Stability analysis of sugarcane (*Saccharum* spp) genotypes for matric and quality traits by AMMI Model

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ABSTRACT

The experiment across nine environments (three cuttings × three locations) was conducted during 2009-10 and 2010-11 crop seasons to study the effect of genotype × environment interaction (GEI) on a cane, CCS yield and sucrose (%) in sugarcane (*Saccharum* spp). Analysis of variance of 10 genotypes revealed that genotype, environment and GEI were highly significant. The additive main effects and multiplicative interaction (AMMI) model was used to interpret the behaviour of genotype, environment and their interaction. In fact, the objective of this study was to identify stable and adaptable genotypes across the locations and to determine the magnitude of G×E interaction. AMMI analysis of variance showed that 52.93% of the total SS for cane yield, 60.48% for CCS yield ad 56.0% for sucrose (%) was attributed to the environmental effects, indicating that the locations were diverse. The PCA-1 and PCA-2 were also significant and both sums contributed cumulatively to 66.84% to the total of G×E interaction. The genotype CoP 05437 (4) exhibited high cane and CCS yield along with wider stability and adaptability to the different environments. However, BO 91 (8), CoSe 092423 (10), CoSe 05452 (5), Co 05019 (2) and CoBln 04174 (7) genotypes showed instability and specific adaptability to the environments, while CoP 09301 (9) genotype showed higher sucrose (%) and greater stability across the environments for this trait.

Key words: Adaptability, AMMI model, G×E interaction, IPCA, *Saccharum* spp, Stability

Sugarcane (*Saccharum* spp) is an important cash crop of the country cultivated over about 5.0 million ha area including both sub-tropical and tropical regions. The sub-tropical region contributes more than 55% area of the sugarcane in India but sugar production in this region is less than 40%. The productivity in the sub-tropical region is substantially low (50 tonnes/ha) as compared to the tropical region (80 tonnes/ha) of the country (Nair and Govindraj 2007). The tillering and formative phase of sugarcane is the most critical for water requirement which coincides with high temperature and hot wind in sub-tropical India. Delayed and skipping irrigation during this phase severely affects tillering and subsequent growth of the crop at a later stage, the crop has a commanding position in the economy in the country supporting the livelihood of millions of farmers and landless labour.

Higher polyploidy combined with highly heterozygous nature makes sugarcane breeding highly complex. The most important objective of sugarcane breeder is to tape genotypes with a high cane and CCS (Commercial cane sugar) yield adopted in the most varied environments. However, great emphasis and priority remain on developing location specific varieties to capitalize on their inherent genetic potential. In multi-location experiments, the rank of the genotypes varies from one location to another in terms of yield as well as quality which indicate the strong role of genotype (G) × Environments (E) interaction in their performance. The importance of G×E interaction in sugarcane clone selection is widely recognized (Milligan *et al*. 1990). The phenotype of an individual plant determined by both of its genotype and its growth environments. These two effects are not always additive because of the presence of genotype and environment interaction (GEI) measured as the inconsistent performance of a genotype across environments. A stable variety should have high mean yield with the low magnitude of GEI when grown over the varied environments. Breeder's deals with the GEI challenge by evaluating genotypes in many diverse environments to ensure that particular genotype with high yield and stable performance are selected (Kumar *et al*. 2007).

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Indeed, highest cane yielding environmentswere E7 and E4, whereas E4, E5 and E7 recorded highest CCS yield and sucrose per cent.

Several methods have been proposed to analyze GEI and phenotypic stability (Singh *et al.* 2001, Kumar *et al.* 2007). The additive main effects and multiplicative interaction (AMMI) model involves correlation or regression analysis that relates the genotypic and environmental score derived from a principal component analysis (PCA) of the GE matrix to genotypic and environmental covariates (Zobel *et al.* 1988). The AMMI is widely used in GEI studies for different crops (Crossa *et al.* 1990, Queme *et al.* 2001) to separate the additive portion from the interaction by way of an analysis of variance. AMMI biplot analysis is considered to be an effective tool to diagnose GEI pattern graphically, whereby a PCA provides a multiplication model to analyze the interaction effects. The results of AMMI analysis are useful in supporting the decision in a breeding programme for selection of stable genotypes and selection of environment for location-specific genotypes in sugarcane.

The objectives of this investigation were to (i) Study genotype-environment interactions for cane and CCS yield of sugarcane genotypes tested across environments; (ii) Assessing stability performance of sugarcane genotypes in terms of cane and CCS yield across the tested environments.

MATERIALS AND METHODS

A set of seven advanced genotypes of sugarcane (mid-late group) developed by different research centers of North Central Zone along with three standard checks were evaluated for cane yield, CCS yields and sucrose (%) in juice under the All India Coordinated Research Project (AICRP) on sugarcane for three crops (First plant crop, second plant crop and ratoon crop) during 2009-10 and 2010-11 at three locations, viz. ICAR-IISR, Regional Centre, Motipur (28°03' latitude 81°4' longitude), Sugarcane Research Institute, RAU, Pusa (25°9' latitude 85°7' longitude) and GSSBRI, Seorohi, Kushinagar (26°7' latitude 84°2' longitude).

The experimental material consisted of Co 05018, Co 0519, Co 05020, CoP 05437, CoSe 05452, CoBln 05502 and CoBln 04174 along with three cultivars of sugarcane BO 91, CoP 09301 and CoSe 092423 as checks. The experiment at three different locations over two crop seasons with three crops constituted nine environments. The experiments were laid out in randomized block design (RBD) with three replications at each location. Plots were of eight rows with 6.0m length having 0.90 m spacing between rows. Three budded sets were used for planting with a seed rate of 12 buds/m^2 at all the three locations. Six rows were harvested for measuring cane yield in each plot across replication and calculated as tonnes/ha. 10 stalk samples were randomly taken from each plot and weighed. The clarified juice was analyzed with digital automatic saccari-meter autopol 880 and J 57 automatic refractometer for sucrose (%). A combined analysis of variance across test environment and an AMMI analysis were carried out using the programme IRRISAT Version 5.

RESULTS AND DISCUSSION

The AMMI analysis of variance for cane yield revealed that the effect of sources of variation, genotype, environment and GE interaction was significant. The analysis of variance of cane yield across three cutting and nine environments showed that 52.93% of the total SS was attributable to the environmental effects, 13.48% to genotypic effects and 33.59% to G×E interaction effects (Table 1). A large value of SS for environments indicated that the environments were diverse with large differences in their mean causing most of the variation in cane yield. The significant G×E indicated differential and inconsistent responses of the genotypes across environments (Gauch and Zobel 1996, Kumar *et al.* 2009, Rea *et al.* 2011).

Results from AMMI analysis also showed that the PCA-1 and PCA-2 axes explained 18.87% and 8.92% of the total G×E Interaction. The mean square for PCA-1 and PCA-2 were significant at P<0.01 and P<0.05 respectively, and cumulatively contributed to 66.84% of the total G×E interactions. The F-test at P<0.01 and P>0.05 suggested that the two principal component axes from the interaction were significant to the model. Hence, the AMMI model with only two PCA interactions was the best predictive model, which is in agreement with Zobel *et al.* (1988) and Annicchiarico (1977).

An ideal genotype should have an invariably high average yield across the environments where it has been tested. The mean cane yield of sugarcane genotypes varied among environments ranging from 35.40 tonnes/ha in E3 to 77.88 tonnes/ha in E7. The mean cane yield for the 10 genotypes extended from 54.69 to 70.02 tonnes/ha. However, the G×E interaction was a crossover type as revealed by the differential ranking of genotype, across the environment (Table 2). CoP 05437 clone was the top ranking genotype across all nine environments and recorded the top yield of 77.88 tonnes/ha at the highest yielding environment

Table 1   AMMI analysis of variance for cane yield (tonnes/ha) across nine environments

Source of variations	df	Sum of squares (SS)	Mean squares (MS)	(%)
Trial	89	11370.02	127.75	
Genotypes	9	1532.75	170.31**	13.48
Environments	8	6017.93	752.24**	52.93
G*E Interaction	72	3819.34	53.05**	33.59
PCA I	16	2145.64	134.10**	18.87
PCA II	14	1015.22	72.52**	8.92
PCA III	12	455.93	37.99	
PCA IV	10	140.76	14.08	
PCA V	8	45.24	5.65	
PCA VI	6	11.51	1.92	
PCA VII	4	4.90	1.22	
Residual	2	0.16	0.08	
Pooled residual	72	3819.34	530.46	

** 1% level of significance

Table 2   Mean cane yield (tonnes/ha) of ten sugarcane genotypes across nine environments

Genotypes/ Environments	E1 (First plant crop, Motipur)	E2 (Second plant crop, Motipur)	E3 (Ratoon crop, Motipur)	E4 (First plant crop, Pusa)	E5 (Second plant crop, Pusa)	E6 (Ratoon crop, Pusa)	E7 (First plant crop, Kushinagar)	E8 (Second plant crop, Kushinagar)	E9 (Ratoon crop, Kushinagar)	Adj. mean
Co 05018 (1)	50.92	61.20	35.40	62.12	59.55	51.42	62.54	57.84	51.24	54.69
Co 05019 (2)	55.66	65.94	40.14	66.86	64.29	56.16	67.29	62.58	55.99	59.44
Co 05020 (3)	59.58	69.85	44.06	70.78	68.21	60.08	71.20	66.50	59.90	63.35
CoP 05437 (4)	66.25	76.53	50.73	77.45	74.88	66.75	77.88	73.17	66.58	70.02
CoSe 05452 (5)	56.43	66.71	40.91	67.64	65.07	56.93	68.06	63.35	56.76	60.21
CoBln 05502 (6)	50.94	61.22	35.42	62.15	59.58	51.44	62.57	57.86	51.27	54.72
CoBln 04174 (7)	57.26	67.54	41.74	68.46	65.89	57.76	68.89	64.18	57.59	61.03
BO 91 (8)	55.49	65.77	39.97	66.69	64.12	55.99	67.11	62.41	55.81	59.26
CoP 09301 (9)	57.48	67.76	41.96	68.68	66.11	57.98	69.11	64.40	57.81	61.25
CoSe 092423 (10)	55.78	66.06	40.26	66.98	64.41	56.28	67.41	62.70	56.11	59.55
Adj. mean	56.58	66.86	41.06	67.79	65.21	57.08	68.21	63.50	56.91	

(E7). Meanwhile, again CoP 05437 genotype was the highest yielder (50.73 tonnes/ha) at the lowest yielding environment (E3).

The biplot from AMMI analysis is a useful tool in explaining the specific pattern of main effects and G×E interaction, of genotypes and environments simultaneously (Crossa *et al.* 1990, Kempton 1984). The IPCA-1 scores for both genotypes and environments were plotted against the mean cane yields. The IPCA-1 scores of a genotype in the AMMI analysis are an indication of adaptability over the environments. The genotypes with high mean yield positioned near the line showing IPCA=0 suggests negligible or no G×E interaction, consequently, such genotypes will have general adaptability over all locations (Naroui Rad *et al.* 2013). On the other hand, the genotypes which are away from the line with IPCA-1=0 would be adapted to a specific environment (Fig 1). The clone CoP 05437 (4) scattered at the right-hand side of the grand mean level and
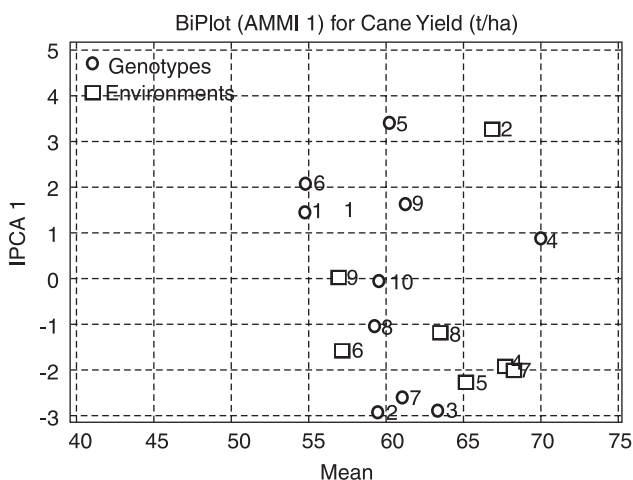

Fig 1 AMMI-1 biplot showing the first principal axis of interaction (IPCA-1) versus mean cane yield (tonnes/ha) from the 10 genotypes across nine environments.

close to IPCA-1=0 line was declared by the AMMI model as having general adaptability in all the environments. But, this genotype is the most suited in E7, E4 E5 and E2. However, four genotypes: Co 05020 (3),CoBln 04174 (7), CoP 09301 (9) and CoSe 05452 (5) have performed better with high and low IPCA scores; hence it indicates that these clones specifically suited to a particular environment. The genotype BO 91 (8), CoSe 092423 (10) did better and the most adapted to low yielding environments.

Although, AMMI model made it possible to construct the bioplot and calculate genotype and environmental effects (Gauch and Zobel 1996). The IPCA score for genotypes that are closer to zero indicates greater stability of the genotype over the testing environments. Two types of biplot, AMMI-1 and AMMI-2 were used to interpret GEI interaction in this study. Indeed, in AMM1-1 the genotype and environmental means were plotted on the abscissa and the IPCA-1 scores for the genotypes and environment on the ordinate. However, in AMMI-2 the IPCA-1 scores were plotted on the abscissa and IPCA-2 scores on the ordinate.

The genotypes stationed near the origin of the bioplot showed greater stability over the environment while those clones were distant from the biplot origin indicates their unstability and specific adaptability over the environments.

Environment (E3) was the largest contributor to the phenotypic stability of the genotype (Table 2). In this environment, no differences (P>0.05) were found among genotypes. Additionally, this environment recorded one of the lowest cane yield tonnes/hamean. On the other hand, environments E8 and E9 mostly contributed to the G×E interaction because they were positioned distant/far for from the origin in the AMMI-2 biplot (Fig 2). Genotypes and environments positionedclose to each other in the bioplot have positive associations thus, created acongenial location for the clones. Genotype CoP 05437 (4) being close to the origin of the plot is the most stable across the environments.

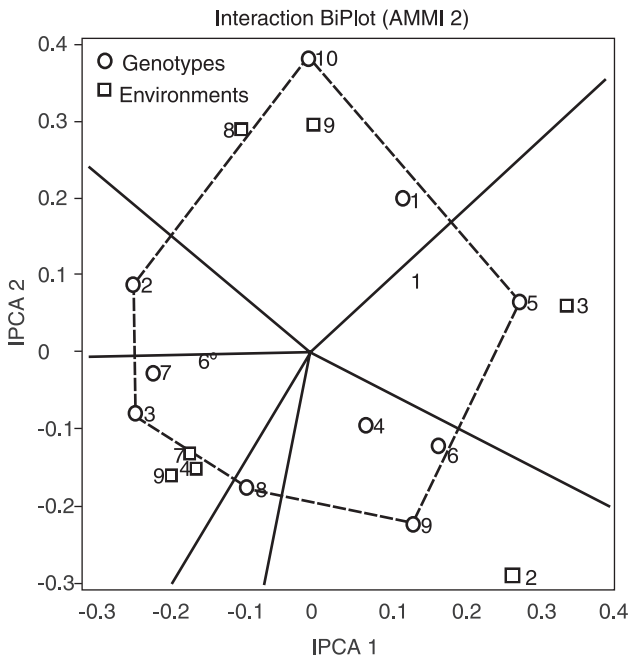The genotype and environment can be seen as vectors

Fig 2 AMMI-2 biplot showing the first two principal axes of interaction (IPCA-1 and IPCA-2) corresponding to cane yield (tonnes/ha) from 10 genotypes across nine environments.

Table 3   AMMI analysis of variance for CCS yield (tonnes/ha) under nine environments

Source of variations	df	Sum of squares (SS)	Mean squares (MS)	(%)
Trials	89	195.50	2.20	
Genotypes	9	21.88	2.43**	11.19
Environments	8	118.24	14.78**	60.48
G*E Interaction	72	55.38	0.77**	28.33
PCA I	16	27.51	1.72*	14.07
PCA II	14	14.48	1.03*	7.40
PCA III	12	7.09	0.59	
PCA IV	10	2.40	0.24	
PCA V	8	2.15	0.27	
PCA VI	6	1.20	0.20	
PCA VII	4	0.34	0.07	
Residual	2	0.21	0.10	
Pooled residual	72	55.38	0.77	

** 1% level of significance, * 5% level of significance

from the origin of the axis to the endpoints determined by their scores. If any two vectors for the environments form an angle exceeding the right angle, it indicates that genotypes have different interaction pattern in these environments, genotypes with small interactions were located near the origin, e g CoP 05437 (4). In other words, this genotype was less or negligible influenced by the environments. The genotypes those were far from the origin have apositive response tothat environment that was away from the origin but at the same time in the same direction with asmall angle (<90°). The genotypes Co 05018 (1) and CoSe 092423 (10) had shown thepositive response for cane yield with E8 and E9, CoSe 05452 (5) with E1 and E3. For anegative response, the genotype, and environment vectors from the angle between 90° and 270°, e g CoP 05437 (4) CoBln 05502(6) and CoP 09301 (9) with E2 indicate negative interaction with the environment for cane yield. However, genotypes Co 05019 (2), Co 05020 (3), CoBln 04174 (7) and Bo 91 (8) had negative G×E interaction with cane yield. In fact, AMMI-2 biplot represents the G×E in part only and it does not include the main effects of the genotypes. Thus, the biplot showed the best genotypes in each environment with regard to G×E but not with respect to the main effect of the genotypes (Guerra *et al.* 2009, Rao *et al.* 2011).

Analysis of variance for CCS yield revealed significant differences among genotypes, environments and their interaction GEI (Table 3). Bartlett's test for homogeneity of variances indicated significant error variance among environments. GEI resulted from changes in the relative rankings of the genotypes, implying that genotypes responded differently to the environmental conditions. The testing in multi-location experiments will be necessary to understand the adaptation pattern and stability of newly developed available genotypes.

The analysis of variance of CCS yield across three cutting and nine environments showed that 60.48% of the variation was attributable to the environmental effects, 11.19% to the genotypic effects and 28.33% to G×E interaction effects (Table 3). A large portion of SS for environments indicated that the environments were diverse with large differences in their mean value causing most of the variation in CCS yield. The significant G×E indicated differential and inconsistent responses of the genotypes across the environments (Gauch and Zobel 1996, Gauch *et al.* 2006, Pedro *et al.* 2013). At the same time, AMMI analysis also showed that PCA-1 and PCA-2 axes explained 14.07 and 7.40% of the total G×E interaction. The mean square for PCA-1 and PCA-2 was significant at 5% level of significance respectively.

The genotype having high average CCS yield over the environments under which it has been tested. However, the mean CCS yield of sugarcane genotypes ranged among the environments from 3.82 tonnes/ha in E3 to 9.01 tonnes/ha in E7. The mean CCS yield for ten genotypes under study ranged from 6.33 to 8.15 tonnes/ha. Indeed, the G×E interaction was a sporadic type as reflected by the differential position of genotypes across the environments (Table 4). Genotype CoP 05437 (4) attained top position (9.66 tonnes/ha) in CCS yield production in highest yielding environment E4. While in lowest yielding environment E3 the genotype CoP 05437 (4) yielded the highest CCS (5.64

Table 4   Mean CCS yield (tonnes/ha) of ten sugarcane genotypes over nine environments

Genotypes/ Environments	E1 (First plant crop, Motipur)	E2 (Second plant crop, Motipur)	E3 (Ratoon crop, Motipur)	E4 (First plant crop, Pusa)	E5 (Second plant crop, Pusa)	E6 (Ratoon crop, Pusa)	E7 First plant crop, Kushinagar)	E8 (Second plant crop, Kushinagar)	E9 Ratoon crop, Kushinagar)	Adj. Mean
Co 05018 (1)	5.90	7.00	3.98	7.99	7.54	5.69	7.35	6.73	6.19	6.48
Co 05019 (2)	6.42	7.52	4.50	8.52	8.07	6.21	7.87	7.25	6.72	7.01
Co 05020 (3)	6.70	7.80	4.78	8.79	8.34	6.49	8.15	7.53	6.99	7.29
CoP 05437 (4)	7.56	8.67	5.64	9.66	9.21	7.35	9.01	8.39	7.86	8.15
CoSe 05452 (5)	6.77	7.88	4.85	8.87	8.42	6.56	8.23	7.60	7.07	7.36
CoBln 05502 (6)	5.74	6.84	3.82	7.83	7.38	5.53	7.19	6.57	6.03	6.33
CoBln 04174 (7)	6.48	7.58	4.56	8.57	8.12	6.27	7.93	7.31	6.77	7.06
BO 91 (8)	6.37	7.47	4.45	8.47	8.02	6.16	7.82	7.20	6.67	6.96
CoP 09301 (9)	6.98	8.09	5.06	9.08	8.63	6.77	8.44	7.81	7.28	7.57
CoSe 092423 (10)	6.64	7.74	4.72	8.73	8.28	6.43	8.09	7.47	6.93	7.23
Adj. mean	6.55	7.66	4.63	8.65	8.20	6.35	8.01	7.39	6.85	

tonnes/ha) hence, the behaviour of CoP 0547 (4) is the best in low and high input environments and at the same time, it has negligible or low G×E interaction (Rao *et al.* 2011, Sandhu *et al.* 2012). Although, CoP 09301 (9) genotype remained at second pedestal in terms of CCS yield across the environments.

The IPCA-1 scores for both genotypes and environments were plotted against the mean CCS yield (Fig 3). The IPCA-1 scores of a genotype in the AMMI-1 analysis are an indication of adaptability over the environments. The genotype with high CCS yield positioned near the line showing IPCA=0 suggesting negligible or no G×E interaction, as a result, such genotypes will have general adaptability over all locations (Kumar *et al.* 2009, Naouri Rad *et al.* 2013). While, those genotypes which are distant from the line with IPCA=0 would indicate their specific adaptability in the environment (Fig 3). The genotype CoP 05437 (4) BO 91(8) and Co 05019(2) are close to IPCA-1=0 line indicated general adaptability across the nine environments. But the genotype CoP 05437 (4) was most suited in E4, E5 and E7. Although genotype CoSe 05452(5) with high IPCA score had specific adaptability in E2. Similarly, clone CoBln 05502 (6) and Co 05018(1) shown specific adaptability in E1. On the other hand, genotypes with low IPCA score CoBln 04174(7), Co 05019(2), Co 05020 (3), and BO 91 (8) had specific adaptability in E6, E8 and E9. CoBln 04174 (7), BO 91 (8) and Co 05019 (2) had the lowest absolute IPCA-1 score, an indication of a small interaction with environments and hence can be considered stable among genotypes (Fig 3). Despite the fact, genotype CoP05437 (4) performed best in lowest and highest yielding E3 and E4 environments respectively. It indicated that this clone had negligible G×E interaction over the environments.

The genotypes which are away from the biplot origin indicate their unstability and specific adaptability to the environments (Guerra *et al.* 2009, Ramon Rea *et al.* 2011). The genotypes plotted near the origin of biplot showed greater stability over the environments. E3 recorded one of the lowest CCS yield tonnes/ha mean as it was the largest contributor to the phenotypic stability of the genotype (Table 4). Moreover, E5 E4, E2 and E6 largely contributed to the G×E interaction being distant from the origin in the AMMI-2 biplot (Fig 4). Genotype CoP 05437 (4) being more close to the origin of the biplot is the most stable and has negligible G×E interaction across the environments. If genotype and environments positioned close to each other the biplot indicate positive association and reveal favorable condition for the genotype in that environment. The genotype CoBln 05502(6) close to E1, BO 91(8) and Co 05019(2) close to E7 and E8, Co 05020(3), CoBln 04174 (7) are close to E8 suggesting congenial locations for respective clones. If any two vectors for the environment form an angle exceeding the right angle, it indicates that genotypes have different
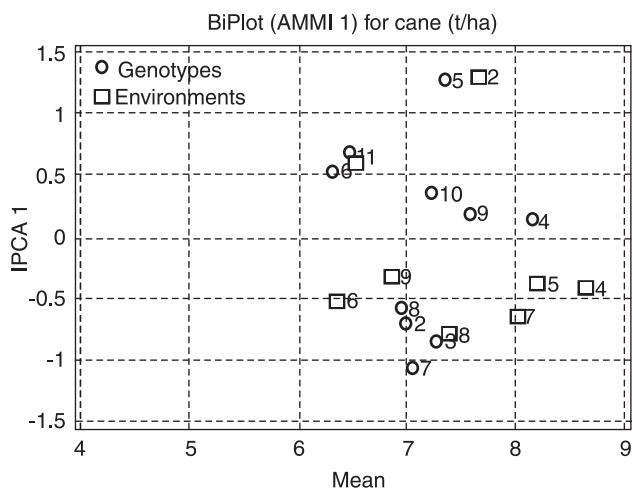

Fig 3 AMMI-1 biplot showing the first principal axis of interaction (IPCA-1) versus mean CCS yield (tonnes/ha) from the 10 genotypes in nine environments
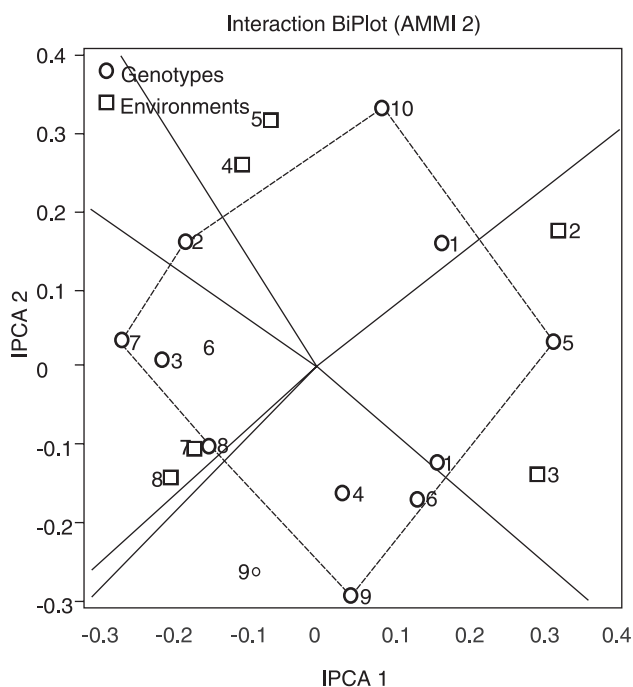
Interaction BiPlot (AMMI 2)

Fig 4 AMMI-2 biplot showing the first two principal axes of interaction (IPCA-1 and IPCA-2) corresponding to CCS yield (tonnes/ha) from ten genotypes across nine environments.

Table 5   AMMI analysis of variance for sucrose per cent across nine environments

Source of variations	df	Sum of squares (SS)	Mean squares (MS)	(%) SS
Trials	89	75.79	0.85	
Genotypes	9	16.49	1.83**	21.75
Environments	8	42.45	5.31**	56.00
G*E Interaction	72	16.86	0.23**	22.24
PCA I	16	6.90	0.43*	9.10
PCA II	14	3.81	0.27*	5.03
PCA III	12	2.75	0.23	
PCA IV	10	1.57	0.16	
PCA V	8	0.71	0.09	
PCA VI	6	0.61	0.10	
PCA VII	4	0.37	0.09	
Residual	2	0.14	0.07	
Pooled residual	72	16.86	0.23	

** 1% level of significance, * 5% level of significance

interaction pattern in these environments. The genotypes those were far from the origin have a positive response with those environments that were away from the origin but a the same time in the same direction with a small angle (<90°). The genotypes CoP 05437 (4), CoP 09301 (9), CoBln 05502 (6) and CoSe 05452 (5) show positive response for CCS yield with E1, E2 and E3. While negative response was shown by the genotype, BO 91(8), Co 05019 (2), Co 05020(3), CoBln 04174 (7) with E9, E8, E7 and E6 since, vectors of both genotype and environment fall between the angle 90° and 270° indicating negative gene interaction with the environments. Indeed, AMMI-2 biplot showed the genotypic behaviour in each environment with regard to GEI.

The AMMI analysis of variance for sucrose (%) revealed significant difference among genotypes, environments and their GEI (Table 5) Bartlett's test for homogeneity of variance indicated a significant error of variance among environments. GEI resulted from changes in the relative ranking of the genotypes, implying that genotypes responded differently to the environmental conditions. The analysis of variance of sucrose (%) across three cutting over nine environments showed that 56% of the total SS was attributable to the environmental effects 21.75% to the genotypic effects and 22.25 to G×E interaction effects (Table 5). A large portion of SS due to environment indicated that the environments were diverse with small differences in their mean (Kumar *et al*. 2007). The significant G×E indicated differential and inconsistent responses of the genotypes to the environment (Gauch and Zobel 1996). AMMI analysis also showed that

PCA-1 and PCA-2 axes explained 9.10% and 5.03% of the total G×E interaction (Table 5).

A genotype having high sucrose (%) across the environments where it is tested assumed to be an ideal (Kumar *et al*. 2009). The mean sucrose (%) of genotypes, hovering among the environments ranged from 15.92% in E6 to 19.30% in E5. The mean sucrose % for 10 genotypes under study in nine environments extended from 16.65% to 18.17%. However, the G×E interaction was differential type across the environments (Table 6). The genotype CoP 9301 (9) was top ranking across all the nine environments and registered highest sucrose (%) (19.30%) in the highest sucrose yielding environment E5, while in low sucrose yielding environment E6, CoP 09301 (9) genotype was also found on a top pedestal (Table 6).

The genotypes with high sucrose mean yield located near the line showing IPCA=0 suggested negligible or no G×E interactions (Guerra *et al*. 2009). Consequently, such genotypes will have general adaptability over all the locations. On the contrary, the genotype which maintains distance from the line with IPCA=0 indicates their specific adaptability across the environments (Fig 3). The genotype CoP 09301(9) closed to IPCA=0 line is stable and performed better in E4 and E5. The genotypes Co 05018 (1), Co 05019 (2) and CoSe 05452(5) are scattered in the biplot indicating poor adaptability over the environments. While, the genotypes like Co P05437 (4), Co 05020(3), CoBln 04174(7) and BO 91(8) are positioned very close to IPCA=0 line indicated that they are stable and did not have any environmental effect on sucrose per cent. However, some genotypes like BO 91(8) did better in E7 and E9. AMMI biplot analysis for sucrose per cent revealed that this trait is less influenced across the locations.

Table 6   Mean sucrose per cent of 10 genotypes across nine environments

Genotypes/ Environments	E1 (First plant crop, Motipur)	E2 (Second plant crop, Motipur)	E3 (Ratoon crop, Motipur)	E4 (First plant crop, Pusa)	E5 (Second plant crop, Pusa)	E6 (Ratoon crop, Pusa)	E7 (First plant crop, Kushinagar)	E8 (Second plant crop, Kushinagar)	E9 (Ratoon crop, Kushinagar)	Adj. mean
Co 05018 (1)	16.45	16.52	16.46	18.16	18.21	16.31	17.27	16.95	17.37	17.08
Co 05019 (2)	16.20	16.26	16.21	17.90	17.96	16.05	17.01	16.69	17.11	16.82
Co 05020 (3)	16.03	16.10	16.04	17.73	17.78	15.88	16.84	16.52	16.94	16.65
CoP 05437 (4)	16.31	16.37	16.32	18.01	18.06	16.16	17.12	16.80	17.22	16.93
CoSe 05452 (5)	16.83	16.90	16.84	18.54	18.58	16.68	17.64	17.32	17.74	17.45
CoBln 05502 (6)	16.25	16.32	16.26	17.96	18.01	16.11	17.07	16.75	17.17	16.88
CoBln 04174 (7)	16.07	16.13	16.08	17.77	17.28	15.92	16.88	16.56	16.98	16.69
BO 91 (8)	16.58	16.65	16.59	18.19	18.33	16.44	17.40	17.08	17.49	17.21
CoP 09301 (9)	17.55	17.62	17.56	19.26	19.30	17.40	18.36	18.04	18.46	18.17
CoSe 092423 (10)	16.61	16.68	16.62	18.32	18.37	16.47	17.43	17.11	17.53	17.24
Adj. mean	16.49	16.56	16.50	18.19	18.24	16.34	17.30	16.98	17.40	

The genotypes stationed near the origin of biplot showed greater stability over the environment for sucrose per cent. BO 91 (8) was the nearest located with the origin of biplot indicated most stable genotype over environments for sucrose per cent and it did not influence by the magnitude of G×E interaction (Ramon Rea *et al.* 2011).

Genotypes CoSe 092423 (10) and CoP 05437 (4) were also positioned near the origin of biplot, it showed these genotypes are less affected by the environment for the trait of sucrose (%) or they showed very low G×E interaction. The environment E5, E6 and E8 largely contributed to the GEI being far from the origin in the AMMI-2 biplot (Fig 3). The genotype CoBln 04174 (7) close with E8, CoP 05020 (3) positioned with E3 and E9 while, CoBln 05502 (6) and CoP 09301(9) close with E1 indicated positive association and reveal favorable environment for the genotype in that location. Genotype Co 05019(2), CoBln 04174 (7), CoSe 05452 (5), CoBln 05502(6) and CoP 09301(9) showed the different magnitude of genotype interaction across the environment falling under a different angle of vectors.

Conclusion

The magnitude of SS due to theenvironment was higher for cane yield, CCS yield and sucrose (%) of 10 genotypes evaluated across nine environments in North Central Zone,India than those SS due to genotype and G×E interactions. The use of biplot in AMMI model helps the selection of stable and high yielding genotypes of sugarcane. The genotype CoP 05437 (4) was discriminated highly adapted and stable over all the environments for cane as well as CCS yield. However, check variety BO 91 (8), was the most stable across environments for sucrose per cent. The environment like E2, E4, E5 and E6 largely contributed to the G×E interaction being away from the origin in the AMMI biplots. However, some genotypes performed differently at different locations owing to the magnitude of G×E interactions.

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