



## RESEARCH ARTICLE

## Genotype × Environment interaction and yield stability analysis in ridge gourd (*Luffa acutangula* L.) using AMMI and GGE approaches

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### Abstract

Ridge gourd (*Luffa acutangula* L. Roxb.) is an economically important cucurbit vegetable cultivated widely in tropical and subtropical regions; however, limited information is available on yield stability across seasons. The present study aimed to assess genetic variability, genotype × year interaction, and yield stability of 64 ridge gourd genotypes evaluated over three consecutive years during rainy season in a randomized block design with three replications. Pooled analysis of variance revealed highly significant ( $p \leq 0.001$ ) differences among genotypes for yield and its component traits, indicating substantial exploitable genetic variability. The effects of year and genotype × year interaction were also significant for most traits, highlighting the influence of seasonal variation and differential genotypic response across years. To elucidate interaction patterns, additive main effects and multiplicative interaction (AMMI) and genotype plus genotype × Environment (GGE) biplot analyses were performed. The AMMI model showed that the first two interaction principal component axes captured 100% of the interaction sum of squares, enabling identification of stable genotypes. GGE biplot analysis ((PC1 = 65.21% and PC2 = 22.73%, totaling 87.94%)) effectively discriminated genotypes based on mean yield and stability, revealed “whichwonwhere” patterns, and identified ideal genotypes namely RDG35 for 2024 (E2), VRRG271 for 2025 (E3), and VRRG817 for 2023 (E1) combining high productivity with wide adaptability. The integration of pooled ANOVA with AMMI and GGE approaches proved efficient in selecting superior and stable genotypes. The findings provide valuable insights for ridge gourd breeding programs focused on developing high-yielding and widely adapted cultivars under variable environmental conditions.

**Keywords:** Ridge gourd, *Luffa acutangula*, genotype × environment interaction, AMMI analysis, GGE biplot, yield stability, multiyear evaluation

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**Citation:** Chaubey, T., Sagar, V., Pandey, S., Gautam, K.K., Kumar, R., & Singh, A.K. (2026). Genotype × environment interaction and yield stability analysis in ridge gourd (*Luffa acutangula* L.) using AMMI and GGE approaches. *Vegetable Science*, 53(1), 79-86.

**Source of support:** Nil

**Conflict of interest:** None.

**Received:** 17/03/2026; **Revised:** 13/04/2026; **Accepted:** 13/04/2026

### Introduction

Ridge gourd (*Luffa acutangula* L. Roxb.), an economically important member of the family Cucurbitaceae (2n = 26), is widely cultivated across tropical and subtropical regions of Asia and parts of Africa for its tender immature fruits. In India, ridge gourd was grown on approximately 10.03 thousand hectares in the 2020-21 seasons, yielding 3.16 million tonnes (NHB 2020-21). The crop plays a significant role in nutritional security due to its richness in dietary fiber, vitamins (especially vitamin C), minerals, and bioactive phytochemicals with antioxidant and medicinal properties (Dhiman et al., 2012). Every 100 g of the palatable part of the ridge gourd contain 0.5 g of fiber, 0.5% protein, 0.35% carbohydrate, 37 mg of carotene, 5.0 mg of vitamin C, 18 mg of calcium, and 0.5 mg of vitamin E (Patel and Bahadur, 2024). Ridge gourd is also known to have medicinal property in Indian traditional medicine system, used to treat anemia, leucoderma, Kaph, Vata and splenic hypertrophy. It is an emetic that has long been used to treat stomach ailments and fevers (Chakravarthy 1959). Ridge gourd contains anti-inflammatory and antibacterial qualities, aids in weight loss and is good for diabetics.

Yield in ridge gourd is a complex quantitative trait influenced by multiple component characters, including flowering time, vine length, fruit size, fruit weight, and number of fruits per plant. The effectiveness of breeding for high yield depends on the magnitude of genetic variability and the stability of trait expression across environments (Suresh *et al.* 2022). In vegetable crops, significant phenotypic variability has been widely reported for yield and yield-contributing traits, indicating ample scope for genetic improvement through selection and hybridization (Singh *et al.* 2015).

A major constraint in breeding for enhanced productivity is the presence of genotype  $\times$  environment interaction ( $G \times E$ ), which results in differential genotypic responses across environments. Significant  $G \times E$  interaction reduces the predictability of genotype performance and complicates selection decisions (Allard & Bradshaw, 1964; Yan & Kang, 2003). In ridge gourd, seasonal fluctuations across years can substantially alter vegetative growth, flowering synchronization, and fruit development, thereby affecting yield stability. Therefore, multiyear and multienvironment evaluation is essential to obtain reliable estimates of genotypic performance and adaptability (Annicchiarico, 2002; Farshadfar *et al.*, 2011). Pooled analysis of variance (ANOVA) across years enables partitioning of total variation into components attributable to genotypes, environments, and  $G \times E$  interaction. Significant genotypic variance indicates the presence of exploitable variability, whereas significant interaction variance highlights the need for stability analysis (Crossa *et al.*, 2012). However, conventional ANOVA alone does not adequately explain the pattern of interaction. To address this limitation, multivariate statistical models such as the additive main effects and multiplicative interaction (AMMI) model and the genotype plus genotype  $\times$  environment (GGE) biplot methodology have been widely adopted in crop improvement programs (Gauch, 2013; Yan *et al.*, 2007).

In cucurbit crops, significant  $G \times E$  interaction for yield and related traits has been reported in bitter melon (Moharana *et al.*, 2025) and sponge melon (Chaubey *et al.*, 2025), emphasizing the necessity of multienvironment testing. However, comprehensive multiyear phenotypic evaluation combined with AMMI and GGE biplot analysis in ridge gourd remains limited. In the context of climate variability and increasing environmental unpredictability, breeding for resilience and stability has become even more critical (Ceccarelli, 2015). Multiyear evaluation, coupled with robust statistical models such as AMMI and GGE biplot, provides a powerful framework to dissect complex interaction effects and enhance selection efficiency. Therefore, the present study was undertaken to (i) assess the magnitude of genetic variability among ridge gourd genotypes under multiyear evaluation, (ii) quantify genotype  $\times$  year interaction through pooled ANOVA, and (iii) identify high-yielding and stable genotypes using AMMI and GGE biplot analysis.

## Materials and Methods

### Experimental material and design

The present investigation was conducted using 64 ridge gourd genotypes (Table 1) evaluated over three consecutive years during the *Kharif* season of 2023 (E1), 2024 (E2) and 2025 (E3), under open field conditions at ICAR-IIVR, Varanasi. Standard agronomic and plant protection practices were followed uniformly in all years to raise a healthy crop. The experiment was laid out in a randomized block design (RBD) with three replications during each year. Each genotype was grown in a plot consisting of 10 plants with spacing of 150  $\times$  50 cm on flat bed. Observations were recorded on five randomly selected plants from each replication on fruit colour and 9 quantitative traits such as days to first male flower appearance (DFMF), days to first female flower appearance (DFFF), days to first harvesting (DFH), average fruit weight (g; AFW), average fruit length (cm; AFL), average fruit diameter (cm; AFD), average vine length (cm; AVL), number of fruits per plant (NFPP), yield (q/ha). The mean values of five plants per plot were used for statistical analysis.

### Pooled analysis of variance (ANOVA)

Individual year-wise ANOVA was first performed to test homogeneity of error variances. Upon confirmation of homogeneity, pooled analysis across years was conducted. The linear statistical model for pooled ANOVA across years was:

$$Y_{ijk} = \mu + Y_i + R_j(Y_i) + G_k + (GY)_{ik} + \varepsilon_{ijk}$$

Where:

- $Y_{ijk}$  = observation of  $k$ th genotype in  $j$ th replication of  $i$ th year
- $\mu$  = overall mean
- $Y_i$  = effect of  $i$ th year
- $R_j(Y_i)$  = effect of  $j$ th replication nested within  $i$ th year
- $G_k$  = effect of  $k$ th genotype
- $(GY)_{ik}$  = genotype  $\times$  year interaction effect
- $\varepsilon_{ijk}$  = experimental error

Years and replications were treated as random effects, while genotypes were considered fixed.

### Additive main effects and multiplicative interaction

The additive main effects and multiplicative interaction (AMMI) model was used to further partition the genotype  $\times$  year interaction.

The AMMI model is expressed as:

$$Y_{ge} = \mu + G_g + E_e + \sum_{n=1}^N \lambda_n \alpha_{gn} \gamma_{en} + \rho_{ge}$$

Where:

- $Y_{ge}$  = mean of genotype  $g$  in environment  $e$
- $\mu$  = grand mean
- $G_g$  = genotype effect

**Table 1:** Showing the name of ridge gourd genotypes used for the study of genotype × environment interaction

| Genotype     | Genotype     | Genotype     | Genotype        | Genotype       | Genotype       |
|--------------|--------------|--------------|-----------------|----------------|----------------|
| VRRG-3-10    | VRRG-12-10   | VRRG-8-17    | VRRG-8-10       | VRRG-35-2016   | Ridge gourd-29 |
| VRRG-6       | VRRG-4-10    | VRRG-17-17   | VRRG-17-2016    | Ridge gourd-82 | Ridge gourd-67 |
| VRRG-26      | VRRG-9       | VRRG-25-2016 | VRRG-181        | Ridge gourd-66 | Ridge gourd-57 |
| VRRG-83      | VRRG-88      | VRRG-1-22    | VRRG-29         | Ridge gourd-19 | Ridge gourd-23 |
| VRRG-39      | VRRG-46-2016 | VRRG-1-16    | VRRG-103        | Ridge gourd-65 | Ridge gourd-12 |
| VRRG-10-2016 | VRRG-46      | VRRG-7-2016  | VRRG-23         | Ridge gourd-28 | RDG-35         |
| VRRG-7-2     | VRRG-5A      | VRRG-55-2016 | VRRG-2-18       | Ridge gourd-27 | RDG-41         |
| VRRG-112     | VRRG-13-17   | VRRG-12-17   | VRRG-110        | Ridge gourd-74 | RDG-57         |
| VRRG-4-17    | VRRG-37-2016 | VRRG-6A      | VRRG-41         | Ridge gourd-24 | RDG-22         |
| VRRG-28-2016 | VRRG-27-1    | VRRG-76-2016 | VRRG-68-2016    | Ridge gourd-45 |                |
| VRRG-42-2016 | VRRG-75-2016 | VRRG-59-2016 | VRRG-25-10-2016 | Ridge gourd-20 |                |

**Table 2:** Pooled analysis of variance for different traits of ridge gourd

| Source of Variation | df  | DFMF     | DFFF     | DFH      | AFW      | AFL       | AFD        | AVL       | NFPP      | Yield    |
|---------------------|-----|----------|----------|----------|----------|-----------|------------|-----------|-----------|----------|
| Year                | 2   | 900.1*** | 969.2*** | 881.2*** | 42615*** | 279.20*** | 0.3127***  | 443859*** | 0.472     | 56914*** |
| Genotype            | 63  | 7.2***   | 8.7***   | 5.1**    | 1752***  | 65.87***  | 0.0584***  | 2041***   | 2.236***  | 3192***  |
| Rep (Year)          | 6   | 43.0***  | 71.0***  | 21.7***  | 918***   | 32.55***  | 0.0266***  | 699       | 1.045**   | 1467***  |
| Year × Genotype     | 126 | 9.7***   | 5.0***   | 6.2***   | 601***   | 9.85***   | 0.00782*** | 2120**    | 0.7669*** | 957***   |
| Error               | 378 | 2        | 1.8      | 3.2      | 36       | 1.31      | 0.0021     | 680       | 0.3388    | 98       |

Where: \*\*\* Significant at  $p \leq 0.001$ , \*\* Significant at  $p \leq 0.01$ , \*Significant at  $p \leq 0.05$ , ns = non-significant

Where: DFMF (days to first male flower appearance), DFFF (days to first female flower appearance), DFH (days to first harvesting), AFW (average fruit weight), AFL (average fruit length), AFD (average fruit diameter), AVL (average vine length), NFPP (number of fruits per plant), yield (q/ha).

- $E_e$  = environment (year) effect
- $\lambda_n$  = singular value of  $n^{\text{th}}$  interaction principal component axis (IPCA)
- $\alpha_{gn}$  and  $\gamma_{en}$  = genotype and environment PCA scores
- $\rho_{ge}$  = residual

### GGE biplot analysis

GGE biplot analysis was conducted to visualize genotype performance and stability across years. Unlike AMMI, GGE focuses on genotype main effects and genotype × environment interaction.

The GGE model is represented as:

$$Y_{ge} - \mu - E_e = \sum_{k=1}^2 \lambda_k \xi_{gk} \eta_{ek} + \delta_{ge}$$

Where:

- $Y_{ge}$  = mean performance
- $E_e$  = environment effect
- $\lambda_k$  = singular value
- $\xi_{gk}, \eta_{ek}$  = genotype and environment scores

All statistical analyses were performed using R software (R Core Team, 2024) with the packages: agricolae, lme4, metan, GGEbiplotGUI, ammistability and graphs were generated using ggplot2 where necessary.

## Results

The current investigation was conducted to investigate the 64 Ridge gourd genotype for nine quantitative traits, to decipher the genotype × environment interaction and to select the most promising and stable genotypes.

### Mean performance of genotypes

Based on the final 3-year mean yield (q/ha) values, VRRG-8 to 10 recorded the highest mean yield (180.03), followed by VRRG-17-2016 (177.67) and VRRG-13-17 (177.27). Other high-yielding genotypes were VRRG-42-2016 (175.37), VRRG-12-17 (175.10), VRRG-27-1 (174.80), VRRG-25-10-2016 (174.23), and VRRG-8-17 (174.17). The remaining entries in the top ten were VRRG-7-2016 (167.77) and VRRG-181 (167.40).

### Pooled analysis of variance

The pooled analysis of variance across three years (Table 2) revealed highly significant differences among genotypes for all the traits studied, indicating the presence of substantial genetic variability in the experimental material. The effect of Year was highly significant ( $p \leq 0.001$ ) for all traits except number of fruits per plant (NFPP), indicating considerable environmental influence on trait expression across years. The

significant year effect for traits such as DFME, DFFF, DFH, AFW, AFL, AFD, AVL, and yield suggests that seasonal variations contributed markedly to phenotypic performance. The Genotype mean squares were highly significant ( $p \leq 0.001$ ) for all traits except DFH, which was significant at  $p \leq 0.01$ . This indicates the existence of sufficient genetic variability among genotypes for yield and its component traits, thereby offering scope for effective selection and genetic improvement. The year  $\times$  genotype interaction was highly significant ( $p \leq 0.001$ ) for all traits studied, demonstrating that genotypes responded differently across years. This differential response suggests the presence of genotype–environment interaction and indicates the need to evaluate genotypes across multiple environments to identify stable performers. The effect of replications within Year was also significant for most traits, except for average vine length (AVL), where it was non-significant. Overall, the significant variation due to genotype and genotype  $\times$  year interaction highlights the importance of multi-year evaluation for identifying stable and high-performing genotypes for yield and related traits.

#### AMMI ANOVA

The AMMI analysis of yield revealed highly significant effects of environment, genotype, and their interaction. The environment main effect was significant, indicating that mean yield differed markedly among the three test environments. The replicate effect within environments was also significant, confirming the presence of within-environment experimental variation. Genotypic differences were highly significant, demonstrating substantial genetic variability for yield among entries. Importantly, the genotype  $\times$  environment interaction (GEN  $\times$  ENV) was highly significant, evidencing differential genotype performance across environments and justifying stability and adaptation analyses. Decomposition of the interaction showed that the first two interaction principal components were both highly significant and together captured the entire interaction pattern, with IPCA1 (PC1) explaining 66.7% ( $p < 0.001$ ) and IPCA2 (PC2) explaining 33.3% ( $p < 0.001$ ) of the GE sum of squares (Table 3). Thus, the AMMI model based on the first two IPCAs provided an adequate description of G  $\times$  E for yield in this trial.

#### AMMI analysis

The AMMI1 biplot for yield (q/ha) revealed distinct genotype  $\times$  environment (G  $\times$  E) patterns, with the first interaction principal component (IPCA1/PC1) explaining 66.7% of the G  $\times$  E interaction sum of squares, indicating that most crossover responses among genotypes were captured by this axis. Mean yield was displayed on the horizontal axis, such that genotypes positioned to the right exhibited higher average productivity across environments, whereas those to the left were comparatively low yielding. Genotype stability

**Table 3:** Analysis of variance (ANOVA) for the AMMI model showing the effects of environment (ENV), genotypes (GEN), and genotype  $\times$  environment interaction (GEN  $\times$  ENV), with decomposition of the interaction into the first two interaction principal component axes (IPCA1/PC1 and IPCA2/PC2).

| Source           | Df  | Sum Sq | Mean Sq | F value | Proportion (%) |
|------------------|-----|--------|---------|---------|----------------|
| ENV              | 2   | 113828 | 56914.1 | 38.79   | –              |
| REP(ENV)         | 6   | 8804   | 1467.4  | 14.99   | –              |
| GEN              | 63  | 201065 | 3191.5  | 32.61   | –              |
| GEN $\times$ ENV | 126 | 120547 | 956.7   | 9.77    | –              |
| PC1 (IPCA1)      | 64  | 80459  | 1257.2  | 12.84   | 66.7           |
| PC2 (IPCA2)      | 62  | 40089  | 646.6   | 6.61    | 33.3           |
| Residuals        | 378 | 36998  | 97.9    | –       | –              |
| Total            | 701 | 601791 | 858.5   | –       | –              |

was inferred from proximity to the PC1 = 0 line, where genotypes near the origin showed minimal interaction and thus broad adaptation, while large positive or negative PC1 scores indicated specific adaptation. The test environments were strongly contrasting: E1 had a large positive PC1 score and E2 a large negative PC1 score, demonstrating that both environments were highly interactive and discriminating, with E1 tending to favor genotypes with positive PC1 scores and E2 favoring those with negative PC1 scores; in contrast, E3 was located close to the origin (PC1  $\approx$  0), suggesting relatively lower G  $\times$  E interaction and a more representative, less discriminating environment. High-yielding genotypes were concentrated on the right-hand side of the biplot, notably VRRG25102016 (142.87 q/ha), VRRG271 (163.51), VRRG462016 (140.65) and VRRG592016 (148.88), with additional high-yielding entries including VRRG1717 (151.35), VRRG817 (153.59), VRRG5A (142.06) and VRRG181 (139.60). Among these, genotypes closest to PC1 = 0, particularly VRRG25102016 (142.87 q/ha) and VRRG122 (132.19), combined high mean yield with greater stability and are therefore promising candidates for broad adaptation, whereas low-yielding genotypes clustered on the left side included Ridge gourd28 (99.95), Ridge gourd66 (96.69) and RDG22 (74.7) (Figure 1).

The AMMI2 biplot (IPCA1 vs IPCA2) for yield partitioned the genotype  $\times$  environment (G  $\times$  E) interaction into two principal components, with PC1 and PC2 explaining 66.7 and 33.3% of the interaction, respectively ( $\approx$ 100% jointly), indicating that the first two IPCAs adequately captured the interaction pattern. The three test environments were well separated and positioned in different sectors of the biplot, demonstrating strong differential genotypic responses. Environment E1 was located in the positive quadrant for both PC1 and PC2, E2 in the negative PC1 but positive PC2 region, and E3 in the positive PC1 but strongly negative

PC2 region, confirming that E1 and E2 were contrasting and that E3 represented a distinct interaction pattern. In AMMI2 interpretation, genotypes located near the origin exhibited minimal interaction and thus greater stability across environments, whereas genotypes located closer to an environment vector showed specific adaptation to that environment. Accordingly, genotypes positioned toward the E1 sector (e.g., Ridge gourd65, Ridge gourd24, Ridge gourd19 and VRRG552016) showed better adaptation to E1, while those closer to E2 (e.g., VRRG88, RDG22 and Ridge gourd74) were more suited to E2. Genotypes oriented toward the E3 vector (e.g., VRRG810, VRRG762016 and VRRG83) expressed specific adaptation to E3. Overall, the clustering of several genotypes around the biplot origin suggests the presence of broadly adapted entries, while the dispersion of others along the E1, E2 and E3 vectors highlights opportunities for targeted genotype recommendation by environment (Figure 2).

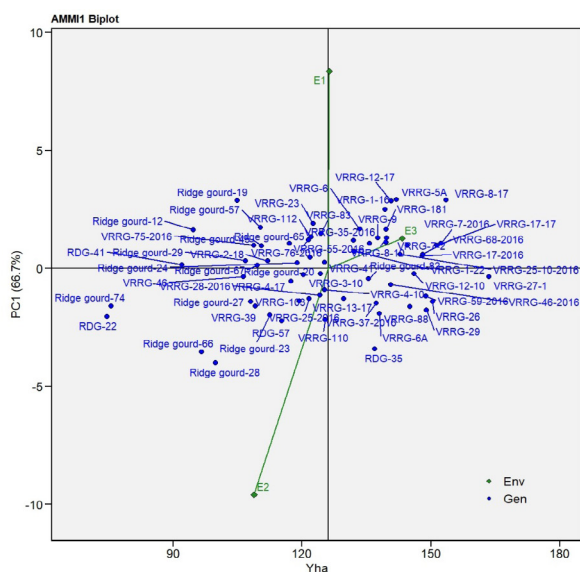
### GGE biplot analysis

The GGE biplot for yield showed that the first two principal components explained a substantial proportion of the genotype plus genotype  $\times$  environment variation (PC1 = 65.21% and PC2 = 22.73%, totaling 87.94%), indicating that the biplot provided an adequate summary of genotype performance and interaction across environments. The environment vectors were long and well separated, demonstrating that the test sites were discriminating and differed in their ability to separate genotypes. E2 and E3 were positioned in the positive PC1 region with a relatively acute angle between them, suggesting a generally

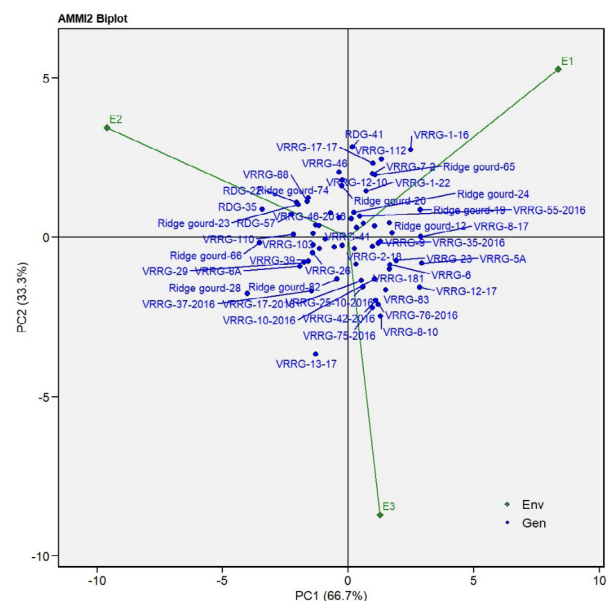
positive association in genotype ranking between these environments, whereas E1 was located in a contrasting direction (negative PC2), indicating differential genotype responses and a stronger crossover interaction relative to E2 (and, to a lesser extent, E3). Genotypes located near the origin exhibited comparatively high stability (low interaction), while those projected toward a given environment vector expressed specific adaptation to that environment. In this regard, VRRG271 was positioned far along the positive PC1 axis and close to the E3 direction, indicating superior performance and specific adaptation to E3. Genotypes such as VRRG29, RDG35, VRRG88 and VRRG372016 were oriented toward E2, suggesting better adaptation to E2, whereas VRRG116, VRRG5A and VRRG817 tended to align more with the E1 sector, indicating preferential performance under E1. Conversely, entries clustered on the negative PC1 side (e.g., Ridge gourd28, Ridge gourd66 and RDG22) were associated with low yield across environments (Figure 3).

### Which won where biplot

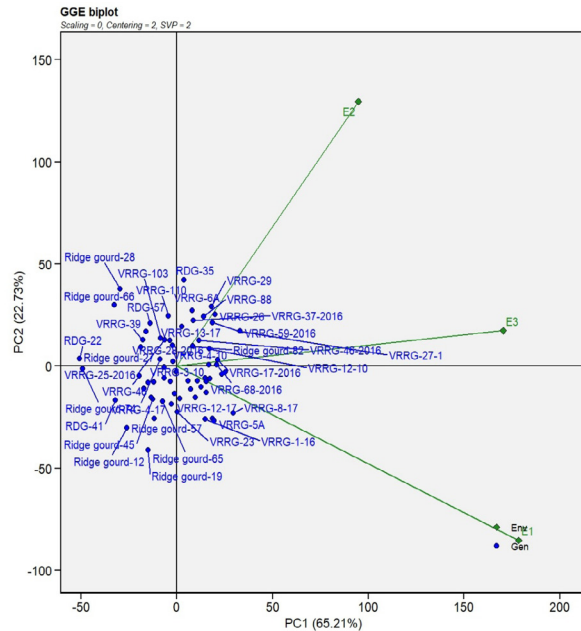
The which-won-where view of the GGE biplot for yield revealed clear crossover genotype responses and allowed the identification of winning genotypes for each test environment (Figure 4). The polygon drawn by the outermost (vertex) genotypes and the perpendicular rays partitioned the biplot into sectors (mega-environments), and environments located within the same sector shared the same winning genotype. The three environments were positioned in different sectors, showing that they constituted distinct mega-environments with different genotype winners. Environment E2 was located in the



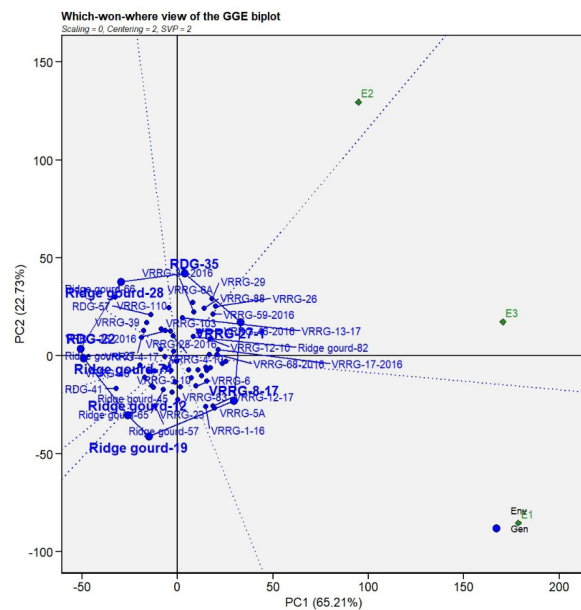
**Figure 1:** AMMI1 biplot for yield ( $\text{Yha}^{-1}$ ) of ridge gourd genotypes evaluated across three environments (E1–E3). The horizontal axis represents genotype and environment mean yield (Yha), while the vertical axis shows the first interaction principal component (PC1/ IPCA1), which explains 66.7% of the genotype  $\times$  environment (G $\times$ E) interaction.



**Figure 2:** AMMI2 biplot for yield (Yha) showing genotype  $\times$  environment interaction patterns of ridge gourd genotypes across three environments (E1–E3).



**Figure 3:** GGE biplot for yield (q/ha) of ridge gourd genotypes evaluated across three environments (E1–E3). The biplot is based on environment-centered data (centering = 2) with singular value partitioning (SVP = 2) and displays the first two principal components, PC1 (65.21%) and PC2 (22.73%), which together explain 87.94% of the genotype plus genotype  $\times$  environment (G+GE) variation.



**Figure 4:** Which-won-where view of the GGE biplot for yield of ridge gourd genotypes evaluated across three environments (E1–E3) (scaling = 0, centering = 2, SVP = 2). The biplot displays PC1 (65.21%) and PC2 (22.73%), explaining 87.94% of the genotype plus genotype  $\times$  environment (G + GE) variation.

upper sector, indicating that the vertex genotype in that direction (e.g., RDG35) was the best performer under E2 conditions. Environment E3 fell in a separate right-hand sector, suggesting a different winning genotype for E3 (e.g., genotypes positioned toward the E3 sector such as VRRG27-1).

Environment E1 was placed in another distinct sector (lower-right), confirming that the highest-yielding genotype under E1 differed from those favored in E2 and E3. The VRRG 8-17 was winner for the E1 environment. Overall, the separation of environments into different sectors highlights substantial G $\times$ E interaction and supports environment-specific genotype recommendation rather than a single universally superior genotype.

## Discussion

The pooled analysis of variance across three years revealed highly significant differences among genotypes for all the traits studied, indicating the presence of substantial genetic variability in ridge gourd. The existence of significant variability for days to flowering (DFMF, DFFF), days to harvest (DFH), average fruit weight (AFW), average fruit length (AFL), average fruit diameter (AFD), average vine length (AVL), number of fruits per plant (NFPP), and yield suggests ample scope for genetic improvement through selection. Similar findings of significant genotypic variability in ridge gourd have been reported by earlier workers (Kumar *et al.*, 2013; Singh *et al.*, 2015; Yadav *et al.*, 2017), confirming that the crop possesses considerable exploitable genetic diversity.

The highly significant effect of years for most traits indicated strong environmental influence on trait expression. Ridge gourd, being a warm-season cucurbit, is highly sensitive to seasonal variation, particularly temperature and rainfall fluctuations, which influence flowering behavior, fruit set, and yield (Rai *et al.*, 2008). The significant environmental effect observed in the present study emphasizes the importance of multi-season evaluation to obtain reliable estimates of genotypic performance. The non-significant year effect for number of fruits per plant suggests comparatively stable expression of this trait across seasons, indicating that it may be less influenced by environmental fluctuations.

The genotype  $\times$  year interaction was highly significant for all traits, including yield, demonstrating differential genotypic response across years. This indicates the presence of considerable genotype–environment (G  $\times$  E) interaction in ridge gourd. Similar significant G  $\times$  E interactions for yield and yield-contributing traits have been reported in cucurbits (Hanchinamani *et al.*, 2011; Kumar *et al.*, 2018). The presence of significant interaction implies that selection based solely on single-season data may not be effective. Therefore, stability analysis using models such as AMMI or GGE biplot would be useful to identify genotypes with broad or specific adaptation.

The significant genotypic differences observed for yield and major yield-attributing traits such as average fruit weight, fruit length, and number of fruits per plant suggest that these traits can be effectively utilized as selection criteria in breeding programs. Yield in ridge gourd is a complex trait governed by several component characters; therefore,

improvement in yield can be achieved through indirect selection for highly heritable and positively associated traits (Pandey *et al.*, 2009). Traits showing significant genetic variation with relatively lower environmental influence can be prioritized for direct phenotypic selection.

The AMMI analysis for ridge gourd (*Luffa acutangula*) indicated that environment (ENV), genotype (GEN), and genotype  $\times$  environment interaction (GEI) were highly significant, confirming differential genotype responses across test locations/seasons. The significant GEI justified the use of AMMI to partition interaction patterns into principal components (Zobel *et al.*, 1988; Crossa, 1990). PC1 and PC2 together explained 100% of the GEI sum of squares, with PC1 accounting for 66.7% and PC2 for 33.3%, suggesting that most crossover interaction could be summarized by the first axis, while the second axis captured additional, meaningful complexity. This pattern implies that ridge gourd yield performance is strongly influenced by specific adaptation, and genotype recommendations should consider both mean performance and stability across environments (Gauch, 2013).

In the AMMI1 biplot (genotype/environment mean on the x-axis and IPCA1 score on the y-axis), ridge gourd genotypes positioned to the right generally represent higher mean yield, while those close to the zero IPCA1 line show greater stability across environments. Thus, high-yielding genotypes with near-zero IPCA1 values are desirable for broad adaptation because they combine productivity with minimal interaction sensitivity. Conversely, genotypes with large positive or negative IPCA1 scores exhibit stronger GEI and are better suited to specific environments, where their interaction aligns with the corresponding environment scores. Environments with larger IPCA1 values are more discriminating (they separate genotype performance more clearly), whereas those near zero are less interactive and more representative for general testing (Crossa, 1990; Gauch, 2013).

The AMMI2 biplot (IPCA1 vs IPCA2) provides a clearer view of interaction patterns by displaying both major GEI axes simultaneously. For ridge gourd, genotypes located near the origin are relatively stable, showing limited interaction across environments, while those farther from the origin are more responsive and may express specific adaptation (Zobel *et al.*, 1988). The angle and proximity between genotype and environment points indicate association: genotypes plotted in the same direction as an environment tend to perform better there, whereas opposite directions suggest poorer relative performance. Because PC1 and PC2 captured all GEI variation in the present analysis, the AMMI2 biplot should reliably describe the major crossover patterns, enabling identification of mega-environments and targeted genotype recommendations (Gauch, 2013; Yan & Kang, 2003).

The GGE biplot for ridge gourd yield captured most of the genotype plus G $\times$ E signal (PC1 = 65.21% and PC2 = 22.73%, total = 87.94%), indicating that the first two PCs provided a reliable graphical summary of genotype performance and crossover interaction across environments. The long, well-separated environment vectors confirmed that E1, E2, and E3 were highly discriminating test sites, with contrasting genotype rankings among locations, an expected outcome when environmental heterogeneity drives differential expression of yield potential in ridge gourd (Yan *et al.*, 2001; Yan & Kang, 2003). The acute angle between E2 and E3 suggested similarity in genotype ranking and a positive correlation, whereas the contrasting placement of E1 (negative PC2) indicated stronger crossover interaction, implying that selection decisions would differ substantially if based only on E1 *versus* E2/E3 (Yan, 2001).

Genotypes near the biplot origin showed greater stability (low interaction), while those projecting toward an environment vector expressed specific adaptation. VRRG271 aligned strongly with E3, indicating superior and targeted performance in that environment. Similarly, VRRG29, RDG35, VRRG88 and VRRG372016 were oriented toward E2, supporting their recommendation for E2-like conditions, whereas VRRG116, VRRG5A and VRRG817 were associated with the E1 sector, indicating preferential adaptation to E1. Poor performers (Ridge gourd28, Ridge gourd66 and RDG22) clustered on the negative PC1 side, reflecting generally low yield across sites. The “which-won-where” polygon view separated the three environments into distinct sectors (mega-environments), confirming substantial G $\times$ E and identifying different winners for each: RDG35 for E2, VRRG271 for E3, and VRRG817 for E1. Collectively, these patterns support environment-specific cultivar recommendation in ridge gourd rather than reliance on a single broadly superior genotype (Yan *et al.*, 2001; Yan & Kang, 2003).

From a breeding perspective, the presence of substantial genetic variability indicates good prospects for developing improved varieties through selection and hybridization. The significant G  $\times$  Y interaction further suggests that breeding strategies should focus on developing either widely adapted genotypes with stable performance or specifically adapted genotypes suited to particular seasons. For commercial cultivation, stable high-yielding hybrids or open-pollinated varieties with consistent performance across environments would be desirable. Overall, the results confirm that the experimental material possesses adequate genetic variability for yield and its component traits in ridge gourd. However, due to the significant environmental and G  $\times$  Y interaction effects, multi-environment testing should be an integral part of ridge gourd breeding programs to ensure the development of stable, high-yielding cultivars.

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## सारांश

नसदार तोरई एक आर्थिक रूप से महत्वपूर्ण कुकुर्बिट सब्जी है, जिसकी खेती उष्णकटिबंधीय और उपोष्णकटिबंधीय क्षेत्रों में व्यापक रूप से की जाती है; हालांकि, विभिन्न मौसमों में इसकी उपज स्थिरता के बारे में सीमित जानकारी उपलब्ध है। वर्तमान अध्ययन का उद्देश्य 64 नसदार तोरई जीनोटाइप्स में आनुवंशिक विविधता, जीनोटाइप × वर्ष अंतःक्रिया तथा उपज स्थिरता का मूल्यांकन करना था। इन जीनोटाइप्स का मूल्यांकन वर्षा ऋतु के दौरान लगातार तीन वर्षों तक यादृच्छिक ब्लॉक डिजाइन में तीन पुनरावृत्तियों के साथ किया गया। संयुक्त विचरण विश्लेषण (pooled ANOVA) में उपज और उससे संबंधित घटक लक्षणों के लिए जीनोटाइप्स के बीच अत्यधिक महत्वपूर्ण ( $P \leq 0.001$ ) अंतर पाए गए, जो पर्याप्त उपयोगी आनुवंशिक विविधता की उपस्थिति को दर्शाते हैं। वर्ष तथा जीनोटाइप × वर्ष अंतःक्रिया के प्रभाव भी अधिकांश लक्षणों के लिए महत्वपूर्ण पाए गए, जिससे मौसमी विविधता और विभिन्न वर्षों में जीनोटाइप्स की भिन्न प्रतिक्रियाओं का प्रभाव स्पष्ट हुआ। अंतःक्रिया पैटर्न को स्पष्ट करने के लिए योगात्मक मुख्य प्रभाव एवं गुणात्मक अंतःक्रिया (AMMI) तथा जीनोटाइप तथा जीनोटाइप × पर्यावरण अंतःक्रिया (GGE) बाइप्लॉट विश्लेषण किए गए। AMMI मॉडल ने दर्शाया कि पहले दो इंटरैक्शन प्रिंसिपल कंपोनेंट अक्षों ने अंतःक्रिया वर्गों के योग का 100% भाग स्पष्ट किया, जिससे स्थिर जीनोटाइप्स की पहचान संभव हुई। GGE बाइप्लॉट विश्लेषण ( $PC1 = 65.21\%$  और  $PC2 = 22.73\%$ , कुल  $87.94\%$ ) ने औसत उपज और स्थिरता के आधार पर जीनोटाइप्स को प्रभावी रूप से अलग किया, “कौन-सा जीनोटाइप कहाँ विजयी रहा” जैसे पैटर्न को प्रदर्शित किया तथा उच्च उत्पादकता और व्यापक अनुकूलनशीलता वाले आदर्श जीनोटाइप्स की पहचान की, जिनमें 2024 (E2) के लिए RDG35, 2025 (E3) के लिए VRRG271 और 2023 (E3) के लिए VRRG817 शामिल हैं। संयुक्त ANOVA के साथ AMMI और GGE विधियों का एकीकृत उपयोग श्रेष्ठ और स्थिर जीनोटाइप्स के चयन में प्रभावी सिद्ध हुआ। इस अध्ययन के निष्कर्ष परिवर्तनीय पर्यावरणीय परिस्थितियों में उच्च उपज देने वाली और व्यापक रूप से अनुकूलित किस्मों के विकास पर केंद्रित तोरई प्रजनन कार्यक्रमों के लिए महत्वपूर्ण जानकारी प्रदान करते हैं।