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## Deciphering Genotype $\times$ Environment Interaction of barley genotypes by AMMI and GGE analysis

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### Abstract

AMMI analysis of 25 barley genotypes at 12 locations evaluation had observed the significant the effects to the tune of 50% 21.4% 3.71% by environment, interaction of genotype with environments and genotype respectively. Further the interaction effects were partitioned into six components which accounted for 90.8% of the total interactions sum of squares. The total share of first two components was of 58.9% which justified the use of PC1 and PC2 for plots. Out of 25 only G10, G12, G18, G7 genotypes had been identified by most of the measures defined on AMMI analysis. Mean vs stability analysis of GGE had observed genotypes G19, G22, G5, G7 had yields above the average values. The angle between the vector and the average environment axis reflected the representativeness of the environment, with a smaller angle of E4, E9 and E12 environments had indicated stronger representativeness. The elongated vectors of environments observed for E10, E06 and E12 explained their robust discriminative power. Genotypes like G16, G2, G17, G12 belonged close to environments E7, E8 would be good to identify for their sustainable high yield. Genotype G02 was located within the inner circle and considered to be optimal. The genotypes that exhibited close spatial closeness to the inner circle were G16, G12 and G23. A straight line angle between E6 and E12 suggested the opposite behaviour of evaluated genotypes at these two environments like of G16 with G22, G02 with G19, G23 with G5, G12 with G19.

**Keywords:** AMMI, Association analysis, Biplot analysis, Discriminative, which won where GGE

### Introduction

The crop improvement programs revolve around the clear understanding of genotype-environment interaction to exploit for better yielding genotypes (Rahmati *et al.*, 2024) [16]. Under the vagaries of environmental conditions coupled with unpredictable genotype behaviour, often masks the identification of stable and high-yielding genotypes for their cultivation at large areas (Singh *et al.*, 2025) [17]. Initial the statistical models have provided linear frameworks for assessing adaptability and stability, but were unable to capture the multidimensional nature of G $\times$ E interactions. The advent of the Additive Main effects and Multiplicative Interaction (AMMI) and the Genotype + Genotype-Environment (GGE) approaches had revolutionized the interpretation of multi-environment trials (Pereira *et al.*, 2025) [14]. During multi location yield trials, an additive main effect and multiplicative interaction (AMMI) model has been widely exploited to analyze G  $\times$  E interaction (Kumar *et al.*, 2024) [10]. AMMI is capable of detecting G $\times$ E interaction in a multi-dimensional environment and displaying it using a biplot. GGE biplots-based multi-environment trial (MET), genotype evaluation environmental valuation has been successfully executed for varietal stability analysis experimented by several researchers (Kindie *et al.*, 2022) [9]. GGE biplot analysis has been used by several researchers to classify the mega environment, assess genotype rankings, and decide the discriminative and representative among the tested environments (Ashwini *et al.*, 2021) [1]. The discriminative ability and representativeness of the GGE biplot serve as vital metrics for test environments, offering unbiased insights into the tested genotypes. GGE biplots analysis, on the other hand, is regarded as a useful statistical technique for producing phenotypically stable and superior cultivars, identifying stable genotypes across several environments, and achieving crop yield stability across multiple locations. The current study aimed to identify promising genotypes with stable yield

performance over a wide range of environments by assessing the association analysis of various stability analysis methodologies by utilizing both AMMI and GGE biplots (Gonçalves *et al.*, 2025) [6].

## Materials and Methods

Twenty barley genotypes were evaluated under field trials during 2024-25 cropping seasons at twelve major locations of the country. The parentage details of the evaluated barley genotypes along with the major locations were reflected in table 1 for ready reference. Simple lattice incomplete block designs were laid out with two replications. Recommended

agronomic interventions were followed in toto to harvest the good crop yield. AMMI analysis had been exploited to estimate the proportion of genotypes, environments and their interactions effects share in total variance by combined analysis. Afterwards GGE biplots had been employed for visualizing the interaction between genotype (G) and environmental conditions (E) across multiple sites. Complete statistical analysis and biplots carried out by METAN software on R studio platform. Moreover the details of commonly used AMMI analysis based measures had been mentioned below for completeness.

|                              |                                                                              |                                                                                                                                          |
|------------------------------|------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|
| Zobel 1994                   | Sums of the averages of squared eigenvector values (EV)                      | $EV = \sum_{n=1}^{N'} \frac{\gamma_{in}^2}{N'}$                                                                                          |
| Annicchiarico 1997           | Annicchiarico D parameter values (Da)                                        | $D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$                                                                                 |
| Sneller <i>et al</i> 1997    | Sums of the absolute value of the IPC scores (SIPC)                          | $SIPC = \sum_{n=1}^{N'}  \lambda_n^{0.5} \gamma_{in} $                                                                                   |
| Zhang's <i>et al</i> 1998    | Zhang's parameter (Dz)                                                       | $D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$                                                                                             |
| Purchase <i>et al.</i> 2000  | AMMI stability value(ASV)                                                    | $ASV_i = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1)^2 + (IPCA2)^2}$                                                                     |
| Raju 2002                    | Stability measure based on fitted AMMI model (FA)                            | $FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$                                                                                         |
| Farshadfar 2011              | Yield stability index (YSI)                                                  | YSI = RASV + RY<br>RASV is the rank of AMMI stability value and RY is the rank of mean grain yield of genotypes (RY) across environments |
| Zali <i>et al</i> 2012       | Absolute value of the relative contribution of IPCs to the interaction (Za)  | $Za = \sum_{i=1}^{N'}  \theta_n \gamma_{in} $                                                                                            |
| Zali <i>et al</i> 2012       | Sum across environments of absolute values of GEI modelled by AMMI(AV(AMGE)) | $AV_{(AMGE)} = \sum_{j=1}^E \sum_{n=1}^{N'}  \lambda_n \gamma_{in} \delta_{jn} $                                                         |
| Jambhulkar <i>et al</i> 2017 | AMMI stability index (ASI)                                                   | $ASI = \sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$                                                                   |
| Ajay <i>et al</i> 2018       | Modified AMMI stability index (MASI)                                         | $MASI = \sqrt{\sum_{n=1}^{N'} PC_n^2 \times \theta_n^2}$                                                                                 |
| Olivoto <i>et al</i> 2019    | Weighted average of absolute scores (WAAS)                                   | $WAAS_i = \frac{\sum_{k=1}^p  IPCA_{ik}  \times EP_k}{\sum_{k=1}^p EP_k}$                                                                |
| Ajay <i>et al</i> 2019       | Modified AMMI stability value (MASV)                                         | $MASV = \sqrt{\sum_{n=1}^{N'-1} \left( \frac{SS_{IPC_n}}{SS_{IPC_{n+1}}} \right) \times (PC_n)^2 + (PC_{N'})^2}$                         |

Three major components would be elucidated nicely by using the biplot (a) 'which-won-where' pattern or MET, an effective approach to visualize the pattern of G×E interactions based on the correlation between G and E; (b) stability vs mean performance over the environment for genotype evaluation; (c) representativeness and discriminating ability for test environments utilized for genotypes assessment (Yan *et al.*, 2007) [21]. Biplot is a 2D visualization matrix that has two axes, first data was centered afterward sectionalizing the singular value (SV) into G×E scores for individual principal components viz. PC1 and PC2 followed by intrigue the PC1 scores contrary to the PC2 scores to create a biplot (Yan and Tinker, 2006) [20].

## Results and Discussion

### AMMI analysis

The analysis of variance showed that the effects of genotype (G), environment (E) and their interaction (G × E) on yield were statistically significant. The environment (E) effect was a predominant source of the variation and accounted for 50% of the total sum of squares (TSS), while GE interaction and G sources of variation accounted for 21.4% and 3.71% of the total variation, respectively (Verma and Singh, 2021) [19]. Further the interaction effects were partitioned into six components which accounted for 90.8% of the total interactions sum of squares. Moreover the first four components had augmented to the tune of 38.8%, 20.1%, 11.1% and 10.3% respectively. The total share of first two

components was of 58.9% which justified the use of PC1 and PC2 for plots (Pour *et al.*, 2022) [15].

### Performance of genotypes as per AMMI analysis based measures

Higher yield (Y) had been expressed by G24 followed by G21 & G16 while lowest yielders were G4, G22, G25 whereas the consistent performance as judged by least values of CV measure had identified G9, G21, G2 out of evaluated 25 barley genotypes besides more variable yield had been observed for G6, G7, G5 genotypes. Ammi stability index (ASI) had found suitability of G10, G2, G7 genotypes and unsuitability of G24, G17, G22 while the same genotypes G10, G2, G7 had been identified by Ammi stability value (ASV) measure as based on first two interaction principal components (Mohammadi *et al.*, 2023) [12]. Sum across Environments of Absolute Value of G×E interaction modelled by AMMI (AVAMGE) had selected G10, G18, G12 genotypes and next two measures Annicchiarico's D Parameter values ( $D_a$ ) and Zhang's D

Parameter ( $D_z$ ) had pointed towards barley genotypes. In the series of AMMI analysis based measures Sums of the Averages of the Squared Eigenvector Values (EV) and Stability Measure Based on Fitted AMMI Model (FA) had expressed differences in the ranking of genotypes but both had identified the same genotypes G10, G18, G12 (Gauch *et al.*, 2008) [5]. Modified AMMI Stability index (MASI) and Modified AMMI Stability Value (MASV) had pointed towards G10, G18, G7 and G18, G10, G12 respectively. The least values of Sums of the Absolute Value of the IPC Scores (SIPC) had been found for G10, G18, G12 genotypes and lower values for Absolute Value of the Relative Contribution of IPCs to the Interaction ( $Z_a$ ) had been exhibited by G10, G18, G7 out of 25 barley genotypes evaluated under multi location trials at twelve locations of the zone. The values of last measure i.e. Weighted average of absolute scores had pointed for G10, G18, G7 genotypes only for their suitability besides the not to good performance by G24, G17, G16 genotypes (Daba *et al.*, 2023) [3].

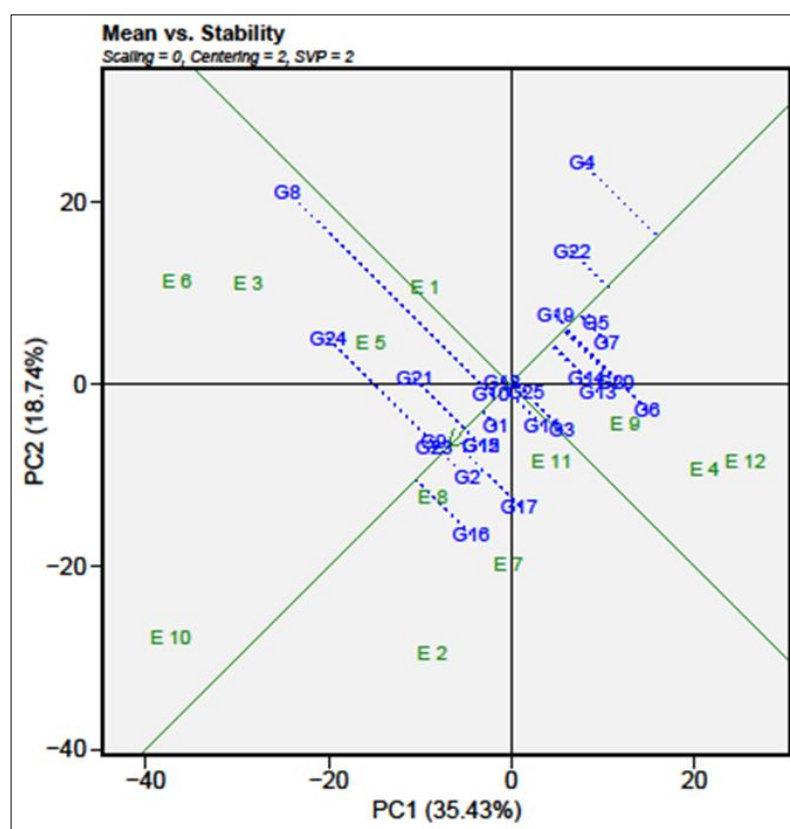


Fig 1: Mean yield vis-à-vis stability of genotypes

### Mean and stability as per GGE biplot

Visualization of the mean performance and stability of genotypes is always an important issue in cultivar evaluation. It was pointed out that if PC1 of a GGE biplot approximates the genotype main effects (i.e., mean performance), PC2 must approximate the GE effects associated with each genotype, which is a measure of instability (Dehghani *et al.*, 2006) [4]. The ideal genotype demonstrates both high and stable yields in specific environments. The "Mean vs. Stability" method is employed to concurrently identify the high-yielding and stable

characteristics of materials. In figure, the direction along the arrow indicated higher yields. Genotypes on the left side of the vertical axis G8, G24, G21, perpendicular to the horizontal axis, had yields below the average, while those on the right side G19, G22, G5, G7 had yields above the average (Azam *et al.*, 2020) [2]. The length of the perpendicular line from a genotype to the average environment axis reflected the genotype's stability, with longer lines G1, G23, G9, G2 indicated less stability and vice versa.

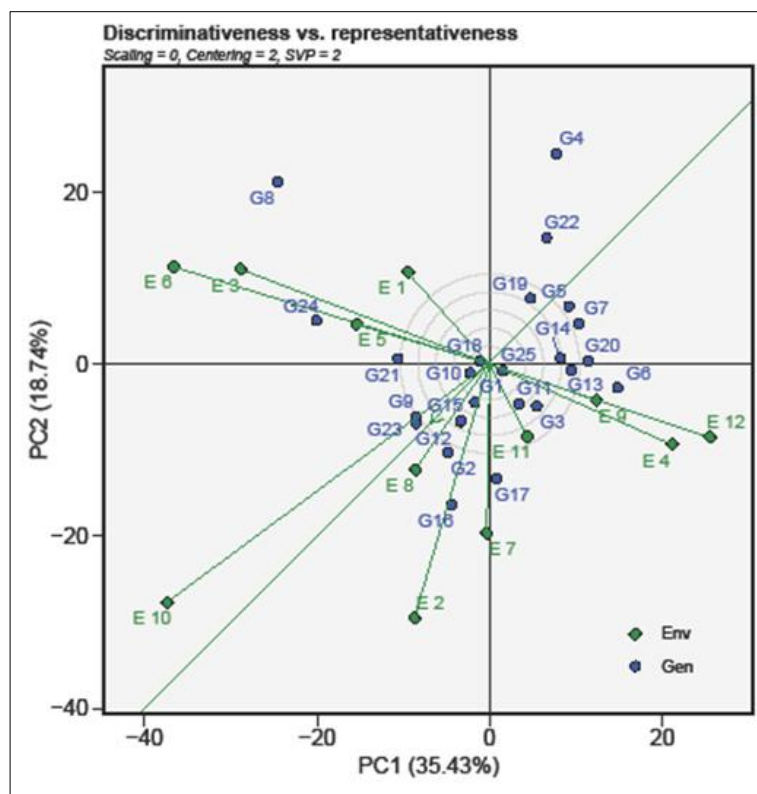


Fig 2: Discriminative vis-a-vis Representativeness

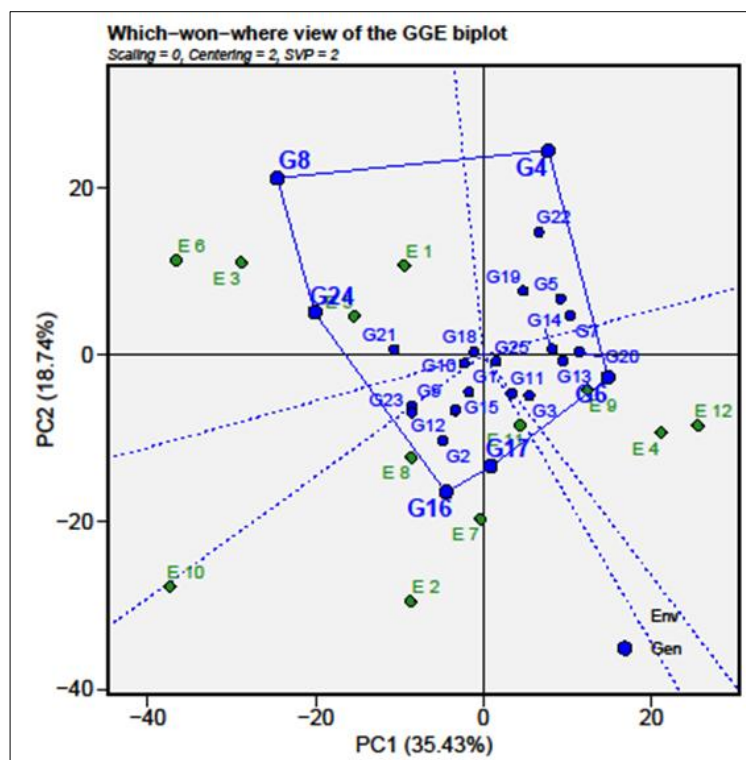


Fig 3: Which-won-where polygon view

### Discriminative and which won where analysis as per GGE

The "Discriminativeness vs. Representativeness" analysis method employed to illustrate the association of different locations in the assessment of genotypes adaptability. The lines originated from the origin represented vectors, with the length of the vector indicated discriminative power (Güngör *et al.*, 2022) [7]. Longer vectors of environments E10, E6, E12 suggested a stronger discriminative ability of the

location for the studied genotypes. The lines with arrows passed through the circles represented the "average environment axis." The angle between the vector and the average environment axis reflected the representativeness of the environment, with a smaller angle of E4, E9, E12 indicated stronger representativeness. Furthermore, the angle between testing points could unveil the correlation between environments. An angle less than 90° indicated a positive correlation, suggested similar effects of

environments on the evaluated genotypes at E2, E7, E8. Conversely, an angle greater than  $90^\circ$  signified a negative correlation, indicated opposing effects of environments E6, E3, E1 on the genotypes. An angle equal to  $90^\circ$  represented no correlation between environments E12 with E8. In the current study, the elongated vectors observed in both E10, E06 and E12 indicated a robust discriminative power. The angles between the vectors and the average environment axis were less than  $90^\circ$ , highlighted the strong representativeness of E10, E06. Nevertheless, the angle

between the E10 and E04 was close to  $90^\circ$ , indicated that the impacts of the two locations on the genotypes were independent of each other. Genotypes like G16, G2, G17, G12, etc. belonged very near to environments E7, E8 would be good to identify for sustainable high production. Fig. 2 (which won where/what) indicates that genotypes are located close to centre of figure are very stale in response to yield can be select and recommend to the farmers for cultivation across the locations.

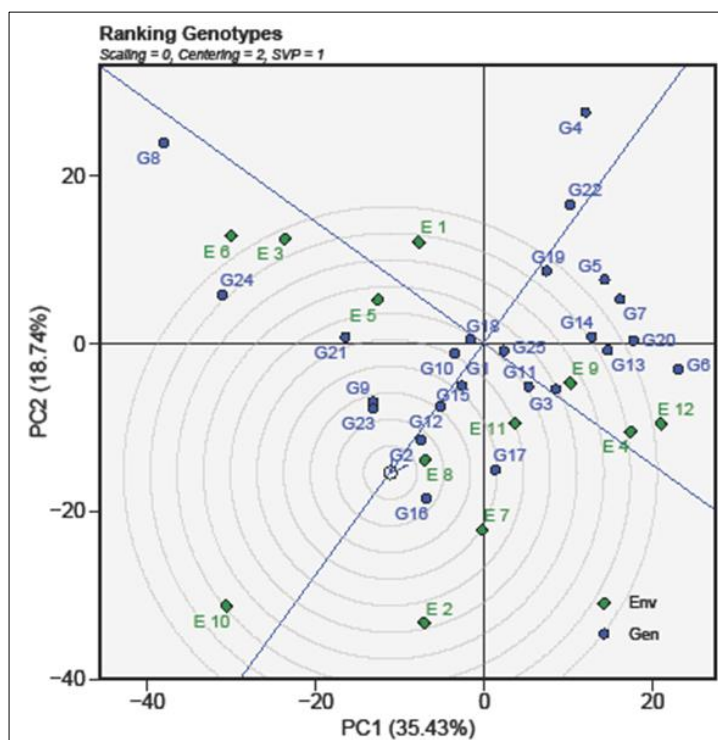


Fig 4: Ranking of genotypes

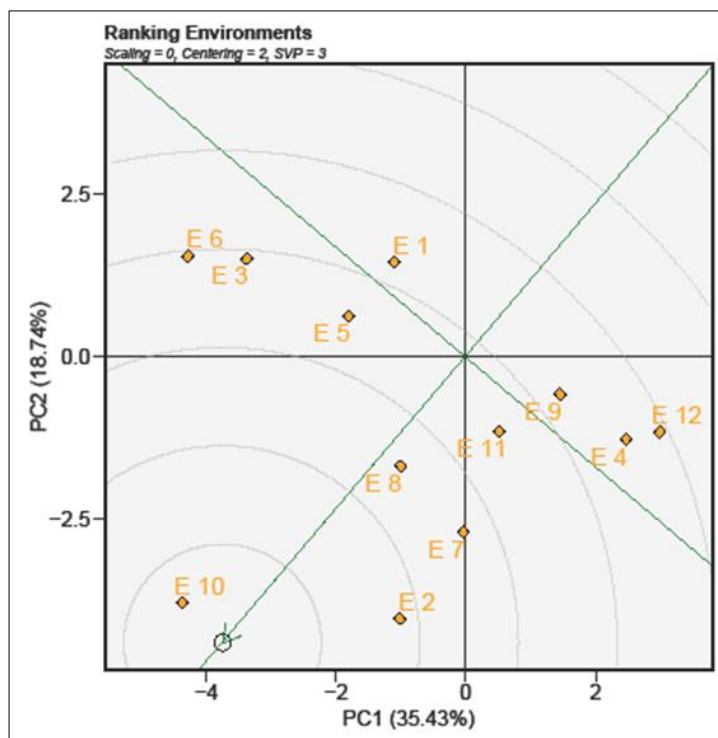


Fig 5: Ranking of environments

### Ranking of genotypes and environments

The application of a biplot enabled the determination of optimal and most desirable genotype from a set of 25 genotypes that were assessed. The ideal genotype is consistently located within the middle region and in close proximity to the peak of the arrow within the circular band, as illustrated in Fig. 4. It was noted that genotype G02 was located within the inner circle and considered to be optimal. The genotypes that exhibited close spatial closeness to the inner circle were G16, G12 and G23. In contrast, it was seen that G24, G19 exhibited the greatest distance from the arrowhead in the plot. The length of concentric circles on the biplot helps to visualize the length of the environment vectors which is proportional to standard deviation with in the respective environments on the biplot and also shows the discriminating ability of the environments (Hossain *et al.*, 2023) [8]. Fig. 3 showed Average Environment Axis (AEA)

view of biplot. Average Environment Axis (AEA) is the line that passes through the average environment (represented by small circle) and biplot origin. The average environment has the average coordinates of all test environments. A test environment that has a smaller angle with the AEA would be more representative of other test environments. Thus, E2 was the most representative environments, whereas E11 and E7 with the large deviation from AEA were the least representative. Testing environments that are discriminating but non representatives are useful for selecting specifically adapted genotypes. Hence, E11 was useful for selecting specifically adapted genotypes. Non-discriminating testing environments are those with very short vectors and are less useful. Thus, E7 was less useful test environment. The ideal test environment (the center of concentric circles) should be both highly discriminating and most representatives of the target environments.

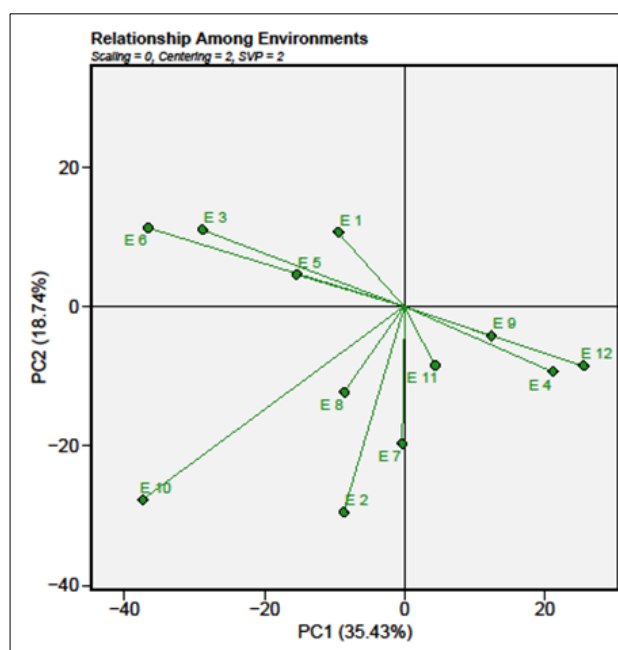


Fig 6: Association among the environments

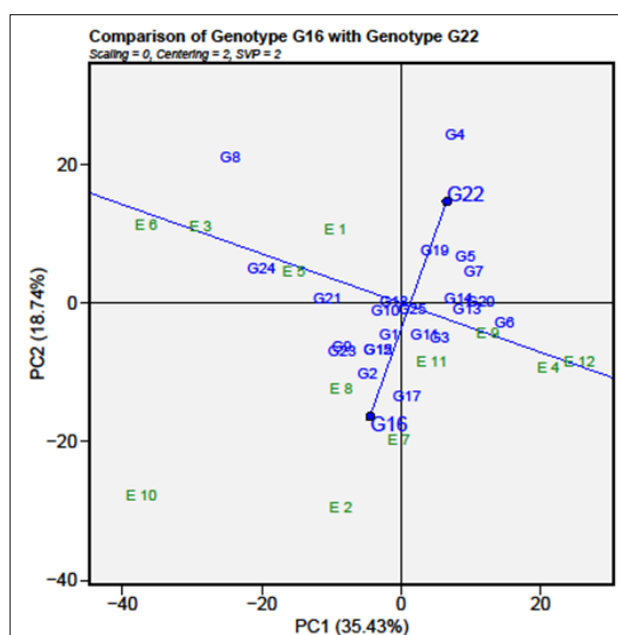


Fig 7: Performances of genotypes as compared to G16 genotype

### Association analysis among environments

A straight line angle between E6 and E12 suggested the opposite behaviour of evaluated genotypes at these two environments like of G16 with G22, G02 with G19, G23 with G5, G12 with G19. Furthermore, the angle between rays unveils the correlation between environments (Mndolwa *et al.*, 2019) <sup>[11]</sup>. An angle less than 90° indicate a positive correlation E12 with E4 & E9 and of E3 with E5 & E6, suggesting similar effects of environments on materials. Conversely, an angle greater than 90° signifies a negative correlation, indicate opposing effects of environments on materials as of E02 with E01, E10 with E12. An angle equal to 90° represents no correlation between environments E10 with E01 implied the impacts of the two test points on the materials were independent of each other. In this investigation, the elongated vectors observed E10, E12, E6 indicated a robust discriminative power. The association

among 11 test environments were indicated in the vector view of the GGE- biplot (Fig. 2) gives a succinct summary of the relationships among the environments. Thus, all environments which were found in the quadrant II were positively correlated to each other as the angle between them was less than 90° (i.e., acute angle) which was also true for environments in quadrant I. In addition to this, E10 E11 and E7 were positively correlated with E3 of quadrant II and there was also positive relation between E10 and E3, E6 and E2. However, since the angle between E11 or E7 and E6 was nearly 90°, hence the correlation between them was close to zero. Similarly, the correlation between E10 and E4 approaches to 90° indicating near zero associations (Olanrewaju *et al.*, 2021) <sup>[13]</sup>. This weak association was also shown in Table 3. However, there were some inconsistencies.

**Table 1:** Parentage and locations details of the study

| Genotype  | Code      | Parentage                    | Location    | Latitude  | Longitude | Mean Sea Level |
|-----------|-----------|------------------------------|-------------|-----------|-----------|----------------|
| UPB-1133  | IVT-MB-1  | DWRUB136/UPB1008/RD2794      | Bawal       | 28° 10'N  | 76° 50'E  | 266            |
| BH-1069   | IVT-MB-2  | IBON-17-16/BH 946            | Bathinda    | 30° 09' N | 74° 55 'E | 211            |
| BH-1068   | IVT-MB-3  | UPB 1058/BH 393              | Bulandshahr | 28° 40'N  | 77° 84'E  | 195            |
| BH-1068   | IVT-MB-4  | UPB 1058/BH 393              | Durgapura   | 26° 51'N  | 75° 47'E  | 390            |
| RD-3113   | IVT-MB-5  | BH 1013/DWR 101//DWRUB 52    | Hissar      | 29° 10' N | 75° 46'E  | 229            |
| DWRB-2404 | IVT-MB-6  | DWRUB52/IRINA                | Karnal      | 29° 43' N | 70° 58'E  | 245            |
| BH-1066   | IVT-MB-7  | RD 2946/BH 946               | Ludhiana    | 30° 54' N | 75° 48 'E | 247            |
| DWRB-2402 | IVT-MB-8  | PL426/DWRB101                | Meerut      |           |           |                |
| PL-970    | IVT-MB-9  | RD2917/ DWRB137              | Navgaon     | 26° 35'N  | 74° 61'E  | 508            |
| RD-3114   | IVT-MB-10 | PL705/RD2668// DWR46//BCU 73 | Pantnagar   | 29° 02'N  | 79° 48'E  | 243.8          |
| PL-972    | IVT-MB-11 | RD2917/DWRB101               | SG Nagar    | 29° 66'N  | 75° 53'E  | 175.6          |
| DWRB-2401 | IVT-MB-12 | DWRB123/RD2849               | Tabijji     | 26° 35'N  | 74° 61'E  | 508            |
| RD-3112   | IVT-MB-13 | RD 2962//DWRB 101/PL 805     |             |           |           |                |
| RD-2849   | IVT-MB-14 | DWRUB52/PL705                |             |           |           |                |
| PL-974    | IVT-MB-15 | RD2917/DWRB123               |             |           |           |                |
| PL-969    | IVT-MB-16 | DWRUB52/ DWRB128             |             |           |           |                |
| DWRB-2405 | IVT-MB-17 | DWRB101/SLOOP SAWL3167       |             |           |           |                |
| PL-971    | IVT-MB-18 | DWRB127/ RD2849              |             |           |           |                |
| UPB-1132  | IVT-MB-19 | BH902/UPB1066                |             |           |           |                |
| RD-3115   | IVT-MB-20 | RD 2904/UPB 1059//RD 2849    |             |           |           |                |
| DWBR-219  | IVT-MB-21 | BETZS/DWRB88                 |             |           |           |                |
| RD-3116   | IVT-MB-22 | DWRUB 52/DWRB 101//RD 2963   |             |           |           |                |
| BH-1067   | IVT-MB-23 | RD 2919/BH 946               |             |           |           |                |
| DWRB-2403 | IVT-MB-24 | DWRB123/SK1                  |             |           |           |                |
| BH-1070   | IVT-MB-25 | IBON-17-16/BH 885            |             |           |           |                |

**Table 2:** AMMI analysis of barley genotypes evaluated under multi location trial

| Degree of freedom | Mean Sum of Squares | Significance | Respective Proportion in total | Accumulated share by components | Degree of freedom |
|-------------------|---------------------|--------------|--------------------------------|---------------------------------|-------------------|
| ENV               | 11                  | 5424.53      | ***                            | 50.04                           |                   |
| REP(ENV)          | 12                  | 16.94        | ***                            |                                 |                   |
| GEN               | 24                  | 184.38       | ***                            | 3.71                            |                   |
| GEN:ENV           | 264                 | 96.83        | ***                            | 21.44                           |                   |
| PC1               | 34                  | 292.01       | ***                            | 38.80                           | 38.80             |
| PC2               | 32                  | 160.56       | ***                            | 20.10                           | 58.90             |
| PC3               | 30                  | 94.87        | ***                            | 11.10                           | 70.10             |
| PC4               | 28                  | 94.48        | ***                            | 10.30                           | 80.40             |
| PC5               | 26                  | 55.79        | ***                            | 5.70                            | 86.10             |
| PC6               | 24                  | 50.13        | ***                            | 4.70                            | 90.80             |
| PC7               | 22                  | 38.55        | ***                            |                                 |                   |
| PC8               | 20                  | 37.08        | ***                            |                                 |                   |
| PC9               | 18                  | 24.06        | ***                            |                                 |                   |
| PC10              | 16                  | 14.25        | ***                            |                                 |                   |
| PC11              | 14                  | 7.15         | ***                            |                                 |                   |
| Residuals         | 288                 | 13.28        |                                |                                 |                   |
| Total             | 863                 | 138.18       |                                |                                 |                   |

**Table 3:** Ranks of genotypes based on AMMI analysis based measures

| GEN | Y  | CV | ASI | ASV | AVAMGE | DA | DZ | EV | FA | MASI | MASV | SIPC | ZA | WAAS |
|-----|----|----|-----|-----|--------|----|----|----|----|------|------|------|----|------|
| G1  | 18 | 9  | 6   | 6   | 9      | 7  | 19 | 19 | 7  | 5    | 8    | 14   | 6  | 6    |
| G2  | 5  | 3  | 2   | 2   | 7      | 11 | 21 | 21 | 11 | 4    | 19   | 19   | 5  | 4    |
| G3  | 14 | 11 | 5   | 5   | 12     | 13 | 14 | 14 | 13 | 8    | 21   | 7    | 8  | 8    |
| G4  | 25 | 14 | 11  | 12  | 10     | 18 | 20 | 20 | 18 | 13   | 20   | 22   | 15 | 14   |
| G5  | 19 | 23 | 21  | 21  | 20     | 14 | 6  | 6  | 14 | 21   | 11   | 10   | 18 | 19   |
| G6  | 21 | 25 | 19  | 19  | 21     | 15 | 10 | 10 | 15 | 19   | 15   | 16   | 16 | 18   |
| G7  | 22 | 24 | 3   | 3   | 4      | 4  | 11 | 11 | 4  | 3    | 7    | 6    | 3  | 3    |
| G8  | 12 | 8  | 12  | 11  | 13     | 10 | 12 | 12 | 10 | 10   | 9    | 9    | 11 | 9    |
| G9  | 10 | 1  | 9   | 9   | 8      | 5  | 5  | 5  | 5  | 9    | 4    | 5    | 7  | 7    |
| G10 | 11 | 22 | 1   | 1   | 1      | 1  | 1  | 1  | 1  | 1    | 2    | 1    | 1  | 1    |
| G11 | 20 | 12 | 8   | 8   | 6      | 6  | 16 | 16 | 6  | 7    | 6    | 12   | 10 | 10   |
| G12 | 15 | 13 | 7   | 7   | 3      | 3  | 3  | 3  | 3  | 6    | 3    | 3    | 4  | 5    |
| G13 | 6  | 21 | 22  | 22  | 19     | 19 | 4  | 4  | 19 | 22   | 17   | 8    | 20 | 20   |
| G14 | 8  | 16 | 16  | 16  | 16     | 17 | 9  | 9  | 17 | 15   | 10   | 13   | 19 | 17   |
| G15 | 4  | 4  | 13  | 13  | 15     | 9  | 23 | 23 | 9  | 11   | 14   | 17   | 12 | 12   |
| G16 | 3  | 17 | 20  | 20  | 17     | 21 | 22 | 22 | 21 | 20   | 23   | 24   | 23 | 23   |
| G17 | 7  | 15 | 24  | 24  | 24     | 24 | 15 | 15 | 24 | 24   | 24   | 18   | 24 | 24   |
| G18 | 13 | 6  | 4   | 4   | 2      | 2  | 2  | 2  | 2  | 2    | 1    | 2    | 2  | 2    |
| G19 | 17 | 20 | 10  | 10  | 5      | 8  | 13 | 13 | 8  | 12   | 5    | 15   | 13 | 13   |
| G20 | 9  | 18 | 14  | 14  | 11     | 16 | 7  | 7  | 16 | 14   | 13   | 4    | 9  | 11   |
| G21 | 2  | 2  | 18  | 18  | 14     | 12 | 8  | 8  | 12 | 16   | 12   | 11   | 14 | 16   |
| G22 | 24 | 19 | 23  | 23  | 23     | 22 | 18 | 18 | 22 | 23   | 22   | 20   | 21 | 22   |
| G23 | 16 | 7  | 15  | 15  | 22     | 23 | 25 | 25 | 23 | 18   | 18   | 23   | 17 | 15   |
| G24 | 1  | 5  | 25  | 25  | 25     | 25 | 24 | 24 | 25 | 25   | 25   | 25   | 25 | 25   |
| G25 | 23 | 10 | 17  | 17  | 18     | 20 | 17 | 17 | 20 | 17   | 16   | 21   | 22 | 21   |

Y—Genotype average yield; CV- Coefficient of Variation, ASV—AMMI Stability Value; AMGE—Sum across environments of GEI modelled by AMMI; ASI—AMMI Stability Index; ASTAB—AMMI-based stability parameter; AVAMGE—Sum across environments of the absolute value of genotype × environment interaction model by AMMI; DA—Annicchiarico's D parameter; DZ—Zhang's D parameter or AMMI statistic coefficient; FA—Stability measure based on fitted AMMI model; MASI—Modified AMMI Stability Index and MASV—Modified AMMI Stability Value; SIPC—Sums of the absolute value of the IPC scores; Za—Absolute value of the relative contribution of IPCs to the interaction

## Conclusion

The G×E effect was greater than the G effect, which suggested the differential response of genotypes among the considered environments. The AMMI and GGE biplot analysis considered to be one of the better method being used for many purposes like stability analysis, multi environment testing, genotype by environment interaction study, genotype by pathogen interaction study, genotype by trait interaction study and selection of best parent and parental combination study etc. which are directly helpful to the researchers during experimentation to recommend the better adapted genotypes to sustain the farmers income.

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