# AMMI analysis for stability of grain yield of pearl millet (*Pennisetum typhoides* L.) hybrids

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## Abstract

**Nine pearl millet (*Pennisetum typhoides* L.) genotypes (eight hybrids and one variety) were tested over fourteen environments (years/locations) in different zones of Maharashtra. Grain yield data were subjected to the Additive main-effects and multiplicative interaction (AMMI) analyses. Results indicated a significant genotype × environment interaction (GEI) that influenced the relative ranking of the hybrids across the environments. It was evident from AMMI analysis that genotype, environment and the first principal component of interaction effect accounted for 95.20% of treatment sum of squares and the first three principal components of interaction effect were found significant. As per the AMMI model, four genotypes (RHRBH-9802, RHRHH-8609, RHRBH-9807 and RHRBH-9808) were identified as having general adaptability. Further, two environments i.e. 1998/Rahuri-II and 2000/Rahuri-II were found ideal for stable performance of the hybrids.**

## Introduction

The genotype × environment interaction structure is an important aspect of both plant breeding programmes and the introduction of new crop cultivars [1]. ANOVA which is an additive model is effective in partitioning the total sum of squares into i) the genotypic main effect, ii) the environment main effect and iii) the GEI, but it does not provide insight into GEI structure. To study the underlying interaction component, more advance techniques such as principal component analysis are required. The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure. The AMMI model separates the additive variance and then applies principal component analysis (PCA) to the interaction portion to extract a new set of coordinate axes which explain in more detail the interaction pattern. The effectiveness of AMMI procedure has been clearly demonstrated by various authors *viz.*, in soybean Zobel *et al.*, [2], in maize Crossa *et al.*, [3], Nichit *et al.*, [4] and Crossa *et al.*, [5] in wheat, and Sharma *et al.*,

[6], Vijaykumar *et al.*, [7], Zavala-garcia *et al.*, [8] in pearl millet, rice and sorghum, respectively using multilocational trial data.

Using the AMMI analysis and biplot facility therefrom, the pearl millet yield trial data were analyzed to determine the nature and magnitude of G × E interaction effects on grain yield in diverse production environments, to identify high yielding, stable genotypes adapted to diverse production environments and to determine the areas where pearl millet cultivars would be adapted and produce economically competitive yields.

## Materials and methods

Nine pearl millet genotypes (eight hybrids including two hybrid checks RHRBH-8609 and RHRBH-8924 developed at MPKV., Rahuri and a check variety ICTP-8203) were evaluated at fourteen environments. The locations were *kharif*-1998 (Rahuri I, Rahuri II, Dhule, Mohol and Niphad); *kharif*-1999 (Rahuri I, Rahuri II, Dhule and Mohol) and *kharif*-2000 (Rahuri II, Dhule, Chas, Solapur and Niphad). Rahuri I and Chas locations are characterized by shallow soil and Rahuri II location has medium soil and these two locations are in central Maharashtra. Dhule is in North Maharashtra, Niphad is under plain zone and Solapur and Mohol is in southern Maharashtra. All the locations except Niphad are in scarcity zone. Each entry at each location was sown in randomized block design with three replications at 45 × 15 cm spacing. Yield data (Kg/plot) for each replication were recorded for each entry at all the locations during Kharif 1998-2000 and used for statistical analysis.

The AMMI model is :

$$Y_{ij} = \mu + g_i + e_j + \Sigma\, hk\, \alpha_{ij}\, \tau_{ik} + R_{ij}$$

where, $Y_{ij}$ is the yield of *i*th genotype *j*th environment, $g_i$ is the mean of the *i*th genotype as a deviation from the grand mean $\mu$; $e_j$ is the mean of the *j*th environment minis the grand mean ($\mu$), *hk* is the eigen value of the PCA axis *k*, $\alpha_{ij}$ and $\tau_{ik}$ are the principal component

scores for *k* of the *i*th genotypes and the *j*th environment respectively and $R_{ij}$ is the residual. The GE interaction sum of squares was subdivided into PCA axis, where axis *k* is regarded as having *t* + *s*-1-2*k* degrees of freedom and *t* and *s* are the number of the genotypes and environments respectively. The data was analyzed by using INDISTAT statistical package at Mahatma Phule Krishi Vidyapeeth, Rahuri.

## Results and discussion

The AMMI analysis of variance is presented in Table 1. It clearly indicated that the mean sum of squares for genotypes, environments and G × E interactions were found to be highly significant. This suggested that broad range of diversity existed among genotypes and among environments and that the performance of genotypes was differential over the locations (environments).

**Table 1.** AMMI analysis of variance of grain yield of six pearl millet hybrids and two hybrid checks and one variety check tested at 14 environments

| Source | d.f. | Sum of squares | Mean squares | Percentage SS |
|---|---|---|---|---|
| Treatment combinations | 125 | 60.28 | 0.48** | 100 |
| Genotype | 8 | 1.68 | 0.21** | 2.80 |
| Environment | 13 | 54.34 | 4.18** | 90.15 |
| GE interaction | 104 | 4.25 | 0.04** | $7.05 |
| PCA 1 | 20 | 1.36 | 0.07** | $32.07 |
| PCA 2 | 18 | 1.27 | 0.07** | $29.85 |
| PCA 3 | 16 | 0.72 | 0.04** | $16.87 |
| Residual | 50 | 0.90 | 0.02** | $21.21 |
| Error | 252 | 1.64 | 0.006** | |
| Total | 377 | 61.91 | 0.164** | |

*,** = Significant at 5% and 1% level of significance, respectively
$ = As percent of GE interaction SS

Out of the total treatment variation (Trial SS), the proportion of variance due to differences in environments was largest (90.15 per cent) followed by the variance due to G × E interactions (7.05%) and variance due to genotypes (2.80%). Thus, ordinary ANOVA model accounted only 92.95% of the treatment combination SS attributed to genotypes and environment effects.

The GEI which was highly significant was further partitioned into three PCA axes (IPCA) with contribution of 32.07, 29.85, and 16.87 per cent to the total GEI Variance. All the three IPCA axes representing the interaction pattern were highly significant and jointly accounted for 78.79% of interaction component with 51.33% of the df for GEI. The residual SS which accounted for only 21.21% of the interaction SS and 48.77% of df for GEI was also found to be highly significant. This situation seems to arise due to presence

of high level of uncontrolled variations but not due to the real GEI.

The above analysis, however seems to suggest the presence of a complex, multidimensional variation in genotype-by-environment data as the first three axes were demonstrated to be highly significant. The AMMI models with many IPCA axes are expected to involve rather more noise than the highly complex interactions among genotypes and environments. Further, if the AMMI model includes more than one PCA axes, assessment and presentation of genetic stability are not as simple as that of AMMI model [4-7]. The second and third ICPA axes, despite significant in the present study, were pooled into residual. Thus, AMMI model with first IPCA axis was accepted for further study.

The results of the AMMI analysis can also be easily comprehended with the help of AMMI biplot as represented in Fig. 1. The mean performance IPCA1 score for both the genotypes and environments used to construct the bioplot (Fig. 1) are presented in Table 2. The main effects (genotype means and environment means in Fig. 1) are shown along the abscissa (X-axis), and the ordinate (Y-axis) represents the first PCA. Both main effects and interaction component are very clearly depicted in the figure. The usual interpretation of such a biplot assay is that if a genotype or an environment has a PCA score of nearly '0', it has small interaction effects and when the genotype and environment have the same sign on the PCA axis, their interaction is positive; if different their interaction is negative. The biplot helps in visual interpretation of the GE patterns and identify genotypes or locations that exhibit low, medium or high levels of interaction effects. [2, 5, 6, 9].

According to the AMMI model, the genotypes, which are characterized by mean greater than the grand mean and the PCA scores nearly zero, are
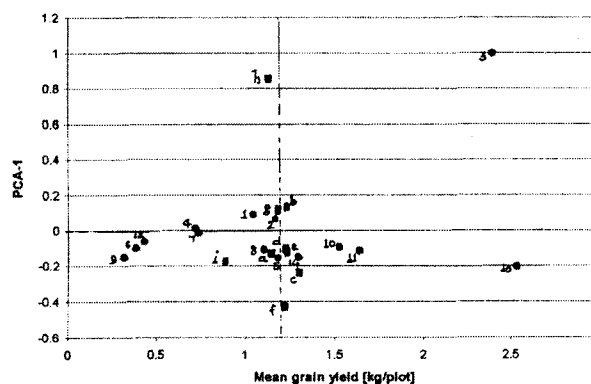


Fig. 1. Bioplot of AMMI-1 model for a pearl millet yield trial with nine genotypes (■) and 14 environments (•). The vertical line represents the grand mean of the experiments and horizontal lines is IPCA-1 = 0

**Table 2.** Mean grain yield (Kg/plot) of six pearl millet hybrids and two hybrid checks and one variety check grown in 14 environments and the first PCA scores for the GE interaction effect as derived from AMMI model.

| Sr. No. | Hybrid/Variety | E1 | E2 | E3 | E4 | E5 | E6 | E7 | E8 | E9 | E10 | E11 | E12 | E13 | E14 | Gen. mean | First PCA |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | *kharif* 1998 | | | | | | *kharif* 1999 | | | | *kharif* 2000 | | | | | |
| | | Rahuri I | Rahuri II | Dhule | Mohol | Niphad | Rahuri I | Rahuri II | Dhule | Mohol | Rahuri II | Dhule | Chas | S'pur | Niphad | | |
| a | RHRBH-9801 | 1.24 | 1.03 | 2.46 | 0.88 | 1.18 | 0.34 | 0.56 | 1.08 | 0.26 | 1.30 | 1.35 | 0.41 | 2.70 | 1.17 | 1.14 | −0.122 |
| b | RHRBH-9802 | 1.20 | 1.42 | 2.19 | 0.65 | 1.08 | 0.37 | 0.83 | 1.18 | 0.32 | 1.80 | 2.06 | 0.46 | 2.42 | 1.38 | 1.24 | 0.154 |
| c | RHRBH-9803 | 1.08 | 1.52 | 2.70 | 0.90 | 1.48 | 0.39 | 0.85 | 1.05 | 0.25 | 1.77 | 1.81 | 0.54 | 2.78 | 1.18 | 1.31 | −0.239 |
| d | RHRBH-9807 | 1.20 | 1.03 | 2.66 | 0.77 | 1.33 | 0.38 | 0.89 | 1.18 | 0.31 | 1.52 | 1.43 | 0.48 | 2.63 | 1.45 | 1.24 | 0.111 |
| e | RHRBH-9808 | 1.09 | 1.17 | 2.77 | 0.74 | 1.18 | 0.43 | 0.91 | 1.02 | 0.35 | 1.59 | 1.43 | 0.47 | 2.23 | 1.93 | 1.24 | −0.114 |
| f | RHRBH-9810 | 1.18 | 1.34 | 2.83 | 0.65 | 1.20 | 0.33 | 0.88 | 1.17 | 0.23 | 1.69 | 1.86 | 0.31 | 2.43 | 1.17 | 1.23 | −0.424 |
| g | RHRBH-8609 | 1.05 | 1.35 | 2.09 | 0.96 | 1.15 | 0.60 | 0.55 | 1.03 | 0.51 | 1.53 | 1.85 | 0.44 | 2.76 | 0.97 | 1.20 | 0.128 |
| h | RHRBH-8924 | 0.91 | 0.94 | 1.56 | 0.58 | 1.43 | 0.34 | 0.87 | 1.19 | 0.31 | 1.59 | 1.50 | 0.40 | 2.60 | 1.67 | 1.14 | 0.905 |
| i | ICTP8203 | 0.44 | 0.76 | 2.26 | 0.38 | 0.69 | 0.21 | 0.36 | 1.10 | 0.30 | 1.01 | 1.49 | 0.35 | 2.28 | 0.77 | 0.88 | −0.178 |
| | Location mean | 1.04 | 1.17 | 2.39 | 0.72 | 1.19 | 0.38 | 0.74 | 1.11 | 0.31 | 1.53 | 1.64 | 0.43 | 2.54 | 1.30 | 1.18[*] | |
| | PCA 1 | 0.090 | 0.064 | 0.995 | 0.008 | −0.155 | −0.107 | −0.013 | −0.111 | −0.148 | −0.094 | −0.116 | −0.06 | −0.208 | −0.147 | | |

[*]Overall

considered as generally adaptable to all the environments. However, the genotypes with high mean performance and with large value of IPCA scores are considered as having specific adaptability to the environments.

Biplot assay presented in Fig. 1 thus, identified four hybrids *viz.*, (b) RHRBH-9802, RHRHH-8609, RHRBH-9807 and RHRBH-9808 as having general adaptability as they were scattered at the right-hand side of the grand mean level and close to IPCA1 = 0 line. Hybrid, (h)-RHRBH-8924 was specially adapted to favourable environments.

Further, Fig. 1 presents the biplot corresponding to the environment means and first PCA. It clearly indicated that environment E-10 (2000/Rahuri-II) and E-2 (1998/Rahuri-II) had good conditions for all the hybrids while at the same time, the PCA score for these two environments were near zero indicating all the genotypes are expected to be fairly stable. While, environments E-4, E-7 and E-12 also had zero score on the PCA axis but their yield potential was below average. The environments E-3, E-13 and E-11 had excellent potential for yield levels, but were exhibiting high interaction effects and therefore they are most suitable for specially adapted hybrids or genotypes. On the other hand, the environments such as E-1, E-8, E-5, E-6 and E-9 differed for both main effects and interactions, thus ranking in such environments are likely to be quite variable.

AMMI analysis carried out for studying the performance and stability of pearl millet hybrids has clearly indicated the usefulness of this model to have greater insight into the magnitude and nature of genotype × environment interaction. This model is effective in identifying the genotypes that have specific adaptation (interacting) and those which are adaptable (non-interacting). It is also useful for characterizing the environments/locations which are suitable for growing a specific or group of the hybrids.

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