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### Genotype × environment interaction and stability analysis for fruit yield and its components over environments in eggplant (*Solanum melongena* L.)

## Raval Kalpesh, Akshay I Patel, Rajesh Panchal, Chirag Solanki, Hardik Patel and Harsiddhi B Limbani

#### Abstract

The present investigation was designed in order to estimate the G×E interaction and stability parameters for fruit yield and its components over environments in eggplant. The experimental material comprised of 8 parents, their resultant 28 hybrids produced following half diallel mating design and a standard hybrid check "GJBH-4" of eggplant, which were evaluated in randomized block design with three replications. The experiment was conducted at three different locations of Navsari Agricultural University, Navsari during *rabi* 2020-21. Stability analysis results indicated that both linear and nonlinear component played an important function in building up G × E interaction in our experiment. The stability ANOVA deciphered that genotypes (parents, hybrids and check) mean squares had displayed highly significant trend for all of the characters while G × E was highly significant only for branches per plant when tested against pooled error. The environmental index study revealed that Waghai (L3) has the most auspicious location and had well-nourished majority of the characters. The stability parameters analysis for branches per plant character confirmed that BPG-3 displayed above average response and specifically adapted to unfavorable locations in comparison to all the other parents. GJBH-4 (check) displayed average response along with high stability under all locations for branches per plant.

Keywords: Brinjal, eggplant, environmental index,  $G \times E$  interaction and stability

#### Introduction

First and foremost, objective of eggplant is to develop high-yielding varieties, mostly  $F_1$  hybrids but it is also to be kept in mind that the hybrids produced should be having a high degree of adaptation and stability in their yield and its related characters. Thus, study the performance of a crop in more than one environment to identify genotypes, which give high stability for various yield related traits over a wide range of environment (Jindal *et al.*, 2008) <sup>[10]</sup>.

The phenomenon of genotype  $\times$  environment interaction is a common problem in plant breeding programme and has long been a challenge to plant breeder. A variety developed by a plant breeder is usually grown at different locations for many years under different conditions. Assessing any genotype without including its interaction is incomplete and thus limits the accuracy of yield estimates. It is usually preferable to estimate yield stability and reliability values with reference to all genotype  $\times$  environment interaction effects (Ezekiel *et al.*, 2011) <sup>[16]</sup>. Therefore, breeding efforts are directed towards stepping up the yield levels through the development of high yielding varieties and hybrids for different environment. Hence, there is a need for development of different environment (location) specific hybrids in addition to identification of stable hybrids over environments.

Multi-location testing of genotypes provides an opportunity to plant breeders to identify the adaptability of genotype to a particular location and so stability of genotype over different locations. There are number of statistical methods for consideration of genotype  $\times$  environment interaction and its relation with stability. From all these methods, regression of mean of each genotype on environmental index is one of the most applicable methods (Tesemma *et al.*, 1998) <sup>[17]</sup>. This method has been suggested by Finley and Wilkinson (1963) modified by Eberhart and Russel (1966) <sup>[9]</sup>. In the present investigation, this approach was used to understand the G  $\times$  E interaction of different genotypes, and to access stability of individual genotype. For determining adaptability and stability of genotypes in this method, parameters like mean genotype yield, regression coefficient (bi) and variance of deviation

from regression (S<sup>2</sup>di) are used. In this model various amounts of bi *i.e.*, bi=1, bi<1 and bi>1 are expressing average, high and low stability, respectively (Eberhart and Russel, 1966) <sup>[9]</sup>. According to this model, a genotype is encountered as the most stable that its regression coefficient is equal to unit, variance of deviation from regression is the least (non-significant with zero) and its average yield is highest (Sreedhar *et al.*, 2011) <sup>[18]</sup>.

#### **Materials and Methods**

The present investigation was designed in order to estimate the G×E interaction and stability parameters for fruit yield and its components over environments in eggplant. The experimental material comprised of 8 parents, their resultant 28 hybrids produced following half diallel mating design and a standard hybrid check "GJBH-4" of eggplant, which were evaluated in randomized block design with three replications. The experiment was conducted at three different locations viz., College Farm, N. M. College of Agriculture, Navsari (L1), Wheat Research Station, Bardoli (L2) and Hill Millet Research Station, Waghai (L3), Navsari Agricultural University, Navsari during rabi 2020-21. The observations were taken using five competitive plants from each entry in each replication which were randomly selected and tagged for the purpose of recording observations on different characters expect for days to 50% flowering, which was recorded on plot basis. Their average values were used in the statistical analysis in WINDOSTAT 9.1 software.

#### A) Analysis of variance for G × E interactions

The statistical analysis for  $G \times E$  interactions and stability parameters were carried out according to the method of Eberhart and Russell (1966)<sup>[9]</sup>. According to them, the mean performance of i<sup>th</sup> genotype in j<sup>th</sup> location, Y<sub>ij</sub> is defined as:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

The model provides means of partitioning the genotypelocation interactions into two parts.

- 1. The variation due to response of i<sup>th</sup> genotype to varying locational indices *i.e.*, sum of square due to regression
- 2. The deviation from regression

#### **B**) Estimation of stability parameters

According to Eberhart and Russell (1966) <sup>[9]</sup>, the ideal genotype is one which has high mean ( $\overline{X}_i$ ), unit regression coefficient ( $b_i = 1$ ) and the least deviation from regression ( $S_{d_i}^2 = 0$ ).

Stability parameters were calculated by following formula:

#### Mean $(\overline{X}_i)$

The mean value of i<sup>th</sup> genotype over all the locations,

$$\overline{X}_i = \frac{\Sigma Y_{ij}}{e}$$

#### **Regression co-efficient** (b<sub>i</sub>)

The regression coefficient  $(b_i)$  is the regression of the performance of each genotype under different locations on the locational means over all the genotypes.

$$b_i = \frac{\Sigma Y_{ij} I_j}{\Sigma I_j^2}$$

Where

I\_j=Environmental index

The environmental index was calculated by following formula:

$$I_{j} = \left[ \left( \frac{\Sigma Y_{ij}}{g} \right) - \left( \frac{\Sigma \Sigma Y_{ij}}{ge} \right) \right], \Sigma I_{j} = 0$$

The significance of the deviation of each regression coefficient from zero and unity was tested by 't' test by following formula:

$$t_{(n-2)} = \frac{b_i - 0}{S. E_{\cdot b_i}}$$
 and  $t_{(n-2)} = \frac{1 - b_i}{S. E_{\cdot b_i}}$ 

Where

S. E.<sub>bi</sub> = 
$$\sqrt{\frac{\Sigma \delta_{ij}^2 / (e - 2)}{\Sigma I_j^2}}$$

#### Deviation from regression $(S_{d_i}^2)$

Non-linear component of stability can be calculated by following formula:

$$S_{d_i}^2 = \left[\frac{\sum_j \delta_{ij}^2}{(e-2)}\right] - \frac{\sigma_e^2}{r}$$

Where

$$\sum_{j} \delta_{ij}^{2} = \left[\sum_{j} Y_{ij}^{2} - \frac{Y_{i}^{2}}{e}\right] - \frac{\left(\sum_{j} Y_{ij}I_{j}\right)^{2}}{\sum_{j} I_{j}^{2}}$$

 $\sigma_e^2$  = Estimate of the pooled error

The significance of the deviation from regression for each genotype was tested by 'F' test using following formula:

$$F = \frac{\left(\frac{\sum_{j} \delta_{ij}^{2}}{e - 2}\right)}{\text{Pooled error mean square}}$$

The calculated 'F' values of each genotype were compared with table values of 'F' at (e-2) and pooled error degrees of freedom.

S. E. (mean) = 
$$\sqrt{\frac{\text{M. S. due to pooled deviation}}{(e-1)}}$$

#### **Results and Discussion**

#### 1) Analysis of variance for phenotypic stability

The ANOVA for phenotypic stability is a technique that separate various environmental and genetic components of stability and provide relative measures of stability. The analysis of variance for Genotype  $\times$  Environment interaction

and stability parameters were estimated and are presented in Table 1 for different characters.

In our study, genotypes (parents, hybrids and check) mean squares had displayed highly significant trend for all of the characters when tested against pooled error and pooled deviation, assuring that there is ample amount of variability present among the genotypes. Significant values of genotypes for one or more characters were also obtained by Chaudhari et al. (2015)<sup>[7]</sup> for fruit diameter; Vasu and Mulge (2015)<sup>[15]</sup> for fruit yield per plant and number of fruits per plant; Bhushan and Samnotra (2017b)<sup>[4]</sup> for total phenol content and ascorbic acid; Akhtar et al. (2019)<sup>[1]</sup> for plant height, days to 50% flowering, fruit length, fruit weight, number of fruits per plant, fruit yield per plant; Chaitanya and Reddy (2021)<sup>[6]</sup> for plant height, branches per plant, days to 50% flowering, fruit length, fruit weight, number of fruits per plant, fruit vield per plant and Dhaka and Kaushik (2022)<sup>[8]</sup> for fruit length, number of fruits per plant, fruit weight and fruit yield per plant. This implies significant genetic difference among the all genotypes and there was a potent scope to select promising stable genotypes (Akhtar et al., 2019)<sup>[1]</sup>.

In the same analysis, environments mean squares for plant height was significant and branches per plant, days to 50 % flowering, flowers per plant and total phenol content had also marked higher extent of significance with both pooled error and pooled deviation. Analogy for the result was also demonstrated by Vaddoria et al. (2009)<sup>[14]</sup> for days to 50 % flowering, plant height, number of primary branches per plant; Akhtar et al. (2019)<sup>[1]</sup> for days to 50 % flowering, plant height, number of primary branches per plant and Bhushan and Samnotra (2017b)<sup>[4]</sup> for total phenol content. It indicates there was considerable difference amongst the locations for the above characters and that these characters were influenced greatly by that environments thereby suggesting that large difference amid locations along with greater part of genetic response was linear function of environments *i.e.*, the environment created by sowing at different locations (Vaddoria et al., 2009)<sup>[14]</sup>. This justified the necessity of carrying out this investigation since location exerted influence on the performance of the genotypes (Akhtar et al., 2019)<sup>[1]</sup>.

Highly significant mean sum of squares due to  $E + (G \times E)$ was observed for branches per plant, days to 50 % flowering while the fruit yield per plant was simply significant, when verified against pooled error and pooled deviations and which was also in favour with the results of Vaddoria et al. (2009) <sup>[14]</sup> for all these three characters; for fruit yield per plant -Vasu and Mulge (2015)<sup>[15]</sup>, Akhtar et al. (2019)<sup>[1]</sup> and Dhaka and Kaushik (2022)<sup>[8]</sup>; for days to 50 % flowering - Akhtar et al. (2019)<sup>[1]</sup>, Chaitanya and Reddy (2021)<sup>[6]</sup>, respectively. It depicts variable genotypic response to environmental fluctuation over locations and independent nature of genetic system governing the stability parameters (Dhaka and Kaushik, 2022)<sup>[8]</sup>. This satisfied the requirements of stability analysis, against pooled error; therefore, it was further partitioned into three components i) Environment (Linear) ii)  $G \times E$  (Linear) and iii) Pooled deviation ( $G \times E$ ; Non-linear). Environment (linear) component was also found highly significant for the traits like plant height, branches per plant, days to 50 % flowering, flowers per plant, total phenol content while, significant for fruit yield per plant and ascorbic acid as soon as examined against pooled error and pooled deviation, depicting considerable difference among the locations with their predominant effect on this characters and

also pointing out to additivity of the environmental effects for these characters (Akhtar *et al.*, 2019)<sup>[1]</sup>. Similar results were earlier reported by Vaddoria *et al.* (2009)<sup>[14]</sup>, Chaudhari *et al.* (2015)<sup>[7]</sup>, Vasu and Mulge (2015)<sup>[15]</sup>, Bhushan and Samnotra (2017a)<sup>[3]</sup>, Akhtar *et al.* (2019)<sup>[1]</sup>, Chaitanya and Reddy (2021)<sup>[6]</sup> and Dhaka and Kaushik (2022)<sup>[8]</sup> with significance at pooled error for one or more characters. Higher Magnitude of environment (linear) effect as compared to genotype × environment (linear) interaction depicted that major part of the total variation was linear function of locations which might be responsible for high adaptation in relation to yield and its attributes in eggplant genotypes (Dhaka and Kaushik 2022)<sup>[8]</sup>.

 $G \times E$  (linear) was highly significant for branches per plant and fruit yield per plant while significant for days to 50 % flowering at both pooled error and pooled deviation. proposing that genotypes had divergent linear response to locational alteration and the difference among the regression co-efficients of the genotypes on the environmental indices was real (Dhaka and Kaushik, 2022)<sup>[8]</sup>. Therefore, prediction of performance over locations was possible for these characters on the basis of regression analysis. Interestingly fruits per plant, found to be significant only at pooled deviation for  $G \times E$  (linear). The results were in resemblance with Vaddoria et al. (2009) [14] for days to 50 % flowering, fruit yield per plant; Bhushan and Samnotra (2017a)<sup>[3]</sup> for fruit yield per plant; Akhtar et al. (2019)<sup>[1]</sup> for days to 50 % flowering, fruits per plant, fruit yield per plant and Chaitanya and Reddy (2021)<sup>[6]</sup> for number of branches per plant, total yield per plant, fruits per plant.

Pooled deviation had revealed an extra ordinary result by staying non-significant for all the characters under study, indicating that deviation for linear regression had not contributed substantially towards the differences in stability of genotypes. The results are in partial accordance with Vasu and Mulge (2015) <sup>[15]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> and Dhaka and Kaushik (2022) <sup>[8]</sup>. It implies that in character like branches per plant {which marked highly significant for G × E and non-significant for pooled deviation} confirms an ideal condition of predictability and hence the variation in the performance of genotypes is entirely predictable in nature and there is chance to isolate the best genotype.

 $G \times E$  is one of the most important parameters of this ANOVA as it depicts the reality of interaction between genotypes and locations which leads to resultant phenotype (Dhaka and Kaushik, 2022)<sup>[8]</sup>. Here, the outcomes of  $G \times E$ was highly significant only for branches per plant against pooled error and pooled deviation both, suggesting that there is significant difference among the genotypes as there is high influence of location in defining the phenotype of the character and hence its necessary to examine different stability parameters like bi and S<sup>2</sup>di, so that the best stable genotype could be isolated (Chaitanya and Reddy, 2021)<sup>[6]</sup>. This significant result at pooled error for branches per plant was also observed earlier by Vaddoria et al. (2009) [14], Chaudhari et al. (2015)<sup>[7]</sup> and Chaitanya and Reddy (2021)<sup>[6]</sup>. In consideration to all above outcomes, the stability parameters were worked out and interpreted only for branches per plant. The stability parameters employed for identification of stable genotypes were high or low mean values than population mean as the character has economic importance, a regression coefficient (bi) equals to unity and its significant deviation from unity and a mean square deviation from linear regression coefficient statistically equal to zero (S<sup>2</sup>di).

#### 2. Environmental Index (Ij)

The effect of environment in a stability analysis study is quantified through environmental index (Bhusan and Samnotra, 2017a)<sup>[3]</sup>. The estimates of environmental indices for different characters are presented in Table 2.

The environmental index was observed to be most congenial for plant height, branches per plant, days to 50% flowering, flowers per plant, fruits per plant, fruit length, fruit weight, fruit yield per plant, total phenol content and ascorbic acid content at Waghai (L3). While, Navsari (L1) was also found to be favorable for branches per plant, flowers per plant and fruit weight and interestingly reacted as most suitable location for fruit diameter, alone. The location of Bardoli (L2) was also somewhat in favour of characters like plant height, total phenol content and a magical thing was that, this location stood as the highly apposite location for the total soluble sugars, alone.

Estimates of environmental index given in the Table 4.29, suggested a trend that Waghai (L3) has the most auspicious location and had well-nourished majority of the characters followed by Navsari (L1) while, Bardoli (L2) has reacted as most unfavorable location for the expression of one or more characters. High and desirable *per se* performance of the genotype over different environments was also an important consideration for ranking it as better and stable genotype (Akhtar *et al.*, 2019)<sup>[1]</sup>.

The environmental index study is of much importance to know the real trend in which the particular character is favored in at certain location/environment, that can help us for better evaluation of the character, as well as accuracy in the study of data could be ascertained. Waghai (L3) location had been preferred by majority of the characters for their better development and phenotypic expression which ultimately leads to higher fruit yield in eggplant, which is the vital need of breeder for a good breeding programme. Environmental index study to interpret favorable environment for different characters in eggplant was also done by Vaddoria *et al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Bhusan and Samnotra (2017a) <sup>[3]</sup>, Akhtar *et al.* (2019) <sup>[1]</sup> and Dhaka and Kaushik (2022) <sup>[8]</sup>.

#### **3. Stability parameters**

The stability performance is one of the most desirable properties of a genotype for its wide adaptation. Hence, three stability parameters *i.e.*, mean performance, regression coefficient (bi) and deviation from regression (S<sup>2</sup>di) for parents and their hybrids were estimated and computed as per Eberhart and Russel (1966)<sup>[9]</sup> to appraise relative stability over different locations. The estimates of stability parameters for branches per plant in eggplant was computed to evaluate relative stability of hybrids as per Eberhart and Russell (1966) <sup>[9]</sup>. In present study, linear regression is considered as measure of responsiveness and deviation from regression as measure of stability of particular genotype. As per Eberhart and Russell (1966)<sup>[9]</sup>, a genotype is believed to be stable for the trait and adaptable to varied environmental conditions in its performance if it exhibits high mean performance, regression co-efficient is around unity (bi=1) and non-significant deviation from linear regression (S<sup>2</sup>di=0). However, genotypes with a higher mean value and value of regression coefficient more than unity with non-significant deviation

from linear regression were considered to be responsive and suitable for favourable environmental conditions. Further, the genotypes with higher mean values and regression coefficient less than unity or negative and non-significant deviations from linear regression were considered to be responsive and suitable for poor locational conditions. Accordingly, the genotypes were classified as suitable for varied locational conditions.

#### 3.1 Branches per plant

The result of ANOVA for phenotypic stability showed that G  $\times$  E interaction was significant only for branches per plant explaining the genotypes unstable response towards the different location/environment for this character. Hence, it become necessary to the stability parameter in order to identify stable genotypes for branches per plant (Chaitanya and Reddy, 2021)<sup>[6]</sup>. So, the stability parameter values (mean, bi and S<sup>2</sup>di) for branches per plant are provided in Table 3 and the results are explained here under:

Deviation from regression for branches per plant was nonsignificant for the all eight parents and twenty-seven hybrids, indicating that prediction of performance would be possible for these parents and hybrids.

Out of eight parents only two parents *viz.*, GNRB-1 (bi = -0.613) and BPG-3 (bi = -0.935) were significantly deviating from bi = 0 but, only BPG-3 (5.689) displayed mean value higher than the parental mean (5.529) value for branches per plant and had regression coefficient less than one (bi < 1) and non-significant S<sup>2</sup>di, indicating that BPG-3 displayed above average response in performance with high stability under unfavorable locations in comparison to all the other parents.

Out of twenty-seven hybrids (having non-significant S<sup>2</sup>di), sixteen hybrids were significantly deviating from bi = 0. Out of these sixteen hybrids, only six hybrids *viz.*,  $GJB-3 \times GJB-2$ (5.778), AB  $8/5 \times$  Swarna Mani (6.044), GJB-3  $\times$  Swarna Mani (5.978), GNRB-1 × IC 110662 (5.756), GJB-3 × IC 110662 (6.133) and GJB-2  $\times$  Swarna Mani (5.822) had higher mean values for branches per plant as compared to hybrid mean (5.529). In these hybrids,  $GJB-3 \times GJB-2$  (bi = -3.040), AB  $8/5 \times$  Swarna Mani (bi = -1.895), GJB-3 × Swarna Mani (bi = -0.480) had exhibited regression coefficient less than unity (bi < 1) with higher mean than hybrid mean and nonsignificant S<sup>2</sup>di indicating their above average response along with high stability under unfavorable locations. Whereas, GNRB-1 × IC 110662 (bi = 1.200), GJB-3 × IC 110662 (bi = 5.016) and GJB-2  $\times$  Swarna Mani (bi = 8.082) unveiled regression coefficient greater than unity (bi > 1), higher mean than population mean and non-significant S<sup>2</sup>di indicating their below average response along with high stability under favorable locations.

The only genotype *viz.*, GJBH-4 (bi = 0.587) with higher mean than population mean and non-significant  $S^2$ di with significant deviation from bi = 0 but not from bi = 1 *i.e.*, regression coefficient equals to unity (bi = 1) indicating its average response along with high stability under all locations. Vaddoria *et al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> had also explained similar result as above for branches per plant in eggplant.

 $G \times E$  interaction is a category coming from quantitative genetics and it is used in plant breeding. It reflects genotype adaptability and stability. Variation of the genotype in different environments is manifested as a change in phenotype. Changes in the phenotypic values result from the

reaction of the genotype to the prevailing environmental conditions (Chaitanya and Reddy, 2021)<sup>[6]</sup>.

In the present study, the pooled analysis of variance for genotype × environment interaction uncovered that there is significant difference among the genotypes, environments and  $G \times E$  interaction for one or more characters indicating the inconsistent performance of genotypes across the environments, but none of these parameters were significant for all the characters except genotypes. The results are analogous with Vaddoria *et al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Akhtar *et al.* (2019) <sup>[1]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup>

The result of ANOVA for phenotypic stability also projected that  $G \times E$  interaction was significant only for branches per plant explaining the genotypes unstable response towards the different location for this character. The major portion of  $G \times$ E interaction was attributed by the linear component (predictable) for this character as compared to non-linear (unpredictable) component, because of lower magnitude of pooled deviation as compared to  $G \times E$  (linear) for this character. Thus, this result indicates that the linear functions play an important role in building up  $G \times E$  interaction here. The result showing significant  $G \times E$  interaction along with higher magnitude of linear component as compared to nonlinear component for branches per plant was also observed by Vaddoria *et al.* (2009) <sup>[14]</sup>. The lack of significant  $G \times E$ interaction for rest of the characters under study indicated that genotypes responded consistently over the locations for that characters and location had not influenced that characters significantly, that's why these characters were not considered for stability parameter analysis (Chaudhari et al., 2015)<sup>[7]</sup>. The non-significant  $G \times E$  variance for various characters was also indicated in the results of Vaddoria et al. (2009) [14], Chaudhari et al. (2015)<sup>[7]</sup>, Bhusan and Samnotra (2017b)<sup>[4]</sup> and Chaitanya and Reddy (2021)<sup>[6]</sup>.

The magnitude of environment (linear) over  $G \times E$  (linear) for all characters were high (except fruits per plant, fruit weight and fruit diameter) which might be the reason for higher adaptation in relation to yield and other characters (Chaitanya and Reddy, 2021) <sup>[6]</sup>. The higher magnitude of location (linear) over  $G \times E$  (linear) for different characters was also observed by Vaddoria *et al.* (2009) <sup>[14]</sup>, Mehta *et al.* (2011), Bhusan and Samnotra (2017a)<sup>[3]</sup>, Akhtar *et al.* (2019)<sup>[1]</sup>, Chaitanya and Reddy (2021)<sup>[6]</sup> and Dhaka and Kaushik (2022)<sup>[8]</sup>.

The major portion of  $G \times E$  interaction was attributable to linear component (predictable) for branches per plant, days to 50% flowering, fruits per plant, fruit length, fruit weight, fruit diameter and fruit yield per plant while, major portion of  $G \times E$  interaction was attributable to non-linear component (unpredictable) for the plant height, total phenol content, total soluble sugars and ascorbic acid. This indicates that both linear and non-linear component function play an important function in building up  $G \times E$  interaction in our experiment. The findings are in agreement with Vaddoria *et al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Akhtar *et al.* (2019) <sup>[1]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> and Dhaka and Kaushik (2022) <sup>[8]</sup>.

The mean squares of  $G \times E$  remained non-significant for majority of the yield attributing traits (except branches per plant), suggesting that non-significance of  $G \times E$  mean squares for these component traits (specially for fruits per plant and fruit weight) might be the reason for nonsignificance of  $G \times E$  interaction for fruit yield per plant. This result was in *vice-versa* relation with the results of Vaddoria *et al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Bhusan and Samnotra (2017a) <sup>[3]</sup>, Akhtar *et al.* (2019) <sup>[11]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> and Dhaka and Kaushik (2022) <sup>[8]</sup>.

According to Eberhert and Russell (1966)<sup>[9]</sup>, identification of stable genotypes suited to different environmental conditions is the ultimate aim of the estimation of the stability parameters of individual genotype. So, according to the model of Eberhert and Russell (1966)<sup>[9]</sup>, a variety is said to be stable over different environments, if it shows unit regression coefficient (bi = 1.0) with lowest deviation (non-significant) from the linear regression ( $S^2di = 0$ ). With these conditions, high and desirable per se performance of variety over environments is also a positive point to rate the variety/hybrid as a better and stable genotype. Later on, Breese (1969)<sup>[5]</sup>, Samuel et al. (1970) <sup>[13]</sup> and Paroda and Hayes (1971) <sup>[12]</sup> suggested that linear regression (bi) should be regarded as measure of response of a particular genotype, whereas, the deviation from regression (S<sup>2</sup>di) as measure of stability and suggested the methodology to classify the different genotypes into four different groups as below:

Group	Mean	bi	S <sup>2</sup> di	Behavior
Ι	High	Around unity	Around zero	Average response, high stability
	High	Significantly deviating from unity	-	-
Π		i) bi > 1	Around zero	Below average response, specifically adapted to favorable environments
		ii) bi < 1	Around zero	Above average response, specifically adapted to unfavorable (poor) environments
III	High	Significantly deviating from unity	Significantly deviating from zero	Unpredictable / unstable
IV	High	Around unity	Significantly deviating from zero	Unpredictable / unstable

Result of stability parameters of 37 genotypes (parents + hybrids + standard check) publicized that none of the genotype was stable for all the traits studied. Similar results were reported by Vaddoria *et al.* (2009) <sup>[14]</sup>, Mehta *et al.* (2011), Chaudhari *et al.* (2015) <sup>[7]</sup>, Bhusan and Samotra (2017a) <sup>[3]</sup>, Akhtar *et al.* (2019) <sup>[1]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> and Dhaka and Kaushik (2022) <sup>[8]</sup>. Thus, any generalization regarding stability of genotypes for all the traits is too difficult since the genotype may not simultaneously exhibit uniform responsiveness and stability patterns for all the traits. Therefore, it should be kept in mind that in order to

produce stable hybrids, actual testing of hybrids over wide range of environment is necessary, while decision for actual use of parents should be based on their combining ability.

Stability performance is one of the most desirable properties of a genotype for its wide adaptation (Chaudhari *et al.*, 2015)<sup>[7]</sup>. For branches per plant based on the stability parameter data, revealed that only one parent *i.e.*, BPG-3 was found to fit under the above stability criteria indicating its above average response in performance with high stability under unfavorable locations.

In consideration to hybrids, six hybrids found to be suited

under that given criteria. The hybrids GJB-3 × GJB-2, AB 8/5 × Swarna Mani, GJB-3 × Swarna Mani had exhibited above average response along with high stability under unfavorable locations. Whereas, GNRB-1 × IC 110662, GJB-3 × IC 110662 and GJB-2 × Swarna Mani came up with below average response along with high stability under favorable locations. These results are comparable with Vaddoria *et al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> for branches per plant in eggplant.

The  $F_1$  hybrids of eggplant are heterozygous and heterogeneous in nature. Such populations depend heavily on physiological homeostasis to stabilize yield and its components over a wide range of changing environments due to higher degree of individual buffering ability (Allard and Bradshaw, 1964)<sup>[2]</sup>.

The chance for selection of stable genotypes could be strengthened by selection in favour of stability in some yield component. The mean yield of each genotype depends on the particular set of environmental conditions. It is therefore, suggested that in order to identify stable genotype, actual testing over a wide range of environments including poor and good ones would be advantageous while making selection and attention should be paid to the phenotypic stability of traits directly related to fruit yield, particularly fruits per plant, fruit weight etc. So as to achieve maximum stability for the end product *i.e.*, fruit yield per plant in eggplant. But in present investigation yield contributing traits and other all traits (except branches per plant) also reported as consistence performance in stability analysis, which showed lack of association to achieve maximum stability for fruit yield per plant in eggplant. The result was in contrast with Vaddoria et *al.* (2009) <sup>[14]</sup>, Chaudhari *et al.* (2015) <sup>[7]</sup>, Akhtar *et al.* (2019) <sup>[1]</sup>, Chaitanya and Reddy (2021) <sup>[6]</sup> and Dhaka and Kaushik (2022) <sup>[8]</sup>.

The yield is polygenically controlled complex trait and is being determined by the joint action of a number of component traits. Therefore, a proper understanding of relationship between fruit yield and its component traits could be of great help in choosing the proper components that may contribute not only towards the manifestation of complex trait but also towards its stability and association with high heterosis and desirable SCA effects. The identification of parents having high mean, good GCA effects and high stability across the locations is of great value to the plant breeders while formulating breeding programme.

It can be also concluded from the study that stability of fruit yield per plant is the result of stability for its component traits like fruits per plant, fruit weight etc. and hence utilization of stable and potential genotypes in plant breeding is of major importance for incorporation of stability as per Vaddoria *et al.*  $(2009)^{[14]}$ .

Above result came out with an excellent parent and hybrids that was really stable and having quantifiable good yielding capacity as well. The same parent and hybrids were also good for many other characters, which suggests that use of these genotypes could be beneficial for further crop improvement programmer in eggplant for developing stable and high yielding variety and improvement of other characters as well. Since the yield stability is genetically controlled, the stable hybrids could be exploited in future improvement programmes to incorporate genes for stability through recombination breeding (Dhaka and Kaushik, 2022)<sup>[8]</sup>.

Source of variation	DF	PH	BPP	DFF	FLPP	FPP	FL
Repl./Env	6	17.51*+	24.60**++	3.17	37.50*+	8.57**++	0.25
Genotypes (G)	36	68.47**++	96.81**++	50.04**++	122.61**++	43.00**++	6.52**++
$(E) + (G \times E)$	74	5.53	23.60**++	5.37**++	12.48	1.61	0.31
Environments (E)	2	24.56*+	94.69*++	81.37**++	89.21**++	0.92	0.41
$G \times E$	72	5.00	21.63**++	3.26	10.34	1.63	0.31
E (linear)	1	49.13**++	189.38**++	162.75**++	178.42**++	1.84	0.83
$G \times E$ (linear)	36	3.83	37.89**++	4.39*+	5.18	2.05+	0.34
Pooled deviation	37	6.00	5.22	2.07	15.09	1.18	0.27
Pooled Error	216	7.27	10.66	2.81	13.21	3.83	0.45
Sources	DF	FW	FD	FY	TPC	TSS	AA
Repl./Env	6	58.98**++	12.71	8.01**++	24.99**++	2.95**++	1.47
Genotypes (G)	36	$205.58^{**++}$	103.26**++	31.01**++	4.95**++	38.23**++	6.79**++
$(E) + (G \times E)$	74	17.47	10.59	1.25*+	0.29	0.64	0.67
Environments (E)	2	9.04	1.29	2.11	5.95**++	0.44	1.43
$G \times E$	72	17.70	10.85	1.23	0.13	0.65	0.65
E (linear)	1	18.09	2.58	4.22*+	11.91**++	0.88	2.86*+
$G \times E$ (linear)	36	18.48	12.69	1.69**++	0.05	0.50	0.58
Pooled deviation	37	16.47	8.77	0.75	0.20	0.77	0.69
Pooled Error	216	21.96	15.31	3.54	0.53	1.26	0.74
PH= Plant height (cm)		BPP= Branches	per plant D	FF= Days to 50 % t	flowering		
FLPP= Flowers per plant	FPP = Fruits per plant FL= Fruit length (cm)						
FW= Fruit weight (g)	FD= Fruit diameter (cm) FYP= Fruit yield per plant (kg)						
TPC= Total phenol content (1	ng/100 g)	TSS= Total solu	ble sugars (%) A	A= Ascorbic acid (	mg/100 g)		

Table 1: Analysis of variance over the locations (Eberhart and Russel, 1966)<sup>[9]</sup> for different characters in eggplant

\* and \*\* indicate significance at 5% and 1% level of probability at pooled error, respectively + and ++ indicate significance at 5% and 1% level of probability at pooled deviation, respectively

	Characters	Env	<b>Environmental index</b>			
Sr. No.		$L_1$	L <sub>2</sub>	L <sub>3</sub>		
		Navsari	Bardoli	Waghai		
1.	Plant height (cm)	-0.940	0.415	0.525		
2.	Branches per plant	0.082	-0.184	0.102		
3.	Days to 50 % flowering	0.532	1.144	-1.676		
4.	Flowers per plant	0.116	-1.608	1.492		
5.	Fruits per plant	-0.121	-0.058	0.178		
6.	Fruit length (cm)	-0.048	-0.074	0.122		
7.	Fruit weight (g)	0.166	-0.555	0.390		
8.	Fruit diameter (cm)	0.020	-0.002	-0.017		
9.	Fruit yield per plant (kg)	-0.009	-0.018	0.027		
10.	Total phenol content (mg/100 g)	0.046	-0.021	-0.025		
11.	Total soluble sugars (%)	-0.008	0.013	-0.005		
12.	Ascorbic acid (mg/100 g)	-0.002	-0.019	0.020		

Table 3: Stability parameters of different genotypes for branches per plant in eggplant

Sr. No.	Genotypes	μι	bi	S <sup>2</sup> di
1.	GNRB-1	5.489	-0.613**++	-0.109
2.	GJB-3	5.689	0.454	-0.100
3.	NBL-50	4.822	0.905	-0.060
4.	AB8/5	4.778	-0.107++	-0.108
5.	IC110662	5.889	0.133++	-0.108
6.	GJB-2	5.689	-0.266++	-0.102
7.	BPG-3	5.689	-0.935*++	-0.099
8.	S. Mani	6.044	-0.429	-0.072
	Parent Mean	5.511		
9.	$GNRB-1 \times GJB-3$	6.689	1.496	-0.044
10.	$GNRB-1 \times NBL-50$	5.111	1.012	-0.080
11.	$GNRB-1 \times AB8/5$	5.244	-0.480*+	-0.110
12.	GNRB-1 × IC110662	5.756	$1.200^{**++}$	-0.110
13.	$GNRB-1 \times GJB-2$	5.333	0.321	-0.089
14.	$GNRB-1 \times BPG-3$	5.444	-0.828**++	-0.107
15.	GNRB-1 $\times$ S. Mani	6.867	-0.026+	-0.102
16.	$GJB-3 \times NBL-50$	5.400	1.067**	-0.107
17.	$GJB-3 \times AB8/5$	5.489	1.097	0.044
18.	GJB-3 × IC110662	6.133	5.016**++	-0.083
19.	$GJB-3 \times GJB-2$	5.778	-3.040**++	-0.101
20.	$GJB-3 \times BPG-3$	6.156	-1.475	0.492*
21.	GJB-3 $\times$ S. Mani	5.978	-0.480*+	-0.110
22.	NBL-50 $\times$ AB8/5	4.778	2.697*	-0.035
23.	NBL-50 × IC110662	4.956	1.703	0.135
24.	NBL-50 $\times$ GJB-2	5.022	-1.308**++	-0.106
25.	NBL-50 $\times$ BPG-3	5.289	1.496	-0.044
26.	NBL-50 $\times$ S. Mani	5.333	3.524*	0.000
27.	AB8/5 × IC110662	4.644	0.188	-0.074
28.	$AB8/5 \times GJB-2$	5.133	1.415**	-0.097
29.	$AB8/5 \times BPG-3$	5.089	1.522*	-0.084
30.	$AB8/5 \times S.$ Mani	6.044	-1.895**++	-0.096
31.	IC110662 × GJB-2	5.267	-0.296	-0.053
32.	IC110662 × BPG-3	5.222	-2.298	0.058
33.	IC110662 × S. Mani	6.600	0.321	-0.089
34.	$GJB-2 \times BPG-3$	4.778	9.605**++	-0.092
35.	$GJB-2 \times S.$ Mani	5.822	8.082**++	-0.110
36.	BPG-3 $\times$ S. Mani	5.467	7.628**++	-0.094
t i	Hybrid Mean	5.529		
37.	GJBH-4 (check)	6.511	0.587*	-0.107
	General Mean	5.552		
	S.E. ±	0.161	1.010	

 S.E. ±
 0.161
 1.010

 \*, \*\* indicates significance at 5 and 1 percent levels, respectively as tested as bi/SE(bi)
 5
 5

+, ++ Significant deviation of bi from unity at 5 and 1 percent levels, respectively as tested as 1-bi/SE(bi)

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