Electronic Journal of Plant Breeding, 8(4): 1223-1228 (Dec 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00175.2

Research Article

Assessment of Genotype-Environment Interaction Using Additive Main Effects and Multiplicative Interaction Model (AMMI) in Maize (Zea mays L.) Hybrids

G. Usha Rani, V. Satyanarayana Rao*, Lal Ahmad M* and K.L. Narasimha Rao**
Department of Genetics and Plant Breeding, Agricultural College, Bapatla.
Department of Plant Physiology, Agricultural College, Bapatla

(Received: 30 Aug 2017; Revised: 1 Dec 2017; Accepted: 4 Dec 2017)

Abstract

The present study was performed to analyze the Genotype-Environment (G x E) interaction for 21 maize hybrids over 3 locations to identify suitable and stable hybrids. Grain yield data were subjected to the AMMI analysis. Analysis revealed significant G x E interaction which could be attributed to differential ranking of the genotypes across the environments. The G x E interaction was further axis captured into PCA axes, of which the first PCA 52-69% to the total G x E variance. Perusal of the biplot analysis indicated that five hybrids *Viz.,* Seed tech, Super-36, Vivek QPM-9, Prakash and Vivek hybrid-33 were identified as having general adaptability with high mean yields and PCA scores nearer to zero.

Key words
G x E interaction, AMMI, Stability, Hybrid, Maize

Introduction

The impact of environment on any crop is very much prominent particularly in case of flowering traits. An understanding of G x E interaction is fundamental to any crop improvement programmes, where the performance of a cultivar is judged based on the yield trials conducted over locations / year or location and year combinations. Traditional statistical analysis is not always effective with this data structure (Zobel, *et al.,* 1998, Crossa, *et al.,* 1991, Shinde, *et al.,* 2002). The usual ANOVA, having a merely additive model, identifies the GE interaction as a source but does not analyze it, on the other hand PCA (Principle component analysis) is a multiplicative model and hence contain no sources for additive genotype or environment main effects, and the most widely used LR (Linear regression) analysis is able to effectively analyze interaction terms only where the pattern fits a specific regression model. Raising these theoretical and applied problems in estimating and comparing the G x E interaction, different statistical models have been developed, of which AMMI model is worth to be considered. AMMI offers a more appropriate first statistical analysis of yield trials that may have a genotype x environment interaction, since ANOVA, PCA and LR are sub cases of the more complete AMMI model. The effectiveness of this AMMI model has been applied to maize data and detailed discussions were also made by Crossa *et al.* (1990). Hence the present study was undertaken to use AMMI model to determine the nature and magnitude of G x E interaction effects in order to compare the maize hybrids and predicting the high yielding and stable ones before recommending to diverse productive environments.

Materials and methods

Twenty one maize genotypes including check were included in the present study. The experiment was conducted at Agricultural College Farm, Bapatla during *kharif* 2011, *late kharif* 2011 *and rabi* 2011, thus making three environments. The experimental material was planted in randomized block design with three replications in each environment. At each environment, experimental plot consisted of three rows of 5m length each with a row to row distance of 75cm and plant to plant distance of 25cm. Yield data (g/plant) was recorded by averaging ten individual plants data for each hybrid in each location at three environments and used for the AMMI analysis, analysis of variance was performed for grain yield per plant. The analysis of variance (ANOVA) was used and the GE interaction was estimated by the AMMI model. Thus, the mean response of the genotype i in environment j (Y_{ij}) is modelled by

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

Where, Y_{ij} is the yield of genotype; μ is the grand mean, g_i is the deviation of the mean of genotype i from μ; e_j is the deviation of environment j from μ; Residual deviation not explained by the components μ, g_i and e_j. The G x E interaction sum of squares was subdivided into PCA axes. The F tests to determine the significance of the PCA MS, degrees of freedom were calculated by the simple method of Gollob (1968). *i.e.* df = G+E-2n, where G is the genotypes; E is the environments and N is the PCA axes.

Results and discussion

The AMMI analysis of variance revealed that mean sum of squares for environments was found significant (Table 1 & 2), indicating the differential effect of environments on the performance of the genotypes. Out of the total treatment variation due to differences in environments was maximum followed by the variance due to genotypes.

The ANOVA table indicated that G x E interaction was partitioned into three interaction principle component axes (IPCAs). The ANOVA table indicated that all the three IPCAs were not significant and explained 51.06%, 48.85% and 0.00% of the total G x E interaction sum of squares percentage.

The AMMI models with many IPCA axes are expected to involve rather noise than the highly complex interactions among the genotypes and environments. Further, if the AMMI model includes more than one IPCA axes, assessment and presentations of genetic stability become complex. Hence in the present AMMI model first IPCA axis was adopted for further study.

The AMMI biplot provides a visual expression of the relationships between the first interaction principal component axis (IPCA 1) and means of genotypes and environments. The IPCA 1 explained the interaction pattern better than other interaction axes. The biplot showed that two genotypes Vivek hybrid-23 and Buland as low yielding and unstable, CMH-08-284 is the highest yielder but less stable and Seed tech and Super-36 were identified as high yielding and stable genotypes. Since IPCA 2 also play a significant role in explaining the GEI, the IPCA 1 were plotted against the IPCA 2 explore for further adaptation (Figure 1). In AMMI 2 biplot (Figure 2), the hybrids HQPM-1, CMH-08-284 and Bio-9637 are unstable due to their dispersed position. DHM-117, Vivek QPM-9, Prasad and Vivek hybrid-33 were nearer to IPCA origin, hence these genotypes were stable over environments. Among the environments *(kharif* 2011, *late kharif* 2011 *and rabi* 2011), environment III (*rabi* 2011) is most suitable as indicated by high mean value of IPCA 1 and low value of IPCA 2.

Genotypes with IPCA 1 values near zero had little interaction across environments while genotypes with very high IPCA values had considerable interactions across environments. Out of the 21 genotypes, four had negligible interactions characterised by DHM-117, Vivek QPM-9, Prasad and Vivek hybrid-33 (Table 2) and relatively showing broad adaptation across environments. Three genotypes with higher IPCA values were highly interactive and were unstable across environments; these were Vivek hybrid-23, Buland and JH-3457. The underlying causes of the interaction observed can therefore be based on both the genetic differences between these genotypes and the different environments (Banic, *et al.*, 2010). *Kharif* was more stable than others and had the best performances for grain yield.

The AMMI statistical model has been used to diagnose the G x E interaction pattern of grain yield of hybrid maize. Genotypes Seed tech, Super-36, DHM-117, Vivek QPM-9, Prasad and Vivek hybrid-33 showed adaptation with high yield. They were hardly affected by GEI and thus will perform well across a wide range of environments.

.

References

Crossa, J., Gauch, H.G and Zobel, R.W. 1990. Additive main effects and multiple interaction analysis of two international maize cultivar trials. *Crop Science.* 30: 493: 500.

Gallob, H.F. (1968). A statistical model which combines features of factor analysis and analysis of variance techniques. *Psychometrika.* 33: 73-115.

Sharma, P.K., Gupta, P.K and Govila, O.P. 1998. AMMI analysis of a pearl millet yield trial. *Indian Journal of Genetics and Plant Breeding.* **58**(2): 183-192.

Shinde, G.C., Bhingarde, M.N., Khairnar and Mehetre, S.S. 2002. AMMI analysis for stability of grain yield of pearlmillet (*Pennisetum typhoides* L.) hybrids. *Indian Journal of Genetics.* 62: 215-217.

Zobel, R.W., Wright, M.J and Gauch, M.G. 1988. Statistical analysis of a yield trial. *Agronomy Journal.* 80: 388-393.

Banik, B.R., Khaldum, A.B.M., Mondal, A.A., Islam, A and Rohman, M.M. 2010. Assessment of genotype-by environment interaction using Additive Main effects and Multiplicative Interaction model (AMMI) in maize (*Zea mays* L.) hybrids. Academic Journal of Plant Sciences. 3(4): 134-139.

Table 1. ANOVA of AMMI model for Oil content(%), Seed yield per plant(g), Seed yield per ha in maize (Zea mays L.)

Source of Variations	Oil content(%)			Seed yield per plant(g)			Seed yield per ha		
	df	MSS	% explained	df	MSS	% explained	df	MSS	% explained
Trials	62	0.522	-	62	70.696	-	62	24.849	-
Genotypes	20	0.424	26.153	20	72.781	33.210	20	45.238**	58.726
Environments	2	2.577	15.895*	2	200.078	9.129	2	50.326*	6.533
G*E Interaction	40	0.469	57.952	40	63.184	57.661	40	13.381	34.741
PCA I	21	0.686	76.683	21	63.416	52.693	21	13.015	51.063
PCA II	19	0.231	23.317	19	62.873	47.266	19	13.761	48.850
PCA III	17	0.000	0.000	17	0.061	0.041	17	0.0273	0.087
Residual	-17	0.000	0.000	-17	0.000	0.000	-17	0.000	0.000
Pooled residual	19	0.469		40	62.928		40	13.381	

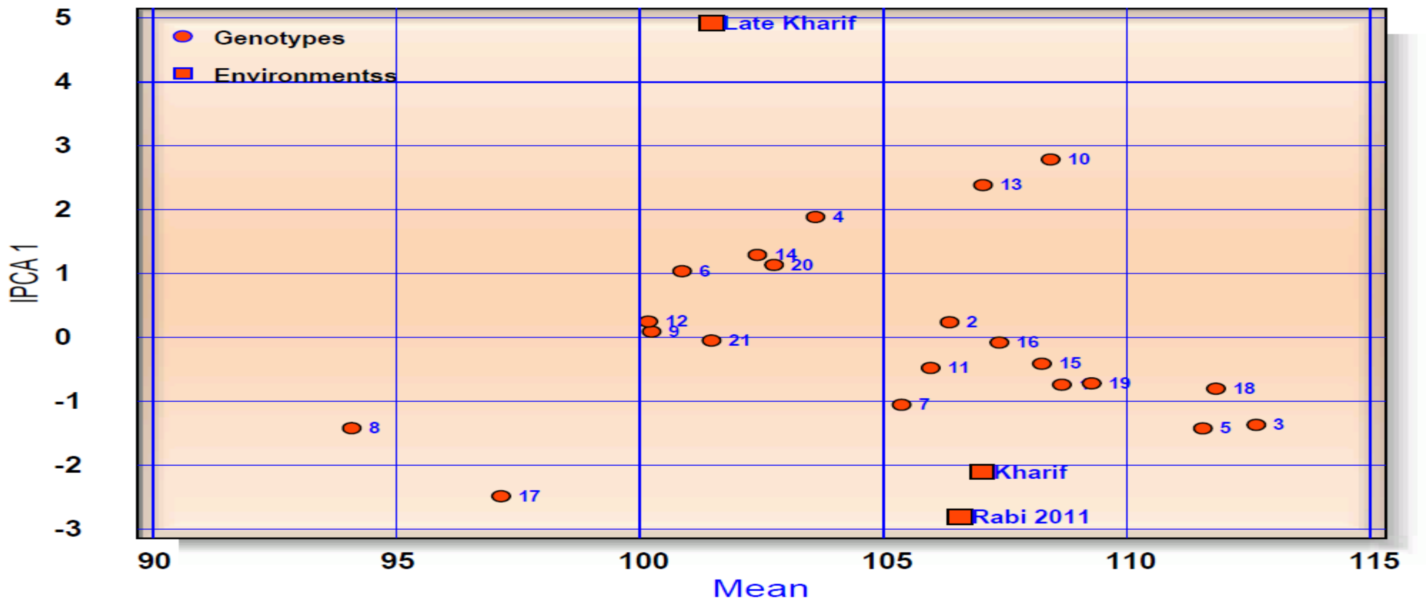
Significant at 0.05 level** * Significant at 0.01 level**

Table 2. ANOVA of AMMI model for Kernel rows per cob, 100 seed weight(g), Biological yield per plant(g), Harvest index(%) in maize (*Zea mays* L.)

Source of Variations	**Kernel rows per cob**			**100 seed weight(g)**			**Biological yield per plant(g)**			**Harvest index(%)**		
	df	**MSS**	**% explained**	**df**	**MSS**	**% explained**	**df**	**MSS**	**% explained**	**df**	**MSS**	**% explained**
Trials	62	1.270	-	62	7.479	-	62	197.682		62	17.648	
Genotypes	20	2.886*	73.290	20	6.399	27.598	20	163.060	26.608	20	29.289*	53.536
Environments	2	0.905	2.297	2	30.382*	13.104	2	906.759*	14.797	2	12.063	2.205
G*E Interaction	40	0.481	24.412	40	6.874	59.298	40	179.540	58.595	40	12.107	44.259
PCA I	21	0.479	51.995	21	8.499	64.910	21	230.932	67.525	21	16.965	73.564
PCA II	19	0.489	48.005	19	5.077	35.086	19	122.753	32.475	19	6.738	26.436
PCA III	17	0.000	0.000	17	0.000	0.005	17	0.000	0.000	17	0.000	0.000
Residual	-17	0.007	0.000	-17	-0.000	0.000	-17	0.016	0.000			0.000
Pooled residual		0.481										

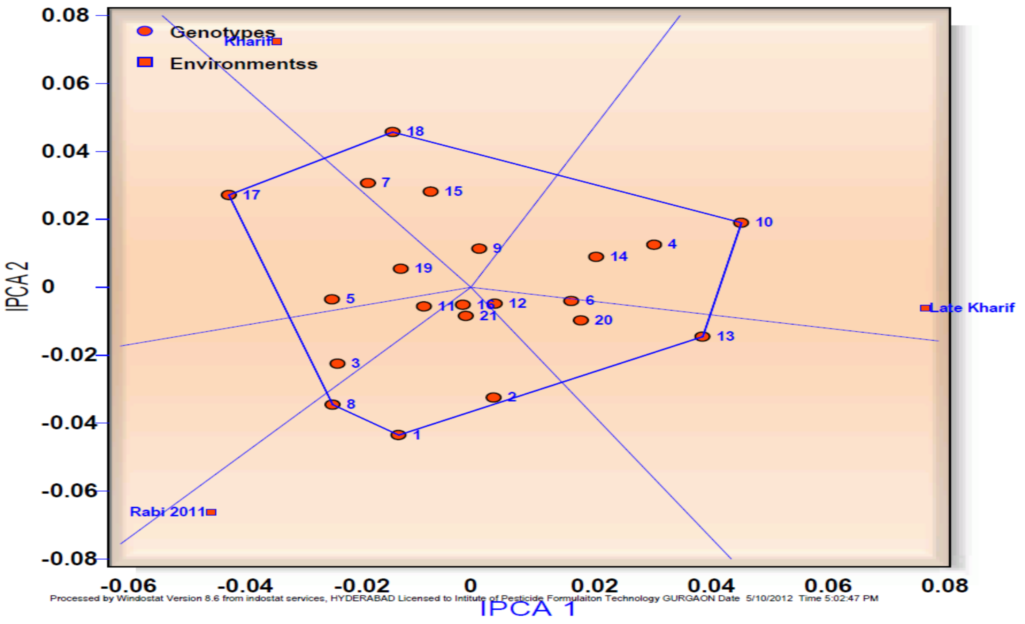
Significant at 0.05 level** * Significant at 0.01 level**

Fig1. **Biplot of the first AMMI interaction (IPCA 1) plotted against mean grain yield (X-axis) for 21 hybrids**



DOI: 10.5958/0975-928X.2017.00175.2

Fig 2. **Graphic of Ammi biplot interaction of twenty one genotypes over environments**



Genotypes : 1. HQPM-7 2.Vivek hybrid-9 3.CMH-08-284 4.Bio-9637 5. HM-4 6.Seed tech 7.HQPM-1 8. Vivek hybrid-23 9.CMH-08-282 10.JH-3457 11.Vivek hybrid-33 12.Prakash 13. HM-9 14.PMH-3 15. Bio-9681 16. Vivek QPM-9 17.Buland 18.Kaveri 19.Manisha 20.Super-36 21. DHM-117