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Genotype × environment interaction analysis of multi-location trial data of sugarcane using variance components and Perkins & Jink model

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Abstract

Sugarcane is one of the most important long duration commercial crops grown in India, with large number of varieties. Indian placed second rank in sugarcane production after Brazil. Primary industries such as sugar mills, jaggery producing units, and chemical industries are largely depend on this crop. Multi-Location Trials (MLT) are being conducted for performance testing of genotypes. Differential performance of genotypes over environments is called as Genotype× Environment Interaction (GEI). The problem of Genotype× Environment Interaction poses a significant challenge when it comes to select and recommend the best genotypes for crop cultivation. This challenge becomes even more pronounced in the case of long duration crop like sugarcane. Unstable cultivar of sugarcane selected for cultivation leads to considerable financial risks for farmers over an extended period. The present study has been carried out using secondary data of 17 different genotypes grown in 6 locations over two years in Randomized Complete Block Design (RCBD) with two replication conducted at G. B. Pant University of Agriculture and Technology, Pantnagar for assessing the Genotype × Environment Interactions analysis using Analysis of variance (ANOVA) and Perkins and Jinks model. The results revealed that there are highly significant variations among the genotypes, GEI and heterogeneity components indicating the presence of substantial diversity within the genotypes of sugarcane and the influence of different environmental conditions. The contribution of variation due to G × E Interaction in total variation found to be significant at 5% level of significance which are varies from characters to characters for all the nine traits under study. Ranking of the genotypes obtained by Perkins stability measures (Bi) found to be significantly correlated with ranks obtained by means. The correlation varied from 0.67 to 0.92 character to character.

Keywords: MLT, GEI, pooled ANOVA, Perkins and jink model, and sugarcane.

Introduction

Sugarcane (*Saccharum officinarum)* is indeed an important commercial crop grown in India and belongs to the family Poaceae. India's climate provides favourable conditions for the growth of sugarcane, making it a significant crop in the country. This crop plays a vital role in various primary industries, such as sugar mills, jaggery (a traditional form of cane sugar) producing units, and chemical industries. The farmers prefer to grow sugarcane for sugar production over sugar beets or other fruits for several reasons like climate requirements, high sugar content, yield and productivity etc. Also it can offer several health benefits due to antioxidant properties. Apart from medical importance and sugar production, sugarcane can also be used for ethanol production, as animal feed, for biogases production.

India placed second rank after Brazil in sugarcane production. India is producing 419.25 million tonnes sugarcane from approximately 54.55 lakh hectares. The efficiency of sugarcane production in India is measured at approximately 82 tonnes per hectare (Statista Research Department, 2022) [6]. Achieving such productivity levels is essential to meet the demands of various industries which are dependent on sugarcane.

Multi-Location Trials (MLT) are being conducted for performance testing of genotypes to identify stable genotypes to meet these requirements and targeted productivity. Unstable cultivar of sugarcane selected for cultivation leads to considerable financial risks for farmers over an extended period. The presence of Genotype Environment Integration is one the challenge for the breeder to select the genotypes which performed better in all the environments. Since, the presence of GEI affects the ranking pattern of the genotypes in different locations. Many study have been carried out in the context of GEI by

Crossa, J. (1990) [4], Acuna, T. L. B and Wade, L. J. (2013) [1], Akcura, *et. al.* (2006) [2], Baraki, *et. al.* (2016) [3], K S Krishna *et. al*. (2022) [7, 8, 9] etc. Various methodologies have been suggested for statistically analyzing the GEI. The first approach, known as the variance components approach, estimates the effects of genotypes, environment, and their interactions by comparing observed mean squares in a pooled ANOVA to their expectations based on a random model. The second approach involves the use of regression techniques to partition the variability of G × E interaction into linear and non-linear components. This helps assess the stability of genotypes across various environmental conditions. This approach is often referred to as regression analysis and is widely adopted in plant breeding. Pioneering contributions to this approach were made by researchers like Eberhart and Russell (1966) [5], Perkins and Jinks (1968) [11], and Shukla (1972) [14] and others. The third approach is based on non-parametric statistics. It involves identifying the best genotype by evaluating the ranks of genotypes across all environments. Genotypes that consistently rank in the top three across all environments are considered as the best performers. The fourth approach involves using multivariate techniques, with the Genotype plus Genotype × Environment Interaction (GGE) biplot and Additive Main Effects and Multiplicative Interaction (AMMI) models, Rao, A.R., and Prabhakaran, V.T. (2005) [12] being particularly prominent in this context. These techniques allow for a comprehensive assessment of G × E interaction patterns.

In the present study Variance components through ANOVA technique and Perkins and Jink Model (1968) [11] have used to assess the GEI in the Multi-Location Trial data of sugarcane. Analysis have been carried out on secondary data of the 17 different genotypes grown in 6 locations in Randomized Complete Block Design (RCBD) with two replication conducted at G. B. Pant University of Agriculture and Technology, Pantnagar. There were nine traits namely cane yield at harvest, single cane weight at harvest, sugar content at harvest, germination% at 45 days after planting, number of tillers at 120 days after planting, number of millable canes at harvest, brix% at 10 months, juice extraction% at 10 months, polarization %. The ranking of the genotypes have be obtained mean, perkin' regression co-efficient (B_i) and deviation from the regression co-efficient stability measures. Rank correlation has used to assess ranking patterns of genotypes affected by GEI. The analyses have been carried out using MS-excel and R-package writing code.

Materials and Methods

Source and extent of data

Secondary data on sugarcane crop from Multi-Location Trials (MLTs) conducted at G B Pant University of Agriculture and Technology, Pantnagar has been collected. The data were included information on 17 different genotypes grown in 6 locations over multiple years. The MLTs were conducted using a Randomized Complete Block Design (RCBD) with two replications, ensuring randomized allocation of genotypes within blocks. Replication-wise data is available for nine traits such as cane yield at harvest, single cane weight at harvest, sugar content at harvest, germination% at 45 days after planting, number of tillers at 120 days after planting, number of millable canes at harvest, brix% at 10 months, juice extraction% at 10 months, polarization%. This comprehensive dataset allows for in-depth analysis and comparison of genotypes performance across different locations and years, providing valuable insights into the variability and stability of the genotypes traits.

Experimental site

The field trials were performed at three different locations: the Norman E. Borlaug Crop Research Centre of G. B. Pant University of Agriculture & Technology in Pantnagar, Uttarakhand; the Sugarcane Research Station in Kashipur; and the Krishi Vigyan Kendra in Dhanauri (Haridwar). These trials took place over the course of two years, 2013-14 and 2014-15. In 2013-14, two sets of trials were conducted at the Norman E. Borlaug Crop Research Centre in Pantnagar, one with normal spring planting (Feb-March) and the other with late planting. The third and fourth sets of trials, involving both normal and late spring planting, were conducted at the same location in Pantnagar during 2014-15. The fifth set of trials took place at the Sugarcane Research Station in Kashipur, which is approximately 65 km away from Pantnagar. The sixth set of trials was carried out at the Krishi Vigyan Kendra in Dhanauri (Haridwar). Both the fifth and sixth sets of trials were conducted during late spring planting in 2014-15.

Table 1: List of the genotypes used in the experiment

SL. No	Genotypes	Code of Genotype
1	'PC2006-07-69'	G1
2	'PC2006-07-28'	G2
3	'PC2006-07-30'	G3
4	'PC2006-07-83'	G4
5	'PC2006-07-56'	G5
6	'PC2006-07-57'	G6
7	'PC2006-07-62'	G7
8	'PC2006-07-101'	G8
9	'PC2006-07-03'	G9
10	'PC2007-08-51'	G10
11	'PC2007-08-59'	G11
12	'PC2007-08-86'	G12
13	'PC2007-08-156'	G13
14	'PC2007-08-266'	G14
15	'CoJ 64 (Check)'	G15
16	'CoPant84211(check)'	G16
17	'CoPant3220(check)'	G17

Table 2: Details of various environment and their code

Sl. No.	Planting condition and places	Code of Environment
1	Normal planting was place at Pantnagar in February–March 2013.	E1
2	Late planting took place at Pantnagar in April–May 2013.	E2
3	Normal planting between February - March 2014 at Pantnagar.	E3
4	Late planting, i.e. in April or May 2014 at Pantnagar.	E4
5	Late planting, i.e. in April-May 2014 at SRS, Kashipur.	E5
6	Late planting, i.e. in April-May 2014 at KVK, Dhanauri (Haridwar).	E6

Analysis of variance

The analysis of variance for each character of sugarcane crop were carried out for the randomized block design as suggested by Fisher (1946). The model used was as follows:

$$Y_{ij} = \mu + g_i + b_j + e_{ij} \; ; \; i = 1, 2, 3 \ldots, g \text{ and } j = 1, 2, 3, \ldots, t \quad (1)$$

Where,

Y_{ij} = Observed response of i^{th} genotype in j^{th} block/ replication.

μ = General mean.

g_i = Effect of i^{th} genotype

b_j = Effect of j^{th} replication

e_{ij} = Random error of i^{th} genotype and j^{th} block/ replication

Basic regression models

Let the average phenotypic value Y_{ijr} of i^{th} genotype (i=1, 2, 3, … g) at j^{th} environment (j=1, 2, 3, … t) and k^{th} replication (k=1, 2, 3, …r)

$$Y_{ijk} = \mu + d_i + e_j + g_{ij} + r_{jk} + \varepsilon_{ijk} \quad (2)$$

Y_{ijk}: average phenotypic value'of i^{th} genotype (i = 1, 2, 3, …, g) at j^{th} environment (j = 1, 2, 3, …, t) in k^{th} replication (k = 1, 2, 3, …, r)

μ is the general mean; d_i is the effect of i^{th} genotype, e_j = effect of j^{th} environment, g_{ij} is the GEI between i^{th} genotype and j^{th} environment, r_{jk} is the replication effect of j^{th} environment in k^{th} replications and ε_{ijk} is the random error.

The basic regression method in stability analysis provides a quantitative approach to evaluate the stability of genotypes across different environments. It helps breeders and researchers in selecting genotypes with desirable stability characteristics for specific target environments and improving crop performance and adaptability. Basic regression model includes two model namely Eberhart and Russell model & Perkins and Jinks model.

Perkins and Jinks Model (1968)

A different stability analysis model was put forth by Perkins and Jinks in 1968. This approach first break down the overall variation into three parts: (1) genotypes, (2) environments, and (3) Genotypes × Environments. The G × E variance is further separated into two categories: (a) heterogeneity resulting from regression, and (b) sum of squares resulting from residuals. Sum of squares due to each genotype is further subdivided from the sum of squares due to remainder. Perkins and Jinks Model is given as:

$$Y_{ij} = \mu + d_i + (1 + \beta_i)e_j + \delta_{ij} + \varepsilon_{ij} \quad (3)$$

Y_{ij}= average phenotypic valueof i^{th} genotype i=1, 2, 3 …, g at j^{th} environment j=1, 2, 3…, t

μ = general means,

d_i = effect of i^{th} genotype,

e_j = effect of j^{th} environment,

$(1 + \beta_i)$ = regression of Y_{ij} on e_j,

δ_{ij} = deviation from regression for the i^{th} genotype in the j^{th} environment

ε_{ij} = random error

Rank correlation

Spearman's rank correlation coefficient, proposed by Spearman (1904) [15] denoted by the symbol ρ (rho), is a statistical measure used to assess the strength and direction of the monotonic relationship between two ranked variables. It is an alternative to Pearson's correlation coefficient when the relationship between variables is non-linear or when the data is in the form of ranks rather than actual numerical values.

Spearman's rank correlation coefficient ranges between -1 and 1. A positive value of ρ indicates a positive monotonic relationship, where higher ranks of one variable tend to correspond to higher ranks of the other variable. A negative value of ρ indicates a negative monotonic relationship, where higher ranks of one variable tend to correspond to lower ranks of the other variable. A value of 0 indicates no monotonic relationship. Spearman's rank correlation coefficient is particularly useful when dealing with ordinal or non-parametric data, as it assesses the strength and direction of the relationship without making any assumptions about the underlying distribution of the data.

Spearman's rank correlation coefficient **(ρ)** has been utilized in the present study to quantify the correlation between ranks of genotype obtained by stability measures. Formula for calculating correlation coefficient is as follows;

$$\boldsymbol{\rho = 1 - \frac{6\sum_{i=1}^{n} d_i^2}{n(n^2 - 1)}}$$

Where,

d_i= Difference between ranks of variables

n = Number of observations

Results and Discussion

To test the significance difference in performance of sugarcane genotypes in different environment were tested using ANOVA in all the 6 environment namely E1, E2, E3, E4, E5, E6 have been performed for all the 9 characters namely cane yield, single cane weight, sugar content, germination% at 45 days after planting, number of tillers at 120 days after planting, number of millable canes at harvest, brix% at 10 months, juice extraction% at 10 months and polarization%. The compiled results are presented in Table 3. The results showed there is a significant difference in the performance of genotypes in all the environments at 5% level of significance for all the 9 characters under this study. It shows that all genotypes are performing differently in all the environments. That may be due to genetic potential of the genotypes and presence of GEI that leads to proceed further analysis by pooled ANOVA.

From the Table 3 the percentage contribution of variation in total variation by genotypes for all the locations have been worked out for all the characters. The contribution of variation for cane yield ranges between 51% to 89%, for single cane weight it ranges from 70% to 98%, for sugar content variation is 42% to 95%, for germination% it varies from 73% to 94%, for number of tillers the variation is ranging from 70% to 96%, the contribution in total variation for number of millable canes varies between 62% to 92%,

for brix% it ranges from 65% to 89%, for juice extraction% and for polarization% it is ranging from 61% to 92%.

The presence of genotype × Environment Interaction have been assessed by pooled analysis of variance and same has been compiled and presented in Table 4 for all the nine traits. The result shown in Table 4 cclearly shows that genotypes and environments are significant for all the six characters at 5% level of significance. The interaction between genotypes and environments also found to be significant for the characters namely cane yield, single cane weight, sugar content, number of tillers, number of millable canes, and for germination%. The interaction between genotypes and environments found to be non-significant for the characters namely brix%, juice extraction, and for polarization%. The significance of the G×E iinteraction implies that the genotypes were unable to maintain consistent performance across different environments, leading to substantial shifts in the relative ranking of the genotypes.

ANOVA explains the contribution of variation to the total variation by Genotype × Environment interaction. The variation for cane yield is 16.5%, for single cane weight is 11.37%, for sugar content is 18.95%, for number of tillers is 25.75, for number of millable canes is 21.5%, and for germination% is 24.52. By this we can conclude that the variation due to Genotype × Environment interaction is maximum for number of tillers (25.75%) and minimum for single cane weight (11.37%).

Table 3: Location wise ANOVA for testing equality of genotype's performance

Characters	Source		E1	E2	E3	E4	E5	E6
Cane yield at harvest	Genotypes	MSS	242.66	154.82	477.65	28.23	50.42	182.65
		F value	12.57*	05.80*	07.84*	03.14*	2.63*	27.73*
Single cane weight at harvest	Genotypes	MSS	00.04	00.04	00.05	00.08	00.02	00.02
		F value	11.62*	08.53*	05.26*	13.54*	34.03*	13.10*
Sugar content	Genotypes	MSS	03.60	02.26	05.88	00.41	00.57	02.24
		F value	14.14*	5.66*	05.92*	03.17*	02.03*	25.08*
Germination% at 45 DAP	Genotypes	MSS	90.98	52.84	361.60	41.32	112.01	108.05
		F value	4.06*	10.49*	21.01*	06.85*	12.98*	5.93*
Number of tillers at 120 DAP	Genotypes	MSS	419.80	407.80	400.77	74.76	246.86	357.42
		F value	18.28*	15.00*	17.27*	06.94*	34.36*	17.48*
Number of millable canes at harvest	Genotypes	MSS	155.47	74.01	717.29	84.99	307.58	433.77
		F value	9.55*	03.07*	25.63*	04.12*	07.62*	23.80*
Brix%	Genotypes	MSS	00.55	00.35	01.28	01.06	00.95	00.89
		F value	09.73*	4.54*	04.32*	07.58*	05.69*	04.60*
Juice extraction at harvest	Genotypes	MSS	29.92	14.50	18.56	07.12	10.06	09.76
		F value	02.39*	02.63*	02.37*	05.00*	03.11*	02.51*
Polarization%	Genotypes	MSS	00.28	00.31	00.72	00.54	00.47	00.63
		F value	08.67*	08.13*	05.01*	10.32*	09.47*	08.09*

Table 4: Assessing the G×E Interaction through ANOVA

Characters	Environment		Genotypes		G × E interaction		Residuals
	MSS	F value	MSS	F Value	MSS	F value	MSS
Cane yield	10600.7	449.33*	503.07	21.32*	156.67	6.64*	23.59
Single cane weight	01.20	324.94*	00.13	36.97*	0.01	3.71*	0.003
Sugar content	140.51	393.09*	06.23	17.45*	2.44	6.57*	0.35
Germination%	1994.01	264.29*	406.90	31.52*	71.98	5.58*	12.91
Number of tillers	2887.69	475.75*	888.36	61.04*	130.55	8.97*	14.55
No. of millable canes	2824.21	99.51*	1170.31	47.58*	120.55	4.90*	24.60
Brix%	04.28	23.98*	04.32	29.53*	0.16	1.12(**NS**)	0.14
Juice extraction %	37.72	5.769*	21.60	4.066*	3.24	0.61(**NS**)	5.31
Polarization%	01.72	19.56*	02.60	39.36*	0.07	1.11(**NS**)	0.06

*significance at 5% level of significance, NS- Non significant

Furthermore, the analysis revealed that the significant pooled deviation, representing the non-linear and unpredictable portion of variance, played a significant role in contributing to the overall variance arising from the genotype × environment interaction. This implies that there are complex interactions between the genotypes and the environments that cannot be easily predicted or explained by linear relationships alone. This finding aligns with similar observations reported by previous studies, such as those conducted by Shahryarinasab and Chogan (2015); Balat *et al*. (2021) in maize and bottle gourd genotypes respectively.

Table 5: GEI analysis through Perkins and jinks model

Characters	Genotype × Environment		Heterogeneity among regression		Remainder
	MSS	F Value	MSS	F Value	MSS
Cane yield	156.67	1.50*	190.42	1.82*	104.22
Single cane weight	0.013	1.54*	0.0209	2.34*	0.0089
Sugar content	2.446	1.50*	3.2635	2.00*	1.6252
Germination%	84.98	1.48*	116.69	2.03*	57.230
Number of tillers	136.55	1.52*	272.09	3.03*	89.566
Num of millable canes	120.55	1.51*	264.72	3.32*	79.533

*significance at 5% level of significance

The results of the analysis carried out for assessing GEI by Perkin's and Jinks (1968) model has been compiled and presented in Table 5. It provides insights into the differences among the genotypes and environments (joint regression). The results revealed that genotypes and environments (joint regression) are significant at 5% level of significance which indicates the presence of substantial diversity within the genotypes and the influence of different environmental conditions. The interaction arising due to genotypes × environments was further observed to be significant. The contribution of variation to total variation is maximum by environments (joint regression) component. The G×E variation is further subdivided into heterogeneity due to regression (linear component) and sum of square due to remainder (non-linear component) and these were also found to be significant at 5% level of significance with respect to the pooled error indicating the performance of genotypes differently to different environments. The magnitude of mean square due to heterogeneity between regressions was greater than the magnitude of mean square of remainder indicating the prediction of the performance of the character is possible.

This finding aligns with the observations from the Eberhart and Russell (1966) [5] model, indicating that the non-linear components are unpredictable. These findings are consistent with the conclusions drawn by Thakur *et al.* (1997) [16] in their study on mustard. It suggests that the presence of significant differences among genotypes and environments, as well as the substantial contribution of non-linear components, is a common phenomenon observed in different crop species.

Table 6: Ranking of genotypes based on Perkins and jink stability measures Bi and Di

GEN	Cane yield						Single Cane weight						Sugar content					
	Mean	R_mean	Bi	Rank Bi	Di	rank di	Mean	R_mean	Bi	Rank Bi	Di	rank di	Mean	R_mean	Bi	Rank Bi	Di	Rank di
G1	63.0183	12	0.1831	9	107.197	15	0.84	14	-0.143	9	0.0099	16	7.3792	13	0.1524	7	1.7462	16
G2	62.8158	13	-0.1278	4	40.4669	9	1.0358	3	0.378	16	0.0061	15	7.4533	11	-0.118	5	0.5983	10
G3	62.7917	14	-0.1775	7	110.859	16	0.8267	15	-0.548	17	0.0017	3	7.1383	15	-0.254	14	1.1902	14
G4	75.7233	2	0.2494	12	27.896	5	0.9775	5	0.061	4	0.0054	12	8.8192	3	0.2101	10	0.4171	6
G5	75.06	4	0.1286	5	43.191	11	0.9392	6	0.2058	11	0.0058	14	8.8992	2	0.1914	8	0.6621	12
G6	76.4025	1	0.1793	8	34.9314	7	1.0017	4	0.2013	10	0.0028	6	8.9658	1	0.2302	12	0.5648	8
G7	70.4608	6	0.212	10	15.7191	1	0.8633	11	-0.254	13	0.001	2	8.5317	4	0.2171	11	0.2719	3
G8	64.755	10	-0.1395	6	102.721	14	0.9333	7	0.3032	14	0.003	8	7.3867	12	-0.1196	6	1.7288	15
G9	68.1483	7	-0.0508	1	54.801	13	0.8458	12	-0.218	12	0.0019	4	7.9625	8	-0.0413	2	0.6909	13
G10	60.11	15	-0.3039	15	118.181	17	1.2125	1	-0.116	7	0.0163	17	7.0217	16	-0.2655	15	1.9145	17
G11	65.3625	9	-0.0896	2	40.4491	8	0.9258	8	0.0183	1	0.003	9	7.7542	10	-0.0566	3	0.5453	7
G12	70.55	5	0.3665	16	26.647	4	0.9192	9	0.067	5	0.0027	7	8.3733	5	0.3993	16	0.3441	4
G13	68.5258	8	0.2625	14	45.4063	12	0.8833	10	-0.040	2	0.0009	1	8.0325	7	0.2534	13	0.6217	11
G14	75.5808	3	0.2179	11	30.9157	6	0.8175	17	-0.124	8	0.0033	10	8.3092	6	0.0291	1	0.3649	5
G15	59.6908	16	-0.1167	3	41.3732	10	0.8225	16	-0.053	3	0.0051	11	7.2008	14	-0.1079	4	0.5925	9
G16	53.8025	17	-0.5356	17	23.2232	3	0.8442	13	-0.112	6	0.0055	13	6.5033	17	-0.5152	17	0.273	3
G17	64.6067	11	-0.2579	13	21.9369	2	1.0742	2	0.373	15	0.0019	5	7.9542	9	-0.2049	9	0.2065	1

GEN	Germination %						No. of tiller						No. of millable cane					
	Mean	R_mean	B_i	rank Bi	Di	rank di	Mean	R_mean	Bi	rank Bi	Di	rank di	Mean	R_mean	Bi	rank B_i	D_i	rank d_i
G1	54.3075	3	0.2304	6	18.858	8	40.628	13	-0.423	10	3.349	3	73.3975	10	0.3645	7	45.270	13
G2	44.6467	9	0.9148	17	30.408	10	29.826	16	-0.652	13	9.045	1	61.1742	15	-0.875	17	29.144	9
G3	43.7033	12	-0.262	7	34.514	13	49.027	3	0.7739	15	73.884	15	75.5092	9	0.458	11	122.582	17
G4	43.5083	13	-0.175	4	26.887	9	42.838	9	0.6101	12	97.928	16	77.2317	5	0.3515	5	37.489	12
G5	53.5633	4	0.3493	11	18.373	7	48.57	6	-0.047	1	9.151	2	80.7317	3	0.1157	3	23.485	6
G6	55.0892	1	0.2835	8	3.0267	2	46.777	7	-0.266	3	58.059	14	76.2867	7	0.0837	1	18.748	2
G7	47.52	6	0.2917	9	14.865	5	63.469	1	1.1967	17	222.612	17	81.1775	2	0.3639	6	27.476	8
G8	38.6008	16	-0.797	16	11.21	3	48.815	5	0.3259	7	25.529	10	70.1192	13	-0.369	8	68.215	14
G9	44.6567	8	0.4845	12	17.611	6	48.83	4	0.8035	16	49.609	13	80.0108	4	0.2625	4	72.687	15
G10	34.6492	17	-0.510	13	33.989	12	29.114	17	-0.668	14	18.223	5	49.3958	17	-1.185	15	81.03	16
G11	45.8433	7	-0.114	3	51.44	15	33.287	15	-0.551	11	22.999	7	70.34	12	-0.449	10	27.837	7
G12	44.3608	10	-0.329	10	9.012	1	41.837	11	-0.268	4	23.248	8	75.9533	8	0.5535	13	12.762	1
G13	48.265	5	-0.012	1	52.225	16	42.835	10	-0.386	8	40.522	11	76.8967	6	0.4966	12	19.428	4
G14	54.4325	2	0.528	14	71.644	17	54.855	2	0.2876	5	14.558	4	92.5117	1	0.8361	16	5.282	3
G15	41.7525	14	-0.102	2	30.763	11	45.0333	8	-0.053	2	46.501	12	72.5608	11	0.0929	2	21.919	5
G16	40.425	15	-0.566	15	48.274	14	41.5033	12	-0.386	9	24.68	9	63.785	14	-0.414	9	32.543	11
G17	43.7358	11	-0.215	5	13.357	4	39.0833	14	-0.295	6	21.409	6	60.8342	16	-0.687	14	30.119	10

Table 7: Top four superior genotypes identified by stability measures B_i and D_i

Mean	Cane yield	Single cane wt	Sugar content	Germi%	Num of tillers	Num of millable canes
	G6, G4, G14, G5	G10, G17, G2, G6	G6, G5, G4, G7	G6, G14, G1, G5	G7, G14, G3, G9	G14, G7, G5, G9
Bi	G9, G11, G15, G2	G11, G13, G15, G4	G14, G9, G11, G5	G13, G15, G11, G4	G5, G15, G6, G12	G6, G15, G5, G9
Di	G7, G17, G16, G12	G13, G7, G3, G9	G17, G7, G16, G12	G12, G6, G8, G17	G2, G5, G1, G14	G12, G6, G14,G13

Table 8: Spearman's rank correlation between ranks of genotypes assigned by B_i and D_i for all the characters

	cane yield			Single cane weight			ugar content		
	Mean	Bi	Di	Mean	Bi	Di	Mean	Bi	Di
Mean	1	0.77**	-0.34	1	0.69**	0.20	1	0.83**	-0.362
Bi		1	-0.24		1	0.19		1	-0.22
Di			1			1			1
	Germination %			No. of tiller			No of millable cane		
Mean	1	0.75**	-0.04	1	0.92**	0.55*	1	0.76**	-0.43
Bi		1	0.05		1	0.68		1	-0.36
Di			1			1			1

**Significant at 1% level of significance.

The analysis using the Perkin's and Jinks (1968) model supports the notion of significant differences among genotypes and environments. The observed significant remainder emphasizes the importance of accounting for non-linear effects and genotype by environment interactions in understanding the performance of the genotypes under different environmental conditions.

Assessment of stability for sugarcane genotypes by B_i and D_i

Assessment of stability for sugarcane genotypes were carried out using stability measures namely Perkin's regression co-efficient (B_i), Perkins's Deviation (D_i) and with the mean yield performance for all the six characters. For this purpose ranking of genotypes based on these stability measures and mean yield were obtained. The genotype with rank 1 is considered as best, indicating high stability and favourable yield performance, while the genotype with rank 17 is considered as worst, suggesting lower stability and less desirable yield performance. The results are presented in Table 6. The top four superior genotypes identified by Bi, Di and Mean performance have been worked out and presented in Table 7.

The results presented in Table 6 and Table 7 revealed that Perkin's regression co-efficient identified G9, G11, G14, G13, G5 and G6 identified as superior genotypes for cane yield, Single cane weight, Sugar content, Germination %, Number of tiller and number of millable canes respectively while G16, G3, G16, G2, G7 and G2 respectively as a poorest genotype since got 17th rank by Bi. However, Perkin's deviation identified G7, G3, G17, G2, G2 and G12 identified as superior genotypes for cane yield, Single cane weight, Sugar content, Germination %, Number of tiller and number of millable canes respectively while G10, G10, G10, G14, G7 and G3 respectively as a poorest genotype. This results clearly shows the changes in ranking patterns of genotypes by these stability measures. The performance of stability measures was assessed by the Spearman's correlation between ranks of genotypes obtained by Perkins stability, deviation and mean performance of genotype the same has been computed and presented in Table 8. Correlation between mean's rank and Bi are highly positively correlated which are varies from 0.69. to 0.92 for different tarits. While, Mean's ranking pattern are negatively correlated with Di except Cane weight and Number of tiller of order -0.04 to -0.43. However it slightly positively correlation between Bi and Di. It means ranking pattern are different by Bi and Di.

Conclusion

Individual environment wise ANOVA revealed that there is a significant differences between genotypes in each environment for all the 6 characters considered for the study. Pooled ANOVA was showed presence of significant G×E interaction by six characters namely cane yield, single cane weigh, sugar content, germination%, number of tillers and number of millable canes while characters like brix%, juice extraction, pol% are shown non-significant for G×E Interaction. The presence of GEI have also been confirmed by Perkins and Jinks model. Perkins Regression coefficient is highly correlated with mean yield while Deviation from the Perkins regression coefficient is less correlated. Hence Perkins deviation more better to identify the stable genotypes than Perkin's co-efficient.

G7, G13, G17, G12, G2 and G12 identified superior genotypes for cane yield, single cane weigh, sugar content, germination%, number of tillers and number of millable canes respectively based on Di.

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