A new index for evaluation of G×E interaction in pearl millet using AMMI and GGE biplot analyses

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ABSTRACT

Performance of a genotype is the result of its genetic constitution and the environment in which it has been grown. In practice, a particular variety may not exhibit the same phenotypic performance under different environments. Also, different varieties may respond differently to a specific environment. Additive Main effects and Multiplicative Interaction (AMMI) and GGE biplot analyses are the most frequently used models to explain G×E interaction of multi-environment cultivar trials. Based on climatic conditions, the pearl millet cultivation in India is divided in 3 major zones A1, A and B for effective evaluation of the pearl millet breeding material. In the present study, the G×E interaction in pearl millet genotypes from zone-A of India has been evaluated using the techniques of AMMI and GGE biplot analyses. A new Weighted Stability Index (WSI) has been proposed for determining the high yielding and stable genotypes based on the normalized indices for grain yield and ASV indices. The three interaction principal component axes (IPCA1, IPCA2 and IPCA3) have been found to be significant for this zone. AMMI Stability Value (ASV) and Stability Index have been used to find the most stable genotypes while indices YSI and WSI have been used to find both the most stable and high yielding genotypes. On the basis of ASV, genotypes MH 2120, MH 2109 and MH 2116 have been found to be the most stable for this Zone. The Spearman’s rank correlation coefficient between YSI and WSI was found to be significant at 1% level of significance indicating that the two indices have almost similar performance in determining high yielding stable genotypes.

Key words: AMMI analysis, GGE biplot analysis, G×E interaction, Stability analysis, Pearl millet, Weighted stability index.

INTRODUCTION

Pearl millet (Pennisetum glaucum L.), also known as bajra in Hindi, is the sixth most important rain fed cereal crop annually cultivated in arid and semi-arid areas of India. It is also a fodder crop of Northern India and forms the staple diet for nearly 10% of the Indian population. Millet variety selection with its production environment is often challenged by the occurrence of significant genotype-by-environment interaction (GEI) in the varietal development process. It is largely affected by G×E interaction, making it difficult and expensive to select and recommend new millet varieties for different environments. Several statistical models have been proposed for increasing the chance of exploiting GEI and supporting breeding program decisions in variety selection and recommendation for target set of environments. Additive Main effects and Multiplicative Interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) models are among the models that effectively capture the additive (linear) and multiplicative (bilinear) components of GEI and provide meaningful interpretation of multi-environment data set in breeding programs. The AMMI model is essentially a combination of ANOVA and Principal Component Analysis (PCA). It applies PCA to the G×E interaction part of the ANOVA. Because of this, the AMMI model is also called Interaction PCA or IPCA. Kempton (1984) seems to have been the first to apply AMMI to the study of G×E interaction. AMMI is theoretically the most effective model to account for the GE interaction sum of squares with a minimum number of degrees of freedom. A full AMMI model (AMMI-F) equates to the ANOVA model, since all the sum of squares due to GE interaction are explained by the principal axes. A GGE biplot (Yan et al., 2000) is a biplot that displays the genotypic main effect (G) and genotype by environment interaction (GE) of a genotype-by-environment data set. GGE biplot analysis is a system that consists of a set of biplot graphs that are designed to address various research objectives when genotypes by environment two-way data are analyzed. A biplot is a scatter plot that graphically summarizes two factors in such a way that relationships among the factors and underlying interactions between them can be visualized simultaneously. To understand GEI, two types of biplot, the AMMI biplot (Crossa, 1990 and Gauch, 1992) and the GGE biplot (Yan and Kang, 2003 and Gauch et al., 2008) are the most commonly used biplots. The measured value of each cultivar in a test environment is the cumulative effect of genotype main effect (G), environment main effect (E) and the GE interaction (Yan and Kang, 2003). Birla and Ramgiry (2015)

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and Khandzadeh et al. (2018) also studied GxE using AMMI and Biplot analysis. Giridhar et al. (2016) studied Stability for seed yield in ajwain based on Gcentotype Selection Index. Kumar et al. (2018) applied GGE Biplot technique for analysis of data from Multi-environment Yield Trials for Wheat in Northern India. The pearl millet cultivation in India is divided in 3 major zones - A, A and Z effective evaluation of the pearl millet breeding material. In the present study, the GxE interaction in pearl millet genotypes from zone-A of India has been evaluated using the techniques of AMMI and GGE biplot analyses. AMMI Stability Value (ASV) and Stability Index have been used to find the most stable genotypes while indices YSI and WSI have been used to find both the most stable and high yielding genotypes. A new weighted index (WI) have been proposed for determining the high yielding and stable genotypes based on the normalized indices for grain yield and ASV indices.

MATERIALS AND METHODS

The yield data for the study were obtained from the annual report of AICRP on pearl millet for the year of 2015-16. Based on climatic conditions, the pearl millet cultivation in the country is divided in 3 major zones-A, A and B. The zone-A includes 15 pearl millet growing locations which receive less that 400mm of annual rainfall. For this study, data on 30 early type genotypes of pearl millet evaluated at 15 locations Mandor (MDR), Jaipur(JPR), Kothara (KTR), S. K. Nagar (SKN), Anand (AND), Jamnagar (JMR), Ahmedabad(AHD), Talaja (TJL), Hisar (HSS), Bawal (BWL), Kalai (KLI), Eglas (ELS), New Delhi, Gwalior (GLR), Ludhiana (LDA) in a randomized complete block design with three replications have been used (Table 1).

AMMI and GGE Biplot Models: The AMMI analysis is a combination of analysis of variance and multiplication effect analysis. The AMMI model (Rao and Prabhakaran, 2005) for T genotypes and S environments is below.

\[
Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{n^*} \lambda_n \alpha_n Y_{jn} + \theta_{ij}
\]

\[
\theta_{ij} \sim N(0, \sigma^2) ; \quad i=1, 2, \ldots, T; \quad j=1, 2, \ldots, S
\]

Where,

\(Y_{ij}\) = mean yield of \(i^{th}\) genotype in the \(j^{th}\) environment/location

\(\mu\) = general mean

\(g_i\) = \(i^{th}\) genotypic effect

\(e_j\) = \(j^{th}\) location effect

\(\lambda_n\) = eigen value of the \(n^{th}\) PCA axis.

\(\alpha_n\) and \(\gamma_n\) are the \(i^{th}\) genotype, \(j^{th}\) environment PCA scores for the \(n^{th}\) axis

\(\theta_{ij}\) = residual

\(n^*\) = number of PCA axes retained in the model

| Genotype | ENTRY | MDR | JPR | KSK | AND | JMR | AHD | TLJ | KLI | ELS | HSS | BWL | GLR | LDA | NDL |
|----------|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| G1       | MH 2103 | 3829 | 1950 | 824 | 2592 | 3913 | 3387 |     |     |     |     |     |     |     |     |
| G2       | MH 2104 | 3412 | 1622 | 801 | 2424 | 3639 | 2935 |     |     |     |     |     |     |     |     |
| G3       | MH 2105 | 2677 | 1300 | 903 | 1715 | 2544 | 2497 |     |     |     |     |     |     |     |     |
| G4       | MH 2106 | 3690 | 2694 | 1153 | 3186 | 4445 | 3516 |     |     |     |     |     |     |     |     |
| G5       | MH 2107 | 3477 | 2667 | 1190 | 3260 | 4356 | 2629 |     |     |     |     |     |     |     |     |
| G6       | MH 2108 | 2556 | 1506 | 838 | 2292 | 3365 | 2629 |     |     |     |     |     |     |     |     |
| G7       | MH 2109 | 3167 | 2683 | 1352 | 3186 | 3647 | 3594 |     |     |     |     |     |     |     |     |
| G8       | MPMH 17 | 3185 | 2433 | 1023 | 2714 | 2942 | 2378 |     |     |     |     |     |     |     |     |
| G9       | MH 2110 | 2986 | 2383 | 1046 | 2892 | 4077 | 2662 |     |     |     |     |     |     |     |     |
| G10      | MH 2111 | 3079 | 2511 | 1093 | 3077 | 3930 | 2567 |     |     |     |     |     |     |     |     |
| G11      | MH 2112 | 2991 | 2467 | 1060 | 3346 | 3615 | 2222 |     |     |     |     |     |     |     |     |
| G12      | MH 2113 | 3338 | 2006 | 1287 | 2759 | 3817 | 2154 |     |     |     |     |     |     |     |     |
| G13      | MH 2114 | 3208 | 1872 | 1190 | 3385 | 3648 | 3093 |     |     |     |     |     |     |     |     |
| G14      | MH 2115 | 3016 | 2300 | 1259 | 2596 | 4176 | 2469 |     |     |     |     |     |     |     |     |
| G15      | MH 2116 | 3104 | 2000 | 1185 | 2199 | 3542 | 2045 |     |     |     |     |     |     |     |     |
| G16      | MH 2117 | 2588 | 1644 | 847 | 1764 | 2991 | 2520 |     |     |     |     |     |     |     |     |
| G17      | RHB 173 | 2685 | 2517 | 1102 | 2523 | 3117 | 2572 |     |     |     |     |     |     |     |     |
| G18      | MH 2118 | 3116 | 2206 | 1134 | 3435 | 3456 | 2998 |     |     |     |     |     |     |     |     |
| G19      | MH 2119 | 2653 | 2379 | 856 | 2929 | 4077 | 2637 |     |     |     |     |     |     |     |     |
| G20      | MH 2120 | 2676 | 1756 | 903 | 2455 | 3708 | 3043 |     |     |     |     |     |     |     |     |
| G21      | MH 2121 | 2509 | 2278 | 1019 | 3025 | 2907 | 2105 |     |     |     |     |     |     |     |     |
| G22      | MH 2122 | 2769 | 2456 | 861 | 2065 | 3611 | 1950 |     |     |     |     |     |     |     |     |
| G23      | GBH 905 | 3324 | 2483 | 1343 | 2484 | 2505 | 3046 |     |     |     |     |     |     |     |     |
| G24      | MH 2123 | 2963 | 2556 | 1111 | 1896 | 4458 | 3617 |     |     |     |     |     |     |     |     |
| G25      | MH 2124 | 2199 | 2372 | 1069 | 1948 | 3168 | 2079 |     |     |     |     |     |     |     |     |
| G26      | MH 2125 | 2880 | 2661 | 1250 | 3188 | 3383 | 2090 |     |     |     |     |     |     |     |     |
| G27      | MH 2126 | 2515 | 2456 | 1574 | 2458 | 2796 | 2510 |     |     |     |     |     |     |     |     |
| G28      | MH 2127 | 2819 | 2344 | 1347 | 2632 | 2953 | 2533 |     |     |     |     |     |     |     |     |
| G29      | MH 2128 | 2571 | 2172 | 958 | 1780 | 2662 | 2109 |     |     |     |     |     |     |     |     |
| G30      | MH 2129 | 3134 | 2350 | 1366 | 3064 | 3393 | 2948 |     |     |     |     |     |     |     |     |
The residual combines the PCA scores from the \( N - n' \) discarded axes, where \( N = \min (T-1, S-1) \). The other constraints in the model (1) are

\[
\sum_{i=1}^{T} \alpha_{in} = \sum_{j=1}^{S} Y_{jn} = 1 \quad \forall n;
\]
\[
\sum_{i=1}^{T} \alpha_{in} \alpha_{in}^* = \sum_{j=1}^{S} Y_{jn} Y_{jn}^* = 0, n \neq n^*\text{ and } \lambda_1 > \lambda_2 > \cdots > \lambda_{n'} > 0.
\]

For many practical situations, the number of PCA axes to be retained is determined by testing the mean square of each axis with the estimate of residual through \( F \)-statistics (Gollob, 1968 and Gauch, 1988). The mean sum of squares of each PCA axis is equal to the ratio of square of the corresponding eigen value and the degree of freedom of each axis obtained as \( T+S-1-2n \).

Further, the \( G \times E \) data for any character can be optimally approximated by SVD in rank two matrix. With above notations, the basic model for constructing a GGE biplot from GE data is given by

\[ Y_{ij} = \mu + g_i + e_j + \phi_{ij} + \theta_{ij} \]  

Where, \( \phi_{ij} \) = interaction between \( g \) and \( e \) and \( \theta_{ij} \) is the residual of the model associated with the genotype \( i \) in environment \( j \). The GGE (i.e. grand mean and environment centered) biplot can also be represented mathematically as

\[ Y_{ij} - \overline{Y}_j = \xi_{i1} \lambda_1 \eta_{ij} + \xi_{i2} \lambda_2 \eta_{ij} + \theta_{ij} \]  

Where, \( \overline{Y}_j \) is the average yield of genotype \( i \) in environment \( j \)

\[ \overline{Y}_j = \frac{1}{n} \sum_{i} Y_{ij} \]  

\( \xi_{i1} \) and \( \xi_{i2} \) are the PC1 and PC2 scores, respectively for genotype \( i \)

\( \lambda_1 \) and \( \lambda_2 \) are the PC1 and PC2 eigenvalues respectively

\( \eta_{ij} \) and \( \eta_{ij} \) are the PC1 and PC2 scores, respectively for environment \( j \).

To display PC1 and PC2 in a biplot, the equation is rewritten as

\[ Y_{ij} - \overline{Y}_j = \xi_{i1} \lambda_1 \eta_{ij} + \xi_{i2} \lambda_2 \eta_{ij} + \theta_{ij} \]  

Where, \( \xi_{i1} = \lambda_n \eta_i \) and \( \xi_{i2} = \lambda_n \eta_i \) with \( n = 1, 2, \cdots \), is the average yield over all genotypes in environment \( j \)

\( \lambda_1 \) and \( \lambda_2 \) are the singular values for PC1 and PC2 respectively

\( \eta_{ij} \) and \( \eta_{ij} \) are the PC1 and PC2 scores respectively for genotype \( i \) in environment \( j \).

**Weighted Stability Index (WSI):** The AMMI model does not provide a quantitative stability measure, much as a measure is essential in order to quantify and rank genotypes according to their yield stability. The AMMI stability value (ASV) proposed by Purchase et al. (2000) is a useful measure to quantify and rank genotypes according to their yield stability. In ASV method, a genotype with the least ASV score is the most stable and is given by

\[ ASV = S \sqrt{ \frac{\text{IPCAsum of squares}}{\text{IPCAscore}} } - \text{(IPCAscore)}^2 + \frac{\text{IPCA2sum of square}}{\text{IPCA2score}}^2 \]  

An index for determining high yielding and stable genotypes, called yield Stability Index (YSI) is given by

\[ YSI = R(ASV) + R(GY) \]  

Where, \( R(ASV) \) is the rank of the AMMI stability value of \( i^\text{th} \) genotype and \( R(GY) \) is the rank of the mean grain yield of \( i^\text{th} \) genotype across all the environments. The yield stability value incorporates both mean yield and stability in a single criterion. Low value of YSI is desirable for genotypes with high mean yield and stability.

Let \( GY \) denote the value of the mean grain yield of \( i^\text{th} \) genotype for all the environments \( (i = 1, 2, \ldots, T) \), then normalized index of mean grain yield (Hooda et al., 2017) of \( i^\text{th} \) genotype for all the environments may be obtained as

\[ NGY_i = \frac{GY_i - \min(GY_i)}{\max(GY_i) - \min(GY_i)} \]  

Where, \( GY_i \) is the mean grain yield of the \( i^\text{th} \) genotype in all the locations and \( \max(GY) \) and \( \min(GY) \) are taken for \( i^\text{th} \) genotype.

Also, let \( ASV \) denote the value of the AMMI Stability Value of \( i^\text{th} \) genotype for all the locations \( (i = 1, 2, \ldots, T) \) where lower the ASV more stable in the genotype then normalized index (Hooda et al., 2017) of \( i^\text{th} \) genotype for all the locations may be obtained as follows:

\[ NASV_i = \frac{\max(ASV_i) - ASV_i}{\max(ASV_i) - \min(ASV_i)} \]  

Where, \( NASV_i \) is the normalized index of AMMI stability value, where higher the value of \( NASV_i \) more stable the genotype; \( ASV_i \) is the AMMI stability value of the \( i^\text{th} \) genotype in all the locations and \( \max(ASV_i) \) and \( \min(ASV_i) \) are taken for \( i^\text{th} \) genotype. The normalized values indices also lie between 0 and 1 and increase or decrease in the direction of the stability i.e. lower values imply lesser stability and higher values imply higher stability.

From the matrix of the normalized indices for grain yield and ASV, we propose the following weighted stability index (WSI) for determining the high yielding and stable genotypes

\[ WSI = w_1 NGY_i + w_2 NASV_i \quad i = 1, 2, \ldots, T \]  

Here, \((0 \leq w_1, w_2 \leq 1)\) and \(w_1 + w_2 = 1\) are the weights associated with the \( NGY \) and \( NASV \) and the weights \( w_1 \) and \( w_2 \) are given by as

\[ w_1 = \frac{s_2}{s_1 + s_2} \quad \text{and} \quad w_2 = \frac{s_1}{s_1 + s_2} \]  

Where, \( s_1 \) is the standard deviation of \( NGY \) and \( s_2 \) is the standard deviation of \( NASV \). The weighted stability index lies between zero and one. A simple ranking of genotypes based on WSI is used for stability of genotype. Genotype with maximum WSI index is the most stable with high
yielding. Spearman’s rank correlation coefficient between the rank based YSI and WSI was used to demonstrate the similarity of inference drawn from the proposed index WSI and index YSI.

RESULTS AND DISCUSSION

The AMMI ANOVA (Table 2) indicates that maximum contribution towards variation (70.35%) was made by environment effect followed by G × E interaction (19.23%) and genotypic variation (10.40%). The axes IPCA1, IPCA2 and IPCA3 were found significant using the Gollob’s F-test. These axes accounted for 21.90 percent, 17.23 percent and 12 percent of the interaction sum of squares, respectively.

Based on the yield stability values (Table 3), the genotype G3 was found to be the most stable genotype with high yield followed by genotype G16 on the basis of stability index. Based on YSI value, the most stable genotypes with higher grain yield were found to be G7 and G5. Similarly, based on weighted index (W1), G7 was found to be most stable genotype with higher yield followed by genotype G5.

On the basis of SI values, only two groups of stable genotypes were found. Low SI (%) was recorded in genotype G21 whereas moderate SI (%) in G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G22, G23, G24, G25, G26, G27, G28, G29 and G30.

Table 2: AMMI analysis of variance for Zone A pearl millet grain yield (kg/ha) data.

| Source                          | D.F | Sum of squares | Mean square | F_cal | Sum of squares (%) |
|---------------------------------|-----|----------------|-------------|-------|--------------------|
| Genotype                        | 29  | 38015171.11    | 1310867.96  | 7.57**| 10.40              |
| Environment                     | 14  | 257009456.07   | 18357818.29 | 106.04**| 70.35           |
| G × E interaction               | 406 | 70283020.81    | 173110.88   | 1.44**| 19.23             |
| IPCA1                           | 42  | 15392625.92    | 366491.09   | 3.052**| 21.90             |
| IPCA2                           | 40  | 12112644.84    | 302816.12   | 2.522**| 17.23             |
| IPCA3                           | 38  | 8477731.98     | 222045.57   | 1.849**| 12.00             |
| Residual                        | 286 | 34340018.08    | 120069.99   |        |                    |
| Total                           | 449 | 365307648      | 813602.77   |        |                    |

Table 3: Yield-stability indices for Zone A Pearl millet genotypes.

| Genotype | GY   | ASV   | YSI  | WI    |
|----------|------|-------|------|-------|
| G1       | 3114(9) | 27.63(27) | 36(21) | 0.39(24) |
| G2       | 3066(12) | 16.22(17) | 29(13) | 0.56(14) |
| G3       | 2423(30) | 26.09(25) | 55(30) | 0.10(30) |
| G4       | 3466(3)  | 32.12(30) | 33(17) | 0.48(17) |
| G5       | 3403(5)  | 9.33(7)   | 12(2)  | 0.85(2)  |
| G6       | 2637(26) | 13.40(14) | 40(23) | 0.44(22) |
| G7       | 3468(2)  | 4.70(2)   | 4(1)   | 0.89(1)  |
| G8       | 2977(15) | 8.59(5)   | 20(4)  | 0.67(4)  |
| G9       | 2836(22) | 16.77(18) | 40(24) | 0.45(21) |
| G10      | 3226(7)  | 26.99(26) | 33(18) | 0.47(20) |
| G11      | 3078(11) | 21.58(23) | 34(19) | 0.48(19) |
| G12      | 2999(14) | 10.20(9)  | 23(8)  | 0.64(8)  |
| G13      | 3242(6)  | 30.76(29) | 35(20) | 0.40(20) |
| G14      | 2935(18) | 17.56(19) | 37(22) | 0.48(18) |
| G15      | 2917(19) | 6.52(3)   | 22(7)  | 0.67(6)  |
| G16      | 2467(29) | 11.27(11) | 40(25) | 0.37(26) |
| G17      | 2971(16) | 10.88(10) | 26(10) | 0.61(11) |
| G18      | 3027(13) | 8.22(4)   | 17(3)  | 0.68(5)  |
| G19      | 3079(10) | 11.58(13) | 23(9)  | 0.64(8)  |
| G20      | 2737(25) | 2.15(1)   | 26(11) | 0.64(9)  |
| G21      | 2875(21) | 29.54(28) | 49(28) | 0.25(29) |
| G22      | 2761(24) | 8.92(6)   | 30(15) | 0.54(15) |
| G23      | 3168(8)  | 20.77(22) | 30(16) | 0.53(16) |
| G24      | 3406(4)  | 15.75(16) | 20(5)  | 0.73(3)  |
| G25      | 2856(27) | 13.77(15) | 42(26) | 0.38(25) |
| G26      | 2935(17) | 11.34(12) | 29(14) | 0.58(13) |
| G27      | 2878(20) | 9.70(8)   | 28(12) | 0.58(12) |
| G28      | 2769(23) | 4.67(24)  | 47(27) | 0.28(27) |
| G29      | 2581(28) | 19.55(21) | 49(29) | 0.28(28) |
| G30      | 3509(1)  | 18.77(20) | 21(6)  | 0.72(4)  |
The ranks of the genotypes as per various stability indices and mean grain yield are given in parentheses. The Spearman's rank correlation coefficient between YSI and WSI was found to be 0.981 which was significant at 1% level of significance. It shows that the two indices have almost equal performance in determining high yielding stable genotypes.

Graphical presentation of stability and high grain yield of genotypes for Zone A: A quick idea about high yielding stable genotypes can be had from the simple scatter plot of the Normalized Grain Yield (NGY) and Normalized ASV values (NASV). Fig 1 gives the scatter plot of NGY taken along x-axis and NASV taken along y-axis. The scatter plot represents the most stable, high yielding and the most stable with high yielding genotypes. It was observed that the genotype G20 was the most stable (on the basis of NASV), G30 was high yielding (on the basis of NGY) and G7 was the most stable as well as high yielding.

GGE biplots for Zone A pearl millet genotypes included the following major three aspects:

i) Mega-environment analysis based on genetic correlation between location and the which-won-where pattern.

ii) Test location evaluation based on their discriminating ability and representativeness.

iii) Genotype evaluation based on their mean performance and stability across a mega-environment.

Mega-environment analysis for Zone A: In column metrics preserving biplot, properties of environments were retained exactly. Lines are added to extract extra information from column metrics preserving GGE biplot. An irregular convex polygon has been formed such that all the genotypes come inside the polygon. Perpendicular lines were added on all sides of polygon. Now the genotypes and environments in between two perpendicular lines provide positive yield with the environments since angle between any pair of genotype and environment in this region is less than 90 degree. So, the genotype at the vertex of the polygon in this region often provides maximum yield that is why each sector formed by these perpendicular lines has a superior genotype at vertex than any other genotype in this sector. The total environment got divided into different sectors which have their own superior genotypes. The superior genotype is called winner genotype in respective regions. The sectors formed by perpendicular lines enclose similar type environment which has specific performer and those environments which falls in this region are called mega-environment. The “which won where” biplot (Fig 2) for Zone A pearl millet data identified AHD, AND, MDR, JMR, GLR and TLJ forming one mega environment and KLI, BWL, ELS, SKN, JPR, LDA, HSR,
NDL and KTR forming second mega environment. The genotypes G4 (MH2106) and G30 (MH2129) have been observed to be the winner genotypes in the respective mega environments.

**Test-environment evaluation for Zone A:** The relationship among the environments is evaluated by correlation value measured by the cosine of the angle between them as shown in Fig 3. So, for evaluation of representativeness, target environment is depicted as arrow on AEC by taking average of all environments and angle between target and test environment is representativeness of one another. The discriminating property is observed by the variance of the variable (environment). More the variance of environment more is the discriminating power of environment for genotypes.

It was observed that BWL and KLI had the highest representativeness of the trial while AHD and ELI had the highest discriminating power. NDL and TLJ had low representativeness as well as low discriminating power. The environment KLI was observed to be the most fruitful trial while NDL the least fruitful trial.

**Genotype evaluation for Zone A:** Breeding programs have main focus on enhancement of agricultural production and search of superior genotypes. Varieties are evaluated not only by performances in a mega-environment but also by mean yield of genotypes along with their stability for general recommendation of cultivar in experimental region. For general release as a breed, evaluation of a genotype is performed with respect to average performance and stability of all genotypes.

The test environment evaluation axis (Fig 4) is helpful in evaluation of genotypes. The axis passing through this virtual environment is called average environment axis (AEA) while a perpendicular axis is also overlaid on biplot which is called average coordination axis (AEC). The arrow shown on the axis of the AEC abscissa points in the direction of higher mean performance of the genotypes and consequently ranks the genotypes with respect to mean performance. Unless the genotypic effect (G) is too small to be meaningful, the ranking of the genotypes on the AEC abscissa is always perfectly or highly correlated with G. The Fig 4 indicates that the genotypes G10 (MH2111) and G29 (MH2128) were favourable for the trial region in view of both average yield and stability of genotypes. In contrast, G21 (MH2121) and G28 (MPMH17) were least stable genotypes.
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