G1	16	13	14	16	16
Suvarnarekha	G2	2	10	5	5	1.5
Neelum	G3	5	16	16	11	10
Totapuri	G4	1	8	11	3	5
Fazli	G5	13	12	2	13	7.5
Chousa	G6	15	11	8	14.5	13
Mallika	G7	8	3	1	4	3
Zardalu	G8	3	2	7	1	4
Bombay	G9	9	7	4	9	6
Bombay Green	G10	14	1	12	7.5	15
Himsagar	G11	7	6	15	6	11.5
Kishan Bogh	G12	12	5	10	10	11.5
Alphanso	G13	10	14	6	12	9
Kesar	G14	6	9	9	7.5	7.5
Mankurad	G15	4	4	3	2	1.5
Vanraj	G16	11	15	13	14.5	14

genotypes are known as stable genotypes according to ASV and ASTAB$_i$, respectively. G3 was recognized as an unstable genotype due to higher scores of ASV and ASTAB$_i$. The genotypes with the lowest and highest ranks of SSIYS are considered the best and the poorest genotypes, respectively. G8, G15 and G4 were identified as the best genotypes by Index 1, while G2, G15 and G7 were identified as the best genotypes by Index 2. However, the SSIYS (Index 1, Index 2) found G1 as the poorest genotype.

Correlations among the stability measures and SSIYS have been computed and presented in Table 5. Correlations were quantified using Spearman's rank correlation coefficient, and these correlations were tested for significance using a student t-test at a 1% level of significance (Zali et al., 2012). Index 1 and Index 2 have a significant correlation with each other and with mean yield, while ASV and ASTAB$_i$ have no significant correlation with mean yield. Index 1 has a significant correlation with ASV; however, Index 2 has a significant correlation with ASTAB$_i$. For the present study, only SSIYS such as Index1 and Index 2 were chosen to identify superior genotypes among the stability parameters because of their ability to identify the genotypes simultaneously for yield and stability. In contrast, ASV and ASTAB$_i$ rank the genotypes only based on stability, irrespective of their yields. Spearman's rank correlation coefficient between SSIYS (Index 1 and Index 2) is highly significant (p<0.01), which implies either of the indices may invariably be used for identifying the best genotypes. The present study's findings agreed with the report stated by Zali et al. (2012) considered thirteen different stability measures, and Verma et al. (2021) considered different AMMI based stability measures and simultaneous selection index in stability assessment of wheat genotypes. Final ranking order of mango genotypes based on AMMI analysis (Index 1) is G8 > G15 > G4 > G7 > G2 > G11 > G14 > G10.

Table 5: Spearman's correlation coefficients among different stability parameters

	Mean yield	ASV	ASTAB$_i$	Index 1	Index 2
Mean yield	1				
ASV	0.19^{NS}	1			
ASTAB$_i$	0.12^{NS}	0.30^{NS}	1		
Index 1	0.80^{**}	0.73^{**}	0.31^{NS}	1	
Index 2	0.78^{**}	0.32^{NS}	0.71^{**}	0.75^{**}	1

**: Significant at $p\leq 0.01$; NS: Non significant

3.3. *GGE biplot analysis*

3.3.1. *"Which-won-where" view of GGE biplot*

Figure 1 illustrates the "Which-won-where" view of the GGE biplot for the yield variable. Each sector of the biplot forms a unique mega environment. The environments falling in the same sector belong to the same mega environment. The genotypes which share the same sector with the test environments in a biplot are specially adopted to those environments (Kang, 2002, Siddi et al., 2022).

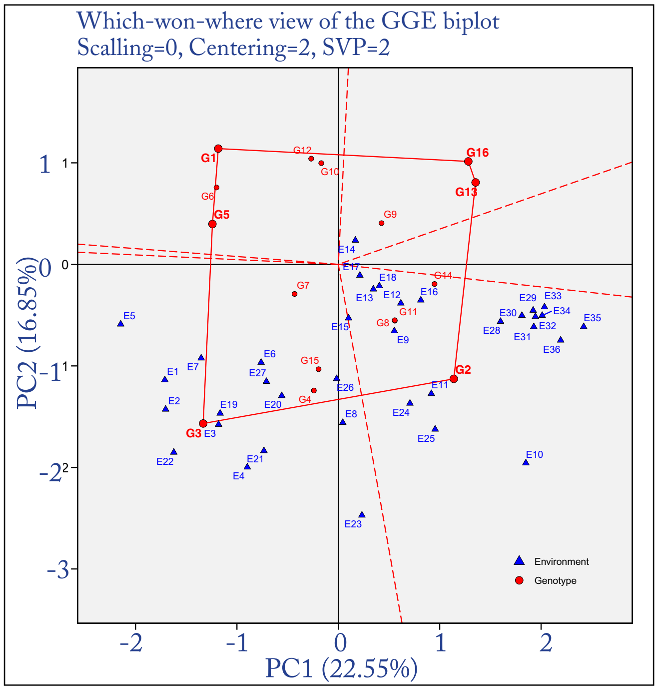

Figure 1: "Which–won–where" view of the GGE biplot for 16 genotypes of mango tested over 36 environments

Three mega environments have been identified as environmental indicators positioned in 3 sections of the biplot, with different genotypes winning in each segment. A single test environment, E14, formed the first mega environment with G16 and G13 as winners, and the test environments E9, E10, E11, E12, E13, E15, E16, E17, E18, E24, E25, E28, E29, E30, E31, E32, E33, E34, E35 and E36 collectively formed as the second mega environment with G2 as winner genotype. While remaining test environments, i.e., E1, E2, E3, E4, E5, E6, E7, E8, E19, E20, E21, E22, E23, E26 and E27 constitute the third mega environment with G3 as the winner genotype. The present study's findings agreed with the report stated by Oladosu et al., 2017, who considered two different cropping seasons across five locations in Malaysia. Comparably, Mary et al. (2019) reported that the biplot for grain yield during the wet season showed that PSBRc82 was the winner genotype in E4 and MS13 in E8 and E9. Rukmini Devi et al. (2020) reported the rice genotypes WGRH-6 and WGRH-10 had better performance in mega environment E3, and the genotype WGRH-18 exhibited better performance in the second mega environment consisting of E1 and E2. Similar results have been reported by Yan et al. (2010).

3.3.2. Ranking genotypes view of GGE biplot

This kind of GGE biplot describes the ranks of genotypes based on their position from the ideal genotype. For an effective selection, an ideal genotype should have both high mean and stability properties (Khan et al., 2021). The genotype located in the innermost concentric circle is highly desirable compared to the genotypes of the outer circle. However, no genotype was positioned within the inner circle in some cases. Consequently, genotypes closer to the inner circle are considered the best ones (Gauch, 2006, Siddi et al., 2022). The genotypes G4, G15, G2, G8, G11, G14, and G7, were regarded as the best genotypes across all test environments because of their closeness to the ideal genotype (Figure 2). So, the genotype ranking based on ideal genotype for yield variable is G4 > G15 > G2 > G8 = G11 > G14>G7. Oladosu et al. (2017) and Chandra Mohan et al., 2021 reported similar findings across mutant rice varieties.

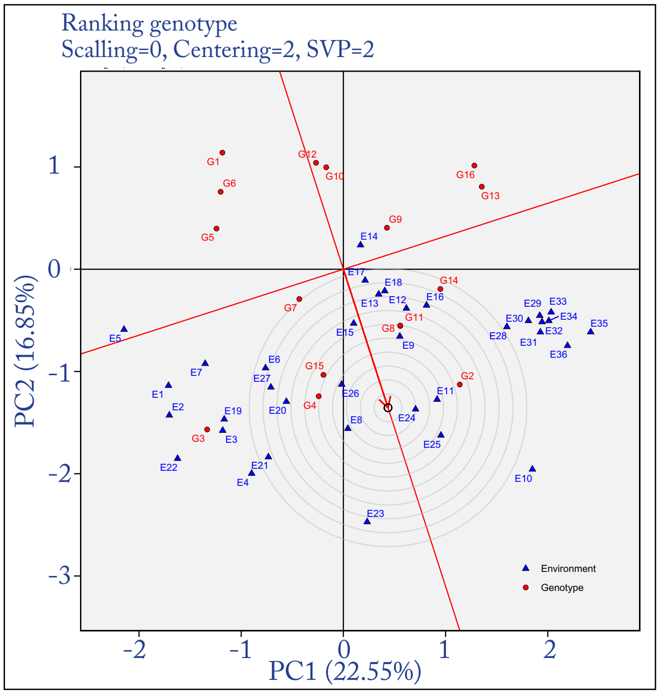

Figure 2: "Genotypes ranking" view of the GGE biplot for 16 genotypes of mango tested over 36 environments

4. CONCLUSION

AMMI analysis recommended Zardalu, Mankurad and GGE biplot analysis recommended Totapari, Mankurad as superior genotypes of mango for all the test locations in India. GGE biplot analysis also revealed that Suvarnarekha was the best-performed genotype in Sabour and Vengurla, while Neelum was the best-performed genotype in Rewa and Sangareddy. The present study concluded that AMMI and GGE biplot analyses were the most valuable tools for identifying the superior genotypes in perennial crops.

6. ACKNOWLEDGMENT

Authors wish to acknowledge AICRP-STF, CISH, Lucknow, India and its centres, Rewa, Sangareddy, Vengurla and Sabour for providing data.

7. REFERENCES

Anonymous, 2019. Transforming agriculture for challenges of 21st century. Available at https://www.niti.gov.in/sites/default/files/2020-01/Presidential_Address.pdf. Accessed on 4th September, 2021.

Anonymous, 2020a. Food and agriculture organization of the United Nations. Available at https://www.fao.org/faostat/en/#data/QCL. Accessed on 4th September, 2021.

Anonymous, 2020b. Multi environment trials analysis (metan): An R package for multi-environment trial analysis. Available at https://tiagoolivoto.github.io/metan/. Accessed on 4th September, 2021.

Bozovic, D., Popovic, V., Rajicic, V., Kostic, M., Filipovic, V., Kolaric, L., Ugrenovic, V. and Spalevic, V., 2020. Stability of the expression of the maize productivity parameters by AMMI models and GGE-biplot analysis. Notulae Botanicae Horti Agrobotanici Cluj-Napoca 48(3),1387–1397.

Chandra Mohan, Y., Krishna, L., Sreedhar, S., Satish Chandra, B., Damodhar Raju, C., Madhukar, P., Rathod, R., Virender Jeet Singh, T., Ramana, M.V., 2021. Stability analysis of rice hybrids for grain yield in Telangana through AMMI and GGE bi-plot model. International Journal of Bio-Resource and Stress Management 12(6), 687–695.

Chandrashekhar, S., Babu, R., Jeyaprakash, P., Umarani, R., Bhuvaneshwari, K., Manonmani, S., 2020. Yield stability analysis in multi-environment trials of hybrid rice (*Oryza sativa* L.) in Northern India using GGE biplot analysis. Electronic Journal of Plant Breeding 11(02), 665–673.

Farias, F.J.C., De Carvalho, L.P., Da Silva Filho, J.L., Teodoro, P.E., 2016. Biplot analysis of phenotypic stability in upland cotton genotypes in Mato Grosso. Genetics and Molecular Research 15(2), 1–10.

Gabriel, K.R., 1971. The biplot graphic display of matrices with application to principal component analysis. Biometrika 58(3), 453–467. DOI https://doi.org/10.2307/2334381.

Gauch Jr., H.G., 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, 278. ISBN 0444892400 9780444892409.

Gauch Jr., H.G., 2006. Statistical analysis of yield trials by AMMI and GGE. Crop Science 46(4), 1488–1500. DOI https://doi.org/10.2135/cropsci2005.07-0193.

Gauch, H.G., Zobel, R.W., 1988. Predictive and postdictive success of statistical analyses of yield trials. Theoretical and Applied genetics 76(1), 1–10. DOI https://doi.org/10.1007/BF00288824,

Giridhar, K., Kumari, S.S., Babu, K.N., Thankamani, C.K., Sastry, E.V.D., Singh, D., Lal, G., Singh, S.P., Tehlan, S.K., Pandey, V.P., Singh, D., 2016. Mega environment analysis and cultivar selection for resource optimization. International Journal of Bio-resource and Stress Management 7(4),798–806.

Jeberson, M.S., Kant, L., Kishore, N., Rana, V., Walia, D.P., Singh, D., 2017. AMMI and GGE biplot analysis of yield stability and adaptability of elite genotypes of bread wheat (*Triticum aestivum* L.) for Northern Hill zone of India. International Journal of Bio-resource and Stress Management 8(5), 635–641.

Kang, M.S., 2002. Genotype- environment interaction: Progress and prospects. In: Kang, M.S. (Ed.), Quantitative genetics, genomics, and plant Breeding. CABI Publishing, Wallingford, Oxon, 221–244.

Kaya, Y., Akcura, M., Taner, S., 2006. GGE-biplot analysis of multi-environment yield trials in bread wheat. Turkish Journal of Agriculture and Forestry 30(5), 325–337.

Khan, M.M.H., Rafii, M.Y., Ramlee, S.I., Jusoh, M., Al Mamun, M., 2021. AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. Verdc.) genotypes under the multi-environmental trails (METs). Scientific reports 11(1), 1–17. DOI https://doi.org/10.1038/s41598-021-01411-2

Kumar, M., Patel, M.P., Chauhan, R.M., Tank, C.J., Solanki, S.D., Gami, R.A., Rani, K., 2020. Delineating G×E interactions by AMMI method for root attributes in ashwagandha [*Withania somnifera* (L.) Dunal]. Indian Journal of Genetics and Plant Breeding 80(4), 441–449.

Kumar, M.N., Ramya, V., Kumar, C.S., Raju, T., Kumar, N.S., Seshu, G., Sathish, G., Bhadru, D., Ramana, M.V., 2021. Identification of pigeonpea genotypes with wider adaptability to rainfed environments through AMMI and GGE biplot analyses. Indian Journal Genetics and Plant Breeding 81(1), 63–73.

Mary, A.I.A., Mallikarjuna Swamy, B.P., Amparado, A.F., Gwen Iris, L., D.E., Emily, C.A., Reinke, R., 2019. Stability and GGE analysis of zinc-biofortified rice genotypes evaluated in diverse environments. Euphytica 215, 1–17.

Mendiburu, F.D., 2020. Agricolae: statistical procedures for agricultural research. Available at https://CRAN.R-project.org/package=agricolae.

Oladosu, Y., Rafii, M.Y., Abdullah, N., Magaji, U., Miah, G., Hussin, G., Ramli, A., 2017. Genotype×environment interaction and stability analyses of yield and yield components of established and mutant rice genotypes tested in multiple locations in Malaysia. Acta Agriculturae Scandinavica, Section B-Soil & Plant Science 67(7), 590–606. DOI https://doi.org/10.1080/09064710.2017.1321138.

Oliveira, R.L.D., Von Pinho, R.G., Balestre, M., Ferreira, D.V., 2010. Evaluation of maize hybrids and environmental stratification by the methods AMMI and GGE biplot. Crop Breeding and Applied Biotechnology 10(3), 247–253.

Pagi, N., Prajapati, N., Pachchigar, K., Dharajiya, D., Solanki, S.D., Soni, N., Patel, P., 2017. GGE biplot analysis for yield performance of grain amaranth genotypes across different environments in western India. Journal of Experimental Biology and Agricultural Sciences 5(3), 368–376.

Peterson, R.A., Cavanaugh, J.E., 2019. Ordered quantile normalization: A semiparametric transformation built for the cross-validation era. Journal of Applied Statistics 47(13–15), 2312–2327. DOI https://doi.org/10.1080/02664763.2019.1630372

Pham, H.N., Kang, M.S., 1988. Interrelationships among and repeatability of several stability statistics estimated from international maize trials. Crop Science 28(6), 925–928. DOI https://doi.org/10.2135/cropsci1988.0011183X002800060010x

Purchase, J.L., Hatting, H., Van Deventer, C.S., 2000. Genotype×environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil 17(3), 101–107. DOI https://doi.org/10.1080/02571862.2000.10634877.

Rao, A.R., Prabhakaran, V.T., 2005. Use of AMMI in simultaneous selection of genotypes for yield and stability. Journal of Indian Society of Agricultural Statistics 59(1), 76–82.

Rao, P.J.M., Sandhyakishore, N., Sandeep, S., Neelima, G., 2022. AMMI and GGE biplot analysis for stability of yield in mid-early pigeonpea [*Cajanus cajan* (L.) Millspaugh] genotypes. Legume Research 1, 8. DOI https://doi.org/10.18805/LR-4667.

Reddy, B.D., Kumar, B., Reddy, M.S.S., Krishna, K.S., Karthik, S., Kumar, R., 2022. Identification of elite pigeonpea genotypes against fusarium wilt and sterility mosaic disease through AMMI and GGE biplot analyses. Legume Research. DOI https://doi.org/10.18805/LR-4838.

Rukmini Devi, K., Venkanna, V., Lingaiah, N., Rajendra Prasad, K., Satish Chandra, B., Hari, Y., Jagan Mohan Rao, P., 2020. AMMI Biplot analysis for genotype×environment interaction and stability for yield in hybrid rice (*Oryza sativa* L.) under different production seasons. Current Journal of Applied Science and Technology 39(48), 169–175.

Sabaghnia, N., Sabaghpour, S.H., Dehghani, H., 2008. The use of an AMMI model and its parameters to analyse yield stability in multi-environment trials. The Journal of Agricultural Science 146(5), 571–581. DOI https://doi.org/10.1017/S0021859608007831.

Sharma, M., Ghosh, R., Telangre, R., Rathore, A., Saifulla, M., Mahalinga, D.M., Jain, Y.K., 2016. Environmental influences on pigeonpea- *Fusarium udum* interactions and stability of genotypes to fusarium wilt. Frontiers in Plant Science 7, 253.

Siddi, S., Anil, D., Lingaiah, N., 2022. GGE biplot analysis for stability in diverse maturity groups of rice (*Oryza sativa* L.) advanced lines. International Journal of Bio-Resource and Stress Management 13(1), 114–121.

Singh, C., Gupta, A., Gupta, V., Kumar, P., Sendhil, R., Tyagi, B.S., Singh, G., Chatrath, R., Singh, G.P., 2019. Genotype×environment interaction analysis of multi-environment wheat trials in India using AMMI and GGE biplot models. Crop Breeding and Applied Biotechnology 19(3), 309–318.

Verma, A., Singh, G.P., 2021. Simultaneous consideration of AMMI analysis and yield of wheat genotypes for stability assessment evaluated under Central Zone of Indian Journal of Crop and Weed 17(2), 160–169. https://doi.org/10.22271/09746315.2021.v17.i2.1466

Yan, W., Fregeau-Reid, J., Pageau, D., Martin, R., Mitchell-Fetch, J., Etienne, M., Rowsell, J., Scott, P., Price, M., de Haan, B., Cummiskey, A., 2010. Identifying essential test locations for oat breeding in eastern Canada. Crop Science 50(2), 504–515. DOI https://doi.org/10.2135/cropsci2009.03.0133.

Zali, H., Farshadfar, E., Sabaghpour, S.H., Karimizadeh, R., 2012. Evaluation of genotype×environment interaction in chickpea using measures of stability from AMMI model. Annals of Biological Research 3(7), 3126–3136.