



Genotype x environment interaction and yield stability analysis of sugarcane (*Saccharum officinarum* L.) genotypes

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Abstract

Twelve sugarcane genotypes (eight local collections, two exotic and two standard checks) were evaluated at three locations (Wonji, Metehara and Finchaa Sugar Estates of Ethiopia) using RCBD with three replications during 2015/2016. The objective was to study the G x E interaction, adaptability and phenotypic stability of sugarcane genotypes at three locations. Data was collected on quantitative traits and sugar quality characters. The analyses of variance showed significant difference among genotypes at the three environments and when locations were combined. The Genotype x environment interaction (GEI) was also significant for all traits, indicating inconsistency of performance of the genotypes over the three locations. The genotypes Aladi, Nach Shenkora, Kay Sidanecho, N55/805, Kay Shenkora and Erero gave cane and sugar yield statistically at par with the two checks and had mean advantage over the rest of genotypes. The mean performance of genotypes in sugar yield was also analyzed using univariate and multivariate stability parameters. The genotypes N55/085 and NCO334 were identified as stable and widely adapted genotypes by five univariate stability parameters and also by AMMI-II. Moreover, GGE identified NCO334 as specifically adapted to Wonji and Finchaa Sugar Estates while B52298 and Yebskula Shenkora were specifically adapted to Metehara Sugar Estate.

Keywords: AMMI, GGE; Sugarcane; Stability Parameters

1. Introduction

Sugarcane (*Saccharum officinarum* L.) is a major economically important crop in tropical and sub-tropical countries (Khan *et al.*, 2013). Sugarcane plays a significant role in the Ethiopian socio economy. Sugar and its byproduct are used for local consumption and export. The industry created job opportunity for a large number of people. Today in the country sugar consumption outstrips its production. To alleviate this problem today there are many expansion projects in the existing sugar estates and new sugar development projects are underway in different parts

of the country. The sustainable supply of new sugarcane varieties adaptable to various agro-ecologies is vital to realize surplus sugar production in the country.

The development of sugarcane and other crops is affected by effects of the environment (E), genotype (G) and their interaction (GEI), of which the latter causes significant variation in cultivar performance among different locations (Mohammadi *et al.*, 2007). The observation and analysis of genotype-by-

environment (G x E) interaction in multi environment yield trials (MEYT) are very important for evaluation, selection and recommendation of crop varieties (Mattos et al., 2013; Regis et al., 2018).

Genotype x environment interaction (GEI) is known by worldwide sugarcane breeding programs, as the phenomenon that influences the selection of superior genotypes in trials and these rank changes confound the determination of the overall true genetic value of the prospective varieties (Kimbeng *et al.*, 2009). Kang (2002) indicated that the effect of GEI in sugarcane is dependent on traits and is more pronounced for quantitatively inherited traits, such as cane and sugar yield affecting their relative rankings in different environments.

The statistical methods of analyzing sugarcane G x E interactions have included conventional analysis of variance, regression analysis, additive main effects and multiplicative interaction (AMMI) and variance components analyses (Crossa, 1990). Newer methods such as GGE (genotype + G x E) biplot analysis have been evaluated with sugarcane in a number of studies (Kang, 2008; Guilly et al., 2017; Todd et al., 2018). Combine analysis of variance procedure is the most common used to identify the existence of GEI from replicated multiplication trails (Sanesh Ramburan, 2012).

The stability of a cultivar refers to its consistency in performance across environments and is affected by the presence of GxE interactions. Estimation of stability of a new genotype for yield and quality traits is a pre-requisite in plant breeding program prior to its release for commercial planting. Productivity of a genotype in favorable environments does not indicate its adaptability and stability whereas performance of a genotype in diverse environments is a true evaluation of its inherent potential for adaptativeness (Pandey *et al.*, 1981). Therefore varietal trials are normally conducted over various locations for different years before deciding the release of a new cultivar in a particular region.

Various statistical approaches have been so far to measure the stability of genotypes over environments. However, it was shown that no single method can adequately explain cultivar performance across environments (Dehghani et al., 2006). The stability parameters are not informative and useful in selection unless they are combined with mean performance of genotypes. Thus, stability must be used along with

performance measurements to give reliable results. The multivariate stability measures, AMMI and GGE, are the most commonly methods used to estimate stability of genotypes in multi-location trials. Other univariate stability parameters include regression coefficient (bi) and deviation from regression (Sd_i^2) (Eberhart and Russel, 1966), coefficient of variation, CV_i (Francis and Kannenberg, 1978), Wricke's covalence (Wricke, 1962), stability variance σ_i^2 (Shukla, 1972) and genotypic superiority index P_i (Lin and Binns, 1988).

In Ethiopia, with the establishment of new sugarcane plantations in different agro-ecologies, the need for superior varieties that meet the requirements of various environmental conditions increases. Sugarcane genotypes should be evaluated over many environments to determine their adaptability to the diverse agro-climatic and edaphic conditions to satisfy varietal requirements of the sugar estates. Therefore, this study was conducted to study the G x E interaction, adaptability and phenotypic stability of different sugarcane genotypes at three sugar estates of Ethiopia.

2. Materials and Methods

Description of the study area

The experiment was conducted at three sugarcane plantations of Ethiopia during 2015/2016 cropping season. Wonji Sugar Estate is situated, (8° 3' N; 39° 20' E), Metahara, (8° N; 39° 52' E) and Finchaa (9° 30' N; 37° 30' E); The estates has altitudes measuring 1540, 950 and 1350 to 1600 m.a.s.l., respectively. The areas receive an annual average rainfall of 800, 554, 1300 mm, and minimum and maximum temperature of 15.3/26.9, 17.5/32.6, and 15/31 C°, respectively.

Experimental materials and design

Eight locally collected genotypes (Kay Sidancho, Tafach Shenkora, Wotete, Kay Shenkora, Nach Shenkora, YeBeskula Shenkora, Aladi, Erero) and two introduced sugarcane genotypes (B4425 and N55/805) were evaluated including two standard checks (NCO334 and B52-298). The local collections were selected among other genotypes based on field performance on observation plots in the previous year. The experiment was laid out in RCBD with three replications. Each plot was comprised of six rows, each 5 m long, and spaced 1.45 m apart with total plot area of $6 \times 1.45 \times 5\text{m} = 43.5\text{m}^2$. The two border rows

were considered guard rows whereas the 4 middle rows were sampling rows and were used for data collection.

Data collected and statistical analysis

Data was collected on sprouting (germination percent), number of tiller, millable stalk count, stalk height (m), stalk diameter (cm), single cane weight (kg), cane yield (ton/ha), brix%, pol%, recoverable sugar percent and sugar yield (ton/ha). The data were subjected to analyses of variance (ANOVA) using statically analysis system (SAS, 2002) version 9.

Due to their ability to produce bi-plots that allow for rapid visualization of the patterns of G x L interactions, multivariate techniques such as the additive main effects and multiplicative interaction (AMMI) and GGE (genotype + G x E) bi-plot analysis have been used to assess similarity and dissimilarity among the three environments and interaction patterns between genotypes and locations. The AMMI model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_k \lambda_k a_{ik} b_{jk} + R_{ij}$$

Where Y_{ij} is the value of i^{th} genotype in the j environment; μ is the grand mean; G_i is the deviation of the i^{th} genotype from the grand mean; E_j is the deviation of the j environment from the grand mean; λ_k singular value for pc axis k ; a_{ik} and b_{jk} are the pc scores for axis of k of the i^{th} genotype and in the environment; R_{ij} residual and error term.

GGE biplot was computed as: $Y_{ij} - E_j = \sum_k \lambda_k a_{ik} b_{jk} + R_{ij}$

Where Y_{ij} is the value of i^{th} genotype in the j environment; E_j effect of environment; λ_k singular value for pc axis k ; a_{ik} and b_{jk} are the pc scores for axis of k of the i^{th} genotype and i^{th} environment; R_{ij} residual.

Performance consistency or stability of each genotype was determined after testing the significance of the genotype by environment interaction. By using sugar yield data, univariate stability parameters such as Wricke's ecovalence, genetic superiority index, coefficient of variation, linear regression coefficient (slope) and mean square deviation from regression were employed to observe stability of sugarcane genotypes.

Stability by Wricke's (1962) ecovalence (W_i):

Stability of i^{th} genotype is its interaction with environments expressed as:

$$W_i = \sum_j (y_{ij} - \bar{Y}_i - \bar{Y}_j + \mu)^2$$

Where y_{ij} is the mean performance of genotype i in the j th environment; \bar{Y}_i is means of i^{th} genotype across environments and \bar{Y}_j is means of j^{th} environment across all genotypes and μ is the grand mean. Genotype with lower W_i has smaller deviation from the environmental mean indicating the stability of the genotype. Higher W_i indicates the a higher contribution of a genotype for the genotype by environment interaction which indicates the instability in the performance of the genotype across the environments.

Linear regression coefficients (bi)

The model partitions the G x E interaction in to a component due to linear regression (bi) and a component due to deviations from linear regression (dij) so that equation becomes

$$Y_{ij} = \mu + G_i + E_j + (b_i E_j + d_{ij}) + e_{ij}$$

Regression coefficient close to 1 indicates the average stability of the genotype meaning that good (high mean yield) or poor (low mean yield) general adaptability of the genotype in all environments. When Regression slope is greater than 1 it indicates the sensitivity of the genotype to low yielding environment, whereas if it is less than 1 it indicates genotype better yielder in low yielding environment and more adaptive. Smaller values d_i^2 is associated with more stable genotypes.

Stability by coefficient of variance (CV)

According to Francis and Kannenberg's (1978) coefficient of variability, stable genotypes are those showing lower CV with higher yield.

$CV = \frac{S}{Y} * 100$ Where; S is standard deviation and Y is the grand mean of the experiment.

Stability by superiority index

Lin and Binns (1988) model was used and the P_i parameters obtained by the expression;

$$P_i = [n (X_i - M...)^2 + \sum_{j=1}^n (X_{ij} - X_i - M_j + m...)^2] / 2n$$

Where p_i is superiority index of the i^{th} genotype, X_{ij} is the average response of the i^{th} genotype in the j^{th} environment, X_i is the mean deviation of the genotype i ; M_j is the genotype with maximum response among all the genotypes in the j^{th} environment; M is maximum response among all the genotypes over the environments; n is number of environment. Smaller value of p_i indicates less distance and maximum yield resulting better genotype and stable.

3. Results and Discussion

The combined analysis of variance over locations indicated that there was highly significant ($p < 0.05$) differences among the genotypes for number of tillers, number of millable cane, single cane weight and plant height (Table 1). This reflected the presence of genotypic variability for these major yield components that can be exploited in breeding programs. There was no significant difference for cane and sugar yield and sugar quality parameters (pol percent and brix percent). In a similar study Khan et al. (2004) and

Mohammad et al. (2013) also found significant difference among sugarcane genotypes in multi location trials for number of tillers, number of millable cane, single cane weight and plant height. They also found no significant difference for pol percent and brix percent.

Mean performance of sugarcane genotypes for yield, yield components and sugar quality traits is presented in Table 2. Though statistically there was no difference among genotypes the highest millable cane number and cane and sugar yield was recorded for the check variety NCO344.

The genotype by location (G x L) interaction showed highly significant difference for all traits which indicates the differential response of genotypes across the three locations (Table 1). For example, Figure 1 shows the presence of cross over interaction for sugar yield that indicated change in ranks of genotypes across environments. During cross over interaction both the rank and magnitude of performance of the genotypes changes from location to location. Rank change in performance of quantitative traits of sugarcane genotypes in multi location trials is evident (Kimbeng et al., 2009; Kang, 2002).

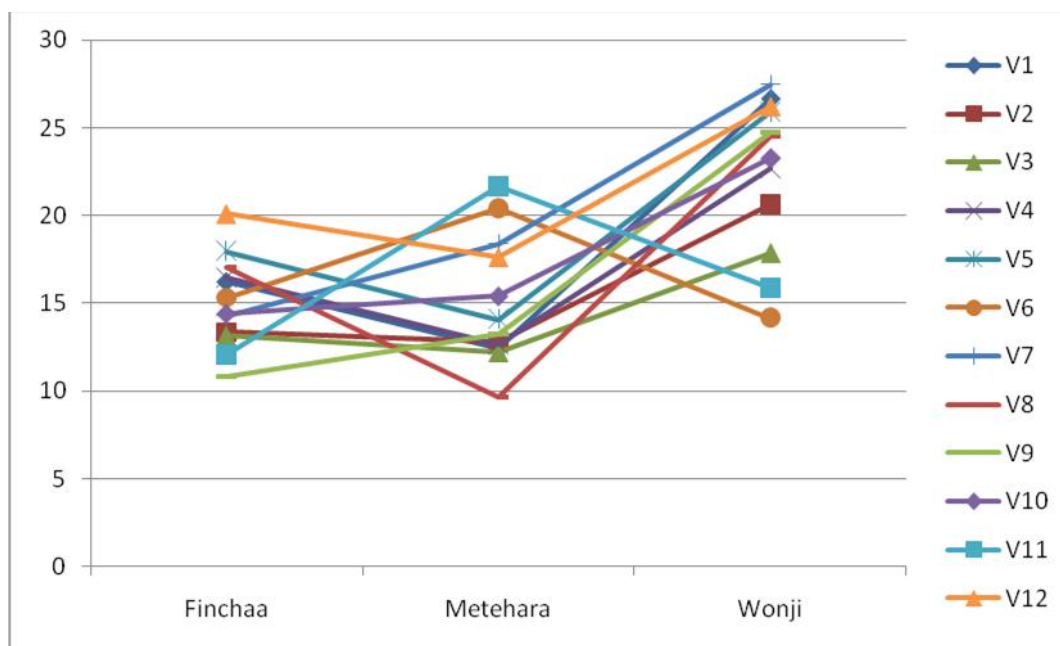


Figure1. Sugar yield performance of 12 sugarcane genotypes tested across three locations

V1 = Key sidanecho; V2 =Tafach shenkora; V3 =Wotete; V4 = key shenkora; V5 = Nech shenkora; V6 = Yebskula shenkora; V7 = Aladi; V8 = Erero; V9 = B4425; V10 = N55/085; V11 = B52298 and V12 = Nco334.

Table 1. Combined analysis of variance for agronomic and sugar quality traits of the 12 sugarcane genotypes

Source	DF	GP	Tiller	MC	PH	DM	SCW	CY	Brix (%)	Pol (%)	SP	SY
Replication	6	59.57	440.37	43.68	0.03	0.04	0.03	516.58	0.79	0.42	0.37	8.84
Location	2	640.02**	83376.16***	2176.70***	0.86***	0.66**	1.06***	29183.78***	38.87***	62.58***	50.51***	661.79***
Genotype	11	414.95ns	15104.70*	4180.36***	0.38***	0.29ns	0.47***	2374.54ns	3.55NS	2.98Ns	3.01Ns	34.07Ns
GXL	22	358.44***	6320.82***	908.91***	0.07***	0.16***	0.12***	2087.01****	4.14***	5.86***	4.89***	43.04***
Error	66	27.6	258.38	55.32	0.02	0.03	0.01	345.43	0.38	0.31	0.45	5.60

Where, GP=Germination percent; Tiller=Number of tillers (ha^{-1}); MC=Number of Millable cane (ha^{-1}); PH=Plant height (m); DM= Cane diameter (cm); SCW=Single cane weight (Kg); CY=Cane yield (t/ha); SP=Sucrose (%);SY= Sugar yield (t/ha); *=significant at ($p \leq 0.05$), ** = significant at ($p \leq 0.01$), and *** = significant at ($p \leq 0.001$), ns=non significant

Table 2. Mean performance of sugarcane genotypes evaluated across environments for yield, yield components and sugar quality traits

Genotype	GP	Tiller	PH	DM	MC	SCW	CY	Brix (%)	Pol (%)	SP	SY
Kay SidaNecho	55.89 ^{ab}	182.57 ^c	2.4 ^a	2.82 ^{abc}	99.43 ^c	1.60 ^{ab}	159.49 ^a	18.34 ^a	16.39 ^a	11.41 ^a	18.43 ^a
Tafach Shenkora	62.22 ^{ab}	213.33 ^{bc}	2.21 ^{abc}	2.87 ^{ab}	103.26 ^c	1.47 ^{abc}	148.85 ^a	17.67 ^a	15.30 ^a	10.39 ^a	15.59 ^a
Wotete	45.11 ^b	180.00 ^c	2.23 ^{abc}	2.59 ^{abcd}	96.51 ^c	1.41 ^{abc}	134.61 ^a	19.65 ^a	16.31 ^a	10.70 ^a	14.42 ^a
Kay Shenkora	60.33 ^{ab}	206.63 ^{bc}	2.31 ^{ab}	2.64 ^{abcd}	107.62 ^{bc}	1.50 ^{abc}	163.24 ^a	18.07 ^a	15.72 ^a	10.71 ^a	17.27 ^a
Nach Shenkora	69.56 ^a	204.48 ^{bc}	2.34 ^{ab}	2.72 ^{abcd}	113.87 ^{bc}	1.49 ^{abc}	171.36 ^a	19.18 ^a	16.56 ^a	11.23 ^a	19.33 ^a
Yebskula Shenkora	54.11 ^{ab}	227.82 ^{abc}	1.89 ^{ef}	2.67 ^{abcd}	138.51 ^{ab}	1.13 ^{cd}	158.88 ^a	17.43 ^a	15.37 ^a	10.61 ^a	16.61 ^a
Aladi	58.11 ^{ab}	259.12 ^{abc}	2.09 ^{bcde}	2.43 ^{bcd}	140.21 ^{ab}	1.29 ^{bc}	178.87 ^a	17.69 ^a	15.92 ^a	11.12 ^a	20.04 ^a
Erero	60.22 ^{ab}	173.37 ^c	2.34 ^{ab}	2.91 ^a	93.75 ^c	1.68 ^a	156.22 ^a	18.04 ^a	15.66 ^a	10.65 ^a	17.06 ^a
B4425	66.78 ^a	302.95 ^a	1.78 ^f	2.38 ^{cd}	156.94 ^a	0.86 ^d	138.35 ^a	18.31 ^a	16.62 ^a	11.69 ^a	16.30 ^a
N55/085	57.44 ^{ab}	224.52 ^{abc}	1.97 ^{cdef}	2.65 ^{abcd}	116.86 ^{bc}	1.36 ^{abc}	158.44 ^a	18.58 ^a	16.20 ^a	11.07 ^a	17.69 ^a
B52298	68.78 ^a	282.57 ^{ab}	1.92 ^{def}	2.64 ^{abcd}	115.69 ^{bc}	1.14 ^{cd}	131.94 ^a	18.44 ^a	17.26 ^a	12.40 ^a	16.53 ^a
NCO334	62.11 ^{ab}	247.7 ^{abc}	2.19 ^{abcd}	2.36 ^d	148.93 ^a	1.23 ^{bc}	181.96 ^a	18.21 ^a	16.52 ^a	11.62 ^a	21.29 ^a
Mean	60.06	225.42	2.14	2.64	119.31	1.35	156.85	18.3	16.15	11.13	17.55
CV (%)	8.7	7.1	6	6.5	6.2	8.3	11.8	3.4	3.5	6	13.5

Where, GP=Germination percent; Tiller=Number of tillers (ha^{-1}); MC=Number of Millable cane (ha^{-1}); PH=Plant height (m); DM= Cane diameter (cm); SCW=Single cane weight (Kg); CY=Cane yield (t/ha); SP=Sucrose (%);SY= Sugar yield (t/ha); Means followed by the same letter in the columns are not significantly different

G x E interaction

Additive Main Effect and Multiplicative interaction (AMMI)

AMMI combines analysis of variance (ANOVA) in to a single model with additive and multiplicative parameters. AMMI bi- plot analysis for sugar yield of sugarcane genotypes is indicated in Figure 2. According to the AMMI model, the genotypes which are characterized by the IPCA1 and IPCA2 scores nearly zero are considered as generally adaptable to all locations (Figure 2). The genotypes close to the origin of the axes are more stable than the most distant ones since they contributed little to the interaction. Combinations of genotypes and environments with the principal components of the same signal have specific positive interactions, whereas combinations of opposing signals have specific negative interactions.

The clones that contributed the least to the GxE interaction and considered stable were b (Tafach Shenkora) which was the most stable followed by l (NCO334), c (Wotete), d (Kay Shenkora) and j

(N55/085). Other than Tafach Shenkora the other genotypes were not strictly close to the origin, but have relatively lower values of IPC1 and IPC2. They were also identified as stable and widely adapted genotypes by univariate stability parameters (Table 3). Therefore these genotypes are considered for wide adaptation. However, these genotypes also had mean sugar yield less than the check variety NCO334 (Table 2). The highest sugar yield and its stability makes this check variety suitable to be recommended for wide adaptation across the tested environments.

The genotype by environment interaction bi-plot of AMMI which captures GXL interaction effects distributed the three locations in to three different sectors (Figure 2). The h, d, and l clones interacted positively with the environment C, because they showed similar signal scores. Using a similar interpretation, the a, i, j, and g clones also had positive specific interaction with environment A and clone k with environment B. A distinct lack of adaptation of the f clone to the A environment was observed in the graph (markers pointing in opposite directions).

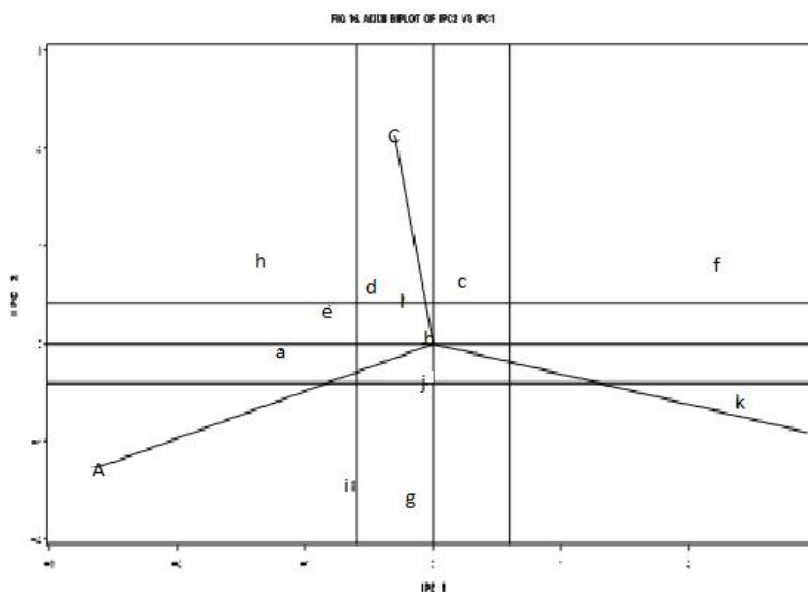


Figure 2. AMMI (Additive Main effects and Multiplicative Interaction) bi-plot analysis for sugar yield.

Where; A, B and C are location Wonji, Metehara and Finchaa respectively. Small letters are genotypes a= Key sidanecho; b=Tafach Shenkora; c =Wotete; d = kay Shenkora; e = Nech Shenkora; f= Yebskula Shenkora; g= Aladi; h= Erero; i = B4425; j= N55/085; k= B52298 and l = Nco334

Genotype + Genotype environment interaction (GGE) bi-plot

GGE biplot displays genotype main effect and G x E interaction effects together that are relevant to

genotype evaluation and must be considered simultaneously for appropriate genotype and test environment evaluation. In this method, genotypes are evaluated for their mean performance and stability and also environmental evaluation, the power to

discriminate among genotypes in target environments. GGE bi-plot for sugar yield of 12 sugarcane genotypes tested over three locations is presented in Figure 3.

A set of lines drawn from the biplot origin and intersecting the sides of the polygon at right angles divided the bi-plot into 6 sectors thereby the bi-plot subdivides the target environment into sub regions (mega-environments). Mega-environments are those sectors which comprise one or more environments. This way the environment markers were grouped into two sectors (i.e. two mega-environments) where sector 1 contained environments A and C and sector 2 had only one environment B (Figure 3). Locations Wonji (A) and Finchaa (C) fell in the same sector and were positively correlated as the angle between the two is less than 90° . There was no correlation between location A (Wonji) and B (Metahara) because the angle between them was more than 90° . Low correlation was also observed between location B (Metahara) and C (Finchaa). In agreement with the results reported by Yan (2002), the genotype(s) vertex in these sectors may have higher or the highest yield compared to other parts in all environments. The genotypes located within the polygon were the least responsive to the stimuli of the environments (Figure 3). That is to say that these genotypes within the polygon had near similar performance across locations.

The genotype on the vertex of the polygon, contained in a mega-environment, had the highest yield in at least one environment and was one of the best-performing genotypes in the other environments (Yan and Rajcan, 2002). Accordingly, genotype NCO334 (l) was the winning genotype in environments A (Wonji) and C (Finchaa). In the environment B (Metahara) genotypes Yebskula Shenkora (f) and one of the check B52298 (k) were positioned on the vertex of the polygon and were the winning genotypes in this environment.

The d (Kay Shenkora), h (Erero) and c (Wotete) genotypes generated the other polygon vertices for sugar yield, but no group of environments was formed within this sector comprising these clones, which were considered unfavorable to the groups of tested environments, with low productivity. Likewise, the genotypes located within the sectors delimited by them were also unfavorable for recommendation.

The most productive genotype was l (NCO334), the check variety, followed by g (Aladi), and e (Nech Shenkora). The least productive were genotypes b (Tafach Shenkora) and c (Wotete) because they were located further away in the opposite direction. The genotype near the center of the bi-plot j (N55/085) can be considered to be stable (Figure 3). It was also shown by AMMI as stable and above average performance and can be a suitable candidate for wide adaptation.

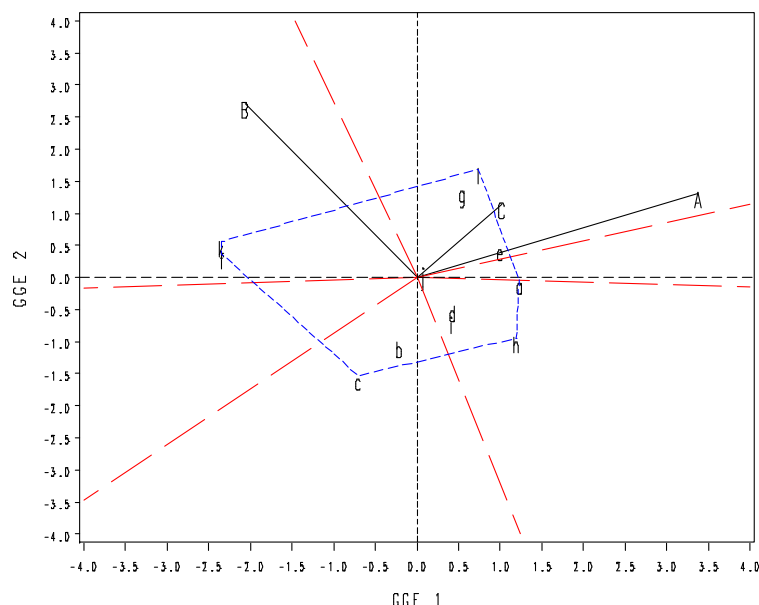


Figure 3. Genotype + genotype environment interaction bi-plot for sugar yield of 12 sugarcane genotypes. Where; A, B and C are environments Wonji, Metehara and Finchaa respectively. Small letters are genotypes a= Key sidanecho; b=Tafach Shenkora; c =Wotete; d = key Shenkora; e = Nech Shenkora; f= Yebskula Shenkora; g= Aladi; h= Erero; i = B4425; j= N55/085; k= B52298 and l = Nco334.

Univariate Stability Analysis

Different stability estimates were determined for sugar yield to examine consistency of performance of genotypes across the test environments (Table 3). In this table mean sugar yield of the 12 sugarcane genotypes and their stability as measured by five univariate stability parameters are presented. Among the 12 sugarcane genotypes NOC334 (21.30 t/ha), Aladi (20.04), Nech Shenkora (19.33t/ha), Key sidanecho (18.43t/ha) and N55/085(17.69 t/ha) gave above average sugar yield. The remaining genotypes gave sugar yield below the grand mean. A stable genotype tends to maintain a constant yield across different environments (Dyke et al., 1995). Therefore genotypes with above average yield performance and are stable by the stability parameters are preferred. The various univariate statistical models to measure yield stability of genotype performance across environments are discussed below.

Wrinkle's ecovalence (Wi)

According to Wrinkle (1962) genotypes with low ecovalence have smaller fluctuation across

environments and are therefore stable. These genotype has limited differential response to the changes in the growing environments. Accordingly, Tafach Shenkora, N55/085, NCO334, Wotete and Kay Shenkora were found to be stable. Among these genotypes, only N55/085 and NCO334 gave above average sugar yield and can be recommended for wide adaptation.

Francis and Kannenberg's coefficient of variability (CV)

According to Francis and Kannenberg's coefficient of variability, stable genotypes are those with below average CV and with above average yield. In this regard genotypes with their CV below the average (30.84) were Yebskula Shenkora, NCO334, Wotete, N55/085 and Tafach Shenkora (Table 3 and Figure 4). As can be observed clearly from Figure 4 which depicts the genotypes sugar yield performance and their CV in different quadrants, only NCO334 and N55/085 fulfilled the criteria with their yield performance above the grand mean and with lower CV. This also holds true with measurement of Wrinkle's ecovalence.

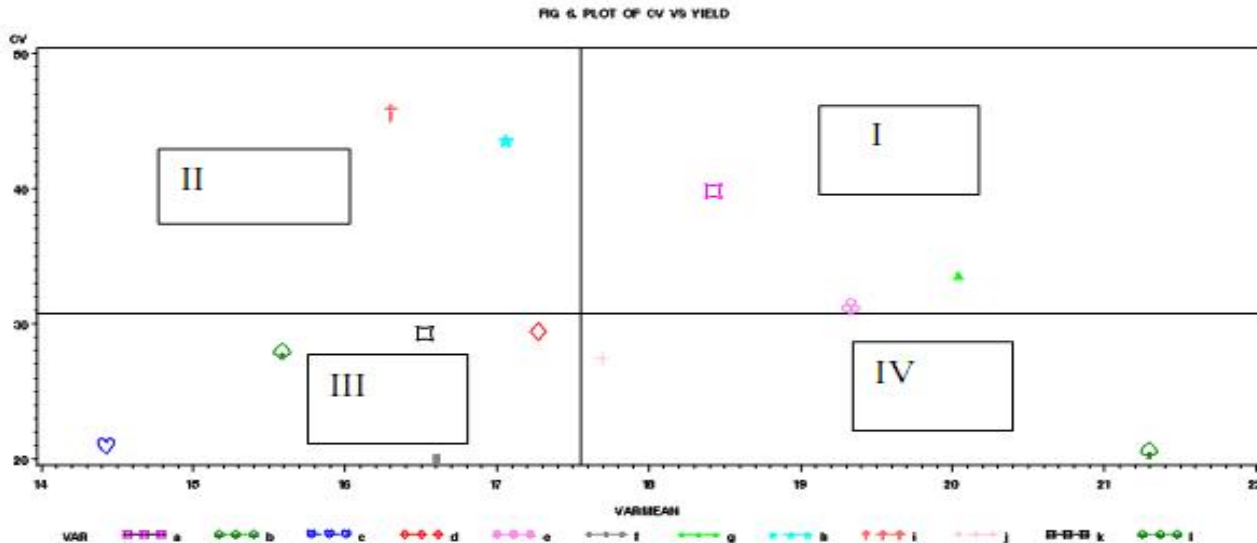


Figure 4. Graph of Francis and Kannenberg for CV and mean sugar yield of 12 sugarcane genotypes averaged over three locations

Key: letters attached to each figure represent genotypes; a = Kay Sidanecho; b =Tafach Shenkora; c =Wotete; d=Kay Shenkora; e=Nach Shenkora; f=Yebskula Shenkora; g=Aladi; h=Erero; i = B4425; j= N55/085 ; k= B52298 and l = NCO334.

Table 3 Stability by five parameters of 12 sugarcane genotypes tested at three locations in 2016

S/No	Genotype	Mean	R	Wi	R	CV	R	Pi	R	Bi	R	S ² d	R
1	Kay Sidanecho	18.43	4	22.77 ^{**}	9	39.86	10	16.81	5	1.66	9	6.83 [*]	6
2	Tafach Shenkora	15.59	11	0.14	1	28.08	5	28.50	9	1.02	2	0.13	1
3	Wotete	14.42	12	3.75	4	21.01	3	38.13 [*]	12	0.69	5	0.14	2
4	Kay Shenkora	17.27	6	7.45	5	29.46	7	19.53	6	1.10	3	7.05 [*]	7
5	Nach Shenkora	19.33	3	11.57 [*]	6	31.28	8	10.76	3	1.34	6	7.39 [*]	8
6	Yebskula Shenkora	16.61	8	95.93 ^{***}	12	20.08	1	33.64 [*]	11	-0.50	12	12.96 ^{**}	10
7	Aladi	20.04	2	17.65 ^{**}	7	33.62	9	7.41	2	1.49	7	8.68 [*]	9
8	Erero	17.06	7	36.45 ^{***}	10	43.57	11	27.17	7	1.51	8	26.96 ^{***}	11
9	B4425	16.30	10	21.67 ^{**}	8	45.61	12	27.16	8	1.71	10	3.19	5
10	N55/085	17.69	5	1.14	2	27.44	4	14.84	4	1.13	4	0.56	3
11	B52298	16.53	9	94.3 ^{***}	11	29.34	6	33.13 [*]	10	-0.14	11	46.29 ^{***}	12
12	NCO334	21.30	1	2.89	3	20.74	2	3.01	1	0.99	1	2.89	4
	Mean	17.55				30.84							

Where; mean = mean sugar yield (t/ha); Wi = Wricks ecovalence; CV = coefficient of variation; Pi = Genetic superiority index; Bi = Linear regression coefficient (slope); S²d = Mean square deviation from regression; R = Rank of genotypes for CV, Wi, Pi and S²d from lowest to highest according to parameter estimates of stability

Mean square deviation from regression

According to Eberhart and Russell (1966), a regression deviation (S^2_d) near to zero indicates average stability. From Table 3 it can be observed that the values of S^2_d for genotypes Tafach Shenkora, Wotete, B4425, N55/085 and NCO334 did not significantly differ from zero and were considered stable genotypes. From these genotypes only N55/085 and NCO334 had sugar yields (17.77 and 21.30 t ha⁻¹, respectively) higher than the grand mean and can be recommended for wide adaptation.

Regression coefficient (bi)

As described by Finlay and Wilkinson (1963), in the regression coefficient (bi) genotypes with their slope not significantly different from unity are stable. From Table 3 and Figure 5, although the slopes varied from

-0.51 (Erero) to 1.71 (B4425), none of the slopes significantly deviated from unity. However genotypes such as Kay Sidanecho ($b=1.66$), Aladi ($b=1.50$), Erero ($b=1.51$) and B4425 ($b=1.71$) were relatively more responsive to improving environment (Figure 5). Genotypes such as Wotete ($b=0.70$) and NCO334 ($b=0.99$) are relatively less responsive to improvement in environmental conditions. The genotypes Yebskula Shenkora and one of the check B52298 with their negative slopes negative (-0.50 and -0.14, respectively) showed low sugar yield performance as environmental conditions improve (Figure 5 and Table 3). These genotypes were the highest yielders under poor environments. NCO334, Tafach Shenkora, Kay Shenkora, N55/085 and Wotete had the smallest deviation from regression and can be declared to be stable. Out of these genotypes, NCO334 and N55/085 had sugar yield higher than the grand mean and could be recommended for wide adaptation.

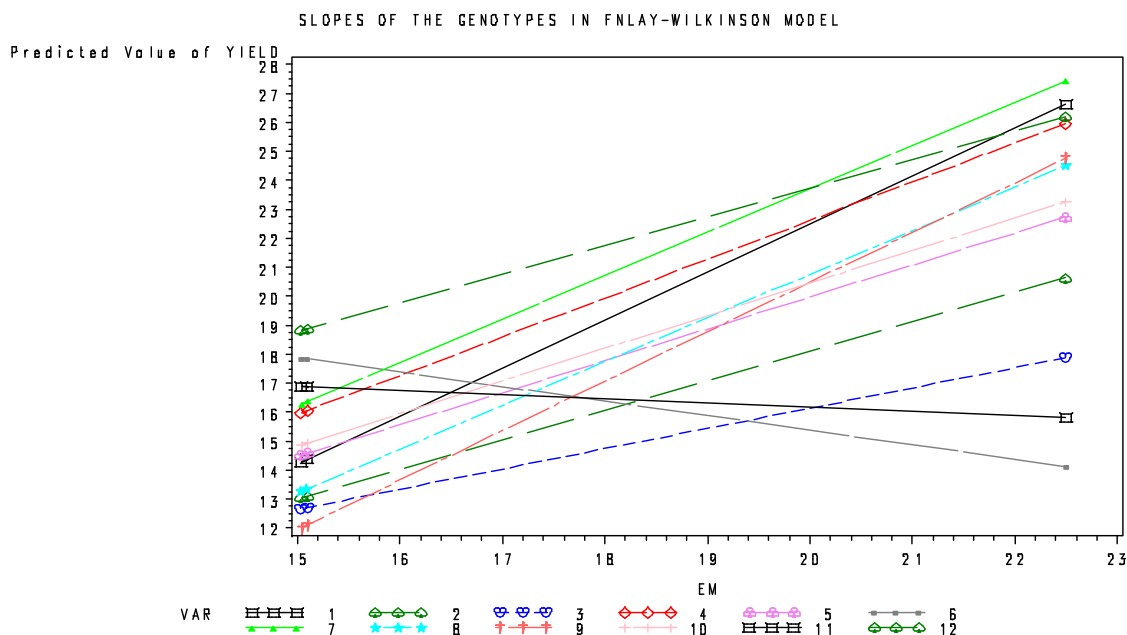


Figure 5. Graph of liner regression model for 12 sugarcane genotypes

Where V1=Kay Sidanecho; V2=Tafach Shenkora; V3 =Wotete; V4=Kay Shenkora; V5 =Nach Shenkora; V6 = Yebskula Shenkora; V7=Aladi; V8=Erero; V9=B4425; V10= N55/085; V11= B52298 and V12 = NCO334.

Lin and Binns Superiority measure of genotype performance (pi)

According to Lin and Binns (1988), Pi characterizes genotypes by associating stability and productivity and defines a superior genotype with performance near the maximum in various environments. Genotypes

NCO334, Aladi, Nach Shenkora and N55/085 had the smallest Pi value and were the most stable (Table 3). These genotypes also gave sugar yields higher than the grand mean. The rank of (Pi) and mean yield were almost similar (Table3). This indicates that cultivar performance measure is more an indicator of yield performance and not an indicator of stability.

Generally from the univariate stability estimates it was observed that the two genotypes NCO334 and N55/085 were the most stable and highly productive in terms of sugar yield to be considered for cultivation in the studied three environments. These stability measurements were used in determination of stability of sugarcane varieties and other crops (Srivastava et al., 1999; Queme et al., 2001; Queme et al., 2005; Adugna, 2008).

Correlation among Stability Parameters

Pearson correlation coefficient was used to determine the closeness of relations between each pair of the different stability parameters (Table 4). Mean yield

was positively correlated with Pi (0.930***), with Wricke's ecovalence ($r=0.055$) and with the slope ($r=0.231$). It was negatively correlated with coefficient of variability (-0.077) and S^2d (-0.209).

Wricke's ecovalence was positively correlated to all stability parameters; with CV and Pi ($r=0.308$), bi ($r=0.923***$) and S^2d ($r=0.853***$). The significant positive correlation with S^2d and bi indicates that the two stability parameters were equivalent for stability purpose. S^2d and bi were positively correlated with each other. The use of mean yield, bi, Pi and Wi as a tool to select would favor simultaneous development of stable and high yielding genotypes.

Table 4 Correlation of stability parameters

	Mean yield	Wi	CV	Pi	Bi	S^2d
Mean yield		0.055	-0.077	0.930***	0.231	-0.209
Wi			0.308	0.308	0.923***	0.853***
CV				-0.209	0.308	0.268
Pi					0.427	0.021
Bi						0.678**
S^2d						

Note; Wi = Wricke's ecovalence; Cv = Francis and Kannenberg's (1978) coefficient of variability; S^2d = Means square deviation from regression; Pi = Lin and Binns's (1988) cultivar superiority index; bi=Wilkinson (1963) regression coefficient.

Based on their high correlation and ranking of genotypes which corresponds to their performance, the best procedure to select most stable genotypes appeared to be Wricke's ecovalence, slope (bi) and mean deviation from regression S^2d . Correlation among the different stability estimates were reported in sugarcane Purchase, 1997; Queme et al., 2001; Queme et al., 2005).

4. Summary and Conclusion

The present study showed the presence of significant G x L interaction for the traits considered. This signifies the need to select genotypes well adapted to specific environment and exceptionally for broadly adapted genotypes. The performance of sugarcane genotypes was analyzed using multivariate methods and univariate stability estimates. The genotypes Aladi, Nach Shenkora, Kay Sidanecho, N55/805, Kay Shenkora and Erero gave higher cane and sugar yield

across locations at par with the two checks and have mean advantage of the rest genotypes. The genotypes N55/085 and NCO334 were identified as stable and widely adapted genotypes by five univariate stability parameters and also by AMMI analysis. However, GGE identified NCO334 as specifically adapted to Wonji and Finchaa while B52298 and Yebskula Shenkora were specifically adapted to Metehara conditions.

Competing Interests

The authors declare that they have no conflict of interests.

Acknowledgments

The authors are grateful for the financial grant of Sugar Corporation of Ethiopia.

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Quick Response Code	
DOI: 10.22192/ijarbs.2020.07.01.003	

How to cite this article:

Abebech Seife and Esayas Tena. (2020). Genotype x environment interaction and yield stability analysis of sugarcane (*Saccharum officinarum* L.) genotypes . *Int. J. Adv. Res. Biol. Sci.* 7(1): 14-26.

DOI: <http://dx.doi.org/10.22192/ijarbs.2020.07.01.003>