

GGE Biplot Analysis and ITS Application to Mango Multi Location Trial Data in India

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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 Genotype plus Genotype \times Environment interaction (GGE) biplot analysis. 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 \times environment interaction (GEI) effects. GGE biplot analysis classified the test locations into two mega environments. The first mega environment includes Rewa, Sabour and Sangareddy with Totapari as the best suitable genotype; the second includes Vengurla with Suvarnarekha as the best suitable genotype. The present study concluded that GGE biplot analysis was the best analytical tool for identifying location-specific genotypes and superior genotypes having high yield with stability across all the test locations.

Keywords Adaptability, Biplot, Environment, GEI, GGE.

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 2020). 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 and 46.68% of world mango cultivated area (Anonymous 2020). The increasing population raises demand for agricultural

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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 (Chand 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). 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, Oladosu *et al.* 2017, Rao *et al.* 2022). Yet there is no single method developed so far that equally satisfies breeders for the study of GEI.

Among various statistical techniques, Genotype plus Genotype \times Environment Interaction (GGE) biplot is being used predominantly for evaluating GEI and identifying superior genotypes (Rakshit *et al.* 2012). GGE biplot model concurrently depicts mean performance and stability and gives a comprehensive assessment of genotypes by creating a biplot. 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, Yan *et al.* 2010). GGE biplot analysis has been carried out in understanding GEI in many crops including Ashwagandha (Kumar *et al.* 2020), Barley (Kendal *et al.* 2019), Ground nut (Khan *et al.* 2021, Lal *et al.* 2019), Lentil (Sabaghnia *et al.* 2008), Maize (Shojaei *et al.* 2022), Oat (Yan *et al.* 2010), Pigeon pea (Kumar *et al.* 2021, Reddy *et al.* 2022), Rice (Alam *et al.* 2021, Chandrashekhar *et al.* 2020, Siddi *et al.* 2022), Sweet potato (Mahmud *et al.* 2021) and others. Although, the usefulness of GGE biplot analysis in determining superior genotypes is huge in annual crops, their ap-

plication in perennial fruit crops, especially in mango is scanty. Genotype environment interaction is a major constraint in selecting and recommending superior genotypes for the cultivation of crops, which further intensifies while dealing with perennial crops like mango because selection of unstable cultivars puts the farmers in a long-term risky income situation. In this connection, the present study has been taken up to avoid such circumstances and to facilitate growth in farmer's income by recommending superior genotypes prior planting.

MATERIALS AND METHODS

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., fruits yield 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 four different locations over nine different years, it gives 36 environments. Codes of mango genotypes, and environments used in the present study were shown in Table 1.

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

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

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 (Oladosu *et al.* 2017, Reddy *et al.* 2022). Genotypes, environments and their interactions were portrayed on the biplot.

For better understanding and easy interpretation, various biplots have been derived from the basic GGE biplot. In the present study, two types of biplots namely, “Which-won-where” 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.

Statistical analysis

To attain normality and homogeneity of error variances across environments, data was transformed using $\log(x+0.5)$ transformation technique. To explain the GEI, the multivariate stability analysis was performed graphically based on GGE biplot (Which-won-where view and ranking genotypes view) using metan pack-

age of R studio (Olivoto and Lúcio 2020).

RESULTS AND DISCUSSION

Combined analysis of variance

One of the vital objectives of crop improvement program is identifying superior varieties which are having high yield and stability across diverse locations. Combined analysis of variance (CANOVA) has been performed to describe the main effects and quantify the interactions among and within the sources of variation (Table 2). 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 (Shojaei *et*

Table 2. Combined analysis of variance for 16 genotypes of mango. Sov: Source of variation, Df: Degrees of freedom, Sum sq: Sum of squares, Mean sq: Mean sum of squares, **Significant at $p < 0.01$, NS Non-significant.

Sov	Df	Sum sq	Mean sq	F value
Environment (E)	35	101.46	2.90	69.21**
Replication within E	72	3.02	0.04	1.22NS
Genotype (G)	15	32.49	2.17	63.07**
G × E	525	123.73	0.24	6.86**
Residuals	1080	37.09	0.03	
Total	1727	297.80		

al. 2021). The mean squares of main effects and their interactions showed significant differences ($p < 0.001$) for the yield variable i.e., fruit yield per tree. Genotypes, Environments and GEI were accounted for 10.91%, 34.07% and 41.54% of the total sum square respectively. CANOVA confirmed the presence of significant interaction effects, additional statistical techniques like GGE biplot analysis was more helpful in unfolding and understanding the GEI (Khan *et al.* 2021). Sabaghnia *et al.* (2008) also observed about 40% of GEI contribution in total variation in the lentil genotypes. Similar findings were reported by Reddy *et al.* (2022) stated that 36.49% of variation contributed by the GEI effect for Sterility mosaic disease. Chandra Mohan *et al.* (2021) observed highly significant difference for 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.

GGE biplot analysis

Which won where view of GGE biplot

This kind of biplot was used to visually identify the highest yielding genotypes for each environment. For this purpose, the genotypes located far away from the biplot origin were connected with straight lines so that a polygon or vertex hull was formed with all other genotypes contained within the polygon. Perpendicular lines to the sides of the polygon are drawn, starting from the biplot origin, to divide the biplot into five sectors, each having a vertex genotype. The vertex genotype for each quadrant is the one which gave the highest yield for the environments that fall within

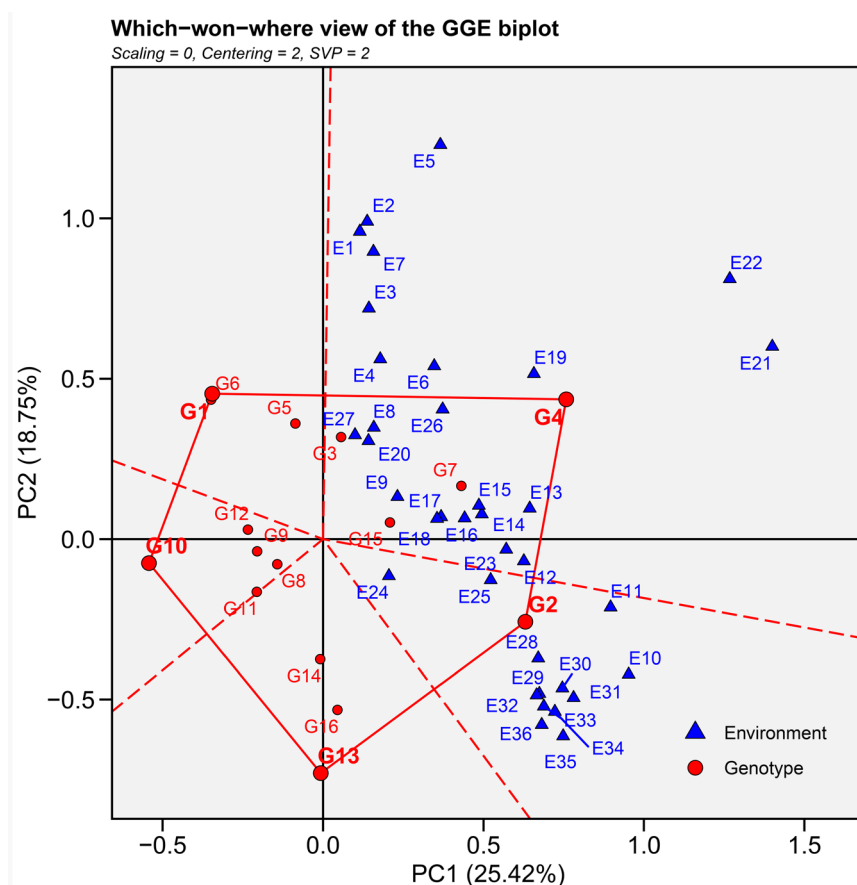


Fig. 1. Which won where view of GGE biplot with mega environments and winner genotypes of mango.

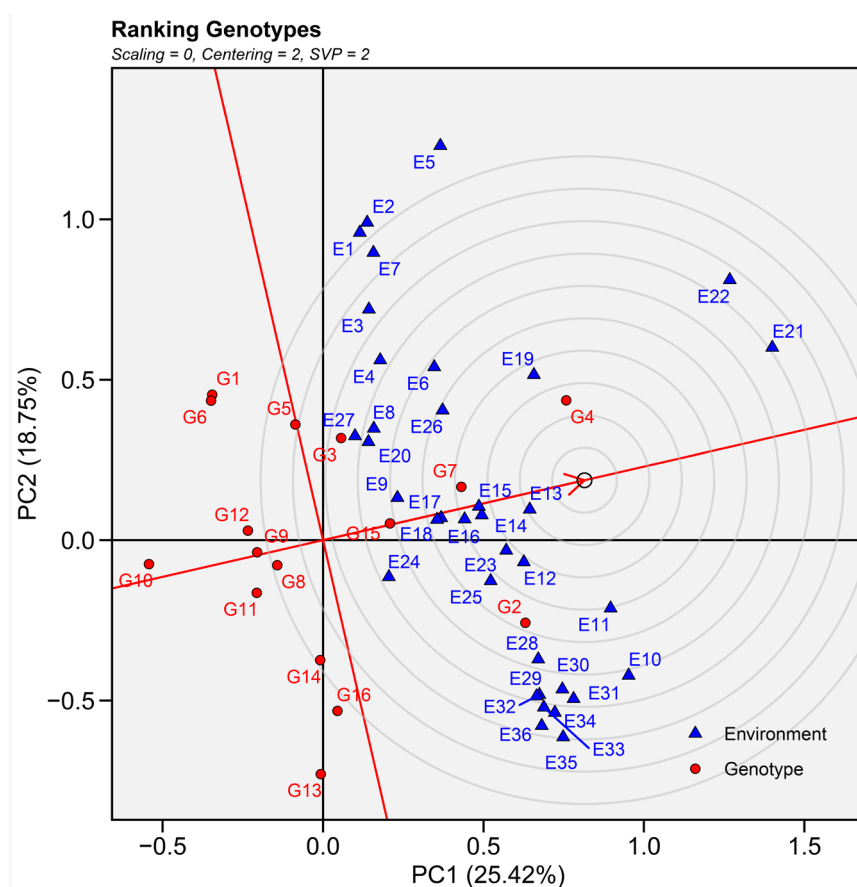


Fig. 2. Ranking genotypes view of GGE biplot for 16 genotypes of mango grown across 36 environments.

the sector. 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). Two mega environments have been identified as environmental indicators positioned in two sections of the biplot, with different genotypes winning in each quadrant (Fig. 1). The test environments E1, E2, E3, E4, E5, E6, E7, E8, E9, E12, E13, E14, E15, E16, E17, E18, E19, E20, E21, E22, E23, E26 and E27 collectively formed as the first mega environment with G4 as winner genotype. While remaining test environments, i.e., E10, E11, E24, E25, E28, E29, E30, E31, E32, E33, E34, E35 and E36 constitute the second mega environment with G2 as the winner

genotype. Most of the environment markers of Rewa, Sabour and Sangareddy were clustered in the same quadrant of the biplot with Totapari as the high yielding genotype and all the environment markers of Vengurla were positioned in one quadrant of biplot with Suvarnakha as high yielding genotype. However, remaining vertex genotypes (G1, G10, G13) were poorly performing genotypes in all test environments and they were considered as unstable genotypes. 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), Chandrashekar *et al.* (2020).

Genotype ranking view of GGE biplot

Ideal genotype is the one with highest mean yield and stability across different environments. Genotypes of mango were ranked based on their position from the ideal genotype. The genotypes situated closer to ideal genotype are said to be the best genotypes and the genotypes located far away from ideal one or outside the concentric circles were considered as undesirable genotypes (Alam *et al.* 2021, Chandrashekar *et al.* 2020, Shojaei *et al.* 2022). From Fig. 2, it is evident that, the genotype G4 followed by G7 were much closer to the ideal genotype, hence these genotypes were considered as the best mango genotypes for all test location under study. Ranking order of genotypes based on the biplot (Fig. 2) was $G4 > G7 > G2 > G15 > G3 > G5 > G8 > G14$. Most of the genotypes were located outside the concentric circles, which explained these genotypes were either below average yielder with high stability or below average yielders with low stability. These findings agreed with the report stated by Chandrashekar *et al.* (2020) who evaluated eight rice hybrids and two check cultivars six different agroclimatic zones of Uttar Pradesh and Bihar and found that H2, H3, H5 as the best rice hybrids for test locations since they situated nearest to ideal genotype while others were located outside the concentric circles. Comparably, Mahmud *et al.* (2021) studied performance four sweet potato varieties across different agroclimatic zones in Bangladesh and found that BARI Mistialu-15 was closest to ideal one in terms of high yielding and stability relative to others. Similar kind of results have been reported by Kendal *et al.* (2019), Lal *et al.* (2019).

CONCLUSION

The present study based on GGE biplot analysis concludes that, Totapari was the best suitable mango genotype for the test locations Rewa, Sabour and Sangareddy, while Suvarnarekha was the best suitable genotype for the location Vengurla. GGE biplot

analysis recommended Totapari as highly stable and high yielding genotype across diverse environments under study. This study also concludes that, GGE biplot analysis was the most valuable and useful tool for identifying the superior genotypes and location specific genotypes in perennial crops.

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