



## A robust non-parametric stability measure to select stable genotypes

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### ABSTRACT

Climate change has a considerable influence on agricultural output, raising farmers' production risk. Nevertheless, the risk can be mitigated by selecting stable genotypes. In countries such as India, where significant proportions of farmers are smallholders or operate on marginal land, the minimization of risk is of paramount importance. Existing methods of stability measures often result in low-yielding varieties. Consequently, there is a need to develop more effective stability strategy to solve this problem without reducing yield. In light of the preceding, the Rank Based Stability Index (RSI) has been proposed for choosing genotypes based on the rank of interaction residuals to mitigate the influence of climatic changes without compromising yield. Through statistical analyses, the RSI approach demonstrates its ability to discern stable genotypes resilient to environmental fluctuations. By evaluating genotype performance across multiple environments and seasons, RSI identifies cultivars with consistent yield performance, thus offering a valuable tool for enhancing crop resilience and ensuring food security. The effectiveness of the proposed RSI approach for selecting stable genotypes from groundnut (*Arachis hypogaea* L.) data has been notably demonstrated in comparison to other methods. RSI emerges as a promising methodology for genotype selection in groundnut, offering a robust framework for mitigating the influence of climatic changes on crop yields.

**Keywords:** Environmental variations, Genotype × Environment, Interaction, Non-parametric stability analysis, Static and dynamic stability concepts

Climate change, from a statistical standpoint, is an alteration in the statistical distribution of weather over time, which can range from decades to millions of years. Melting glaciers, variations in solar radiation, and changes in the earth's orbit and axis are the causes. Increasing population trends draw our attention to the issue of global food security, which is jeopardised by climate change. The development of climate-smart agriculture is critical to the future of agricultural development. Genotype-Environment Interaction (GEI) refers to the interaction of both variations (genetic and non-genetic) on development (Comstock and Moll 1963). GE interactions are considered for strategic management in order to stabilise the farmer's economic conditions. Based on the farmer's primary objective, the trait in question is associated with two fundamental concepts of phenotypic stability. There are two different stability concepts, one biological/static stability concept and other agronomic/dynamic stability concepts.

Large numbers of stability measures were developed in the past six decades. Shukla (1972) introduced the stability variance of the  $i^{\text{th}}$  genotype, defined as its variance across all environments after removing the main effects of genotypes, environments, and the grand mean. Reviewing the literature, we observed that Kang's rank-sum stability measure has some inherent weaknesses where weights assign heavily towards yield performance rather than stability (Kang 1988). It was observed that Huehn's statistics  $S_1^{(2)}$  is highly correlated with Wricke's ecovalence ( $W_i$ ) (Wricke 1962) measures. But here we observed that Huehn's rank variance may give different results if we see the rank sum of interaction residuals for the same. When genotypes are evaluated across a moderate number of environments, the likelihood of selecting subpar genotypes through nonparametric measures is significantly reduced (Rao and Prabhakaran 2000). Therefore, it is required to develop an improved stability measure to address this issue for the betterment of stability measures. The combination of various measures may be a possible solution.

### MATERIALS AND METHODS

*Data description:* The present study was carried out during 2019 to 2022 utilized data from multi-location year trials conducted on released and pre-release groundnut

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Table 1 Rankings based on the mean data of 15 groundnut genotypes across 20 different environments

| Variety/<br>Environment | E1 | E2 | E3 | E4 | E5 | E6 | E7 | E8 | E9 | E10 | E11 | E12 | E13 | E14 | E15 | E16 | E17 | E18 | E19 | E20 |
|-------------------------|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| G1                      | 13 | 5  | 12 | 4  | 5  | 11 | 13 | 4  | 4  | 15  | 12  | 8   | 14  | 14  | 14  | 6   | 10  | 6   | 12  | 7   |
| G2                      | 10 | 4  | 4  | 4  | 3  | 5  | 6  | 2  | 10 | 14  | 4   | 11  | 2   | 6   | 3   | 4   | 7   | 7   | 4   | 1   |
| G3                      | 2  | 1  | 14 | 1  | 10 | 9  | 5  | 1  | 1  | 12  | 3   | 4   | 13  | 13  | 5   | 10  | 15  | 14  | 11  | 8   |
| G4                      | 5  | 6  | 13 | 12 | 13 | 13 | 11 | 11 | 8  | 3   | 13  | 1   | 3   | 1   | 11  | 12  | 2   | 2   | 2   | 10  |
| G5                      | 1  | 15 | 15 | 3  | 6  | 12 | 1  | 15 | 2  | 9   | 10  | 7   | 1   | 2   | 9   | 13  | 1   | 3   | 1   | 2   |
| G6                      | 15 | 13 | 9  | 15 | 11 | 14 | 14 | 13 | 12 | 10  | 14  | 15  | 8   | 15  | 13  | 15  | 6   | 11  | 14  | 15  |
| G7                      | 14 | 11 | 5  | 12 | 6  | 8  | 12 | 7  | 14 | 8   | 7   | 6   | 15  | 11  | 8   | 11  | 9   | 10  | 6   | 2   |
| G8                      | 3  | 7  | 1  | 2  | 1  | 2  | 8  | 2  | 11 | 13  | 9   | 13  | 5   | 9   | 9   | 8   | 4   | 4   | 9   | 5   |
| G9                      | 12 | 3  | 2  | 10 | 8  | 6  | 2  | 6  | 13 | 5   | 15  | 3   | 6   | 7   | 1   | 3   | 13  | 12  | 6   | 6   |
| G10                     | 4  | 2  | 11 | 6  | 9  | 15 | 2  | 10 | 15 | 1   | 8   | 2   | 12  | 3   | 15  | 14  | 5   | 1   | 4   | 12  |
| G11                     | 6  | 8  | 6  | 10 | 12 | 4  | 2  | 8  | 5  | 2   | 5   | 12  | 11  | 12  | 6   | 2   | 3   | 9   | 6   | 13  |
| G12                     | 9  | 12 | 10 | 14 | 14 | 10 | 6  | 9  | 3  | 4   | 6   | 14  | 3   | 5   | 6   | 9   | 7   | 15  | 15  | 9   |
| G13                     | 7  | 9  | 8  | 6  | 15 | 7  | 9  | 12 | 6  | 7   | 2   | 9   | 7   | 8   | 4   | 6   | 13  | 13  | 12  | 14  |
| G14                     | 8  | 14 | 7  | 6  | 4  | 3  | 9  | 14 | 7  | 11  | 11  | 10  | 9   | 4   | 12  | 5   | 12  | 8   | 10  | 11  |
| G15                     | 11 | 10 | 3  | 6  | 2  | 1  | 15 | 5  | 9  | 6   | 1   | 5   | 10  | 10  | 2   | 1   | 11  | 5   | 3   | 4   |

varieties across diverse agro-climatic zones in the former state of Andhra Pradesh, India. Data used in this study for model validation was taken from the Regional Agricultural Research Station (Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana), Palem, Telangana using a randomised block design (RBD) with three replications. The experiment involved 20 different environments and 15 genotypes, focusing on the stability analysis of pod yields, which were measured in kg/ha. Table 1 shows the ranking means data for the 15 genotypes and 20 environments over replicate.

The statistical technique used to quantify the extent of Genotype by Environment (GE) interaction is crucial for analyzing experiments in plant breeding and crop production. Traditionally, the magnitude of the GE interaction is assessed through analysis of variance (ANOVA).

*Statistical model description:* The fundamental model, incorporating replication, for a two-way crossed classification with interaction is as follows (Montgomery *et al.* 2012):

$$Y_{ijr} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijr}, \quad i = 1, 2, \dots, G; j = 1, 2, \dots, E; r = 1, 2, \dots, R.$$

where  $Y_{ijr}$ , Yield of  $i^{\text{th}}$  variety in  $j^{\text{th}}$  environment with  $r^{\text{th}}$  replicate;  $\mu$ , Overall mean;  $\beta_j$ , Random effect of  $j^{\text{th}}$  environment;  $\alpha_i$ , Fixed effect of  $i^{\text{th}}$  variety;  $(\alpha\beta)_{ij}$ , Interaction effect and  $e_{ijr}$ , Error associated with yield  $Y_{ijr}$ . Usually, stability statistic is based on the mean model which is represented as follows:

$$Y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij}, \quad \text{where } i=1, 2, \dots, G; j=1, 2, \dots, E$$

where  $Y_{ij}$ , Mean yield of  $i^{\text{th}}$  genotype at  $j^{\text{th}}$  environments;

$\mu$ , General mean;  $\alpha_i$ , Effects of  $i^{\text{th}}$  genotype;  $\beta_j$ , Effects of environment; and  $(\alpha\beta)_{ij}$ , Effects G×E interaction, respectively.

*Proposed methodology:* Stability analysis measures are classified as parametric or non-parametric (Huehn 1979, Sabaghnia *et al.* 2006). To select the stable variety, a large number of parametric stability measures are available. These measures, however, have some limitations. Non-parametric procedures outperform parametric stability measures in the following ways, (i) It possesses the capability to mitigate the influence of outliers, thereby reducing bias; (ii) There is no necessity to make any assumptions beforehand regarding the distribution of observed values; (iii) They are simple to understand and apply; (iv) The inclusion or exclusion of one or more genotypes has minimal impact on the outcomes.

*A novel statistical method to quantify the magnitude of G×E interaction:* The significance of G×E interaction is intricately linked to the quantitative assessment of genotypic stability across different environments. However, the combined analysis of variance in multi-location yield trials has limitations and fails to explore the underlying structure of the observed non-additive GE interaction. Without additional analysis, the valuable information within (G-1) (E-1) degrees of freedom is essentially forfeited if ANOVA techniques are unable to discern the pattern of response of the Genotype by Environment (GE) interaction (Crossa 1990). Furthermore, if the observations are qualitative in nature, non-normally distributed data, or data fail to meet the assumptions of the parametric test, the ANOVA technique of quantifying the magnitude of G×E interaction over environments is ineffective; in this case, an alternative measure based on rank is required. As a result, a robust

rank-based measure has been developed to quantify the magnitude of  $G \times E$  interaction.

Spearman's rank correlation coefficient was utilized to calculate the correlations between genotypes based on their rankings (Garde et al. 2023). In this approach,  $G$  genotypes are arranged in a similar order in both parameters i.e.  $x_i$  (first parameter) indicates the order of ranking of the  $i^{\text{th}}$  genotype for the first environment,  $y_i$  (second parameter), indicates the ranking order of the  $i^{\text{th}}$  genotype of the second environment. Further, Spearman's rank correlation coefficient (RS) can be computed as follows:

$$1 - \frac{6 \sum d_i^2}{n(n^2 - 1)}$$

where  $d_i$ ,  $x_i - y_i$  ( $i = 1, 2, \dots, n$ ). The average of these correlation coefficients (excluding self) may be designated as Index for Genotype-Environment Interaction (IGEI).

$$\text{IGEI} = \frac{[\sum \sum (r_{ij} - 1)]}{(ij - j)}; I = j = [1, \dots, E]$$

where  $E$ , Number of environments. IGEI value near 1 indicates higher  $G \times E$  interaction.

*An improved non-parametric approach to measure the stability:* With the genotype supposed to be stable if  $\sigma_i^2$ , the variability based on interaction residual  $V_{ij}$  associated with that genotype is small. A plethora of stability measures are documented in the literature, often interpreted as indicators of the spread of  $V_{ij}$ 's. The main drawback of existing measures is the residuals are assumed to be normal. Many times the parent distribution of the  $V_{ij}$ 's effects departs from normality (Piepho 1992), under such conditions the existing measures are not useful. To overcome this problem, the following method has been proposed in this work.

The proposed algorithm is as follows:

Step 1: Calculate the rank of all genotypes in each environment based on the interaction residual ( $V_{ij}$ ) denoted as  $r_{ij}$  i.e.  $i^{\text{th}}$  genotype rank in  $j^{\text{th}}$  environment where,  $i=1, \dots, G$  and  $j=1, \dots, E$ .

Step 2: Compute the rank sum of genotypes across all environments that is  $i^{\text{th}}$  genotypes across environments based on absolute value of  $V_{ij} = Y_{ij} - \mu - \alpha_i - \beta_j$ ;

$$RS_i = \sum r_{ij}$$

Step 3: Rank all the Rank-Sum of genotype calculated in step 2 in which lower rank is given for lower value.

Step 4: Compute the variance ( $S_i^2$ ) of each genotype across environments based on the absolute value of  $V_{ij}$ .

$$S_i^2 = \frac{\sum_{j=1}^E \square(v_{ij} - v_i)}{E - 1}; j = 1, \dots, E$$

where  $v_{ij}$ , Value of interaction residual of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment.

Step 5: Rank all the variances of genotypes ( $rs_i^2$ ) calculated in 3<sup>rd</sup> step in which lower rank is given for lower value.

Step 6: Linear combination of rank of RS (step 2) and  $S_i^{(2)}$  (step 4) are used in the proposed algorithm, which is

denoted as rank based stability index (RSI).

$$RSI_i = \frac{(r_{RS_i} + rs_i^2)}{2}$$

Lower rank of statistic RS gives more stable variety and lower rank of statistic  $S_i^{(2)}$  also gives more stable variety. But both statistics give different ranks for the same experiments.

where  $r_{RS}$ , Rank of statistic based on rank-sum and  $rs_i^2$ , Rank of statistic based on variance.

Step 7: Re-rank the proposed estimator computed in step 6 and which is denoted as  $r_{RSI}$  in which lower rank is given for lower value. Lower rank of RSI indicates more stable genotypes.

## RESULTS AND DISCUSSION

*Empirical illustration:* To assess the influence of environment (E), genotype (G), and their interaction  $G \times E$ , a two-way combined analysis of variance (ANOVA) was conducted using SAS software version 9.4, accessible at the ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India. The significance of ANOVA lies in its capability to estimate the variance components associated with different sources of variation, including genotype and  $G \times E$  interaction. If the  $G \times E$  interaction effect is found to be significant, we will conduct additional research on genotype variation in terms of stability.

*Results of rank based stability Index (RSI):* Stability measures utilizing rank-based indices offer a feasible alternative to existing parametric and non-parametric measures based on absolute value of ( $V_{ij} = Y_{ij} - \mu - \alpha_i - \beta_j$ ). We observed the ranks of interaction residuals of 15 groundnut genotypes in each environment. Here, we can see the genotype G14 has minimum rank-sum ( $RS_{14}=103$ ) across 20 environments and described as from E1–E20 is 2, 13, 5, 4, 7, 12, 3, 12, 1, 3, 2, 3, 2, 7, 2, 7, 8, 1, 8 and 1 which has been seen most stable but their variance ranked as 6 out of 15 genotypes. Similarly, genotype G5 has maximum rank-sum (209) across environments and described as from E1–E20 is 14, 14, 15, 5, 4, 13, 14, 15, 6, 6, 6, 5, 15, 13, 8, 14, 15, 5, 14 and 8 which has been seen least stable but their variance ranked as 9 out of 15 genotypes which gives some contradict results. Hence, here we developed a modified stability index as explained in the methodology section. According to the proposed rank based stability index (RSI) it has been seen the genotype G2 is most stable. By comparing with other measures of stability for multi-location trials, rank based stability index (RSI) has been found as a satisfactory measure of stability for selecting stable varieties.

Further, Table 2 indicates the value of Y-mean, value of ecovalence ( $W_j$ ) (Wrike 1962), value of rank based stability index (RSI) (proposed method) and  $S_i^{(2)}$ ,  $S_i^{(3)}$ ,  $S_i^{(5)}$ ,  $S_i^{(6)}$  (Nassar and Huehn 1987) are the stability measures of all 15 groundnut genotype in each 20 environments respectively.

*Ecovalence is straightforward to calculate and is expressed as:*

$$W_i = \sum_j \square(Y_{ij} - Y_i - Y_j + Y_{..})^2$$

where  $Y_{ij}$ , Mean performance of the  $i^{th}$  genotype in the  $j^{th}$  environment;  $Y_{.j}^-$  and  $Y_{i.}^-$ , Environment and genotype mean deviations, and  $Y^-$ , Overall mean.

Rank variance in each environments ( $S_i^{(2)}$ ):

$$S_i^{(2)} = \frac{\sum_{j=1}^E (r_{ij} - \bar{r}_i)^2}{(E-1)}$$

where E, Total environments count;  $\bar{r}_i$ , Mean of ranks over environments;  $r_{ij}$ , Rank of genotypes in each environment based on interaction residual  $V_{ij}$ ; and ranks are assigned in ascending order from lowest to highest.

The sum of absolute rank differences ( $S_i^{(3)}$ ) of a genotype per unit of  $\bar{r}_i$ :

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

where E, Total number of environments;  $\bar{r}_i$ , Mean of ranks across all environments for genotype;  $r_{ij}$ , Rank of  $i^{th}$  genotypes in  $j^{th}$  environment based on mean yield and , and ranks are lated in ascending order from lowest to highest.

Mean deviation in rank in each environments ( $S_i^{(5)}$ ):

$$S_i^{(5)} = \frac{\sum_{j=1}^E |r_{ij} - \bar{r}_i|}{E}$$

where E, Number of environments;  $\bar{r}_i$ , Mean of ranks over environments;  $r_{ij}$ , rank of  $i^{th}$  genotypes in  $j^{th}$  environment based on mean yield.

Rank variance/unit of  $\bar{r}_i$  ( $S_i^{(6)}$ ):

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

where E, Number of environments;  $r_{ij}$ , Rank of genotypes in each environment based on interaction residual  $V_{ij}$  and

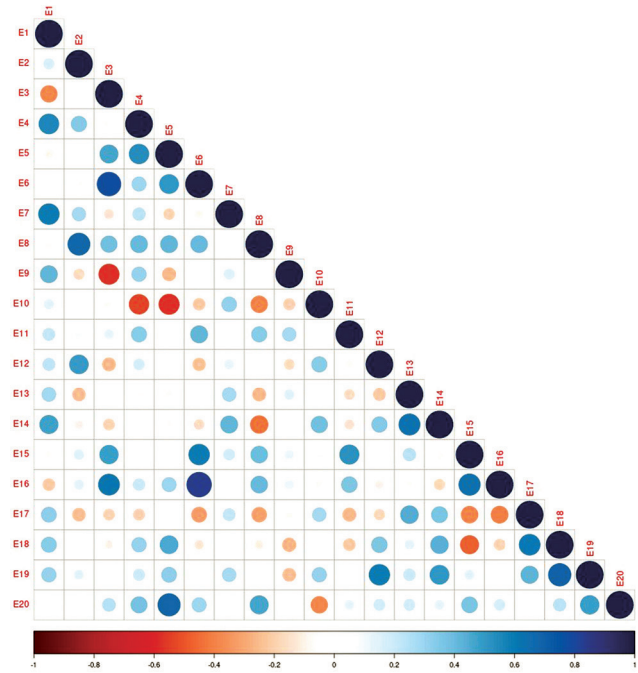


Fig. 1 Correlogram showing the correlation among all environments (E1–E20).

ranks are assigned from lowest to highest.

We observed the correlation among the considered environment to know the diverse effect of various environments on genotypes (Fig. 1). The conventional Wricke’s Ecovalence ( $W_i$ ) parametric stability approach shows genotype G14 is most stable. The Rank-sum also shows genotype G14 is most stable and Rank variance  $S_i^{(2)}$  show the genotype G7 is most stable. These measures give contradictory results about the stability of a given genotype. As different stability measures give different results, therefore, we proposed a ranked based stability

Table 2 Calculated value of stability measures for 15 groundnut genotypes across 20 environments

| Genotypes | Y-mean  | $W_i$    | RSI | $S_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(5)}$ | $S_i^{(6)}$ |
|-----------|---------|----------|-----|-------------|-------------|-------------|-------------|
| G1        | 1514.7  | 1061047  | 6.5 | 13.4        | 7.11        | 3.04        | 29.82       |
| G2        | 1312.4  | 741384.4 | 2   | 13.4        | 9.15        | 2.995       | 38.92       |
| G3        | 1386.7  | 3050912  | 13  | 20.8        | 8.33        | 4           | 41.13       |
| G4        | 1321    | 3877588  | 12  | 19.5        | 8.00        | 4           | 37.00       |
| G5        | 1304.25 | 4191730  | 12  | 19.0        | 7.86        | 4.105       | 34.54       |
| G6        | 1694.25 | 1009306  | 5   | 17.7        | 10.75       | 3.6         | 50.18       |
| G7        | 1468.5  | 632958.4 | 3.5 | 11.1        | 7.50        | 2.755       | 28.65       |
| G8        | 1269.5  | 1074312  | 8   | 20.6        | 11.09       | 3.855       | 56.25       |
| G9        | 1373.55 | 1547303  | 7.5 | 14.6        | 7.76        | 3.26        | 32.95       |
| G10       | 1365.2  | 2351611  | 13  | 22.7        | 8.55        | 4.02        | 45.83       |
| G11       | 1368.95 | 1003308  | 5.5 | 13.7        | 7.77        | 2.99        | 33.79       |
| G12       | 1498.95 | 1103088  | 12  | 24.0        | 10.24       | 4.225       | 55.24       |
| G13       | 1464.45 | 1518851  | 6.5 | 18.0        | 9.71        | 3.4         | 48.86       |
| G14       | 1443.15 | 598202.3 | 3.5 | 15.2        | 12.74       | 3.28        | 56.03       |
| G15       | 1273.5  | 1639291  | 9.5 | 20.1        | 9.46        | 3.76        | 47.92       |

RSI, Rank based stability index;  $S_i^{(2)}$ , Huehn’s variance;  $S_i^{(3)}$ ,  $S_i^{(5)}$ ,  $S_i^{(6)}$ , Huehn’s non-parametric stability index.

index (RSI) which shows genotype G2 is more stable than other genotypes. In support of the results of the proposed method, the correlation coefficient based on Spearman's rank correlation was calculated to compare the stability measures used. Table 3 depicts a strong Spearman's rank correlation (0.84) between ranked based stability index (RSI) and Wricke's Ecovalence ( $W_i$ ). Further, biplot has been obtained on the same data set for visual interpretation using R programming by the package 'GGEBiplotGUI'.

The same data sets were also subjected to a biplot the graphical method of stability analysis (Fig. 2). It also suggests that genotypes G2, G6, G7, and G14 are stable genotypes. Another disadvantage of biplot is that it does not offer a magnitude of stability.

We can also see that the biplot only explains 55.69% of the variation, indicating that it does not contain enough variation to provide adequate results. Despite the fact that the data under consideration violates the parametric assumption, the proposed method outperformed conventional methods.

Kang *et al.* (2009) undertook a review examining the impacts of climate change on crop yield, crop productivity, and food security. He discussed the utilization of climate and crop yield models for evaluating multi environmental trails and its impacts on crop productivity. This model requires the integration of uncertainties and the formulation of risk management strategies. Crop yields can be increased or maintained by using proper crop production management and agronomic practices, including the selection of appropriate genotypes. Future breeding technologies must focus on developing lines that are more adaptable to climatic variations. Climate change is expected to reduce major world crop yields due to water stress, droughts, and floods, according to the BBC. The identification of superior varieties for improved production is critical to the success of crop breeding improvement activities. A variety is considered stable if it has the ability to produce a consistent yield in a variety of environments while also exhibiting high phenotypic stability. Phenotype is determined by

Table 3 Correlation coefficient based on Spearman's rank correlation employed to statistically compare the stability indices with proposed measures RSI

| Stability measures | RS    | $S_i^{(2)}$ | RSI   | $W_i$ | $S_i^{(3)}$ | $S_i^{(5)}$ | $S_i^{(6)}$ |
|--------------------|-------|-------------|-------|-------|-------------|-------------|-------------|
| RS                 | 1     |             |       |       |             |             |             |
| $S_i^{(2)}$        | 0.38  | 1           |       |       |             |             |             |
| RSI                | 0.99  | 0.45        | 1     |       |             |             |             |
| $W_i$              | 0.84  | 0.64        | 0.84  | 1     |             |             |             |
| $S_i^{(3)}$        | -0.58 | 0.48        | -0.50 | -0.17 | 1           |             |             |
| $S_i^{(5)}$        | 0.53  | 0.92        | 0.60  | 0.74  | 0.36        | 1           |             |
| $S_i^{(6)}$        | -0.45 | 0.61        | -0.37 | -0.06 | 0.98        | 0.48        | 1           |

RS, Rank-Sum;  $S_i^{(2)}$ , Huehn's variance; RSI, Rank based stability index;  $W_i$ , Wricke ecovalence;  $S_i^{(3)}$ ,  $S_i^{(5)}$  and  $S_i^{(6)}$ , Huehn's non-parametric stability measures.

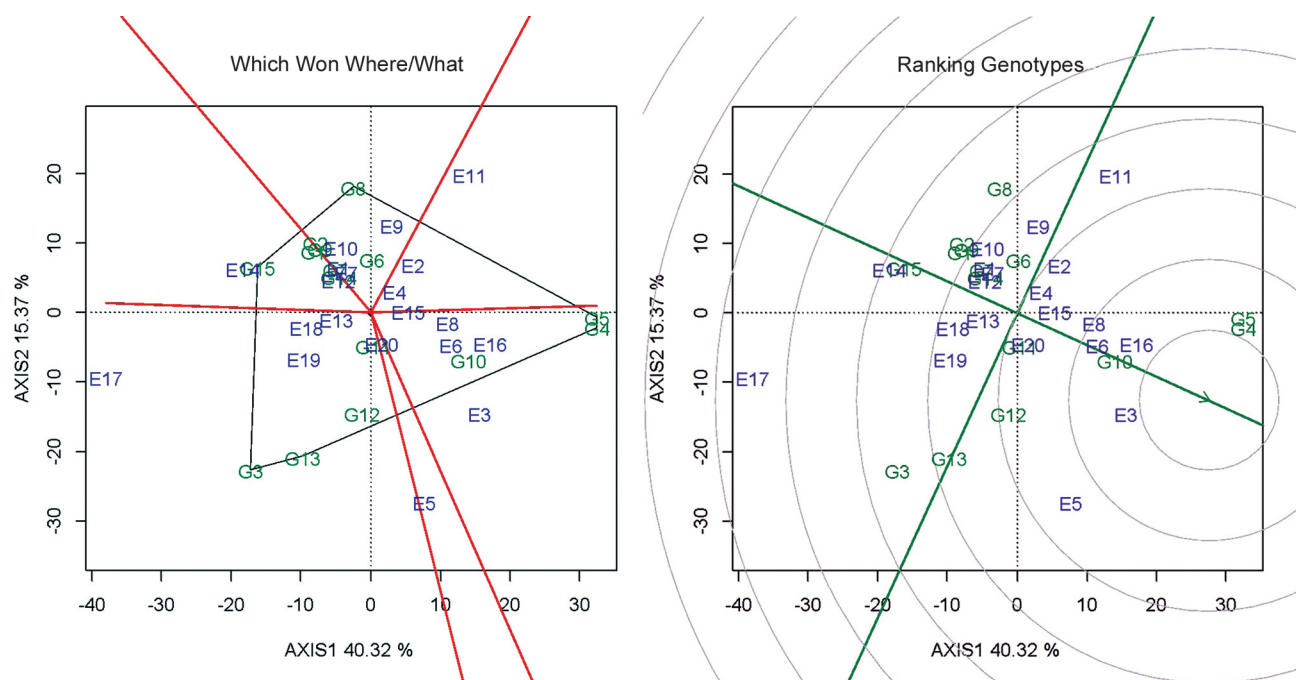


Fig. 2 Biplots for visual analysis of stability.

genotype (G), environment (E), and their interactions noted as Genotype × Environment Interaction (GEI). To understand the concept of stability, we must first understand the phenotypic stability, yield stability, and adaptation in various contexts (Becker and Leon 1988). Different varieties respond differently across a range of environments, implying that the relative performance of varieties varies depending on the environment. The phenotypic response to environmental change differs between varieties. Pour-Aboughadareh *et al.* (2022) developed various new stability indices to study the GEI effect. Evaluation of maize hybrid stability with univariate parametric approaches (Habib Shojaei *et al.* 2022). From a statistical standpoint, the significance of big data in agriculture was explored (Kumar *et al.* 2018). Composite stability measure through the utilization of Multi Criteria Decision Making (MCDM) techniques was proposed and real dataset was also analysed (Kumar *et al.* 2018). Stability analysis was conducted for cane and sugar yield in advanced sugarcane genotypes (Kumar *et al.* 2018). Discovering stable safflower genotypes in variable environments using both parametric and non-parametric methodologies (Afzal *et al.* 2021).

The combined analysis of variance revealed significant magnitude in the Genotype by Environment (GE) interaction effect, which was corroborated by rank correlation analysis. Stability measures based on ranks offer a valuable alternative to current methods. This involves calculating the rank sum of each genotype across environments based on interaction residuals and determining the variance of each genotype across environments using the absolute values of interaction residuals. High concordance of proposed stability measure with Wricke's ecovalence ( $W_i$ ) and Shukla's stability variance ( $\sigma^2$ ) which are largely used stability measures. Proposed rank based stability index (RSI) provides a useful alternative for the biological/static stability concept. The RSI is a non-parametric stability measure that provides a reliable and robust stability measure. It can be used for qualitative data in the future because it is a rank-based measure that is simple to calculate and understand.

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