

## RESEARCH ARTICLE

# GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS FOR SUGARCANE GENOTYPES EVALUATED IN MULTI-LOCATION TRIALS

Sanjeev Kumar\*, D.K. Pandey, P.K. Singh and J. Singh

## Abstract

*Selection for wider adaptability of sugarcane varieties to specific production environments is often challenged by the occurrence of significant genotype by environment interactions (GEI). Several statistical models have been proposed for exploiting positive GEI and supporting decisions in varietal selection and recommendation for target environments. Additive main effects and multiplicative interactions (AMMI) model effectively captures the additive and multiplicative components of GEI and provides meaningful interpretation of multi-environment data sets in breeding programs. The objective of this study was to assess the significance and magnitude of GEI effects on cane yield and suggest the exploitation of the positive GEI effects using AMMI biplot analysis. Cane yield data of nine sugarcane genotypes evaluated at seven locations for two crop seasons (2008-09 and 2009-10) across north-west zone of sub tropical India were used for this purpose. AMMI analysis of variance of cane yield ( $t\ ha^{-1}$ ) showed that 61.11% of the total sum of squares was attributable to GEI effects indicating high interaction among genotypes and environments. However, 22.34% and 16.05% of the total sum of squares were attributable to environments and genotypes, respectively. The sum of squares of interaction principal component analysis axis -I (IPCA-I) and IPCA-II were significant and cumulatively contributed to 69.40% at 38 df. According to*

*the AMMI biplots, none of the varieties had superior performance in all the environments. However, genotype CoS 767, combining low absolute IPCA-I score with good cane yield, was the overall winner with less variable yields across the environments which was also confirmed by low estimate of AMMI stability value.*

**Keywords:** AMMI, ASV,  $G \times E$  interaction, stability, sugarcane

## Introduction

Sugarcane (*Saccharum* spp. hybrid complex), owing to its year long crop cycle, suffers quite often with biotic and abiotic stresses, although it is a crop of irrigated agro-eco system. High genotype by environment interaction makes it difficult for breeders to develop widely adapted, stable and high yielding varieties in sugarcane (Rea and De Sousa-Vieira 2002). With its vast distribution for cultivation, the sugarcane crop is influenced by environmental factors and ultimately affects the sugar production scenario of India. The environmental fluctuations are even more significant in subtropical belt specially the north-west zone comprising central and western part of Uttar Pradesh, Uttarakhand, Haryana, Punjab and Rajasthan, which accounts for the maximum acreage of sugarcane in the country. India, being the second largest producer of sugar in the world, can influence the national and international sugar prices if the sugarcane and sugar production in this zone can be stabilized. The stability in the production is again a function of varietal selection and environmental fluctuations. Thus, for any breeding and selection programme, it is a pre-requisite to develop varieties with stable yield performance over the wide range of production

environments. The success of varieties like CoS 767 can be attributed to their wider adaptability with stable performance over the years. The importance and scope of multi-location testing of sugarcane varieties is therefore a reflection of a successful breeding programme which when coupled with a suitable statistical model for genotype x environment interaction analysis can be extremely helpful in the identification of stable varieties adapted to wider cultivable areas distributed throughout the zone. The genotype x environment interaction is an important aspect of both plant breeding programme and the introduction of new crop cultivars (Freeman 1985). Even though the additive models are effective in partitioning the total sum of squares into genotype main effect, environment main effect and the  $G \times E$  interactions (GEI), these do not provide insight into the GEI structure. In order to study the underlying interaction components, more advanced instruments such as principal component analysis (PCA) are required. The AMMI model is a hybrid model involving both additive and multiplicative components. It separates the additive variance from the multiplicative variance and then applies principal component analysis (PCA) to the interaction portion. The effectiveness of AMMI procedure has been clearly demonstrated by various authors in sugarcane (Quemé et al. 2005; Guerra et al. 2009 and Kumar et al. 2009).

## Materials and methods

Nine sugarcane genotypes of midlate maturity group comprising six test entries (Co 0327, Co 0424, CoLk 99271, CoLk 04238, CoPant 04222 and CoS 03222) and three standard varieties (CoS 767, CoS 8436 and Co 1148) were evaluated in multi-location trials under the All India Coordinated Research Project on Sugarcane. The trials were executed at seven locations, viz. Karnal, Pantnagar, Muzaffarnagar, Lucknow, Faridkot, Ludhiana and Sriganaganagar of North West Zone during 2008-09 and 2009-10 crop seasons. The trials were conducted at all seven locations by planting sugarcane in spring season under randomized completely block design (RCBD) with three replications comprising plots of eight 6 m long rows each and a row to row distance of 90 cm. The central six rows were harvested for cane yield measurement. The cane yield was converted to  $t\ ha^{-1}$  for the analysis. The data received from the different centres were considered for the analysis.

The mean cane yield data were subjected to AMMI analysis in Windostat Version 8.6 (Indostat Services, Hyderabad, India). In the analysis, every combination among the seven locations and two years was considered an environment making a total of 14 environments (Table 1).

**Table 1.** Details of environments, mean cane yield, and IPCA I and IPCA II scores for the 14 environments

Code	Location	Year	Mean cane yield ( $t\ ha^{-1}$ )	IPCA-I	IPCA-II
ENV1	Karnal, Haryana	2008-09	71.82	7.06	0.24
ENV2	Karnal, Haryana	2009-10	80.40	0.93	0.64
ENV3	Pantnagar, Uttarakhand	2008-09	67.20	-0.24	-0.37
ENV4	Pantnagar, Uttarakhand	2009-10	67.28	-0.31	-0.01
ENV5	Muzaffarnagar, Uttar Pradesh	2008-09	74.72	1.29	-2.05
ENV6	Muzaffarnagar, Uttar Pradesh	2009-10	77.35	0.41	-1.93
ENV7	Lucknow, Uttar Pradesh	2008-09	80.42	-1.36	-0.59
ENV8	Lucknow, Uttar Pradesh	2009-10	81.61	0.22	-0.22
ENV9	Faridkot, Punjab	2008-09	69.61	-1.68	2.99
ENV10	Faridkot, Punjab	2009-10	69.47	-2.86	0.78
ENV11	Ludhiana, Punjab	2008-09	60.41	-0.83	4.02
ENV12	Ludhiana, Punjab	2009-10	75.68	0.67	2.13
ENV13	Sriganaganagar, Rajasthan	2008-09	70.00	-1.79	-2.69
ENV14	Sriganaganagar, Rajasthan	2009-10	77.77	-1.50	-2.95

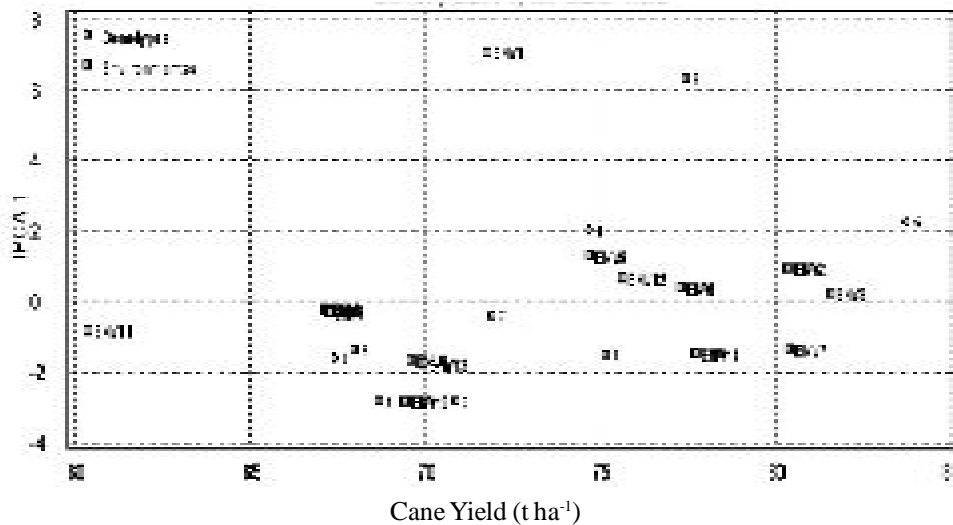
The results were interpreted on the basis of two AMMI graphs (Fig. 1 and 2): the first one that showed the main effect and first multiplicative axis term (IPCA-I) of both genotypes and environments; the second biplot that used IPCA-I scores of environments and genotypes against scores of environments and genotypes of the second multiplicative axis term (IPCA-II). The IPCA scores of genotype in the AMMI analysis are an indication of the stability of genotype over environments. The greater the IPCA scores, either negative or positive, the more specifically adapted a genotype to certain environment. The more the IPCA scores tend towards zero, the more stable the genotype is over

all the environments. In continuation, AMMI's stability value (ASV) was also estimated in order to rank genotypes in terms of stability using the formula as shown below (Purchase 1997).

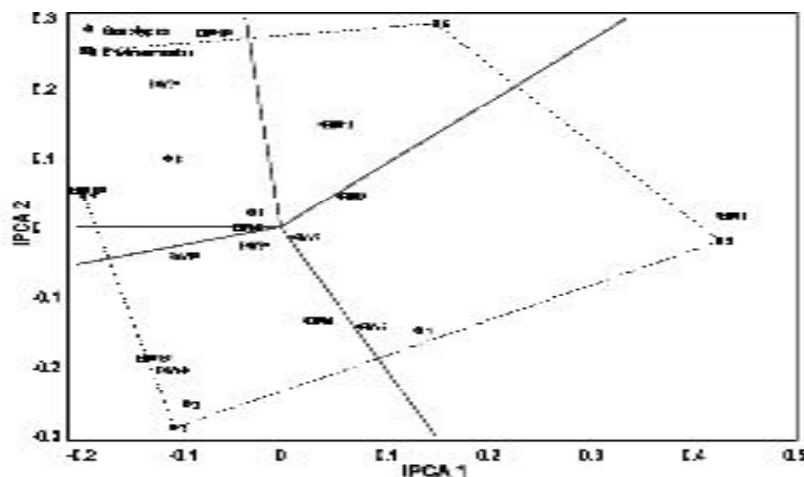
where,

- SS = Sum of squares
- IPCA-I = interaction principal component analysis axis 1 and
- IPCA-II = interaction principal component analysis axis 2

$$ASV = \sqrt{\frac{[SS_{IPCA-I} / SS_{IPCA-II}] * (IPCA-I \text{ Score})^2 + (IPCA-II \text{ Score})^2}{n}}$$



**Fig 1.** AMMI I biplot showing main (cane yield) and interaction (IPCA-I) effects of genotypes and environments. (1- Co 0327, 2- Co 0424, 3- CoLk 99271, 4- CoLk 04238, 5- CoPant 04222, 6- CoS 03222, 7- CoS 767, 8- CoS 8436, 9- Co 1148)



**Fig 2.** AMMI II biplot showing mega-environments and their respective high yielding genotypes (1- Co 0327, 2- Co 0424, 3- CoLk 99271, 4- CoLk 04238, 5- CoPant 04222, 6- CoS 03222, 7- CoS 767, 8- CoS 8436, 9- Co 1148)

## Results and discussion

The mean cane yield, IPCA-I and IPCA-II scores for all the environments under study are given in Table 1. The analysis of variance of AMMI (Table 2) showed that the mean sum of squares due to genotypes, environments and genotype x environment interaction (GEI) were significant indicating broad range of diversity existed among genotypes. Significance of the environments indicated distinctness in different environments. The significance of GEI indicated that genotypes interacted differentially in various environments under test.

**Table 2.** AMMI analysis for cane yield (t ha<sup>-1</sup>) of nine genotypes evaluated in 14 environments

Source	d.f.	Cane yield (t/ha)		
		S.S.	M.S.	Explained (%)
Genotypes (G)	8	3127.58	390.95**	16.05
Environments (E)	13	4451.95	342.46**	22.34
Genotypex Environment (GxE)	104	11909.62	114.52**	61.11
IPCA I	20	5224.83	261.24**	43.87
IPCA II	18	3040.63	168.92**	25.53
IPCA III	16	1755.07	109.69	14.74
IPCA IV	14	874.76	62.48	7.34
Pooled residual	36	1014.39	28.18	8.52
Total	125	19489.15	155.91	

\*\*  $P < 0.01$

AMMI analysis of variance for cane yield (t ha<sup>-1</sup>) of nine genotypes evaluated in 14 environments under multi-location trials showed that 61.11% of the total sum of squares was attributable to GEI effects indicating high interaction among genotypes and environments. However, 22.34% and 16.05% of the total sum of squares were attributable to environments and genotypes, respectively, suggesting the nature of diverse environments and genotypes both resulting in the variation of cane yield. The magnitude of the GEI sum of squares was 3.8 times higher than that for genotypes indicating that there were substantial differences in genotypic response over the environments.

The multiplicative variance of the sum of squares due to GEI was partitioned into IPCA-I, IPCA-II, IPCA-III and IPCA-IV and residual variations.

About 43.87 % of the interaction sum of squares was explained by IPCA-I in 19.23 % of the interaction degree of freedom. Similarly, IPCA-II, IPCA-III and IPCA-IV explained 25.53, 14.74 and 7.34% respectively of the GEI sum of squares. IPCA-I had sum of squares greater than that of genotypes. The sum of squares of IPCA-I and IPCA-II were significant and cumulatively contributed to 69.40 at 38 degrees of freedom. The first principal component factor has a high contribution to the interaction sum of squares while the residual has lower contribution. This indicated that one fundamental factor that affects GEI could

be either genotypic or environmental in nature. It was suggested that AMMI with only two interaction principal component axes was the best predictive model (Zobel et al. 1988; Gauch and Zobel, 1996). Further, interaction principal component axes captured mostly noise and did not help in prediction. Thus interaction of the nine genotypes with 14 environments was best predicted by the first two principal components of GEI.

Biplot analysis is considered the most powerful interpretive tool for AMMI model. There are two basic AMMI biplots, the AMMI 1 biplot, where the main effect and IPCA-I scores for both genotype and environment are plotted against each other (Fig. 1), and AMMI 2 biplot where scores of IPCA-I and IPCA-II are plotted (Fig.2). In AMMI 1 biplot, the usual interpretation of a biplot is that the

displacements along the abscissa indicate differences in additive main effects, whereas displacements along the ordinate indicate differences in interaction effects. Genotypes that group together have similar adaptation while environments which group together influence the genotypes in the same way. If a genotype or an environment has an IPCA score tending towards zero, it has small interaction effects and considered stable. When a genotype and environment have the same sign on the IPCA axis, their interaction is positive and if different, their interaction is negative.

A perusal of IPCA-I scores for different genotypes indicated that some genotypes are adapted to a particular location while others are suitable for cultivation in more than one location (Table 3).

were found to have such specific adaptations. As reported earlier, whatever the direction is, the greater the IPCA scores, the more specifically adapted these genotypes are to certain environments (Crossa et al. 1990). The best genotype needs to combine good cane yield and stable performance across a range of production environments. For example, a genotype like CoS 767 can be judged based on its stability over the environments. CoS 767, which combined low absolute IPCA-I score with good cane yield, was the overall winner with less variable yield across the environments explaining its suitability as one of the leading check varieties for such trials.

The environments showed much variability in both additive main effects and interactions (Table 1). The environment such as Lucknow in 2009-10 was the

**Table 3.** Mean cane yield (t ha<sup>-1</sup>), ASV and ranking orders along with IPCA scores of the nine sugarcane genotypes

Genotype	Cane yield (t ha <sup>-1</sup> )		ASV		IPCA	
	Mean	Rank	Value	Rank	I	II
Co0327	74.70	4	3.94	3	2.00	-1.92
Co0424	68.02	8	4.01	4	-1.34	-3.28
CoLk99271	70.89	6	5.86	8	-2.84	3.25
CoLk04238	68.71	7	4.92	6	-2.84	0.62
CoPant04222	83.77	1	5.39	7	2.25	3.76
CoS03222	75.20	3	4.56	5	-1.53	-3.72
CoS767	71.93	5	0.75	1	-0.41	0.27
CoS8436	67.43	9	3.06	2	-1.62	1.27
Co1148	77.46	2	10.88	9	6.33	-0.26

The IPCA-I score of 6.33 observed for Co 1148 showed that it was well adapted for a single location Karnal explaining its continued cultivation in Haryana even after more than three decades of its release. The genotypes CoLk 99271 and CoLk 04238 with high negative IPCA-I scores (-2.84) were better adapted to Faridkot in 2009-10 which also has high negative IPCA score of -2.86. The genotypes which showed greater main effect to the grand mean with positive IPCA-I scores under those environments, which also had positive IPCA-I scores, are reported to have specific adaptation to these environments. The genotypes CoPant 04222, Co 1148 and Co 0327

most potential and stable with lowest IPCA-I score indicating that genotypes poorly interacted with this particular environment. However, the environment with average potential (ENV1) having high positive IPCA-I score showed differential performance of genotypes for cane yield. The lowest yielding environment (ENV3) had recorded second lowest but negative IPCA I score suggesting that all the genotypes poorly performed under this environment. ENV3 and ENV4 (representing Pantnagar location) had relatively smaller variation in IPCA-I scores from year to year while ENV1 and ENV2 (representing Karnal location) had the largest (Fig. 1).

This indicated that the relative ranking of genotypes was more stable at Pantnagar than at Karnal. Karnal was described as a location that combines larger main effects with larger interaction effects making it a less predictable location for sugarcane variety evaluation during the period considered.

AMMI's Stability Value (ASV) was estimated for all the genotypes (Table 3) in order to rank them in terms of their stability. Low ASV of the genotype indicates its high stability for cane yield over the environments. The stability ranking of genotypes based on ASV was CoS 767 (0.75), CoS 8436 (3.06), Co 0327 (3.94), Co 0424 (4.01), CoS 03222 (4.56), CoLk 04238 (4.92), CoPant 04222 (5.39), CoLk 99271 (5.86) and Co 1148 (10.88).

AMMI 2 biplot (Fig. 2) cross validated the interaction pattern of the nine sugarcane genotypes with 14 environments. The distance from the origin is indicative of the amount of interaction that was exhibited by genotypes either over environments or environments over genotypes (Voltas et al. 2002). The genotypes such as Co 1148, CoPant 04222, CoLk 99271, CoLk 04238 and CoS 03222 had shown highly interactive behavior whether it was positive or negative. The environments ENV8, ENV3 and ENV4 exhibited low interaction. The nearly additive behavior of these environments indicates that genotypic yields were highly correlated with the overall genotypic means across the environments. Among the extreme genotypes, Co 0424 and CoS 03222 were located as a pair indicating their similar response pattern. Connecting the extreme genotypes on AMMI 2 biplot forms a polygon and the perpendiculars to the sides of the polygon form the sectors of genotypes and environments (Hernandez and Crossa 2000). The genotypes at the vertex are the winners in the environments included in that sector. In this biplot, five sectors were formed and each sector had at least one environment. Faridkot in both years (ENV9 and ENV10) clustered in one sector and Sriganagar in both years (ENV13 and ENV14) clustered in another sector indicating repeatable performance of genotypes; these locations, therefore, could be considered separate mega-locations for sugarcane varietal evaluation. Pantnagar in both the test years (ENV3 and ENV4)

was relatively close to biplot origin and hence a less interacting location and could be good enough for selection of genotypes with average adaptation.

In conclusion, GEI is a common phenomenon in multi-location trials and its presence usually complicates varietal selection and identification. This paper demonstrated that AMMI model was very effective for studying the pattern of GEI and interpreting sugarcane yield data from multi-location trials. This model provided relative magnitude and importance of the effects of GEI. It revealed that the GEI was an important source of variation in sugarcane yield and its biplots were effective enough for visualizing the response pattern of genotypes and environments.

### Acknowledgements

The authors are grateful to the breeders of Karnal, Pantnagar, Muzaffarnagar, Lucknow, Faridkot, Ludhiana and Sriganagar for the data provided, Principal Investigator (Crop Improvement) and Project Coordinator, All India Coordinated Research Project on Sugarcane for the compilation and publication of the data in the form of AICRP(S) report.

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