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Analysis of Genotype × Environment Interaction and Identification of Superior Mango (*Mangifera indica* L.) Genotypes using Eberhart and Russell's Stability Model

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ABSTRACT: Mango is one of the most important commercially grown fruit crops in India with greatest collection of varieties. Genotypes does not show same response in all locations due to their interactions with the surrounding environment. Presence of such interactions limits the breeding progress during selection of superior genotypes. Multi location trials are being carried out to study the behaviour of genotypes over different environments. Genotype environment interaction is a major problem in selecting and recommending superior genotypes for the cultivation of crops. This problem gets intensified, when we are dealing with perennial crops like Mango because choosing unstable cultivars to plant in an orchard puts the farmers in a risky income situation for many years. In the present investigation, an attempt has been made to identify the high yielding and stable genotypes of mango by using Eberhart and Russell's stability model. Data on sixteen genotypes of mango tested across four locations viz., Rewa, Sabour, Sangareddy, and Vengurla over a period of nine years is considered for the study. Considering the overall performance, Mallika was found to be the stable genotype for cultivation under unfavourable environmental conditions, while the genotypes Vanraj and Totapari were suitable for cultivation under favourable conditions.

Keywords: Adaptability, Genotype × Environment interaction, Mango, Perennial, Stability.

INTRODUCTION

Mango (Mangifera indica L.) is the most important commercially grown perennial fruit crop in India. Mango belongs to the family Anacardiaceae and it is known as the "King of fruits" because of its versatile uses and taste. Mangoes can be used to prepare pickles, amchur, chutney, jams, jellies, and squashes. Consumption of mangoes helps in boosting immunity, lowering cholesterol, and promoting eye health. India has a huge collection of mango cultivars, and ranks first in the production in the world followed by China, Thailand, Indonesia, Mexico, Pakistan, Brazil, Philippines, Nigeria, and Sudan (FAO, 2020). Mango (including Guava and Mangosteen) is cultivated in a vast area of 2,578 thousand hectares with the production around 24.75 million tonnes, which accounting about 45.13% of total world mango production and 46.68% of world mango cultivated area (FAO, 2020). The increasing population leads to the rise in demand for agricultural produce, and it is expected to enhance agricultural production per unit area. To encounter this requirement various crop improvement programs

have been initiated all over the world. In any crop improvement program, the performance of promising genotypes had been tested over different locations in each year, with an intention to identify the genotypes with not only high yield, but also wider adaptability over different environmental conditions. In Multi location trials (MLTs), most frequently it is noticed that the genotypes respond differently to the diverse environmental conditions, this differential response of genotypes is known as Genotype environment interaction (GEI) (Pham and Kang, 1988). Yet, there is no single method developed so far that equally satisfies plant breeders for the study of GEI. However, there are various 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).

Among various phenotypic stability models, Eberhart and Russell's (1966) stability model is being used predominantly for evaluating GEI and identifying superior genotypes. Shahryarinasab and Chogan (2015) employed different univariate stability models including Eberhart and Russell's stability model (ER

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model) to identify stable and high yielding genotypes of maize and identified KSC705 as the stable genotype. Sowmya et al. (2018) identified superior genotypes of Maize for cultivation in three locations of Karnataka (Dharwad, Sankeshwar and Nippani) using ER model. Manivannan et al. (2019) followed ER model to evaluate and determine the stable genotypes of Cow pea, for consistent seed yield across environments. Raj et al. (2019) applied ER model to identify best hybrids off maize for various environmental conditions and identified the hybrid AU-101 as a stable hybrid for less favorable environmental conditions. Munda et al. (2020); Farag et al. (2019) applied ER model to determine the superior genotypes of Java Citronella and bread wheat, respectively. Milioli et al. (2018); Jain et al. (2019). Two research groups evaluated genotypes of Soybean and Ricefor their stability using ER model along with various multivariate approaches (Milioli et al., 2019; Jain et al., 2019). Naheed and Rahman (2021) assessed the performance and stability of 40 bread wheat lines across six environments in Pakistan using ER model. Likewise, Singh et al. (2021) applied ER model for determining the stability of forty mungbean genotypes across different mungbean growing regions of Uttar Pradesh.

Although, the usefulness of stability models in determining superior genotypes is huge in annual crops, their application 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

This study was based on secondary data of mango fruit crop with common 16 genotypes grown in four locations over a period of 9 years, which have been collected from MLTs of All India Co-ordinated Research Project on Sub-Tropical Fruits (AICRP-STF), Central Institute for Subtropical Horticulture (CISH), Lucknow, India. For the study, we considered one quantitative trait such as the number of fruits per tree. Mango genotypes were tested over four locations namely, Rewa (Madhya Pradesh), Vengurla (Maharashtra), Sangareddy (Telangana), and Sabour (Bihar) over different years in India. Multi-location trials (MLT) were conducted in a Randomized complete block design with 3 replications at each location. These four locations contain common data for 16 genotypes of mango tested over a period of 9 years (i.e., 1997-2005) with 3 replications and the same data were considered for the study. For the present investigation, the yield variable *i.e.*, the number of fruits per tree has been considered for evaluation of MLT data of mango. A combination of years and locations were considered as environments. As mango genotypes were grown in 4 locations over a period of 9 years, it gives thirty-six environments.

In the present study, Eberhart and Russell's stability model was utilised to evaluate genotypic performance across thirty-six environments. A genotype which possesses high mean (μ) , unit regression coefficient (i = 1) with the deviation from regression line approaching zero ($S^2D_i = 0$) or nonsignificant is considered to be stable *i.e.*, possessing average stability, whereas a variety with regression coefficient lower than one has above average stability and is specially adapted to unfavourable (poor) environments. They hardly express response to improved environmental conditions. A variety with regression coefficient greater than one $(_{i}>1)$ has below average stability and is suitable for favourable/rich environments (Eberhart and Russell, 1966; Teja et al. 2021). All the statistical analyses were carried out using Indostat Software.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) for Eberhart and Russell's stability model revealed, highly significant genotypic variance which conveys at least a pair of genotypes are performing differently. Besides highly significant environmental variance confirms the presence of differences in the environmental conditions from location to location and year to year. Genotype environment interaction (GEI) was highly significant, which enable differential performance of different genotypes across environments. Environment (E)+ GEI variance was highly significant against pooled error, which expresses the diverse nature of environments and genotype \times environment interactions. E + GEI variations were partitioned into three parts environments (linear), GEI (linear) and pooled deviations of genotypes; highly significant pooled deviations of genotypes indicates that major portion of GEI was unpredictable. Similar results have been reported by Shahryarinasab and Chogan (2015); Balat et al. (2021) in maize and bottle gourd genotypes respectively.

Stability or consistency in the performance of genotype is one of the most important characters for wider adaptability. The stability parameters viz., overall genotypic mean performance (μ) , regression coefficient $(_{i})$ and deviation from regression (S^2D_i) were estimated as per Eberhart and Russell (1966) for comparative stability assessment of mango genotypes over 36 environments. The genotype Suvarnarekha (2) and Totapari (4) exhibited highest mean yield across different environments, while the genotype Chousa (6) exhibited lowest mean yield among all the genotypes of mango under this study. Genotypes having the regression coefficient of unity or close to unity and lesser deviations from regression are known as stable genotypes (Akcura et al., 2005). From the study, it was clear that the genotypes Fazli (5), Mallika (7) and Alphanso (13) are known as

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specially adopted genotypes for less favourable environments, since they possess values of $_i$ less than 1 (Table 2). However, the genotypes Vanraj (16) and Totapari (4) has the regression coefficient greater than 1, indicating that they are specially adopted to high performance environments with above average yield (Table 2, Fig. 1). Similar genotypic performance had been observed by Sowmya *et al.* (2018); Raj *et al.* (2019); Milioli *et al.* (2018); Jain *et al.* (2019); Teja *et al.* (2021). Behaviour of remaining mango genotypes in the present study were unpredictable because of their significant regression coefficient ($_i$) and highly significant squared deviation (S²D_i). From the biplot (Fig. 1) it is clear that, the genotype Neelum (3) had lower stability across the environments.

Source of variation	df	Sum Sq.	MSS	F value
Replication within Environment.	72	283452.22	3936.84	0.26 ^{NS}
Genotype	15	1589518.96	105967.93	6.85**
Environment + (Genotype × Environment)	560 27225794.88		48617.49	3.15**
Environments	35	16613648.26	474675.66	30.70**
Genotype × Environment	525	10612146.61	20213.61	1.31**
Environments (Linear)	1	16613648.26	16613648.26	1074.63**
Genotype × Environment (Linear)	15	2201968.33	146797.89	9.50**
Pooled deviation	544	8410178.28 15459.89		5.63**
Pooled error	1080	2965389.78	2745.73	
Total		28815313.84	50113.59	

Table 1: Analysis of variance for Eberhart and Russell's stability model.

df: Degrees of freedom; Sum Sq.: Sum of squares; MSS: Mean sum of squares; **Significant at 1% LOS; *Significant at 5% LOS; NS: Non-significant.

Table 2: Estimates of Eberhart & Russell's Sta	ibility parameters and ranking of genotype
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Genotype		Mean		S ² D _i		i	
Name	Code	Yield	Rank	Estimate	Rank	Estimate	Rank
Banganpalli	1	210.19	9	10365.73**	11	1.73**	16
Suvarnarekha	2	328.79	1	15812.32**	13	1.58**	15
Neelum	3	280.53	4	44849.53**	16	0.57	14
Totapari	4	311.90	2	18703.56**	14	1.22	5
Fazli	5	183.36	13	3762.13**	1	0.87	2
Chousa	6	166.01	16	6060.73**	3	0.72**	7
Mallika	7	223.37	8	10351.19**	10	0.86	3
Zardalu	8	297.93	3	11306.97**	12	1.40**	11
Bombay	9	187.13	12	9309.93**	7	0.58**	13
Bombay Green	10	172.74	14	5104.28**	2	0.75**	6
Himsagar	11	224.19	7	22680.18**	15	0.59*	12
KishanBogh	12	169.19	15	7001.88**	4	0.67**	10
Alphanso	13	194.30	11	7590.52**	5	0.83	4
Kesar	14	258.89	6	10206.95**	9	1.29*	8
Mankurad	15	274.42	5	10048.45**	8	1.32**	9
Vanrai	16	200.26	10	9081.02**	6	1.05	1

**significant at 1% LOS; *significant at 5% LOS; ;: regression coefficient; S²D; deviations from regression



Fig. 1. Biplot showing Stability and Performance of genotypes based on i and S²D_i.

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CONCLUSION

Considering the overall performance, Mallika was found to be the stable genotype for cultivation under unfavourable environmental conditions, while the genotypes Vanraj and Totapari were suitable for cultivation under favourable conditions. None of the genotypes were stable across all test environments, hence the emphasis should be laid on the need for environment specific genotypes.

FUTURE SCOPE

Further studies are required to compute the efficiency of ER model. Alternative methods of ER model should be explored for the analysis of unbalanced multilocation trial data. This kind of stability analysis can also be attempted for other perennial fruit crops like Guava, Amla etc.

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