

# International Journal of Statistics and Applied Mathematics

ISSN: 2456-1452  
Maths 2023; SP-8(3): 93-102  
© 2023 Stats & Maths  
<https://www.mathsjournal.com>  
Received: 13-03-2023  
Accepted: 18-04-2023

**Deepankar**  
Department of Mathematics and  
Statistics, CCS Haryana  
Agricultural University, Hisar,  
Haryana, India

**BK Hooda**  
Department of Mathematics and  
Statistics, CCS Haryana  
Agricultural University, Hisar,  
Haryana, India

## Stability assessment of Indian mustard genotypes in north zone of India using TOPSIS technique

**Deepankar and BK Hooda**

### Abstract

Multi-environment trials play a critical role in choosing the best performing genotypes that are stable over several environments. In the present study, stability of 26 genotypes grown at six different environments in north zone of India have been examined using various parametric and non-parametric stability measures as the stability of genotypes revealed by different measures is generally different, researchers have some ambiguity and confusion in selection of stable genotypes. Therefore, a composite measure of stability is required for ranking genotypes on the basis of their stability. Hence TOPSIS, a multicriteria decision making technique has been used to develop composite measures based on scores of various parametric and non-parametric stability measures. For ranking of genotypes according to their stability score of composite measure has been used. The lower value of composite measure indicates higher stability. Association of composite stability measure have been studied with parametric and non-parametric measures. Among parametric measures, the Linn and Binns superiority measure showed strong positive and significant correlation and among non-parametric measures Kang's rank sum and Yule's modified rank sums showed strong positive and significant correlation with composite measure.

**Keywords:** Indian mustard, stability analysis, parametric and non-parametric measures, multicriteria decision making, TOPSIS

### 1. Introduction

Plant breeders are paying attention to a number of oilseed crops around the world. *Brassica juncea* (L.), often known as Indian mustard, is a member of the Brassicaceae (Cruciferae) family of plants, also known as the mustard family. In India, *Brassica juncea* is the most common Rapeseed-mustard crop. The crop thrives in both irrigated and rainfed environments. The seven states, Rajasthan, Madhya Pradesh, Uttar Pradesh, Haryana, West Bengal, Assam and Gujarat, accounts for more than 90% of production and acreage (>80%) out of total production and area coverage over country. This crop has become one of the world's most important suppliers of vegetable oil over the last few decades. Continuous advancement in mustard has resulted in a nutritionally superior edible oil and meal as a major protein source in feed. Mustard seeds are known to have a variety of health benefits, including a high nutritional content as well as antibacterial and antiseptic properties (Beyzi *et al.*, 2019) [5].

Multi-environment trials (METs) are experiments in which a set of genotypes is evaluated in a set of environments that may differ spatially or temporally for selection of genotypes which give stable performance across the set of environments or delineation of mega environments (Mamata and Hooda, 2020) [19]. Genotypes with both stability and high seed yield are determined by growing different genotypes in different environmental conditions (Kumar *et al.*, 2018; Mamata *et al.*, 2019) [21, 18].

In addition to the additive effect of genotype and environment, when several genotypes are tested in different environments, a third effect emerges from the interaction of these variables. This is known as the genotype-environment interaction (GEI). The GEI is linked to the genotype's reaction to various environmental conditions. Interactions between genotype and environment are important sources of variation in any crop, and the term "stability" is sometimes applied to a genotype that produces a relatively constant yield regardless of changing environmental conditions. Genotypes with a low variance in yield across different environments are considered stable (Yan and Kang, 2003) [32].

**Corresponding Author:**  
**Deepankar**  
Department of Mathematics and  
Statistics, CCS Haryana  
Agricultural University, Hisar,  
Haryana, India

Finlay and Wilkinson (1963) <sup>[10]</sup> regressed observed response values on environmental indices defined as the difference between the marginal mean of the environments and the overall mean. The regression coefficient ( $b_i$ ) for each genotype is then taken as its stability parameter. Eberhart and Russell (1966) <sup>[9]</sup> modified the measure suggested by Finlay and Wilkinson (1963) <sup>[10]</sup> with the use of the second parameter ( $S_d^2$ ), which is a function of the squared deviation from regression, in addition to the regression coefficient. Shukla (1972) <sup>[28]</sup> defined the stability variance of  $i^{\text{th}}$  genotype as its variance across environments after the main effects of environmental means have been removed. Lin and Binns (1988) <sup>[17]</sup> proposed cultivar performance measure ( $P_i$ ) for determination of stable genotype, where genotypes with the lowest ( $P_i$ ) values are considered as the most stable.

Nassar and Huehn (1987) proposed four non-parametric stability measures ( $S_i^{(1)}, S_i^{(2)}, S_i^{(3)}, S_i^{(6)}$ ) of phenotypic stability based on the ranking of the genotypes in each environment and defined stable genotypes as those whose position in relation to the others remained unaltered in the set of assessed environments. Kang's (1988) <sup>[15]</sup> rank sum is a non-parametric stability measure where both yield and Shukla's (1972) <sup>[28]</sup> stability variance are used for selecting a stable genotype. Thennarasu (1995) <sup>[29]</sup> considered adjusted ranks of genotypes within each environment. The adjusted ranks depend only on the genotype x environment interaction and error components. Modified rank sum stability measures  $Y^1$  and  $Y^2$  are non-parametric measures given by Yue *et al.* (1997) <sup>[33]</sup> in which they combined the yield and first two Nassar and Huehn's (1987) <sup>[20]</sup> non-parametric stability measures.

Selection of genotypes which are higher yielders as well as stable across the various locations is an ongoing challenge to the plant breeders (Alwala *et al.*, 2010; Kang, 1991, 1993) <sup>[4, 16]</sup>. While examining the stability of genotypes using the various parametric and non-parametric stability measures the dilemma arises because every measure has its own results and it becomes a tedious work for researcher to take decision in such cases (Jamshidmoghaddam and Pourdad, 2011 and Alizadeh *et al.*, 2021) <sup>[14, 3]</sup>. This dilemma can be addressed by the use of multicriteria decision-making (MCDM) techniques. The foundations of modern multi-criteria decision-making procedures was laid in the 1950s, when work on multi-criteria decision-making commenced (Zionts and Wallenius, 1976) <sup>[35]</sup>. In problems dealing with MCDM the main goal is to consider a set of decision criteria and choose the best performing option from a list of available alternatives, which generally show no obvious dominance one over another with respect to the criteria. Research and development in the field of multi-criteria decision-making has accelerated in recent decades and appears to be continuing (Zavadskas *et al.*, 2014) <sup>[34]</sup>. Kumar *et al.* (2018) <sup>[21]</sup> used Technique for Order of Preference by Similarity to Ideal Solution (TOPSIS), a multi-criteria decision analysis method to develop the measure of relative closeness. In Indian mustard, breeding efforts have focused on producing stable genotypes with high seed yield in a variety of environments. Hence the study's aim is to develop a composite measure using TOPSIS technique for timely sown Indian mustard genotypes under irrigated conditions.

## 2. Materials and methods

### 2.1 Data description

For this study, the secondary data on mean yield (Kg/ha) of timely sown Indian mustard genotypes sown under irrigated conditions at different locations (Table 1) have been taken from All India Co-ordinated Research Project (AICRP) report on

rapeseed and mustard (2018). The report has been issued by Directorate of Rapeseed and Mustard, Bharatpur (Rajasthan). The data comprise of 26 genotypes grown at six different locations namely, ABH (Abhor, Punjab), LDH (Ludhiana, Punjab), HSR (Hisar, Haryana), CHT (Chatha, Jammu & Kashmir), NDH (New Delhi) and SGN (Sriganganagar, Rajasthan). The analysis has been done using R and Rstudio.

### 2.2 Stability measures

Over the years, a range of statistical methods have been proposed to evaluate GE interaction and evaluated genotypes for yield stability over environments. In plant breeding, parametric approaches for determining phenotypic stability are generally utilized, and they are largely connected to variance components and associated statistics. Under certain statistical assumptions, such as normal distribution of error and interaction effects, parametric measures have favourable features; but, if these assumptions are ignored, they may not perform well. Non-parametric techniques are based on genotype rankings; they connect environments and phenotypes without imposing any statistical assumptions (Bishnoi and Hooda, 2018) <sup>[7]</sup>. Although non-parametric measures are less efficient than parametric measures, if the number of genotypes is large enough, both procedures can be applied effectively. In general, each of the parametric and nonparametric approaches addresses a unique aspect of the phenomenon of GE interaction, and each method has its own set of strengths and limitations for genotype identification. As a result, plant breeders deploy both parametric and nonparametric approaches to determine genotype stability and adaptability (Vaezi *et al.*, 2019) <sup>[30]</sup>.

#### 2.2.1 Wricke's Ecovalence

Wricke (1962) <sup>[36]</sup> proposed the use of genotype x environment interaction effects for each genotype, squared and summed across all environments, as a stability measure. This statistic was termed as Ecovalence ( $W_i$ ) and expressed as

$$W_i = \sum_j [Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}]^2; 1 \leq i \leq t, 1 \leq j \leq s$$

where,  $Y_{ij}$  is the mean performance of genotype  $i$  in the  $j^{\text{th}}$  environment,  $\bar{Y}_i$  is the marginal mean of  $i^{\text{th}}$  genotype,  $\bar{Y}_j$  is the marginal mean of  $j^{\text{th}}$  environment and  $\bar{Y}$  is the overall mean. Genotypes with a low value of  $W_i$  have smaller deviations from the mean across environments. Therefore, genotypes which have smaller values are more stable.

#### 2.2.2 Finlay and Wilkinson's regression coefficient

Finlay and Wilkinson (1963) <sup>[10]</sup> used regression technique to compare the performance of genotypes grown at several locations for several years. For each genotype, a linear regression of an individual genotype yield on the mean of all genotypes was computed. In order to measure an environment, the mean of all genotypes grown in the environment was used. The assessment allows the grading of the environments from the lowest yielding to the highest yielding. The coefficient of regression ( $b_i$ ) and the mean yield over all the environments were used to classify the varieties for stability. They used two parameters: a) mean performance over environments and b) regression performance in different environments.

$$b_i = 1 + \frac{\sum_i (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}) (\bar{Y}_j - \bar{Y})}{\sum_j (\bar{Y}_j - \bar{Y})^2}$$

The following inferences can be drawn:

- a) the regression coefficient of unity indicates average stability
- b) the regression coefficient is >1, it means below average stability
- c) the regression coefficient is <1, it means above average stability
- d) If the regression coefficient is zero, it means absolute stability.

**2.2.3 Eberhart and Russel’s Model**

Eberhart and Russel (1966) [9] used two parameters to study stability of genotypes a) regression coefficient of Finlay and Wilkinson (1963) [10] and b) Mean square deviation from linear regression ( $Sd_i^2$ ).

$$Sd_i^2 = \frac{1}{e-2} \left\{ \sum_i (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}) - (b_i - 2)^2 \left( \sum_j (\bar{Y}_j + \bar{Y})^2 \right) \right\}$$

Eberhart and Russell (1966) [9] defined stable variety as one with a regression coefficient of unity ( $b = 1$ ) and a minimum deviation from the regression lines ( $Sd_i^2 = 0$ ).

**2.2.4 Shukla’s stability variance**

Shukla (1972) [28] proposed an unbiased estimate of the variance of ( $g_{ij} + \bar{e}_{ij}$ ) for genotype ‘i’. This stability statistic is termed stability variance ( $\sigma_i^2$ ), which is estimated as follows:

$$\sigma_i^2 = \frac{t}{(t-2)(s-1)} W_i - \frac{MS_{GE}}{t-2};$$

where,  $MS_{GE} = \frac{\sum_i \sum_j [Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}]^2}{(t-1)(s-1)}$

Shukla defined stability variance of genotype ‘i’ as its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance thus based on residual matrix in a two-way classification. Stability variance is a linear combination of wricke’s ecovalence and mean square due to genotype by environment interaction. A genotype is called stable if its stability variance ( $\sigma_i^2$ ) is equal to environmental variance ( $\sigma_e^2$ ) which means that  $\sigma_i^2 = 0$ . A relatively larger value of  $\sigma_i^2$  will indicate greater instability of  $i^{th}$  genotype. Negative estimates of  $\sigma_i^2$  can be taken as equal to zero.

**2.2.5 Francis and Kannenberg’s coefficient of variation**

Roemer (1917) [27] proposed the use of variance of each genotype over environments. Therefore, phenotypic stability of  $i^{th}$  genotype across a set of environments can be measured by:

$$S_i^2 = \frac{\sum_j (Y_{ij} - \bar{Y}_i)^2}{s}$$

A stable genotype has small variance. In general, genotypes with high phenotypic stability measured through the environmental variance show low yield. So, this method is not used by plant breeders but its derived quantities can be used for evaluating yield stability across environments. Francis and Francis and Kannenberg (1978) [11] proposed coefficient of variation as a stability measure which is given as:

$$CV = \frac{\sqrt{S_i^2}}{\bar{Y}_i} \times 100$$

Genotype with the smallest value of CV is considered to be stable.

**2.2.6 Linn and Binns’s Superiority measure of cultivar**

Linn and Binns (1988) [17] gave superiority measure of cultivar/genotype. The distance mean square between the cultivar’s response and the maximal response aggregated over all locations is a measure of cultivar general superiority for genotype x location data. Because the maximal response is the ceiling in each location, a small mean square implies that the test cultivar is generally superior. The Linn and Binns superiority measure is denoted by  $P_i$  and calculated as follows:

$$P_i = \sum_{j=1}^s \frac{(Y_{ij} - M_j)^2}{2s}$$

where,  $Y_{ij}$  is the  $i^{th}$  genotype’s response in  $j^{th}$  environment,  $M_j$  is the maximum response in  $j^{th}$  environment and  $s$  is the number of environments. Selection of genotype depends on the value of superiority measure. As  $M_j$  is the maximal response of  $j^{th}$  environment and  $P$  is squared distance between any genotype’s response in specified environment and maximum response of that environment. This difference is desired to be minimum, hence the genotypes with minimal  $P$  values will be considered as stable.

**2.2.7 Nassar and Huehn’s index**

Nassar and Huehn (1987) [20] proposed 4 non-parametric statistics of phenotypic stability, which were based on ranking of genotypes in each environment. Stable genotypes are those whose position in relation to the others remain unaltered in the set of environments assessed. Four measures based on yield ranks of genotypes in each environment are given as:

$$S_i^{(1)} = \frac{2 \sum_{j=1}^{s-1} \sum_{j'+j+1}^s |r_{ij} - r_{ij'}|}{s(s-1)} \quad S_i^{(2)} = \frac{\sum_{j=1}^s (r_{ij} - \bar{r}_i)^2}{(s-1)}$$

$$S_i^{(3)} = \frac{\sum_{j=1}^s (r_{ij} - \bar{r}_i)^2}{\bar{r}_i} \quad S_i^{(6)} = \frac{\sum_{j=1}^s |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

where,  $r_{ij}$  is the rank of  $i^{th}$  genotype in  $j^{th}$  environment,  $\bar{r}_i$  is the mean rank of  $i^{th}$  genotype across all environments.  $S_i^{(1)}$  statistics measures the mean of absolute rank difference of a genotype over environments,  $S_i^{(2)}$  gives the variance among the ranks over environments,  $S_i^{(3)}$  is the sum of square deviations in yield units of each rank relative to mean rank and  $S_i^{(6)}$  is the sum of absolute deviations in yield units of each rank relative to mean rank. Genotypes having smaller value of these measures are the desirable one and those having larger values are the undesirable ones.

**2.2.8 Kang’s modified rank sum**

Kang (1988) [15] proposed rank sum is a non-parametric stability measure where both yield and Shukla’s (1972) [28] stability variance are used for selecting a stable genotype. In this measure a weight of one is assigned to both yield and stability statistics to identify high-yielding and stable genotypes. The genotype with highest yield is given rank of one and a genotype with the lowest stability variance is

assigned a rank of one. After ranking all genotypes in the above stated procedure, the ranks by yield and Shukla's stability variance are added for each genotype. The genotype with lowest rank sum is considered more stable.

**2.2.9 N. P. Thennarasu's index**

Thennarasu (1995) [29] considered adjusted ranks of genotypes within each environment. He suggested that rank of a genotype in a particular environment can't be based purely on the phenotypic values, because the stability has to be measured independently of the genotypic effect. Therefore, the rank of the  $i^{th}$  genotype in the  $j^{th}$  environment is determined on the basis of the corrected phenotypic values which is given as  $Y_{ij}^* = Y_{ij} - \bar{Y}_i$ . The ranks obtained from these corrected  $Y_{ij}$  depend only on genotype by environment interaction and error components. Thennarasu's (1995) [29] stability measures are given as:

$$NP^{(1)} = \frac{1}{s} \sum_{j=1}^s |r_{ij}^* - M_{di}^*|$$

$$NP^{(2)} = \frac{1}{s} \left[ \frac{\sum_{j=1}^s |r_{ij}^* - M_{di}^*|}{M_{di}^*} \right]$$

$$NP^{(3)} = \frac{\sqrt{\frac{1}{s} \sum_{j=1}^s (r_{ij}^* - \bar{r}_i)^2}}{\bar{r}_i}$$

$$NP^{(4)} = \frac{2}{s(s-1)} \left[ \sum_{j=1}^{s-1} \sum_{j=j+1}^s \frac{|r_{ij}^* - \bar{r}_i|}{\bar{r}_i} \right]$$

where,  $r_{ij}^*$  is the rank of  $i^{th}$  genotype in the  $j^{th}$  environment based on  $Y_{ij}^* = Y_{ij} - \bar{Y}_i$ ,  $\bar{r}_i$  and  $M_{di}^*$  are the mean and median ranks respectively of the  $i^{th}$  genotype in the  $j^{th}$  environment, and  $r_{ij}^*$  and  $M_{di}^*$  are obtained from the corrected  $Y_{ij}$ . These measures are obtained simply by adjusting the value of  $Y_{ij}$  and for these measures also ranking is done in same way as explained for Huehn and Nassar's (1987) [20] stability measures. The correction done on data because genotypic effect should not affect the stability of genotype. Thennarasu's first measure was average of rank deviation from median, while Huehn (1979) [12] preferred mean. Its second measure is a ratio of absolute rank deviation of genotypes from their respective median rank to its uncorrected median rank. Third measure is standard deviation of ranks for corrected data relative to its corresponding genotypic mean from uncorrected data. This measure was similar to the one given by Francis and Kannenberg (1978) [11]. Fourth measure corresponds to average successive difference in ranks of a genotype relative to corresponding genotypic mean from uncorrected data. The fourth measure provides insight about the scatteredness prevailing in the data. The genotypes having smaller value these measures are considered as stable.

**2.2.10 Yule's modified rank sum (1997)**

Yule *et al.* (1997) [33] gave a two conjoint measure based on rank of average genotype's response across all environments and ranks of Huehn and Nassar's first and second measures. The Yule's first modified rank sum combines rank of genotype's average response with first measure of Huehn and Nassar whereas the Yule's second measure combines rank of genotype's average response with second measure of Huehn and Nassar. The genotypes yielding lower rank sum are considered to be most stable.

**2.3 TOPSIS - A multi-criteria decision making (MCDM) technique**

The MCDM techniques are useful in taking decision based on the more than one criterion. These techniques are helpful for researchers to visualize, quantify, and increase transparency in the decision-making process by helping to evaluate the criteria influencing the decision and the possible decision alternatives

to implement. The main objective is to consider a set of decision criteria and choose the best performing option from a list of available alternatives (i.e., options to choose from), which generally show no obvious dominance one over another with respect to the criteria. Hwang and Yoon (1981) [13] developed Technique for Order of Preference by Similarity to Ideal Solution (TOPSIS) as a compensatory method measuring the distance to an idealized solution. TOPSIS can be defined as "an approach to identify an alternative which is closest to the ideal solution and farthest to the negative ideal solution in a multi-dimensional computing space" (Qin *et al.*, 2008; Velasquez and Hester, 2013) [24, 31]. Because of its speed, precision, and compatibility, the TOPSIS technique has been used (Pakpour *et al.*, 2013; Kumar *et al.*, 2018; Axelsson *et al.*, 2021) [23, 21].

**Algorithm**

Formation of decision matrix i.e.,

$$X = \{x_{ij}; i = 1, 2, \dots, m \text{ and } j = 1, 2, \dots, n\}$$

$$X = \begin{bmatrix} x_{11} & x_{12} & \dots & x_{1n} \\ x_{21} & x_{22} & \dots & x_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ x_{m1} & x_{m2} & \dots & x_{mn} \end{bmatrix}$$

where,  $x_{ij}$  is score given by  $i^{th}$  stability measure to the  $j^{th}$  genotype.

Normalization of decision matrix

$$R = \{r_{ij}\} = \frac{x_{ij}}{\sqrt{\sum_{i=1}^m x_{ij}^2}}; i=1, 2, \dots, m, j=1, 2, \dots, n$$

Weighted normalized decision matrix

$$W = \{w_{ij}\} = u_j * r_{ij}$$

Where,  $u_j$  is the weight of  $j^{th}$  genotype. It is average of individual ranks of genotypes across all environments. To adjust the entropy measure for the  $i^{th}$  method, related values in the decision matrix are normalised first, and the normalised values are represented as  $r_{ij}$ . The weight of the  $j^{th}$  genotype ( $u_j$ ) is derived using entropy.

Obtaining ideal positive and ideal negative solutions

$$w_i^+ = \max\{w_{ij}, \text{ for all } i = 1, 2, \dots, m\}$$

$$w_i^- = \min\{w_{ij}, \text{ for all } i = 1, 2, \dots, m\}$$

The ideal positive and ideal negative values are the row wise maximum and minimum value of weighted normalized decision matrix corresponding to each measure.

Measuring squared deviation from ideal positive and ideal negative

$$d_j^+ = \sqrt{\sum_{i=1}^n \sum_{i=1}^m (w_{ij} - w_i^+)^2} \text{ and } d_j^- = \sqrt{\sum_{i=1}^n \sum_{i=1}^m (w_{ij} - w_i^-)^2}$$

Measure of degree of closeness

$$C_j^- = \frac{d_j^-}{d_j^+ + d_j^-}; j = 1, 2, \dots, n$$

The lower values of  $C_j$  refers to higher stability of genotypes.

## 2.4 Majority approaches

### 2.4.1 Rank sum of stability measures

The rank sum of different parametric and non-parametric stability has been used to form two new stability measures, one based on rank sum of parametric stability measures ( $RS_P$ ) and other based on rank sum of non-parametric stability measures ( $RS_{NP}$ ). The third measure, overall rank sum stability measure which combines both the parametric and non-parametric stability measures. The genotype having lowest rank sum is considered as stable.

### 2.4.2 Mode-based stability measure

After evaluating performance of a set of genotypes grown at different environments using various parametric and non-parametric stability measures. The mode-based stability measure is defined maximum frequency of a genotype securing place in best five or ten genotypes among all genotypes under study. The genotypes with highest frequencies are considered to be stable among the pool of genotypes.

## 3. Results and Discussion

The preliminary analysis of the average performance of genotypes across all environments provides a broad idea about the overall performance but not a clue about the consistency in performance. The table 1 presents yield (kg/ha) of timely sown 26 mustard genotypes under irrigated conditions across six environments namely, Abhor, Hisar, Ludhiana, New Delhi, Chatha and Sri Ganganagar. The mean yield over the all environments varied from 2045.92 kg/ha to 3648.08 kg/ha. The overall mean yield of all genotypes in study was 2579.54 kg/ha. Genotype G1 was found to be having highest yield (2956.50 kg/ha) averaged over all environments followed up by G24 (2870.50 kg/ha), G21 (2867.67 kg/ha), G22 (2855.67 kg/ha) and so on. While G26 (2030.17 kg/ha) ranked last amongst all 26 genotypes. The variation in performance of genotypes is considered mainly because of environmental conditions but the differences in genetic lineage, cycle and other attributes also contributes in overall expression of genotype. In the following discussion, we used six parametric and eleven non-parametric stability measures to get insights about the consistency in genotype's performance across a series of environments.

### 3.1 Stability of genotypes based on parametric measures

The tables 2 and 3 include the estimates of 6 parametric and 11 non-parametric measures along with mean response of genotype. According to Wricke, the genotype producing minimal squared sum of genotype by environment interaction is considered to be as stable genotype. Therefore, on the basis of Wricke's ecovalence, genotype G19 is more stable in comparison of G8, G13, G11 and so on. According to Finlay and Wilkinson's regression coefficient genotypes G19 and G13 showed average stability while G2, G5, G8, G11, G15, G17, G18 and G25 came out to be near average stability because the regression coefficient lies very close to unity. The genotypes G1, G3, G16, G21 and G24 showed below average stability and are suitable for highly favourable environmental conditions while G4, G12, G14, G20, G23 and G26 fall under above average stability and they are suitable for adverse environments.

According to Eberhart and Russel, the genotype having regression coefficient equals to unity and minimum mean square deviation from regression (preferably equals to zero) is

considered as stable genotype among the all genotypes under the study. It was found that the values of mean square deviation from regression were not close to zero (As desired by Eberhart and Russell's approach). The plausible reason is presence of higher variation in inter-environment performance of genotypes. Hence, Eberhart and Russell's stability measure is not fit for determining stability of genotype. Shukla (1972) [28] gave an unbiased estimate of variance genotype by environment interaction and termed it as "stability variance" and used to determine the stability of a genotype. The scores of stability variance were much higher than desired value i.e., zero. Although the pattern of stability of genotypes is similar to that one given by wricke's ecovalence measure.

According the Francis and Kannenberg's measure the smaller value of coefficient of variation symbolizes the consistency in performance of genotype grown in different environments. The coefficient of variation of genotypes performance across different environment ranged from 19.28 - 30.32 percent. The genotype G26 had lowest score considered as more stable followed by G14 while G21 has highest score hence considered as less stable among all the genotypes. According to Lin and Binns (1988) measure of superiority of cultivar (genotype) genotypes G1, G22, G24, G21 and G25 are found most stable among all the genotypes under study.

### 3.2 Stability of genotypes based on non-parametric measures

On the basis of Huehn and Nassar's first and second measure of stability, the genotypes that found stable among all genotypes are G26, G1, G8, G19 and G10. Based on the third measure of stability by Huehn and Nassar, the genotypes G1, G26, G8, G22 and G19 are to be considered as stable. The fourth stability measure of Huehn and Nassar points out genotypes G1, G22, G24, G17 and G8 are the stables ones amongst all genotypes in trial. Kang (1988) proposed a stability measure as addition of the ranks of average genotype's response across all environment and rank of Shukla's stability variance (1972). On its basis, genotypes G13, G22, G11, G8 and G1 are labelled as stable.

Thennarasu (1995) [29] developed 4 measures to study the stability of genotypes by acknowledging their ranks in individual environments and ranks after removing genotypic effect from the mean data in individual environments. Based on Thennarasu's first measure the genotypes G19, G5, G8, G11, G13 and G17 are found most stable. According to the second measure, the genotypes labelled as most stable are G17, G22, G11, G10 and G13. The score of third measure implies that G19, G22, G1, G8 and G13 are considered most stable genotypes. On the grounds of fourth measure, G1, G22, G17, G24 and G25 are most stable genotypes. According to Yule's first modified rank sum, genotypes G1, G22, G24, G17 and G25 are labelled as most stable. Similarly on the basis of Yule's second measure, genotypes G1, G22, G17, G24 and G25 are most stable.

### 3.3 Stability of genotypes based on composite measures

According to TOPSIS technique the genotype is considered to be stable when it shows maximum deviation from ideal positive solution and minimum deviation from ideal negative solution. The genotypes yielding lowest values of relative closeness measure are the most desirable genotypes. According to the composite measure ( $C_P$ ) based on parametric stability measures (Table 5), the genotypes G1, G22, G26, G3 and G13 are found to be stable. According to the composite measure ( $C_{NP}$ ) based on non-parametric stability measures, the

genotypes G1, G22, G17, G8 and G26 are found to be stable. The genotypes G1, G22, G26, G17 and G24 are the most stable on the basis of composite measure (C) developed using parametric and non-parametric measures.

### 3.4 Stability of genotypes based on majority approaches

According to  $RS_P$ , the G8 was most stable followed up by G14, G1, G22, G11 and so on. Whereas, on the basis of  $RS_{NP}$  genotype G22 followed by G1, G9, G17 and G13 were found most stable in comparison of rest genotypes under study. According to overall rank sum measures the genotypes G1, G8, G13, G17 and G22 are found to be stable among all genotypes. The table 7 consists of best five stable genotypes based on parametric, non-parametric and composite measures. From the modal approach (Fig 1), that genotypes G1, G8, G22, G13 and G19 are most stable in comparison of rest genotypes in multi-environment trial.

### 3.5 Correlation of composite measure (C) with other stability measures

The spearman's rank correlation has been calculated to assess the relationship of the composite measure with parametric and non-parametric measures (Table 6). With parametric measures, the composite measure has been found weakly correlated. The measures of Huehn and Nassar were found moderately correlated while Thennarasu's measures were found to be weak to moderately correlated with composite measure. The composite measure was found moderately correlated with measure based rank sum of parametric measures ( $RS_P$ ) and measure based on rank sum of non-parametric measures ( $RS_{NP}$ ). The composite measure based on parametric measure ( $C_P$ ) and composite measure based on non-parametric measure ( $C_{NP}$ ) were found to be strongly correlated with overall composite measure.

**Table 1:** Two-way mean yield (Kg/ha) data of mustard genotypes grown in different environments

S. NO	Genotype	ABR	HSR	LDH	NDH	CHT	SGN	Mean yield	Range
G1	RH 1550	2170	4424	2644	2975	2239	3287	2956.50 (1)	2170-4424
G2	JM 12-6	1747	3485	2117	2722	2086	2614	2461.83 (21)	1747-3485
G3	AKMS 9026	1639	3709	2249	2286	2004	2682	2428.17 (24)	1639-3709
G4	KMR 17-3	2624	3419	2289	2065	1994	2940	2555.17 (14)	1994-3419
G5	DRMRCI 85	1821	3491	2261	2796	1943	2722	2505.67 (16)	1821-3491
G6	PHR 3278	1783	3659	2540	2253	1922	2353	2418.33 (25)	1783-3659
G7	PR-2015-5	2509	3622	2532	2813	1906	2751	2688.83 (7)	1906-3622
G8	RGN 73 (LR)	1904	3491	2523	2458	1951	2840	2527.83 (15)	1904-3491
G9	KM -927	1645	3317	2307	2688	2185	2469	2435.17 (23)	1645-3317
G10	RB-94	2152	3534	2528	2299	2028	2425	2494.33 (18)	2028-3534
G11	KMR 17-4	2067	3652	2095	2634	1992	2903	2557.17 (12)	1992-3652
G12	PBR 438	2537	3496	2408	1993	2164	2379	2496.17 (17)	1993-3496
G13	DRMR 2017-11	1885	3569	2240	2670	2133	2866	2560.50 (11)	1885-3569
G14	DRMRIJ 16-66	2028	3244	2650	2353	2057	3003	2555.83 (13)	2028-3244
G15	NPJ-212	1681	3573	2577	2537	2016	2380	2460.67 (22)	1681-3573
G16	JMM 991	2153	4251	2276	2535	2351	3181	2791.17 (5)	2153-4251
G17	KRANTI	2197	3876	2511	2598	2103	2384	2611.50 (9)	2103-3876
G18	SVJ-111	2143	3697	1796	2233	2177	2739	2464.17 (20)	1796-3697
G19	PR-2015-1	1920	3511	2360	2543	1885	2587	2467.67 (19)	1885-3511
G20	MAYA	2502	3593	2828	2321	2002	2626	2645.33 (8)	2002-3593
G21	RH 1585	2047	4206	3305	3145	1872	2631	2867.67 (3)	1872-4206
G22	SKM 1328	2371	3963	2865	2691	1985	3259	2855.67 (4)	1985-3963
G23	PCR 400	1967	3441	2184	2426	2315	3159	2582.00 (10)	1967-3441
G24	NPJ-211	2248	4336	2585	3264	1946	2844	2870.50 (2)	1946-4336
G25	RGN-435	2275	3547	2396	3099	1999	3364	2780.00 (6)	1999-3547
G26	TM-179	1683	2744	1842	1776	1939	2197	2030.17 (26)	1683-2744
<b>Mean</b>		2065.31	3648.08	2419.54	2545.12	2045.92	2753.27	<b>2579.54</b>	
<b>Range</b>		1639-2624	2744-4424	1796-3305	1776-3264	1872-2351	2197-3364	2030.17-2956.5	

\*Ranks in parenthesis

**Table 2:** Relative stability of Indian mustard genotypes on the basis of parametric measures

Genotype	Yield	rank	W	Rank	SV	Rank	SDi2	Rank	FWB	Rank	CV	Rank	Pi	Rank	RSP	Rank
G1	2957	1	317748.09	16	66059.58	16	3697.60	2	1.41	1	28.28	22	2235093	1	58	6
G2	2462	21	188606.65	8	38078.93	8	26928.17	12	0.99	15	25.10	17	11966049	20	80	13
G3	2428	24	151030.35	5	29937.40	5	12647.64	4	1.19	5	29.47	24	12415809	22	65	9
G4	2555	14	646164.88	24	137216.55	24	76878.54	25	0.75	24	21.61	6	11361321	19	122	25
G5	2506	16	151265.61	6	29988.37	6	21562.27	9	1.01	12	24.91	16	10208658	15	64	7
G6	2418	25	199309.15	9	40397.81	9	26772.97	11	1.08	7	27.65	21	12318042	21	78	12
G7	2689	7	229864.04	12	47018.03	12	29268.75	13	0.88	19	20.77	4	6093459	7	67	10
G8	2528	15	69478.81	2	12267.90	2	9838.00	3	0.98	16	23.42	11	9253875	11	45	1
G9	2435	23	294443.50	14	61010.25	14	37030.75	18	0.86	21	22.84	9	13020753	24	100	22
G10	2494	18	157388.23	7	31314.94	7	18426.12	7	0.87	20	21.66	7	10607664	16	64	7
G11	2557	12	135567.96	4	26587.22	4	18431.56	8	1.06	8	25.33	18	9325905	12	54	4
G12	2496	17	662900.04	25	140842.50	25	73255.21	24	0.71	25	21.09	5	12881991	23	127	26
G13	2561	11	104710.09	3	19901.34	3	14955.86	5	1.00	13	23.85	12	9179205	10	46	2
G14	2556	13	313807.42	15	65205.77	15	31399.23	15	0.77	23	19.57	2	9669957	13	83	14
G15	2461	22	233631.23	13	47834.26	13	33220.49	16	1.02	11	26.14	19	11257332	18	90	16

G16	2791	5	399218.35	19	83711.47	19	33726.94	17	1.31	3	28.73	23	5626623	6	87	15
G17	2612	9	213942.09	10	43568.28	10	30220.40	14	1.04	9	24.77	15	7735587	9	67	10
G18	2464	20	432166.65	21	90850.27	21	61530.40	22	1.03	10	27.41	20	13562499	25	119	24
G19	2468	19	21903.61	1	1959.94	1	3126.91	1	1.00	14	24.04	13	10688808	17	47	3
G20	2645	8	402955.08	20	84521.09	20	48132.38	21	0.81	22	20.51	3	7466004	8	94	17
G21	2868	3	1002608.85	26	214446.07	26	121568.29	26	1.29	4	30.32	26	3484032	4	112	23
G22	2856	4	214337.15	11	43653.87	11	26541.18	10	1.13	6	24.31	14	2830320	2	54	4
G23	2582	10	359195.59	17	75039.87	17	47977.89	20	0.88	18	22.60	8	10200432	14	94	17
G24	2871	2	561052.24	23	118775.48	23	44657.77	19	1.38	2	29.67	25	3305835	3	95	19
G25	2780	6	495614.51	22	104597.30	22	69984.88	23	0.94	17	23.00	10	5605020	5	99	21
G26	2030	26	398615.19	18	83580.78	18	18016.52	6	0.61	26	19.28	1	28782081	26	95	19

**Note:** W: Wricke’s ecovalence; SV: Shukla’s variance; SDi2: Eberhart and Russell’s deviation from linear regression; FWB: Finlay and Wilkinson’s regression coefficient; CV: Francis and Kannenberg’s coefficient of variation; Pi: Linn and Binn’s superiority measure of cultivar; RSP: Rank sum of parametric measures

**Table 3:** Relative stability of Indian mustard genotypes on the basis of non-parametric measures

Genotype	Si1	Rank	Si2	Rank	Si3	Rank	Si6	Rank	NP1	Rank	NP2	Rank	NP3	Rank	NP4	Rank	KRS	Rank	Y1	Rank	Y2	Rank	RSNP	Rank
G1	3.33	2	8.00	2	1.74	1	0.52	1	7.00	18	0.49	15	0.34	3	0.14	1	17.00	4	3	1	3	1	49	2
G2	8.13	15	48.27	16	23.35	19	3.35	21	5.33	10	0.87	24	0.62	18	0.79	19	29.00	17	36	20	37	20	199	19
G3	8.27	16	45.20	14	22.60	18	3.20	18	4.83	7	0.63	19	0.61	17	0.83	21	29.00	17	40	22	38	21	190	18
G4	10.93	24	81.87	24	33.19	25	3.46	22	7.00	18	0.63	21	0.68	21	0.89	23	38.00	23	38	21	38	21	243	24
G5	6.27	6	33.47	8	16.19	14	2.58	14	3.50	2	0.62	18	0.52	12	0.61	14	22.00	9	22	9	24	13	119	11
G6	8.53	18	56.00	19	31.11	23	4.22	26	5.67	12	1.36	25	0.71	23	0.95	25	34.00	20	43	25	44	25	241	23
G7	8.53	18	54.67	18	16.73	15	1.84	6	6.00	13	0.43	8	0.42	7	0.52	13	19.00	6	25	14	25	14	132	13
G8	4.73	3	15.77	3	7.06	3	1.73	5	3.50	2	0.35	6	0.36	4	0.42	6	17.00	4	18	6	18	7	49	2
G9	10.27	23	70.67	22	33.13	24	3.75	25	7.33	21	0.78	23	0.76	25	0.96	26	37.00	22	46	26	45	26	263	25
G10	5.80	5	23.77	5	9.77	6	2.05	12	5.17	8	0.31	4	0.50	11	0.48	8	25.00	11	23	12	23	11	93	8
G11	6.87	9	34.17	9	12.97	11	2.03	10	4.33	4	0.29	3	0.44	8	0.52	12	16.00	3	21	7	21	9	85	7
G12	11.60	25	88.67	25	35.95	26	3.73	24	8.33	24	0.68	22	0.74	24	0.94	24	42.00	25	42	24	42	24	267	26
G13	6.93	10	32.27	6	11.80	9	2.05	11	4.67	5	0.31	5	0.36	5	0.51	9	14.00	1	21	7	17	4	72	5
G14	9.73	20	62.40	20	22.29	17	2.71	15	6.50	14	0.44	9	0.57	15	0.70	16	28.00	14	33	18	33	17	175	17
G15	7.93	12	44.30	12	19.26	16	2.78	16	5.33	10	0.48	12	0.61	16	0.69	15	35.00	21	34	19	34	19	168	15
G16	8.47	17	48.30	17	13.05	12	1.89	9	8.17	23	0.35	6	0.47	10	0.46	7	24.00	10	22	9	22	10	130	12
G17	6.40	8	33.07	7	10.55	7	1.53	4	4.67	5	0.24	1	0.39	6	0.41	3	19.00	6	17	4	16	3	54	4
G18	10.07	21	69.10	21	27.64	20	3.20	18	6.83	17	0.48	13	0.66	20	0.81	20	41.00	24	41	23	41	23	220	22
G19	4.80	4	17.07	4	9.14	5	1.86	7	2.33	1	0.52	16	0.31	1	0.51	10	20.00	8	23	12	23	11	79	6
G20	8.07	14	44.30	12	14.29	13	2.06	13	6.50	14	0.54	17	0.56	14	0.52	11	28.00	14	22	9	20	8	139	14
G21	11.80	26	97.50	26	29.55	22	2.97	17	11.50	26	0.47	11	0.70	22	0.72	17	29.00	17	29	16	29	16	216	21
G22	6.33	7	34.17	9	8.47	4	1.22	2	5.17	8	0.25	2	0.33	2	0.31	2	15.00	2	11	2	13	2	42	1
G23	10.13	22	73.20	23	28.15	21	3.23	20	7.17	20	0.63	20	0.65	19	0.78	18	27.00	13	32	17	33	17	210	20
G24	8.00	13	47.47	15	12.28	10	1.52	3	7.50	22	0.49	14	0.47	9	0.41	4	25.00	11	15	3	17	4	108	9
G25	7.60	11	41.20	11	11.44	8	1.89	8	9.00	25	0.44	10	0.53	13	0.42	5	28.00	14	17	4	17	4	113	10
G26	2.00	1	3.07	1	6.57	2	3.71	23	6.67	16	6.78	26	3.52	26	0.86	22	44.00	26	27	15	27	15	173	16

**Note:** Si1: Huehn and Nassar first index; Si2: Huehn and Nassar second index; Si3: Huehn and Nassar third index; Si6: Huehn and Nassar fourth index; NP1: Thennarasu’s first index; NP2: Thennarasu second index; NP3: Thennarasu’s third index; NP4: Thennarasu’s fourth measure; KRS: Kang’s rank sum; Y1: Yule’s modified first rank sum; Y2: Yule’s modified second rank sum; RSNP: Rank sum of non-parametric measures

**Table 4:** Weighted Normalized decision matrix

Genotype	W	SV	SDi2	CVi	FWB	Pi	Si1	Si2	Si3	Si6	NP1	NP2	NP3	NP4	KRS	Y1	Y2
G1	0.81	0.81	0.10	1.12	0.05	0.05	0.10	0.10	0.05	0.05	0.92	0.76	0.15	0.05	0.21	0.05	0.05
G2	1.69	1.69	2.54	3.60	3.17	4.23	3.18	3.40	4.02	4.46	2.14	5.08	3.81	4.02	3.67	4.27	4.28
G3	1.08	1.08	0.86	5.18	1.08	4.75	3.46	3.03	3.89	3.90	1.53	4.11	3.67	4.53	3.74	4.79	4.58
G4	4.47	4.47	4.66	1.12	4.47	3.54	4.48	4.49	4.66	4.11	3.39	3.92	3.91	4.28	4.37	3.95	3.95
G5	1.26	1.26	1.89	3.35	2.51	3.14	1.26	1.68	2.93	2.94	0.42	3.78	2.51	2.93	1.92	1.90	2.75
G6	2.06	2.06	2.51	4.80	1.60	4.80	4.13	4.36	5.26	5.96	2.77	5.72	5.26	5.71	4.66	5.76	5.78
G7	1.63	1.63	1.76	0.54	2.57	0.95	2.45	2.45	2.03	0.82	1.78	1.08	0.95	1.76	0.83	1.91	1.92
G8	0.40	0.40	0.60	2.19	3.18	2.19	0.60	0.60	0.60	1.00	0.40	1.19	0.80	1.19	0.81	1.20	1.41
G9	2.90	2.90	3.73	1.87	4.36	4.98	4.78	4.58	4.98	5.20	4.40	4.78	5.19	5.39	4.65	5.44	5.45
G10	1.32	1.32	1.32	1.32	3.77	3.01	0.94	0.95	1.13	2.27	1.52	0.75	2.07	1.51	2.11	2.28	2.09
G11	0.70	0.70	1.41	3.16	1.41	2.11	1.59	1.59	1.93	1.76	0.71	0.53	1.41	2.11	0.54	1.24	1.60
G12	4.66	4.66	4.47	0.93	4.66	4.28	4.67	4.67	4.84	4.48	4.51	4.10	4.47	4.47	4.75	4.51	4.52
G13	0.51	0.51	0.85	2.03	2.20	1.69	1.70	1.02	1.52	1.87	0.85	0.85	0.85	1.52	0.17	1.20	0.68
G14	2.48	2.48	2.48	0.33	3.80	2.15	3.31	3.31	2.81	2.48	2.33	1.49	2.48	2.64	2.36	3.00	2.84
G15	2.56	2.56	3.15	3.74	2.17	3.54	2.37	2.37	3.15	3.16	1.99	2.36	3.15	2.95	4.22	3.77	3.78
G16	2.05	2.05	1.84	2.48	0.32	0.65	1.84	1.84	1.30	0.97	2.51	0.65	1.08	0.76	1.10	0.98	1.09
G17	1.44	1.44	2.01	2.16	1.30	1.30	1.15	1.01	1.01	0.58	0.73	0.14	0.86	0.43	0.88	0.58	0.44
G18	3.87	3.87	4.05	3.68	1.84	4.60	3.88	3.88	3.68	3.32	3.16	2.40	3.68	3.68	4.51	4.27	4.28
G19	0.22	0.22	0.22	2.92	3.14	3.81	0.90	0.90	1.12	1.58	0.23	3.59	0.22	2.24	1.83	2.72	2.49

G20	2.92	2.92	3.07	0.44	3.21	1.17	2.05	1.76	1.90	1.90	2.06	2.49	2.04	1.61	2.09	1.33	1.18
G21	3.47	3.47	3.47	3.47	0.53	0.53	3.48	3.48	2.93	2.27	3.50	1.47	2.93	2.27	2.31	2.15	2.16
G22	0.95	0.95	0.87	1.21	0.52	0.17	0.61	0.78	0.35	0.17	0.70	0.17	0.17	0.17	0.18	0.18	0.18
G23	3.02	3.02	3.56	1.42	3.20	2.49	3.92	4.10	3.73	3.57	3.59	3.56	3.38	3.20	2.36	3.05	3.05
G24	2.24	2.24	1.85	2.43	0.19	0.29	1.27	1.47	0.97	0.29	2.16	1.36	0.88	0.39	1.09	0.29	0.39
G25	2.51	2.51	2.63	1.14	1.94	0.57	1.26	1.26	0.91	0.92	2.89	1.14	1.49	0.57	1.63	0.46	0.46
G26	5.64	5.64	1.88	0.31	8.14	8.14	0.31	0.31	0.63	7.23	5.06	8.15	8.14	6.89	8.31	4.74	4.75

Note: W: Wricke’s ecovalence; SV: Shukla’s variance; SDi2: Eberhart and Russell’s deviation from linear regression; FWB: Finlay and Wilkinson’s regression coefficient; CV: Francis and Kannenberg’s coefficient of variation; Pi: Linn and Binn’s superiority measure of cultivar; Si1: Huehn and Nassar first index; Si2: Huehn and Nassar second index; Si3: Huehn and Nassar third index; Si6: Huehn and Nassar fourth index; NP1: Thennarasu’s first index; NP2: Thennarasu second index; NP3: Thennarasu’s third index; NP4: Thennarasu’s fourth measure; KRS: Kang’s rank sum; Y1: Yule’s modified first rank sum; Y2: Yule’s modified second rank sum

**Table 5:** Stability of genotypes based on composite measures

Genotype	C <sub>P</sub>	Rank	C <sub>NP</sub>	Rank	C	Rank
G1	0.07	1	0.04	1	0.05	1
G2	0.36	21	0.29	18	0.30	17
G3	0.21	4	0.28	17	0.26	15
G4	0.26	11	0.28	15	0.27	16
G5	0.40	24	0.42	25	0.41	25
G6	0.26	10	0.20	10	0.20	8
G7	0.26	12	0.26	14	0.26	14
G8	0.30	17	0.13	4	0.19	7
G9	0.29	14	0.21	11	0.22	10
G10	0.34	20	0.28	16	0.30	19
G11	0.26	13	0.22	12	0.23	12
G12	0.25	8	0.25	13	0.25	13
G13	0.23	5	0.17	7	0.19	6
G14	0.40	23	0.42	26	0.41	26
G15	0.42	25	0.39	24	0.40	24
G16	0.25	7	0.19	9	0.21	9
G17	0.24	6	0.10	3	0.15	4
G18	0.29	15	0.31	20	0.30	18
G19	0.33	19	0.29	19	0.31	20
G20	0.37	22	0.34	21	0.35	22
G21	0.30	16	0.38	23	0.34	21
G22	0.10	2	0.05	2	0.07	2
G23	0.42	26	0.35	22	0.37	23
G24	0.25	9	0.15	6	0.19	5
G25	0.31	18	0.18	8	0.23	11
G26	0.14	3	0.14	5	0.14	3

**Note:** C<sub>P</sub>: Composite measure on parametric measures; C<sub>NP</sub>: Composite measure on non-parametric measures; C: Composite measure based on parametric and non-parametric measure

**Table 6:** Correlation of overall composite measure with genotypes rank based on yield, parametric and non-parametric stability measures

Stability Indices	r	Stability Indices	r
W	0.04	NP1	-0.04
SV	0.04	NP2	0.16
SDi2	0.31	NP3	0.28
CVi	-0.16	NP4	0.36
FWB	0.31	KRS	0.29
Pi	0.26	Y1	0.43*
RSp	0.21	Y2	0.45*
Si1	0.38*	RSnp	0.42*
Si2	0.39*	C <sub>P</sub>	0.85**
Si3	0.48**	C <sub>NP</sub>	0.98**
Si6	0.36**		

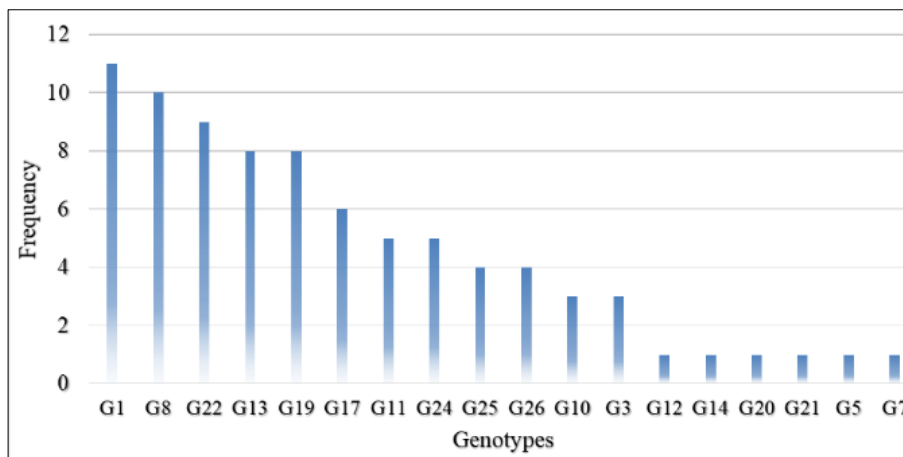
Note: W: Wricke’s ecovalence; SV: Shukla’s variance; SDi2: Eberhart and Russell’s deviation from linear regression; FWB: Finlay and Wilkinson’s regression coefficient; CV: Francis and Kannenberg’s coefficient of variation; Pi: Linn and Binn’s superiority measure of cultivar; RSp: Rank sum of parametric measures; Si1: Huehn and Nassar first index; Si2: Huehn and Nassar second index; Si3: Huehn and Nassar third index; Si6: Huehn and Nassar fourth index; NP1: Thennarasu’s first index; NP2: Thennarasu second index; NP3: Thennarasu’s third index; NP4: Thennarasu’s fourth measure; KRS: Kang’s rank sum; Y1: Yule’s modified first rank sum; Y2: Yule’s modified second rank sum; RS<sub>NP</sub>: Rank sum of non-parametric measures; C<sub>P</sub>: Composite measure on parametric measures; C<sub>NP</sub>: Composite measure on non-parametric measures



**Table 7:** Best five stable genotypes based on parametric and non-parametric measures

Rank	W	SV	SDi2	CV	Pi	Si1	Si2	Si3	Si6	NP1	NP2	NP3	NP4	KRS	Y1	Y2
1	G3	G3	G1	G7	G1	G1	G1	G1	G1	G5	G10	G1	G1	G1	G1	G1
2	G8	G8	G3	G12	G21	G8	G8	G8	G8	G8	G11	G8	G17	G8	G17	G13
3	G11	G11	G8	G14	G22	G10	G10	G19	G17	G11	G13	G13	G22	G11	G22	G17
4	G13	G13	G13	G20	G24	G19	G19	G22	G22	G13	G17	G19	G24	G13	G24	G22
5	G19	G19	G19	G26	G25	G26	G26	G26	G24	G17	G22	G22	G25	G22	G25	G24
										G19						G25

W: Wricke’s ecovalence; SV: Shukla’s variance; SDi2: Eberhart and Russell’s deviation from linear regression; CV: Francis and Kannenberg’s coefficient of variation; Pi: Linn and Binn’s superiority measure of cultivar; Si1: Huehn and Nassar first index; Si2: Huehn and Nassar second index; Si3: Huehn and Nassar third index; Si6: Huehn and Nassar fourth index; NP1: Thennarasu’s first index; NP2: Thennarasu second index; NP3: Thennarasu’s third index; NP4: Thennarasu’s fourth measure; KRS: Kang’s rank sum; Y1: Yule’s modified first rank sum; Y2: Yule’s modified second rank sum



**Fig 1:** Stability of genotypes based on modal approach

**4. Summary and Conclusions**

The present study conducted for assessing the stability of Indian mustard genotypes grown at six different environments. The data for the concerned study was taken from AICRP report 2018 on rapeseed and mustard by Directorate of Rapeseed and Mustard, Bharatpur, Rajasthan. The study included 6 parametric and 11 non-parametric measures to draw conclusion about the stability of genotypes grown at different locations. TOPSIS is a multi-criteria decision analysis method where a lower relative closeness value points towards genotypes that are more stable and high yielding.

The measure of closeness determined by TOPSIS technique uses the information of all measures. Hence it will be useful to use the measure of closeness as a decision-making measure for stability of Indian mustard genotypes. The composite measure ( $C_p$ ) based on parametric measures reveals that the genotypes G1, G22, G26, G3 and G13 are found to be stable. According to the composite measure based on non-parametric measures ( $C_{NP}$ ), the genotypes G1, G22, G17, G8 and G26 are found to be stable. On the basis on overall composite measure (C), the genotypes G1, G22, G26, G17 and G24 are the stable. On the basis of rank sum of parametric measures ( $RS_p$ ) G8, G14, G1, G22 and G11 while on the basis of rank sum of non-parametric measures ( $RS_{NP}$ ) genotypes G22, G1, G9, G17 and G13 were found to be stable. The genotypes G1, G8, G22, G13 and G19 are stable genotypes based on modal approach.

The parametric measures were found weakly correlated while non-parametric measures were found weakly to moderately correlated with overall composite measure. The composite measures based on parametric and non-parametric measures were found to be strongly correlated with overall composite measure.

**4.1 Conflict of interest**

The authors declare no conflict of interests.

**4.2 Acknowledgement**

We thank the Indian Council of Medical Research, New Delhi, for financial support through the ICMR-Junior Research Fellowship (ICMR-JRF).

**5. References**

- Allard RW, Bradshaw AD. Implications of genotype-environment interactions in applied plant breeding. *Crop Science*. 1964;4:503-508.
- Axelsson C, Giove S, Soriani S. Urban Pluvial Flood Management Part 1: Implementing an AHP-TOPSIS Multi-Criteria Decision Analysis Method for Stakeholder Integration in Urban Climate and Stormwater Adaptation. *Water*. 2021;13:2422.
- Alizadeh B, Rezaizad A, Hamedani MY, Shiresmaeili G, Nasserghadimi F, Khademhamzeh HR, *et al.* Genotype x environment interactions and simultaneous selection for high seed yield and stability in winter rapeseed (*Brassica napus*) multi-environment trials. *Agricultural Research*; c2021. p. 1-12.
- Alwala S, Kwolek T, McPherson M, Pellow J, Meyer D. A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable and high yielding maize hybrids. *Field Crops Research*. 2010;119:225-230.
- Beyzi E, Gunes A, Beyzi SB, Konca Y. Changes in fatty acid and mineral composition of rapeseed (*Brassica napus* ssp. *oleifera* L.) oil with seed sizes. *Industrial Crops and Products*. 2019;129:10-14.

6. Breese EL. The measurements and significance of genotype-environment interaction in grasses. *Heredity*. 1969;24:27-44.
7. Bishnoi S, Hooda BK. Yield stability and association among parametric and non-parametric stability measures for wheat (*Triticum aestivum* L.) genotypes in Haryana. *International Journal of Agricultural and Statistical Sciences*. 2018;14(1):323-330.
8. Bishnoi S, Hooda BK. Yield Stability and Association among Parametric and Non-parametric Stability Measures for Wheat (*Triticum aestivum* L.) Genotypes in Northern Region of India. *International Journal of Agriculture, Environment and Biotechnology*. 2018;11(1):103-109.
9. Eberhart SA, Russell WA. Stability parameters for comparing varieties. *Crop Science*. 1966;6:36-40.
10. Finlay KW, Wilkinson GN. The analysis of adaptation in a plant breeding programme. *Australian Journal Agricultural Research*. 1963;14:742-754.
11. Francis T, Kannenberg L. Yield stability studies in short season maize. I. A descriptive method for grouping genotypes. *Canadian Journal of Plant Science*. 1978;58:1029-1034.
12. Huehn M. Beitrage zur erfassung der phanotypischen stabilitat. *EDV Med Biol*. 1979;10:112-117.
13. Hwang CL, Yoon K. *Multiple Attribute Decision Making: Methods and Applications*; Springer: New York, NY, USA; c1981.
14. Jamshidmoghaddam M, Pourdad SS. Genotype x environment interactions and simultaneous selection for high oil yield and stability in rainfed warm areas rapeseed (*Brassica napus* L.) from Iran. *Euphytica*. 2011;180:321-335.
15. Kang MS. A rank sum method for selecting high yielding, stable corn genotypes. *Cereal Research Communications*. 1988;16:113-115.
16. Kang MS. Modified rank- sum method for selecting high yield, stable crop genotype. *Cereal Research Communications*. 1991;19:361-364.
17. Lin CS, Binns MR. A superiority measure of cultivar performance for cultivar x location data. *Canadian journal of plant science*. 1988;68:193-198.
18. Mamata Hooda BK, Hooda E. A new index for evaluation of G x E interaction in pearl millet using AMMI and GGE biplot analyses. *Indian Journal of Agricultural Research*. 2019;53(5):529-535.
19. Mamata, Hooda BK. AMMI and GGE biplot analyses for evaluation of G x E interaction in pearl millet. *Plant Archives*. 2020;20:206-212.
20. Nassar R, Huehn M. Studies on estimation of phenotypic stability: tests of significance for non-parametric measures of phenotypic stability. *Biometrics*. 1987;43:45-53.
21. Kumar B, Hooda E, Hooda BK. GGE Biplot Analysis of Multi-environment Yield Trials for Wheat in Northern India. *Advances in Research*; c2018. p. 1-9.
22. Kumar P, Bhar LM, Paul AK, Das S, Roy HS. Development of Composite Stability Measure using Multi Criteria Decisions Making (MCDM) Techniques. *Journal of the Indian Society of Agricultural Statistics*. 2018;72(2):121-127.
23. Pakpour S, Olishevskaya SV, Prasher SO, Milani AS, Chénier MR. DNA extraction method selection for agricultural soil using TOPSIS multiple criteria decision-making model. *American Journal of Molecular Biology*. 2013;3(04):215.
24. Qin X, Huang G, Chakma A, Nie X, Lin Q. A MCDM-based expert system for climate-change impact assessment and adaptation planning – A case study for the Georgia Basin, Canada. *Expert Systems with Applications*. 2008;34(3):2164-2179.
25. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria; c2020. <https://www.R-project.org/>.
26. RStudio Team. R Studio: Integrated Development for R. RStudio, Inc., Boston, MA; c2019. <http://www.rstudio.com/>.
27. Roemer J. Sinde die ertagdreichen sorten ertagissicherer? *Mitt DLG*. 1917;32:87-89.
28. Shukla GK. Some statistical aspects of partitioning genotype environmental components of variability. *Heredity*. 1972;29:237-245.
29. Thennarasu K. On certain non-parametric procedures for studying genotype-environment interactions and yield stability. Ph.D. thesis. P.J. School. IARI, New Delhi, India; c1995.
30. Vaezi B, Pour-Aboughadareh A, Mohammadi R, Mehraban A, Hossein-Pour T, Koohkan E, *et al.* Integrating different stability models to investigate genotype x environment interactions and identify stable and high-yielding barley genotypes. *Euphytica*. 2019;215:63.
31. Velasquez M, Hester PT. An analysis of multi-criteria decision-making methods. *International Journal of Operations Research*. 2013;10(2):56-66.
32. Yan W, Kang MS. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton; c2003.
33. Yue GL, Roozeboom KL, Schapaugh WT, Liang GH. Evaluation of soybean cultivars using parametric and non-parametric stability estimates. *Plant Breeding*. 1997;116:271-275.
34. Zavadskas EK, Turskis Z, Kildiene S. State of art surveys of overviews on MCDM/MADM methods. *Technological and Economic Development of Economy*. 2014;20:165-179.
35. Zionts S, Wallenius J. An interactive programming method for solving the multiple criteria problem. *Management Science*. 1976;22(6):652-663.
36. Wricke G. Uber eine Methode zur Erfassung der okologischen Streubreite in Feldversuchen. *Z. pflanzenzuchtg*. 1962;47:92-6.