

AMMI analysis for grain yield stability of pearl millet (*Pennisetum glaucum* L.) genotypes

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Improvement in grain yield of pearl millet is one of the focal endeavors of pearl millet (*Pennisetum glaucum* L.) breeding. As pearl millet is grown in tropical and subtropical agro-ecologies, it is important to assess adaptation and yield stability of promising genotypes across environments. Various methodologies have been explored to study genotype x environment (G x E) interaction and to predict the phenotypic response to changes in the environment [1]. The success of identifying high yielding genotypes from yield trials depends on the effectiveness of the statistical analysis used to evaluate parents in data and estimated yields [2].

The G x E interaction is an important aspect of plant breeding [3]. The additive main effects and multiplicative interaction (AMMI) model can effectively explain the role of G x E interaction and it has been used because of its easy interpretation, identification of genotypes for specific and wide adaptation and to measure the genetic gain in plant breeding programmes [4-6]. The AMMI model analyses the additive effects of genotypes (G) and locations (L) by a standard analysis of variance and the multiplicative effects of the G x E interaction by using Principal Component Analysis (PCA).

The model computes the principal component scores for genotypes and environments that represent the G x E interaction. The members of the AMMI family are identified according to the number of PCA axes, for example, with one PCA axis, it is denoted as AMMI1, with two PCA axes AMMI2, and so on. The PCA1 genotype and environment means on x-axis are used

to construct a biplot graph showing the main and interaction effects. Genotypes or environments with large first PCA scores (either plus or minus) have large interaction while those with values close to zero have small interaction [7, 8] and are considered stable. The effectiveness of AMMI already demonstrated by various workers viz., in pearl millet [9, 10], maize [4] and in sorghum [11], using multiplications data. This study was conducted with a view to determine the effect of G x E interaction on the grain yield of genotypes, to identify most stable and adapted genotypes to sustain the yield potentiality across wide environments and seasons.

Twenty eight pearl millet genotypes (Twenty hybrids including five checks and eight population including three checks) were evaluated at five environments during *kharif* 2009 in Maharashtra. The locations were Buldhana, Ambejogai, Dhule, Niphad and Aurangabad. All the locations except Niphad are in scarcity zone. Each entry at each location was sown in randomized block design with three replications at 50 x 15cm spacing, with net plot size 4.20m x 1.50 m. Yield data (kg/plot) for each replication were recorded for each entry at all the locations utilized for computation of statistical analysis.

The AMMI model is :

$$Y_{ij} = \mu + g_i + e_j + \sum_{hk} \alpha_{ij} \alpha_{ij} + R_{ij}$$

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 μ , e_j is the mean of the j^{th} environment minus the grand mean (μ), h_k is the eigen value of the PCA axis k , α_{ij} and γ_{ij} are the principal component scores

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for k of the i^{th} genotypes and j^{th} environment respectively and R_{ij} is residual. The GE interaction sum of squares was subdivided in PCA axis, where axis k is regarded as having $t + s - 1 - 2k$ 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.

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

Out of the total treatment variation (Trial SS), the proportion of variance due to differences in environments was largest with the magnitude of 74.63% followed due to G x E interactions (17.04) and variances due to genotypes (8.33 %). Thus, ordinary ANOVA model accounted only 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 35.62, 30.90, 23.44 percent respectively, to the total GEI Variance. All the three IPCA axes representing the interaction pattern were highly significant and jointly accounted for 89.96 % of interaction component with 77.78 % of df for GEI.

The residual SS which accounted for only 10.04% of interaction SS and 22.22% of 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 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 that of AMMI model [4, 9, 10]. The second and third IPCA axis, despite significant in the present study, were pooled into residual. Thus, AMMI model with first IPCA axis was accepted for further study.

The result of the AMMI analysis can also be easily comprehended with the help of AMMI biplot as represented in Fig. 1. The mean performance ICPCA 1 score for both the genotypes and environments used to construct the biplot (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) represent 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 GE patterns and

Table 1. AMMI analysis of variance of grain yield of twenty eight pearl millet genotypes tested at five environments

Source	df	Sum of Squares	Mean Squares	Percentage SS
Treatment Combination	139	146139584.00	1051363.91	100
Genotype	27	12169082.93	450706.78**	8.33
Environment	4	109071123.61	27267780.90**	74.63
GE interaction	108	24899377.47	230549.79**	\$17.04
PCA 1	30	8868616.19	295620.54**	\$35.62
PCA 2	28	7694655.72	274809.13**	\$30.90
PCA 3	26	5837283.56	224510.91**	\$23.44
Residual	24	2498822.00	104117.58**	\$10.04
Error	280	6513599.02	23262.85**	
Total	419	152653183.02	364327.41**	

*,** = Significant at 5% and 1% level of significance, respectively; \$ = As per cent of GE interaction SS.

Table 2. Mean grain yield (kg/ha) of twenty-eight pearl millet genotypes grown on five environments and the first PCA scores for the first PCA scores for the GE interaction effect as derived from AMMI model

S.No.	Genotype	Environment (for <i>Kharif</i> 2009)					General mean	First PCA
		Buldhana E 1	Ambejogai E 2	Dhule E 3	Niphad E 4	Aurangabad E 5		
1	BBH- 831	3365	1455	3321	1508	2623	2454	3.96
2	BBH -832	3280	3404	3283	878	3667	2902	27.15
3	AHB -903	2275	2318	3070	688	3142	2298	15.08
4	AHB- 961	2540	2047	3163	847	3733	2466	5.61
5	DHBH-7100	3227	1455	3599	1323	4080	2737	-7.71
6	DHBH -7103	3174	1719	3571	1587	4396	2890	-8.96
7	AHB -927	3122	2249	3028	1079	3474	2590	10.58
8	BBH -830	3069	2434	3498	1693	3804	2900	5.13
9	BBH -3	3682	1984	2555	1535	4112	2774	-0.49
10	DHBH- 4/186	2910	1918	3641	2275	4017	2952	-9.13
11	DHBH -7097	2751	1518	3658	1852	3687	2693	-9.01
12	DHBH -7099	3174	1455	3784	1640	3191	2649	-2.75
13	AHB -1666 (C)	2460	1556	2912	873	3687	2297	-1.26
14	Shraddha (C)	2884	1984	2857	1481	3365	2514	3.98
15	Saburi (C)	2222	1905	2945	1222	4254	2510	-4.74
16	Shanti (C)	3254	1545	3647	2699	4632	3155	-22.09
17	ICMH 356 (C)	2963	1656	2774	931	4135	2492	-2.69
18	DHBH -7104	3016	1746	2491	1852	2929	2407	1.99
19	DHBH -7105	3280	1455	3175	1429	4088	2685	-8.3
20	DHBH -7107	3571	1614	3691	1561	4230	2933	-7.7
21	BBC -10	1481	1190	2391	820	3970	1970	-11.08
22	BBC- 12	2486	1249	2415	1328	2694	2035	-0.34
23	ABPC 4-3	1905	1206	2492	715	3119	1887	-1.46
24	ABPC 4-1	2381	1571	2572	423	2741	1938	10.63
25	ABPC 5-7-1	2486	1762	2932	492	3119	2158	9.66
26	92901(C)	2910	2296	2908	487	3166	2353	18.06
27	PPC 6 (C)	2619	1545	2892	587	4442	2417	-5.23
28	ICTP 8203 (C)	1957	1005	2224	577	3804	1913	-8.88
	Location Mean	2802	1759	3053	1228	3654	2499	
	PCA I	8.77	40.53	-0.98	-22.43	-25.89		

identify genotypes or locations that exhibit low, medium or high levels of interaction effects [10, 12].

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

Biplot assay presented in Fig. 1 thus, identified four hybrids *viz.*, BBH 3, DHBH 7099, Shraddha and Saburi as having general adaptability as they were scattered at the right-hand side of the grand mean level and close to IPCA = 0 line. On other hand, the three hybrids *viz.*, BBH 832, AHB 927 and Shanti was

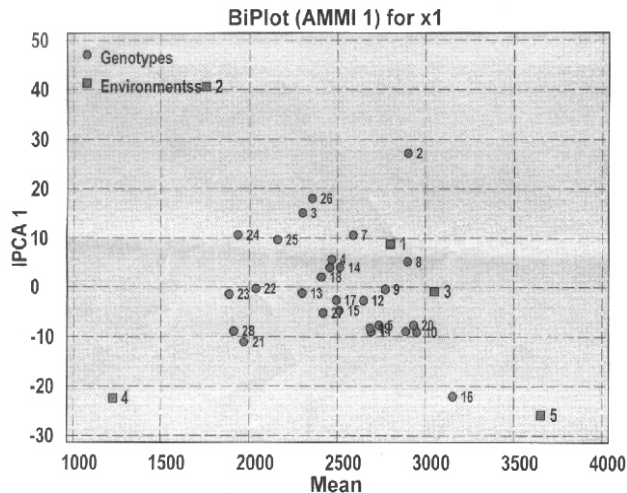


Fig. 1. Biplot of AMMI-1 model for a pearl millet yield trial with nine genotypes(•) and five environments(.). The vertical line represents the grand mean of the experiment and horizontal lines is $IPCA-1=0$

specifically adapted to favourable environments.

Further, Fig. 1 presents the biplot corresponding to the environment mean and first PCA. It clearly indicated that environment, Dhule (E-3) and Buldhana (E-1) had good conditions for most of the genotypes while at the same time, the PCA score for these two environments were nearly zero indicating all the genotypes are expected to be fairly stable. The environment Aurangabad (E-5), had excellent potential for yield levels, but were exhibiting high interaction effects and therefore they are most suitable for specially adapted genotypes. On other hand, the environments, such as Ambejogai (E-2) and Niphad (E-4) had lower grain yield than grand mean and 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 genotypes has clearly indicated the usefulness of this model to have greater insight into the magnitude and nature of genotype x 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 genotypes.

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