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AMMI ANALYSIS OF A PEARL MILLET YIELD TRIAL

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ABSTRACT

The analysis of yield trial data to draw accurate inference is an important aspect of the plant breeding programmes. Grain yield data on 44 pearl millet genotypes tested over 22 locations spread across India were subjected to the ordinary ANOVA and the additive main-effects and multiplicative interaction (AMMI) analyses. The ANOVA model analysed only the main effects (genotypes and environments) while treating the G × E interaction as residual and accounted for the 81.7 per cent of the trial SS while AMMI model analyzed both the main effects and G × E interaction, and accounted for 86.1 per cent of the trial SS. Furthermore, biplot from AMMI1 parameters provided the comprehensive understanding of the pattern of the data. Thus, following the AMMI1 model, 9 genotypes (MH 305, MH 310, MH 328, MH 342, MH 393, MH 401, MH 406, MH 411 and MP 223) were identified as having general adaptability, while 11 genotypes (MH 306, MH 349, MH 351, MH 390; MH 394, MH 402, MH 403, MH 405, MH 408, MH 412 and MH 413) as with specific adaptability to the locations tested. The AMMI (biplot) analysis characterized the four locations, namely Gwalior (M.P.), Patancheru (A.P.), Gulberga (Karnataka) and Aurangabad-(Maharashtra) as the ideal locations for growing the pearl millet crop in general.

Key words: Pearl millet, yield trial, G × E interaction, Additive Main effects and Multiplicative Interaction (AMMI), adaptability.

With an aim to make recommendations about the suitable genotypes to be released as varieties, yield trials in plant breeding programmes are conducted with a set of genotypes at several locations (environments) representing diverse crop growing zones. They are always affected by genotype × environment interactions [1]. A significant G × E interaction for a quantitative trait, such as yield can seriously limit efforts in selecting superior genotypes for both new crop production and improved cultivar development [2], and would reduce the usefulness of subsequent analysis of means and inferences that would otherwise be valid.

The ordinary analysis of variance (ANOVA) is useful for identifying and testing sources of variability, it provides no insight into the particular pattern of the

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underlying interaction. The ordinary ANOVA model is additive and effectively describes the main (additive) effects, while the interaction (residual from the additive model) is nonadditive and requires other techniques, such as principal component analysis (PCA) to identify interaction patterns. Thus, ANOVA and PCA models combine to constitute the Additive Main-effects and Multiplicative Interaction (AMMI) model [3-4]. The AMMI model is, therefore, a hybrid statistical model incorporating both ANOVA (for additive component) and PCA (for multiplicative component) for analyzing two-way (genotype-by-environment) data structure. The model has, in recent past, been recommended for statistical analysis of yield trials, and was preferred over other customary statistical analyses, such as ordinary ANOVA, principal component analysis and linear regression analysis [3-6].

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

MATERIALS AND METHODS

Fourty four pearl millet genotypes (hybrids--MH series, and composite populations--MP series), including a check variety WC C75 were evaluated in a randomised complete block design with three replicates at 22 sites across India during 1989-90 under All India Co-ordinated Pearl Millet Improvement Project (AICPMIP). The grain yield in kg/ha was recorded at maturity.

The basic linear model (the ANOVA model) used in the analysis of yield trial is of the form:

$$Y_{ij} = \mu + g_i + e_j + \delta_{ij}$$

where Y_{ij} is the observed response value (e.g., yield) of genotype (cultivar) i in environment (location) j; μ is the grand mean; g_i is the effect for genotype i (deviation of g from μ), i = 1, ...k; e_j is the effect for environment j (deviation of e from μ), j = 1, ... n; and δ_{ij} is the interaction (= $Y_{ij} - Y_i - Y_j + Y..$).

It is possible to partition the interaction component (δ_{ij}) into the sum of multiplicative functions of i and j [7].

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_k \gamma_{ik} \alpha_{jk} + \varepsilon_{ij}$$

which yields the AMMI model. λ_k is the eigen value of interaction principal component axis (IPCA) k, γ_{ik} and α_{jk} are correspondingly the genotype and environment

eigenvectors (i.e., IPCA scores) for the axis k, N is the number of IPCA axes retained in the model, and ε_{ij} is the residual.

Beginning with the ordinary ANOVA procedure [8] for two-way analysis of variance, the AMMI analysis first separates additive variance (μ, g_i and e_j) from the multiplicative variance (interaction), and then applies PCA to the interaction, i.e. to the residual portion of the ANOVA model to extract a new set of coordinate axes which account more effectively for the interaction patterns [3, 5, 6]. Direct estimation of G × E interaction is obtained by the product of genotype IPCA score(s) ($\lambda_k^{0.5}$ γ_{ik}) times the environment IPCA score(s) ($\lambda_k^{0.5}$ α_{jk}). The eigen values in PCA are equivalent to sum of squares, and the degrees of freedom for IPCA axes were calculated as per Gollob [9] : df = G + E − 1 − 2k for axis k.

AMMI generates a family of models with different values of N. The simplest model with AMMI0 with N equal to zero considers only the additive effects, namely genotypes and enviroments means to explain the data matrix. The second model AMMI1 considers main effects and one interaction principal component axis to interpret residual matrix. Similarly, AMMI2 involves main effects and two interaction principal component axes for nonadditive (interaction) variation, and so on.

When one interaction PCA axis accounts for most of G × E, a feature of AMMI model is the biplot procedure in which genotypes and environments-taking mean values on abscissa and IPCA1 scores on ordinate---are plotted on the same diagram, facilitating inference about specific interactions as indicated by the sign and magnitude of IPCA1 values of individual genotypes and environments.

The statistical analyses were carried out by using the software MATMODEL [10].

RESULTS AND DISCUSSION

PARTITIONING OF VARIANCES

Since AMMI model uses additive ANOVA for partitioning of variance due to genotypes and environments and analyzes its residual (i.e., G × E interaction), analysis for AMMI (Table 1) can also be used for a study of the results of ANOVA. It can be seen from this table that the mean squares for genotypes, locations (environments), and G × E interactions were found to be highly significant (P > 0.001). This suggested that broad range of diversity existed among genotypes and among locations, and that the performance of genotypes was differential over locations.

Table 1. AMMI analysis of variance for grain yield (kg/ha) of 44 pearl millet genotypes tested at 22 locations in India

Source	d.f.	Sum of squares	Mean squares	R^{2a}
Trials	967	2300625562.6	2379137.1**	100.0
Genotype	43	106126849.8	2468066.3***	4.6
Environment	21	1773602333.7	84457254.0***	77.1
GE interaction	903	420896379.1	466108.9***	18.3
IPCA1	63	100103437.4	1588943.4***	23.8
Residual	840	320792941.6	381896.3***	76.2
Error	1892	204377170.5	108021.8	
Block	44	14272704.9	324379.7	
Total	2902	2519275437.9	867817.9	

[a]Fraction of sum of squares associated with each term or interaction

** and *** indicate P>0.01 and P > 0.001, respectively.

Of the total treatment variation (trial SS), the proportion of variance due to differences in locations was largest (77.1 per cent) followed by the variance due to G × E interactions (18.3% : considered as residual in case of ANOVA), and variance due to genotypes (4.6%). Thus, ordinary ANOVA model accounted only for 81.7 per cent of the trial SS concentrating only on the genotype effects and environment effects. Therefore, it could tell us (through statistical tests) whether genotypes, environments and genotype × environment interaction exerted a significant effect, but it did not tell us which genotypes, environments, and genotype × environment combinations were responsible, nor did it tell us how their responses differ. Conclusively, ANOVA provided no insight into the particular patterns of genotypes or environments that gave rise to interactions, but described only the main effects effectively. These results conformed to the observations made by Snedecor and Cochran [4, 8]. Thus, in the present investigation, ANOVA model was not found to be adequate for analyzing the pearl millet yield trial data, as G × E interactions were highly significant. Therefore, ANOVA model was combined with PCA model to further analyze the residuals of the ANOVA model, which infact contains G × E interaction. Gauch [6] suggested further analysis of the effects of G × E interactions even if they are indicated to be non-significant by an F-test in ANOVA.

The G × E interaction was partitioned into seven interaction PCA (IPCA) axes — each explaining, respectively, 23.8, 18.6, 9.1, 7.2, 6.5, 5.2 and 5.0 per cent of the

interaction sum of squares; all the seven IPCA axes were found to be highly significant and jointly accounted for 76% of the interaction SS with only 44% of the total df for G × E interaction. The residual SS which accounted for 24% of the G × E SS with 56% of G × E df was also found to be highly significant. This situation seems to arise due to the presence of high level of uncontrolled variations---the noise---but not due to the real G × E interactions.

The above analysis, however, seems to suggest the presence of a complex, multidimensional variation in the genotype-by-environment data, as the first seven IPCA axes were demonstrated to be highly significant by an F-test (P>0.001). 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 IPCA axes, assessment and presentation of genetic stability are not as simple as that from the AMMI1 model [3, 5, 6, 11-13]. The second and higher IPCA axes, despite significant in the present study, were pooled into residual. Thus, AMMI1 model (AMMI model with first IPCA axis) was

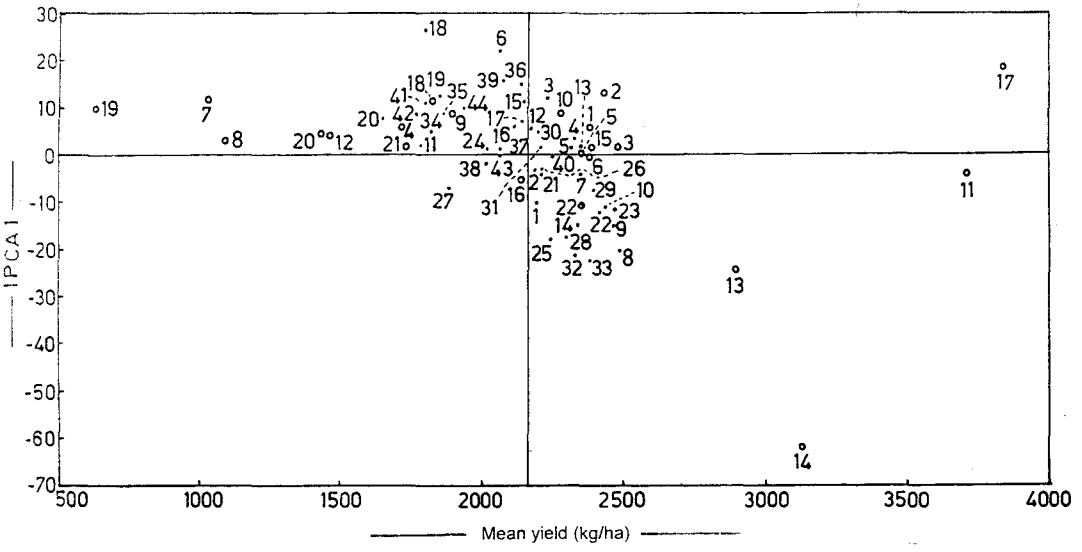

Fig. 1. Biplot of AMMI1 model for a peal millet yield trial with 44 genotypes (•) and 22 locations (o). The vertical line represents the grand mean of the experiment and horizontal line is IPCA1 = 0. For genotype and location names see Table 2a and 2b.

accepted for further study. This model contained 86.1 per cent of the trial SS, leaving the rest 13.9 per cent in the residual, and was more efficient than the ANOVA model which accounted only for 81.7 per cent of the trial SS.

AMMI1 BIPLOT : INTERPRETING SPECIFIC PATTERNS

The results of AMMI analysis can also be easily comprehended with the help of AMMI1 biplot as presented in Fig. 1. The mean performance and IPCA1 scores for both the genotypes and environments used to construct the biplot (Fig. 1) are presented in Table 2a and 2b. The biplot---a graphical representation---from AMMI analysis is a useful tool in understanding more comprehensively the specific patterns of main effects and G × E interactions of both the genotypes and environments simultaneously [4, 12, 14].

Table 2a. Mean yields (kg/ha) and IPCA1 scores for 44 pearl millet genotypes.

S. No.	Genotype	Mean yield	IPCA1 score	S. No.	Genotype	Mean yield	IPCA1 score
1.	MH 298	2196	- 10.1	23.	MH 403	2474	- 11.5
2.	MH 305	2196	- 3.0	24.	MH 404	2029	- 1.2
3.	MH 306	2237	12.0	25.	MH 405	2259	- 18.3
4.	MH 310	2338	3.3	26.	MH 406	2215	- 4.1
5.	MH 328	2329	1.3	27.	MH 407	1895	- 6.9
6.	MH 338	2063	22.4	28.	MH 408	2298	- 17.0
7.	MH 342	2357	- 4.1	29.	MH 409	2401	- 6.4
8.	MH 349	2484	- 20.4	30.	MH 410	2206	5.1
9.	MH 351	2465	- 14.5	41.	MH 411	2217	1.4
10.	MH 390	2438	- 11.2	32.	MH 412	2344	20.7
11.	MH 391	1789	2.4	33.	MH 413	2395	- 21.6
12.	MH 392	2175	5.4	34.	MH 129	1818	4.8
13.	MH 393	2357	1.3	35.	MP 201	1867	9.4
14.	MH 394	2348	- 15.1	36.	MP 204	2112	15.4
15.	MH 395	2159	11.0	37.	MP 205	2076	- 1.3
16.	MH 396	2116	6.5	37.	MP 221	2014	- 2.4
17.	MH 397	2156	6.7	39.	MP 222	2080	15.6
18.	MH 398	1976	26.9	40.	MP 223	2253	- 0.9
19.	MH 399	2026	12.5	41.	MP 224	1974	10.7
20.	MH 400	1993	7.8	42.	MP 225	1774	9.0
21.	MH 401	2213	- 3.9	43.	MP 226	2071	0.7
22.	MH 402	2417	- 12.0	44.	WCC75	1944	9.8

Table 2b. Mean yields (kg/ha) and IPCA1 scores for 22 locations

S. No.	Location (state)	Mean yield	IPCA1 score
1.	Rakh Dhiansar (Jammu & Kashmir)	2381	6.2
2.	New Delhi (Delhi)	2435	12.6
3.	Gwalior (MP)	2497	1.5
4.	Perumallapalli (Andhra Pradesh)	1716	5.6
5.	Patancheru (Andhra Pradesh)	2351	0.3
6.	Gulberga (Karnataka)	2369	- 1.3
7.	Gurgaon (Haryana)	1040	12.0
8.	Mathura (U.P.)	1099	3.3
9.	Bawal (Haryana)	1910	8.5
10.	Jamnagar (Gujarat)	2295	8.5
11.	Rahuri (Maharashtra)	3705	- 4.5
12.	Amaravati (Maharashtra)	1462	4.5
13.	Jalna-Mahendra (Maharashtra)	2902	-24.5
14.	Aurangabad-NATH (Maharashtra)	3140	-62.0
15.	Aurangabad-NARP (Maharashtra)	2393	1.4
16.	Niphad (Maharashtra)	2158	-6.9
17.	Tabiji (Rajasthan)	3845	18.4
18.	Navgaon (Rajasthan)	1815	11.2
19.	Fatehpur Shekhawat (Rajasthan)	645	9.9
20.	Jaipur (Rajasthan)	1438	4.5
21.	Mandor (Rajasthan)	1743	1.8
22.	Narsanda (Gujarat)	2435	- 11.0

The biplot of AMMI1 parameters accounted for 86.1 per cent of the trial SS. It is clear from the biplot that the points for the locations were more scattered than the points for genotypes; this indicated that variability due to locations was higher than that due to genotypes differences. This is also evident from the ANOVA.

In Fig. 1, displacement along the abscissa (horizontal axis) reflects differences in main effects whereas displacement along the ordinate (vertical axis) exhibits differences in interaction effects. When a genotype and an environment fall in the upper or lower portion from the line indicating IPCA1 = 0 in the biplot, their interaction is positive. However, the genotypes and environments of opposite portions

from the IPCA1 = 0 line show negative interaction. In other words, the genotypes and environments with similar signs (either positive or negative) of IPCA1 scores exhibit negative positive and *vice versa*. Thus, with the help of biplot, the results of the present investigation can be interpreted as follows :

1. Identifying high yielding stable genotypes

According to the AMMI model, the genotypes which are characterized by means greater than the grand mean and the IPCA scores nearly zero are considered as generally adaptable to all environments. However, the genotypes with high mean performance and with large value of IPCA scores are considered as having specific adaptability to the environments. Zobel *et al.* [4] in soybean, Crossa *et al.* [12, 15] in maize and wheat, Zavala-Garcia *et al.* [16] in sorghum, and Romagossa *et al.* [17] in barley also conducted AMMI analysis and predicted the stability of genotypes on the basis of mean performance and the magnitude of IPCA1 scores.

On the biplot, the points for the generally adapted genotypes would be at right hand side of the grand mean level (this suggests high mean performance) and close to the line showing IPCA1 = 0 (this suggests negligible or no G × E interaction). However, the points for the specifically adapted genotypes would be away from the line with IPCA1 = 0 and next to the grand mean level. Thus, it was clear from Fig. 1 that 9 genotypes, viz., 2, 4, 5, 7, 13, 21, 26, 31 and 40 (see Table 2a for name of genotypes) which were scattered at the right-hand side of the grand mean level and close to IPCA1 = 0 line, were declared by the AMMI1 model as having general adaptability to all locations. However 11 genotypes, viz., 3, 8, 9, 10, 14, 22, 23, 25, 28, 32 and 33 were equipped with high mean and large IPCA1 scores, hence specifically suited to the favourable locations. Favourable locations for these genotypes can be characterized as with high mean and high IPCA1 scores with same sign as of genotype IPCA1 scores. Similar signs of IPCA1 scores implies positive interaction and thus will suggest higher yield of genotypes. For example, locations 13, 14 and 11 are most favourable for the genotypes 8, 32 and 13, and the locations 17 and 2 are most favourable for genotype no. 3 : high magnitude of positive interaction was observed between these genotypes and locations. On the other hand, genotypes 8, 32 and 33 will show low yields in location no. 2, because they exhibited high magnitude of negative interaction with that environment.

2. Identifying favourable locations for pearl millet

Environments that appear almost in a perpendicular line have similar means and those that fall almost in a horizontal line have similar interaction pattern. AMMI1 biplot (Fig. 1) thus exhibited that locations 19, 7, 2, 18, 9 and 10 (see Table 2b for

name of locations) differed in main effects but they exhibited nearly similar interactions. The locations 1, 2, 15 and 22 had similar main effects but differed in interaction with genotypes.

The sites 7, 3, 13, 14 and 17 differed in both main effects and interactions; the rankings in such locations are likely to be quite variable, thus making it complex to produce variety recommendations. Further, the locations 13, 14 and 17 were highest yielding and highly interacting, hence are most suitable only for the specifically adapted genotypes.

However, sites 3, 5, 6, 15, 11 and 21 all had smallest (near to zero) IPCA1 scores, relative rankings (not absolute yields) of genotypes would be fairly stable in these sites. In addition to the smallest interaction effects, the sites 3, 5, 6 and 15 were high yielding (site mean yield > grand mean), deemed suitable for growing pearl millet crop in general. Selection of sites and requirements of climate for pearl millet crop may, therefore, be recommended on the basis of the main features of these sites.

The results and analyses presented in this paper confirm that AMMI analysis with its biplot is a very useful tool in analyzing yield trial data. It explains comprehensively both the effects due to genotypes and environments and also their interaction patterns. ANOVA could explain only the genotypes and environments but not their interaction which is a significant feature of yield trials.

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