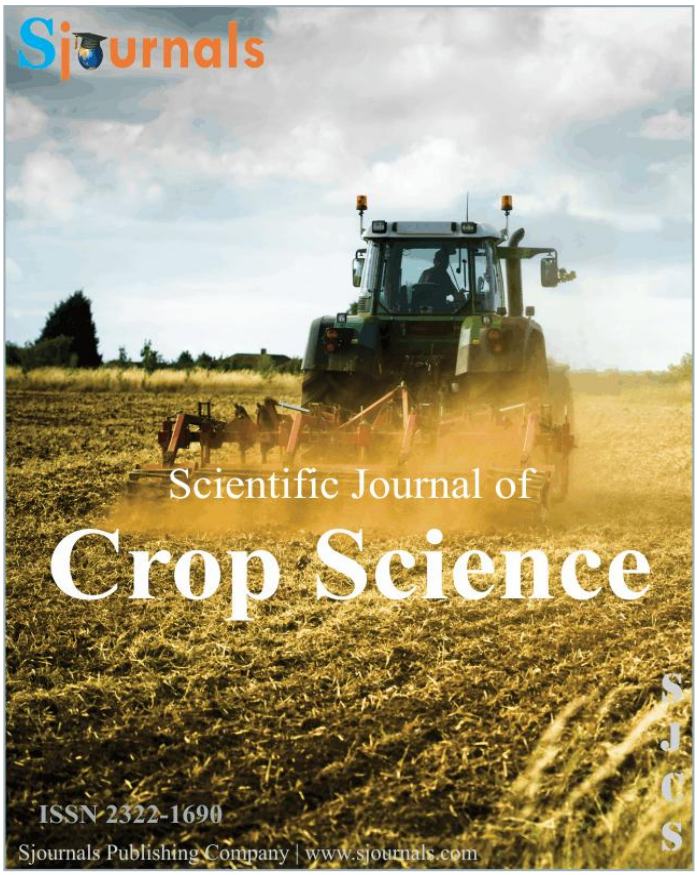

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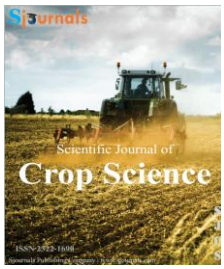

Original article

Genotype x environment interaction and genotype evaluation for yield, yield components and qualities in sugarcane (*Saccharum Spp.*), Ethiopia

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ABSTRACT

The presence of genotype x environment interaction (GEI) and the limited knowledge on the relationships among production environments complicate selection of superior varieties in sugarcane. For this reason, studying about the nature of GEI, genotype evaluation and classification of the production environments in to distinct mega environments is very important in sugarcane breeding program. The study was conducted to investigate the nature of genotype x environment interaction, classify environments in to mega environments and evaluate genotypes based on yield performance and stability. Forty-three genotypes along with six standard varieties were evaluated across location and over crop years using simple lattice design. Data of cane yield, cane yield components and yield qualities were subjected to analysis of variance (ANOVA). Results from ANOVA declared the importance of GEI under Ethiopian agro climatic conditions. When the data was analyzed using the GE model, the f-values were inflated and the genetic variation was under estimated. Thus, for multi-environment trials conducted across locations and over seasons, data analysis based on the GLC model would be appropriate. The genotype + genotype x environment interaction (GGE) bi-plots divided the target environment in to distinct mega environments where a repeatable genotype x

location interaction was observed for recoverable sucrose% and sugar yields. Moreover, GGE bi-plots identified introduced genotypes that have better broad and specific adaptations than the commercial varieties and can be commercially exploited according to their respective regional niche. Moreover, we recommend a breeding strategy for specific adaptation in future sugarcane breeding programs in Ethiopia.

Abbreviations: AEC-Average Environment Coordinate; ATC-Average Tester Coordinate; GGE-Genotype+Genotype by Environment Interaction; GEI-Genotype by Environment Interaction

1. Introduction

Genotype by environment interaction (GEI) is one of the constraints that has a predominant impact on yield and quality of sugarcane and affect the selection efficiency of superior genotypes in sugarcane (Kimbeng et al., 2009). Moreover, GE has differential impact of GxE interaction for quality and cane component traits in sugarcane (Mulema et al., 2008; Ftwi et al., 2017). On the contrary, significant effects of GE interaction for commercial cane sugar (CCS%) and sugar yield t ha^{-1} were reported due to locations, years, genotypes, years by locations and locations x genotypes interaction (Kimbeng et al., 2009; Khan et al., 2013; Tahir et al., 2014). The impact of GEI is differential sugarcane traits which necessitate the inclusion of all traits in multi environment trials in sugarcane. Kang (2002) indicated the effect of GEI in sugarcane is more pronounced for quantitatively inherited traits, such as cane and sugar yields. Similarly, Tahir et al. (2014) indicated that most of the yield components of sugarcane, such as milleable stalk number, and milleable stalk height, stalk diameters and cane yield are highly influenced by the environmental factors than the quality traits.

For trials conducted across locations and over crop years, the components of GEI impose differential impact on sugarcane traits. Productivity declines over successive plant cane crops and subsequent ratoon crops as genotypes differ in their ability to maintain high yields in older ratoon crops (Ramburan et al., 2014). This aggravates the complexity of GE of genotype x location (site), location x crop year in sugarcane (Queme et al., 2010). Moreover, Kimbeng et al. (2009) suggested genotype by location (G x L), genotype by year (G x Y), genotype x location x year (G x L x Y) interaction affects cane yield and cane components in sugarcane. Results reported by Jackson and Hogarth (1992) also indicated genotype x location (GxL) interactions is of greater importance than other interactions, such as genotype x years (G x Y) and genotype x location x years (G x L x Y), which implies testing on several locations is important and testing multiple crops on same location was found to be the reason of minimal gain. This phenomenon demands the GEI to be partitioned into its components; genotype by location (G x L), genotype by crop type (G x C) and G x L x C interactions.

In any sugarcane production command area, a multiple mega environments can be formed due heterogeneity of agro-climatic conditions. As suggested by Gauch and Zobel (1997) mega- environment (ME) may be defined as a portion of a crop species' growing region with a homogeneous environment that causes some genotypes to perform similarly. Using GGE bi-plots, Ramburan and Zhou (2011); Sandhu et al. (2014) and Luo et al. (2015), reported different mega environments in sugarcane under South African, Indian and China agro-ecological conditions, respectively. However, the mega-environments identified may not necessarily be grouped according to any geographical zoning (Ramburan and Zhou, 2011). This could be due the perennial nature of the sugarcane, as an “environment” in sugarcane is often defined as a site x crop year combination where the ratooning has confounding effect (Ramburan, 2012). Moreover, the possibility of formation of distinct mega environment depends on the nature of the target environment for sugarcane production, which in turn depends on the difference of environments for seasonal and site covariates. Under Ethiopian agro-ecological conditions, both seasonal and site covariates are important in separating environments (Ftwi et al., 2017).

Sugarcane is commercially grown in Ethiopia at Wonji Sugar Estate by a Dutch company in 1955 on an initial area of 5,000 ha and currently above 50,000 hectares land is under cultivation (Ethiopian Sugar Corporation, 2017). Ethiopia is one of the potential sugarcane growing countries as the agro ecology of the country is suitable for

sugarcane cultivation. However, the statistical data reported by FAOSTAT (2014) indicated that the productivity of the crop over the 50 years (1977 to 2014) is declining. This could be mainly attributed to lack improved varieties that are yielder, resistant to biotic stresses and tolerant to abiotic stresses. For about 50 years, only six commercial varieties are under cultivation where three of the dominant varieties cover above 50% of the command area. The increasing population and industrialization increases the sugar demand in the country. For this reason, Ethiopia is building additional sugar projects. Development and inclusion of improved sugarcane variety is the major and important step to improve the productivity of the sugar industry. The Ethiopian Sugar Corporation, Research and Development Center, devised a durable sugarcane breeding strategy to improve the variability of sugarcane germplasm by introducing sugarcane genotypes from other potential countries (Feyisa et al., 2014; Mebrahtom, 2017), selecting promising varieties from the existing conservation (Abiy et al., 2014), performing local collections (Esayas et al., 2016) and establishing advanced sugarcane breeding programs (Ethiopian Sugar Corporation, 2017).

The present study focuses on the evaluation of introduced genotypes from different potential sugarcane growing countries. As the yield performance and stability background of the introduced genotypes is unknown, it should be tested under different agro-ecology of the country. Moreover, under Ethiopian agro-ecological conditions, significant and complex GE is reported in sugarcane where both seasonal and site covariates were very important (Ftwi et al., 2017). Furthermore, sugarcane production environments in Ethiopia are not substantially grouped in homogenous groups of environments and similar research experiments are routinely conducted in similar environments, which are resource consuming. Therefore; this study was conducted to investigate the nature of genotype x environment interaction and its repeatability, classify the sugarcane production environments into homogenous groups or mega environments and evaluate the performance of genotypes for yield and yield stability, yield components and yield qualities.

2. Materials and methods

2.1. Description of test environments and genotypes

Eighteen (18) environments (METs) were conducted across five locations or sugarcane production environments (Wonji Sugar Estate, Metahara Sugar Estate, Tendaho Sugar Estate, Finchaa Sugar Estate and Belles Sugar project) and over crop years (2013-2014, 2014-2015 and 2015-2016 crop seasons). The plant cane crop trials (C1 and C2) across all locations were sequentially (on different years) planted and the two successive ratoon crops were raised from the first plant cane crop (C1). The trials are briefly described as shown in Table 1.

Table 1
Descriptions of environments (Locations and crop years) using site factors and seasonal covariates.

Environments		Site factors			Long years seasonal covariates					Seasonal covariates recorded at harvest				
					Pan (mm)	Temperature (C°)		Relative humidity (%)		Pan (mm)	Temperature (C°)		Relative humidity (%)	
Location	Crop year (Trials)	Soil type	Longitude Latitude	Altitude (m.a.s.l)	AEP	Min	Max	Max	Min	AEP	Min	Max	Max	Min
Wonji	C1W	Vertisol	8°31′ N and 39°12′ E	1500	6.52	28.03	14.18	82.32	36.51	6.33	28.3	11.7	86.1	66.85
	C2W									6.31	28.8	9.6	83.6	65.15
	R1W									7.5	29.1	6.58	77.5	60.8
	R2W									6.71	28.73	9.29	82.40	64.27
Finchaa	C1F	Luvisol	9°30′ - 10°00′ N and 37°15′ - 37°30′ E	1350-1600	4.9	30.66	14.72	83.82	24.83	4.58	30.4	14.63	86.3	63.2
	C2F									5.05	31	13.64	85.5	63
	R1F									5.65	31.5	13.25	84.5	57.37
	R2F									5.09	30.97	13.84	85.43	61.19
	C1FCIRAD											NA		
	R1FCIRAD											NA		
Metahara	C1M	F2 Soil fertility unit	08°54′ N and 39°55′ E	947	6.9	32.97	17.36	77.41	27.57	6.7	33.26	16.6	84.3	56.15
	C2M									6.8	32.37	17.3	81.3	75
	R1M									6.97	31.8	17.95	84.4	80
	R2M									6.82	32.48	17.28	83.33	70.38
Belles	C1B	Vertisol	11°30′ N and 36°41′ E	1110	9.11	27.09	13.61	62.21	34.15	5.52	30.56	17.22	86.72	68.16
	C2B									7.23	31.88	13.79	78.33	61.27
	R1B									12.2	34.6	16	69.44	54.44
Tendaho	C2T	Fluvisol	110 20′ - 110 50′ N and Longitude 400 55′to 410 E	340-400	6	NA	NA	NA	NA	6.5	37	23.2	67	56

* PC1=First Plant Cane Crop Trial; PC2=Second Plant Cane Crop Trial; R1=First Ratoon Crop Trial; RF=Rainfall; AT=Average Temperature; AEP=Average Pan Evaporation; ARH=Relative Humidity; SN=Serial Number; C1FCIRAD=Plant Cane Yield Trial for CIRAD Varieties Introduced at Finchaa; R1FCIRAD=First Ratoon Yield for CIRAD Varieties Trial at Finchaa; Sugar Estate=Old Sugar Factory which is under production; Sugar Project=New project which is under establishment and not started sugar production; NA=Not Available.

2.2. Description of test genotypes

Forty-three (43) introduced sugarcane genotypes along with six commercial varieties were included and evaluated (Table 2). Of which, 36 genotypes were introduced from France, where 21, 3, 5, 7 and 7 genotypes were introduced from France, Philippines and Barbados, USA and Cuba origin. The rest of the 6 were the locally grown varieties which had been introduced in to Ethiopia from India, South Africa and Barbados before 50 years. Genotypes other than the initial letter of PG are advanced clones introduced at the final of stages of performance evaluation while the genotypes with the initial letter of PG were clones passed the initial evaluation stages in CIRAD (France). Details of the test genotypes are presented in Table 2.

Table 2
Description of 43 introduced sugarcane genotypes and 6 commercial varieties.

Code	Genotypes (G)	Origin	Code	Genotypes (G)	Origin
1	PSR97 092	PHILSURIN (Philippines)	26	VMC95 212	USA
2	DB70047	WICSCBS (Barbados)	27	NCO-334	South Africa
3	DB66 113	WICSCBS (Barbados)	28	FG03 418	CIRAD (France)
4	FG06 700	CIRAD (France)	29	CO449	India
5	FG06 729	CIRAD (France)	30	FG03 204	CIRAD (France)
6	PSR97 087	Cuba	31	FG02 553	CIRAD (France)
7	PSR97 051	PHILSURIN (Philippines)	32	FG03 103	CIRAD (France)
8	HO95 988	USDA (Louisiana)	33	FG03 318	CIRAD (France)
9	Cp99 1534	USDA (USA)	34	FG04 708	CIRAD (France)
10	FG04 829	Cirad (France)	35	FG04 705	CIRAD (France)
11	DB71 060	Cirad (France)	36	FG02 551	CIRAD (France)
12	TCP93 4245	USDA (Texas/Canal Point)	37	FG03 173	CIRAD (France)
13	CP001 252	USDA (USA)	38	FG04 187	CIRAD (France)
14	VMC95 173	USA	39	FG03 372	CIRAD (France)
15	FG03 447	CIRAD (France)	40	FG03 214	CIRAD (France)
16	CO 740	India	41	C86-56	Cuba
17	CP99 1894	USDA (USA)	42	SP70-1284	Cuba
18	FG03 425	CIRAD (France)	43	C86-165	PHILSURIN
19	FG05 408	CIRAD (France)	44	B78-505	Barbados
20	FG03 520	CIRAD (France)	45	C132-81	Cuba
21	FG04 754	CIRAD (France)	46	C86-12	Cuba
22	FG04 466	WICSCBS (Barbados)	47	C90-501	Cuba
23	FG03 526	CIRAD (France)	48	B52-298	Barbados
24	Mex54/245	Mexico	49	CO-678	India
25	FG03 396	CIRAD (France)			

* FG=CIRAD/Guadeloupe (FRANCE); PSR=PHILSURIN (Philippines); CP=USDA (Canal Point/Florida), USA; TC=USDA (Texas/Canal Point), USA; HO=USDA (Houma, Louisiana); USA, BD=WICSCBS (Barbados/Guyana).

2.3. Experimental design and layout

The experimental design was a 7 x 7 simple lattice square. Each experimental plot consists of six rows (four test rows and two border rows) of 8.7 m width and 6 m length (plot area=52.5 m^2) and total experimental area of used for each location was 0.78 hectare. At planting, 30 two budded sets (end to end) were used for each row of 6 m length and 1.45 m width while the spacing between two adjacent rows was 1 m. All recommended agronomic and cultural practices were uniform to raise the crop across all production environments and crop years.

2.4. Data collection

Sprout% could be calculated the ratio of the number of two-budded sets planted (two/three-budded sets) to the numbers of two/three-budded sets that grow health sprout and multiplied by 100. The numbers of health tillers should also be counted from each plot at 90 and 120 days after planting date and are converted to hectare basis (ha^{-1}). At harvest, milleable stalk population are counted from the four central test rows of each plot and

converted on hectare basis (ha^{-1}). On sample basis, data for numbers of internodes per/stalk, milleable stalk diameter (cm) and milleable stalk height (cm) measurements are collected from 20 randomly selected milleable stalks per plot. On sample basis, about 20 randomly selected milleable stalks should be harvested for fiber and juice analysis. 20 randomly selected milleable stalks are put through a cutter grinder and the ground sample is then placed into a fiber machine where it is washed to remove brix (soluble solids) and fine dirt. The sample is then dried using hot air and weighed. The final weight divided by the initial weight provides a fiber percentage. Example: Original weight of 500 grams, final weight of 75 grams. Fiber percentage = (final weight / original weight) x 100. For juice analysis selected milleable stalks per plot are harvested and milled with Josko and the juice quality is analyzed at Laboratory. Pol in cane = pol in juice x (100-(fiber%+5))/100 and Brix in cane = Brix in juice x (100-(fiber%+3))/100 while Purity of cane can be computed as (pol in cane/brix in cane) x 100.

The milleable stalks from the four central rows per plot are hand trashed to remove the leaves and hand topped at the natural breakpoint of sugarcane stalk. For cane yield estimation, the milleable stalks harvested from the central four test rows were weighted using digital scale balance; the cane weight per plot (kg) was determined and extrapolated to ton ha^{-1} m^{-1}**.** As described by Berg (1972), recoverable sucrose (%) can be estimated as RS% = [Pol % - (Brix - Pol %) 0.61] 0.75), where 0.61 = non-sugar factor, representing the amount of sucrose lost in final process and 0.75 = cane factor, representing the correlation factor between theoretical yields of molasses mixed juice and primary juice for the same genotype and the same cut of cane determined by milling test. Sugar yield (white sugar) can be estimated as the product of cane yield per hectare and average estimated recoverable sucrose content (%) as Sugar yield = [Cane Yield (t/ha) x recoverable sucrose %]/100. As the plant cane crops and ratoon crop were harvested at 17 and 14 months cane age respectively, data for cane and sugar yield were converted to tons $ha^{-1}m^{-1}$ (tons per hectares per month) to bring the crops types to the same productivity unit.

2.5. Data analysis

The block, location and crop year effects were considered random while genotype effect was considered as fixed. Yield, cane yield components and quality data were subjected to analysis of variance. Genotypic means were adjusted using PROC MIXED of SAS, Version 9.2 (SAS, 2009). The LSD and CV were determined based on the average standard error differences of all pair wise mean comparisons and were computed using META-R (2015) V.2.0 CIMMYT software as suggested by Vargas et al. (2013). The two-way mean tables for cane yield, recoverable sucrose% and sugar yield (Table not presented) were analyzed using GGE bi-plot as adopted by Yan (2003) to see average cultivar performance, site representativeness, yield stability and site discriminating ability. In the "which-won-where" and 'discriminating vs. representative" view of the GGE bi-plot, data were not transformed (transform=0), not scaled (scaling=0), environment centered (centering=2) and the bi-plot was based on environment-focused singular value partitioning (SVP=2). The same thing was done in the GGE bi-plot for genotype evaluation except the bi-plot was based on genotype-focused singular value partitioning (SVP=1). The GGE bi-plot was constructed using Gen Stat 17th Edition (Payne et al., 2014).

3. Results and discussion

3.1. Analysis of variance

Means squares obtained from analysis of variances for yield, yield components and qualities are presented as shown in Table 3. Results of the present study indicated the crop year effect was highly significant ($p<0.01$) for number of tillers, milleable stalk height, milleable stalk population, cane yield and sugar yield while the location effect was highly significant ($p<0.01$) for all traits studied except for milleable stalk population, brix%, pol% and recoverable sucrose%. The genotype and LxC interaction effects were also highly significant for all traits. Regarding to the components of genotype x environment interaction, the GxL interaction was significant ($p<0.05$) for number of tillers, milleable stalk height, milleable stalk population, cane yield, brix% and sugar yield while the GxC interaction effect was highly significant ($p<0.01$) for number of tillers and milleable stalk height. Except for milleable stalk diameter, cane and purity%, the GxLxC interaction was highly significant ($p<0.01$) for all traits. Results from the analysis of variance conducted based on the GE model revealed that the environment, genotype and the interaction effects were all highly significant ($p<0.01$) for all traits studied (Table 3).

Percent of the total treatment sum of squares accounted by different effects were also computed for cane yield, recoverable sucrose% and sugar yield under both models (Table 3). In cane yield, the crop year, location, LxC,

genotype, GxL, GxC and GxLxC effects accounted for 14, 35, 5.5, 6.9, 5.7, 3.3 and 7.5% of the treatment sum of squares, respectively while 0.3, 8.9, 12, 26, 15.7, 12.3 and 24.55 of the total treatment sum of squares in recoverable sucrose% were accounted by the crop year, location, LxC, genotype, GxL, GxC and GxLxC effects, respectively. For sugar yield, the crop year, location, LxC, genotype, GxL, GxC and GxLxC effects accounted for 1.1, 44.3, 11, 10, 10.54, 6.33 and 16.61% of the total treatment sum of squares, respectively. Based on the GE model, the environmental effect accounted for the largest variation of 64.85, 57.71 and 55.69% for cane yield, recoverable sucrose% and sugar yield, respectively while the genotype effect accounted for 13.26, 10.3 and 8.3 of the variability in cane yield, recoverable sucrose and sugar yield, respectively, which is the smallest. Moreover, the GEI explained 30.23, 28.84 and 29% of the total variability in cane yield, recoverable sucrose% and sugar yield, respectively.

Table 3

Means squares of 49 sugarcane genotypes (G) evaluated across locations (L) and over crop years (C) for Yield (tons $ha^{-1}m^{-1}$), Yield Components and Yield qualities.

						The GLY Model					
Sources of variation	**DF**	**NT (ha^{-1})**	**MSD (cm)**	**MSH (m)**	**MSP (ha^{-1})**	**Cane yield (t $ha^{-1}m^{-1}$)**	**Brix in juice**	**Pol% in juice**	**Purity %**	**RS %**	**Sugar yield**
Crop year (C)	3	$1.44 \times 10^{12*}$	1.88^{ns}	8.83^{*}	3.74×10^{10ns}	928.06^{*}(14)	18.22^{ns}	1.65^{ns}	100.83^{ns}	1.5^{ns}(0.3)	0.66^{*}(1.1)
Locations (L)	4	1.09×10^{11ns}	5.63^{*}	81.31^{*}	2.51×10^{10ns}	1731.4^{**}(35)	214.76^{ns}	103^{ns}	933.65^{*}	36^{ns}(8.9)	20.19^{**}(44.3)
L x C	7	$1.4 \times 10^{11**}$	0.67^{ns}	3.97^{**}	$1.37 \times 10^{10**}$	155.1^{**}(5.5)	48.87^{ns}	34.31^{**}	110.40^{**}	27.6^{**}(12)	2.88^{**}(11)
Replication	15	$5.16 \times 10^{9**}$	0.62^{**}	0.61^{**}	6.06×10^{8ns}	13.12^{*}	2.79^{ns}	8.32^{ns}	17.90^{*}	3.12^{ns}	0.22^{*}
Block (adj)	180	$1.3 \times 10^{9*}$	0.05^{**}	0.09^{ns}	$4.42 \times 10^{8*}$	4.03^{ns}	1.52^{*}	3.39^{*}	5.08^{*}	1.22^{**}	0.08^{ns}
Genotypes (adj)	48	$2.16 \times 10^{10**}$	0.59^{**}	1.29^{**}	$2.98 \times 10^{9**}$	37.20^{**}(6.9)	9.13^{**}	11.65^{**}	22.75^{**}	8.70^{**}(26)	0.38^{**}(10)
G x L	192	$2.03 \times 10^{9*}$	0.06^{*}	0.16^{**}	$6.04 \times 10^{8**}$	5.89^{**}(5.7)	2.10^{**}	3.36^{ns}	6.09^{ns}	1.30^{ns}(15.7)	0.10^{*}(10.54)
G x C	144	$4.4 \times 10^{9**}$	0.07^{**}	0.13^{ns}	3.26×10^{8ns}	4.63^{*}(3.3)	1.86^{ns}	3.65^{ns}	5.36^{ns}	1.36^{ns}(12.3)	0.08^{ns}(6.33)
G x L x C	336	$1.5 \times 10^{9**}$	0.04^{ns}	0.10^{**}	$2.76 \times 10^{8**}$	4.44^{*}(7.5)	1.49^{**}	3.21^{**}	4.37^{ns}	1.16^{**}(24.5)	0.09^{**}(16.61)
Error	834	8.93×10^{8}	0.14	0.08	2.19×10^{8}	3.75	1.02	2.43	3.96	0.74	0.067
CV		14.37	7.18	11.63	14.79	19.74	5.01	8.59	2.21	6.9	21
Mean		207.99	2.67	2.39	100.15	9.49	20.14	18.16	89.98	12.50	1.20
						The GE Model					
Environment (E)	17	$3.7 \times 10^{11**}$	2.41^{**}	$26.^{**}$	$2.1 \times 10^{10**}$	714^{**}(64.85)	79.4^{**}	48.2^{**}	319^{**}	146^{**}(57.71)	7.20^{**}(55.69)
Replication	18	$5.16 \times 10^{8**}$	0.62^{**}	0.61^{**}	$6.06 \times 10^{8*}$	11.88^{**}	2.79^{**}	7.97^{**}	10.86^{*}	2.9*	0.22^{*}
Block (adj)	216	$1.3 \times 10^{9*}$	0.05^{**}	0.09^{ns}	$4.4 \times 10^{8**}$	3.80^{ns}	0.44^{ns}	03.45^{*}	4.96^{*}	1.52*	0.08^{ns}
Genotypes (G)	48	$2.16 \times 10^{10**}$	10.6^{**}	1.3^{**}	$2.98 \times 10^{9**}$	51.4^{**}(13.26)	9.54^{**}	12.8^{**}	22.6^{**}	9.9^{**}(10)	0.38^{**}(8.3)
GEI	816	$2.18 \times 10^{9*}$	0.05^{**}	0.13^{**}	$3.75 \times 10^{8**}$	4.78^{**}(20.96)	1.55^{**}	3.16^{**}	5.02^{**}	1.7^{**}(32.26)	0.097^{*}(36.01)
Error	648	8.93×10^{8}	0.036	0.08	2.19×10^{8}	3.24	0.87	2.38	5.54	0.85	0.067
CV		14.37	7.17	11.61	14.79	18.94	4.67	8.5	2.16	7.38	21
Mean		207992	2.67	2.39	100153	9.49	20	18.16	90.02	12.46	1.20

** Significant at < 0.001 and ** significant at < 0.01; * significant at < 0.05; ^{ns}=Nonsignificant; E=Environments; adj=Adjusted; NT=Numbers of Tillers; MSD=Milleable Stalk Diameter; MSH=Milleable Stalk Height; MSP=Milleable Stalk Population; numbers in brackets indicate percent of treatment sum of squares accounted.

3.2. Mean performance of genotypes for yield, yield components and yield quality traits

The mean performance of genotypes for cane yield component traits (tillering, milleable stalk height, diameter and population) and yield quality traits (Brix%, Pol% and Purity %) were separated using Tukey's Multiple Test at α=0.05 (Table not shown). As six commercial varieties were included in the study, the means of the introduced genotypes were compared against the better performing commercial variety for each trait studied. Of the commercial varieties included, CO-449 and NCO-334 performed better for yield quality traits and cane yield components, respectively and the test genotypes were compared against these varieties.

3.3. The GGE bi-plot analysis for environment and genotype evaluation

For GGE bi-plot analysis, two-way table data for cane yield (Table 4), recoverable sucrose% (Table 5) and sugar yield (Table not presented) were used. Based on the same dataset, the GGE bi-plots were constructed for mega environment classification (Fig. 1 a, b & c), environment evaluation (Fig. 2 a, b & c), genotype evaluation based yield performance (Fig. 3 a, b & c) and yield stability (Fig. 4 a, b & c) evaluations.

Table 4
G x E two-way table for Cane Yield (tons ha^{-1}m^{-1}).

Genotypes (G)		Environments (E)																	
		Plant Cane 1 (C1)					Plant Cane 2 (C2)					Ratoon crops							
CD	Name	PC1W	PC1F	PC1FCRD	PC1M	PC1B	PC2W	PC2F	PC2M	PC2B	PC2T	R1W	R1F	R1FCRD	R1M	R1B	R2F	R2M	R2W
1	PSR97 092	12.32	13.71	8.57	17.1	9.52	9.9	10.89	15.4	12.3	3.38	7.55	16.47	11.33	12.5	11.6	9.03	9.02	8.32
2	DB70047	6.75	10.28	9.63	10.3	6.14	7.14	9.28	8.6	11.9	3.03	6.66	11.81	8.86	11.26	9.47	6.50	13.31	6.97
3	DB66 113	12.3	13.39	8.13	12.6	11.1	7.19	11.62	10.57	10.3	5.68	5.65	19.36	13.23	14.76	11.9	8.63	8.41	7.22
4	FG06 700	4.69	9.787	6.23	8.84	9.14	6.22	7.164	7.667	7.63	1.02	4.19	11.87	8.57	15.87	9.54	7.72	11.06	4.14
5	FG06 729	7.61	10.51	8.30	11	12.2	4.53	8.77	7.525	11.5	2.05	5.89	14.18	9.55	11.19	11.1	8.27	7.93	5.99
6	PSR97 087	6.46	11.62	7.54	12.3	9.25	6.24	10.78	10.44	10.1	3.37	7.29	12.9	8.42	13.19	10.4	5.42	10.03	7.38
7	PSR97 051	6.28	10.33	7.88	11.5	9.81	5.83	11.18	11.24	10.2	3.16	8.3	15.82	10.53	13.29	11.6	8.44	8.25	8.39
8	HO95 988	5.89	7.606	9.53	11	9.15	7.93	9.02	10.29	7.55	1.72	6.55	12.15	10.36	10.61	9.02	6.52	5.59	6.67
9	CP-99 1534	4.21	10.49	8.06	10.4	7.13	4.67	8.66	7.036	12	1.89	6.37	13.56	10.70	10.09	9.62	7.56	10.26	6.19
10	FG04 829	4.77	10.04	8.34	10.7	7.81	5.16	8.249	9.022	9.43	2.31	6.87	16.13	11.24	13.22	10.4	5.76	6.10	6.65
11	DB71 060	5.78	9.949	9.03	15.3	11.7	5.57	11.27	9.918	14.6	3.1	5.7	14.16	10.06	11.21	11.8	7.48	7.52	6.45
12	TCP93 4245	5.98	9.655	8.09	11.5	7.26	7.43	9.044	10.27	10.4	2.95	5.07	14.41	9.47	12.96	9.78	6.78	9.22	7.53
13	CP001 252	6.84	10.52	8.21	10.5	8.39	6.29	5.902	11.11	12.3	3.25	9.42	12.22	9.55	11.77	11.1	5.65	7.92	8.64
14	VMC95 173	9.84	9.99	10.32	13.8	8.12	10.2	8.81	9.82	4.34	4.06	6.42	10.07	8.12	10.39	7.72	5.39	6.49	7.08
15	FG03 447	6.34	10.06	6.69	13.6	5.01	7.63	8.976	8.935	10.6	5.26	8.57	12.23	9.41	12.71	9.37	8.52	10.00	8.55
16	CO 740	4.94	10.87	9.54	15	10.2	8.46	11.17	12.34	8.06	5.06	8.54	15.68	11.81	14.18	12.6	6.15	12.48	8.90
17	CP99 1894	4.78	8.68	8.57	9.71	7.92	7.74	4.132	9.863	6.5	2.57	3.85	7.588	7.64	12.92	7.68	9.10	7.71	3.91
18	FG03 425	8.35	11.86	9.99	11.7	7.58	7.01	8.449	8.354	4.71	2.26	6.13	15.7	10.41	10.06	8.39	6.41	7.64	6.12
19	FG05 408	4.1	9.128	9.55	10.9	6.73	5.75	7.691	7.543	7.87	2.64	9.44	13.5	8.84	12.05	9.25	4.94	9.55	8.23
20	FG03 520	13.8	9.204	9.61	11	9.33	8.49	11.02	11.1	13.7	4.24	14.1	15.29	10.34	10.81	12.6	6.56	9.01	13.70
21	FG04 754	5.46	11.12	6.65	13.7	11.4	9.07	12.44	11.41	9.98	6.61	5.17	14.95	11.42	16.44	11.4	10.52	13.21	6.61
22	FG04 466	10.6	10.27	8.76	15.2	8	9.32	11.91	16.02	14.5	3.7	6.92	13.24	8.82	13.84	11.3	8.54	11.83	9.20
23	FG03 526	9.02	9.067	8.26	12.9	7.26	7.12	10.58	10.05	9.03	4.06	6.76	12.13	8.41	12.09	9.18	6.19	9.87	6.60
24	Mex54/245	7.88	10.57	9.45	15.4	5.82	7.64	8.149	10.37	13.4	3.57	6.95	14.77	11.40	13.96	10.7	7.81	4.67	7.21
25	FG03 396	9.02	11.79	8.18	8.3	7.94	6.04	11.61	9.034	11.6	4.86	5.07	14.07	11.24	12.73	10.4	10.46	9.72	5.56
26	VMC95 212	5.62	9.686	8.55	13	7.12	7.03	11.8	12.81	12	3.38	6.95	15.61	9.99	12.86	10.6	6.26	15.76	6.82
27	NCO-334	8.99	8.499	8.21	15.3	8.2	9.2	11.62	8.871	10.4	3.88	6.53	14.25	8.89	16.96	10.9	4.97	9.93	7.34
28	FG03 418	8.89	12.86	7.24	12.8	9.64	9.58	13.48	10.45	15.2	5.94	7.51	14.41	10.63	15.24	12.3	9.41	14.92	8.50
29	CO449	5.44	9.087	7.12	14	6.28	6.02	10.17	9.477	6.62	5.16	5.07	13.09	10.33	12.36	8.4	5.05	10.64	4.93
30	FG03 204	10.5	8.408	8.14	12	6.54	8.8	12.03	11.44	7.05	6.34	5.12	13.05	9.20	17.39	9.37	5.38	14.74	5.62
31	FG02 553	4.21	11.2	9.75	11.6	9.86	6.53	9.634	9.757	13.8	4.71	7.55	14.12	11.27	9.643	10.8	7.81	10.66	6.94
32	FG03 103	7.86	7.282	8.15	15.3	10.7	6.96	10.63	12.01	13.3	1.8	7.85	10.23	7.62	16.14	11.6	6.33	11.60	7.43
33	FG03 318	9.84	10.3	8.42	10.6	6.81	9.58	11.6	9.956	10.4	2.67	5.6	14.67	10.71	13.89	10	8.45	12.11	6.20
35	FG04 705	4.68	7.763	8.04	11.9	8.14	4.74	7.707	9.937	12.8	1.55	5.2	11.74	7.82	10.75	9.85	3.03	6.37	5.36
36	FG02 551	7.52	10.39	4.95	9.94	7.94	3.24	10.53	7.65	8.8	2.05	8.38	15.78	10.10	9.14	9.68	4.40	8.09	8.14
37	FG03 173	6.97	8.996	6.56	11.5	8.97	7.37	9.878	8.097	9.95	4.08	4.96	13.28	9.16	10.82	9.56	6.49	6.93	5.09
38	FG04 187	11.5	12.66	7.18	13.4	8.89	10	14.1	15.87	15	4.98	6.45	18.33	11.89	12.97	13.7	9.71	12.86	8.92
39	FG03 372	12.7	11.15	8.76	12.5	7.48	12.9	8.452	11.1	12.8	4.5	4.35	16.12	10.84	14.29	10.9	6.03	12.73	12.66
40	FG03 214	7.54	10.16	9.15	14.8	9.16	6.01	8.627	7.813	5.93	1.83	6.29	11.91	8.55	10.39	8.62	5.76	7.99	6.42
41	C86-56	5.99	11.21	8.01	11.7	7.13	9.17	10.72	11.09	12.3	6.91	5.98	17.66	10.85	13.76	10.2	9.12	10.35	6.14
42	SP70-1284	4.29	10.62	9.87	9.24	8.6	6.57	9.234	9.234	10.2	3.28	5.23	16.45	11.35	5.518	10.3	10.40	9.75	5.70
43	C86-165	4.69	12.31	9.38	9.52	9.95	7.93	10.94	10.91	11.7	3.35	9.87	15.79	9.60	8.876	11.2	6.11	4.90	9.53
44	B78-505	6.95	8.073	6.78	15.2	11.7	8.52	8.264	8.973	10.7	2.81	4.67	12.81	9.87	16.2	11.2	9.82	8.22	5.14
45	C132-81	7.25	9.026	8.71	13.7	9.22	8.87	9.941	9.068	9.29	4.87	8.81	14.21	9.77	12.01	10.6	8.59	11.88	8.63
46	C86-12	8.49	10.81	5.87	13.2	7.89	6.42	12.72	9.579	9.15	5.07	7.53	13.79	9.58	10.76	9.62	8.22	11.47	7.29
47	C90-501	4.3	11.08	6.67	12.9	7.63	7.01	10.5	11.32	10.8	2.97	6.87	14.65	9.61	10.82	9.92	8.28	6.77	6.93
48	B52-298	4.59	7.967	8.13	11.6	8.7	7.86	8.812	7.806	6.65	2.16	6.05	12.83	9.13	14.64	8.81	7.08	9.39	5.65
49	CO- 678	9.61	8.519	10.35	13.5	7.79	8.63	10.33	11.76	10.5	2.86	4.03	15	9.12	10.48	9.55	5.31	11.47	4.66
Mean		7.34	10.18	8.27	12.36	8.51	7.45	9.97	10.19	10.4	3.60	6.67	14.04	9.91	12.50	10.33	7.22	9.72	7.13

* W=Wonji; F=Finchaa; M=Metahara; B=Belles; T=Tendaho; PC1FCRD=Plant cane yield trial for CIRAD varieties introduced at advanced and mid-way selection stages; R1FCRD=First ratoon yield for CIRAD varieties trial introduced at advanced and mid-way selection stages; PC1=First plant cane crop trial; PC2=Second plant cane crop trial; R1=First ratoon crop; R2=Second ratoon crop.

Table 5
G x E two-way table means for recoverable sucrose%.

Genotypes (G)		Environments (E)																	
			Plant Cane 1 (C1)				Plant Cane 2 (C2)					Ratoon crops							
CD	Name	PC1W	PC1F	PC1FCRD	PC1M	PC1B	PC2W	PC2F	PC2M	PC2B	PC2T	R1W	R1F	R1FCRD	R1M	R1B	R2F	R2M	R2W
1	PSR97 092	12.65	12.37	12.91	12.75	11.75	12.88	12.26	10.83	12.11	8.6	13.87	11.43	13.54	10.29	11.82	9.64	11.54	14.02
2	DB70047	14.43	13.12	14.62	13.33	12.89	14.52	13.78	14.18	11.02	4.93	12.88	13.37	13.53	13.14	12.49	11.56	11.09	13.36
3	DB66 113	12.9	12.08	13.24	11.49	11.41	10.88	13.53	12.72	11.11	8.33	13.31	11.37	13.17	10.49	11.51	9.77	10.43	13.16
4	FG06 700	12.91	13.05	12.70	12.5	12.83	12.17	13.64	11.99	11.84	3.05	13.73	12.47	12.16	10.99	12.37	12.08	12.60	13.38
5	FG06 729	14.29	14.06	12.78	13.18	14.11	14.04	14.2	13.23	11.39	5.23	12.7	13.61	13.83	13.86	13.04	11.41	12.36	13.14
6	PSR97 087	15.3	13.39	13.84	13	11.32	11.62	14.3	12.83	11.77	11	13.28	11.66	13.11	11.23	11.79	10.98	12.57	13.32
7	PSR97 051	14.67	13.39	14.27	12.91	12.35	13.69	14.25	13.07	12.08	9.95	13.2	13.53	13.79	11.39	12.45	12.45	12.30	13.68
8	HO95 988	14.23	13.26	12.33	11.56	12.92	12.53	13.5	12.76	11.5	11.6	13.88	14.03	13.80	13.14	12.91	13.61	11.79	13.64
9	CP-99 1534	12.62	12.76	12.96	11.65	12.39	11.01	14.46	13.91	12.48	8.48	11.94	11.95	12.74	10.91	11.99	12.76	12.17	11.90
10	FG04 829	13.46	13.36	12.29	12.34	14.33	12.53	14.24	13.43	11.28	4.37	13.67	13.36	13.63	13.83	13.14	12.18	11.94	12.46
11	DB71 060	13.13	13.45	14.67	12.97	12.64	11.63	14.14	13.24	11.28	10.6	12.95	13.23	13.92	12.25	12.33	11.53	12.85	13.27
12	TCP93 4245	13.89	14.33	14.24	13.11	14.72	12.12	14.28	13.09	12.77	9.97	13.26	13.92	13.90	14.03	13.77	12.45	12.66	13.53
13	CP001 252	13.57	12.28	13.85	12.52	13.48	11.3	11.85	12.03	10.87	7.83	13.44	13.34	12.53	13.35	12.51	12.74	12.61	13.04
14	VMC95 173	12.1	12.35	11.90	13.31	12.43	12.68	12.19	11.17	10.04	6.8	13	12.76	13.75	10.99	11.83	11.72	11.35	12.86
15	FG03 447	14.11	13.46	12.84	12.31	13.69	12.81	13.68	13.27	13.53	5.81	12.01	12.88	13.96	11.28	12.82	12.02	11.31	12.42
16	CO 740	11.76	12.43	11.84	11.68	11.65	12.95	13.52	11.61	8.64	8.79	11.85	12.42	12.78	11.05	11.09	11.47	12.03	10.93
17	CP99 1894	12.17	12.62	11.70	11.61	13.21	14.37	13.66	12.34	11.4	10.4	13.43	13.06	13.23	12.03	12.6	12.10	10.77	13.38
18	FG03 425	12	12.42	12.36	10.99	11.94	11.5	11.99	11.84	12.47	8.42	12.47	12.4	13.60	9.447	11.82	10.96	10.12	12.25
19	FG05 408	12.71	12.84	12.65	12.93	13.06	11.95	12.91	12.82	13.15	9.34	13.66	13.07	13.04	14.36	13.51	12.09	12.24	13.04
20	FG03 520	14.76	12.68	13.67	12.17	13.22	11.37	13.96	12.36	11	11.1	11.72	12.45	13.36	11.04	11.97	10.67	12.06	11.66
21	FG04 754	12.34	13.06	14.16	11.64	12.57	13.75	13.72	13.01	9.43	4.93	13.62	11.82	13.62	11.07	11.53	12.16	12.45	13.43
22	FG04 466	12.07	13.06	13.85	11.14	12.86	12.99	13.88	13.76	11.84	9.12	13.47	12.79	13.80	11.55	12.46	11.15	12.15	13.63
23	FG03 526	13.12	13.86	14.65	12.05	13.13	11.76	13.51	13.15	12.76	8.82	12.77	11.99	13.02	12.73	12.71	11.73	11.98	12.76
24	Mex54/245	12.01	11.79	12.19	11.01	11.42	12.85	12.54	11.46	11.59	7.05	12.22	10.77	11.38	9.75	11.22	10.49	9.92	12.25
25	FG03 396	13.34	12.84	14.13	12.85	14.45	12.22	13.79	13.54	12.17	6.56	13.95	13.25	13.64	13.24	13.13	11.84	12.88	13.33
26	VMC95 212	13.34	13.03	13.80	11.44	12.1	12.66	13.69	13.06	11.35	6.81	12.38	12.95	14.00	8.99	11.52	9.80	12.85	12.31
27	NCO-334	12.9	11.34	13.42	11.93	10.67	10.89	11.68	12.04	10.37	6.83	13.13	12.28	14.57	9.766	11.16	11.20	10.80	12.97
28	FG03 418	13.48	12.97	13.69	13.89	13.22	13.55	13.59	13.44	11.92	11.8	13.55	12.49	13.24	13.36	12.83	10.97	12.22	13.57
29	CO449	12.28	12.46	12.36	12.77	12.32	13.1	12.82	11.94	11.47	6.09	13.52	12.04	12.32	10.51	11.93	10.85	11.34	13.29
30	FG03 204	13.58	12.75	12.92	12.3	13.06	12.97	12.21	13.21	13.32	7.72	11.33	13	13.66	11.84	12.64	11.68	11.76	12.02

31	FG02 553	13.14	11.25	12.46	12.57	11.12	13.15	12.95	13.59	10.76	8.14	12.55	10.89	11.65	13.64	11.87	10.49	11.63	12.80
33	FG03 318	12.53	13.36	12.04	11.66	12.82	12.81	12.91	10.04	11.2	8.34	12.26	12.66	13.27	13.26	12.36	10.64	11.29	12.46
35	FG04 705	13.81	13.6	15.23	12.2	14.74	12.14	14.53	13.5	10.43	11	14.23	14.14	13.86	12.6	13.12	13.54	12.78	13.79
36	FG02 551	12.35	12.08	12.44	11.79	11.88	10.78	13.45	13.3	11.96	11.3	13.5	12.26	12.57	11.84	12.22	11.39	11.88	12.80
37	FG03 173	13.08	12.97	12.92	11.24	12.44	13.16	13.73	12.82	12.99	8.71	12.22	12.59	12.94	12.36	12.56	11.59	10.38	12.52
38	FG04 187	12.02	12.19	13.06	9.889	12.3	12.48	13.06	10.7	10.67	6.86	11.95	11.05	12.87	11.29	11.75	11.26	12.52	13.48
39	FG03 372	13.83	12.16	12.71	12.55	12.76	12.94	11.27	11.49	12.15	7.54	14.59	12.54	12.95	13.01	12.91	11.18	11.62	13.59
40	FG03 214	13.79	12.35	12.23	12.42	12.1	12.85	12.42	12.42	8.082	6.82	12.26	11.95	12.12	13.59	11.43	11.42	11.79	12.66
41	C86-56	11.87	12.07	12.47	10.95	12.26	11.88	13.01	12.52	12.52	7.14	12.15	12.58	12.63	10.59	12.2	11.59	11.19	12.21
42	SP70-1284	13.5	11.96	12.84	11.08	12.23	13.64	13.06	12.94	11.72	8.82	12.93	12.1	12.36	11.51	12	12.18	10.98	13.08
43	C86-165	12.64	12.01	12.55	11.02	13.76	12.4	13.11	12.26	11.85	7.46	12.84	11.54	12.04	9.93	12.07	11.45	12.07	12.72
44	B78-505	12.94	11.95	12.48	11.69	12.4	12.57	13.9	12.18	11.34	5.61	14.63	11.75	12.39	10.81	12.12	10.95	10.23	13.94
45	C132-81	12.36	12.31	12.46	11.97	12.65	10.99	13.55	12.86	9.897	7.65	13.13	11.36	12.09	9.984	11.49	11.96	11.84	12.69
46	C86-12	13.23	12.51	13.12	11.77	13.07	12.08	13.69	13.44	12.16	11.2	13.24	13.01	13.14	12.79	12.82	11.99	12.33	13.06
47	C90-501	13.24	13.26	12.91	12.65	11.84	12.62	13.51	14.88	11.89	11	11	12.87	13.09	13.26	12.11	10.74	11.57	11.59
48	B52-298	12.02	10.69	11.73	11.1	10.6	11.7	11.84	12.86	13.74	9.41	12.61	10.9	14.03	11.21	11.88	9.65	11.10	12.37
49	CO- 678	11.2	11.84	11.90	10.02	9.841	10.7	13.17	9.872	10.7	6.61	12.46	11.22	11.82	10.35	10.77	9.76	10.43	12.06
Mean		13.06	12.65	13.03	12.04	12.57	12.4	13.29	12.62	11.5	8.08	12.95	12.45	13.11	11.78	12.23	11.43	11.72	12.89

* W=Wonji; F=Finchaa; M=Metahara; B=Belles; T=Tendaho; PC1FCRD=Plant cane yield trial for CIRAD varieties introduced at advanced and mid-way selection stages; R1FCRD=First ratoon yield for CIRAD varieties trial introduced at advanced and mid-way selection stages; PC1=First plant cane crop trial; PC2=Second plant cane crop trial; R1=First ratoon crop; R2=Second ratoon crop.

3.4. Mega environment classifications

The "which-won-where" view of the GGE bi-plots for cane yield, recoverable sucrose% and sugar yields are presented (Fig. 1 a, b & c). The GGE bi-plot was constructed based on the two-way GE table of cane yield (Fig. 1 a) explained 43.36% of the genotype + genotype x environment interaction (G+GE) variability in cane yield and was divided into six sectors where the environments located in only of the three sectors. Accordingly, the target environment (sugarcane production environments) was divided into three distinct mega environments. Most of the crop trials from locations Finchaa and Belles were classified in one mega environment where the ratoon crop trials of location Wonji were located and genotype 20 was the top. In the second mega environment, most of the second plant cane crop trials from locations, Wonji, Metahara, Finchaa and Tendaho were grouped where genotype 38 was the best genotypes. In the third mega environment which showed little overlapping with second mega environment; consisted of one plant cane crop and two successive ratoon crop trials from location Metahara where genotype 39 was the winner.

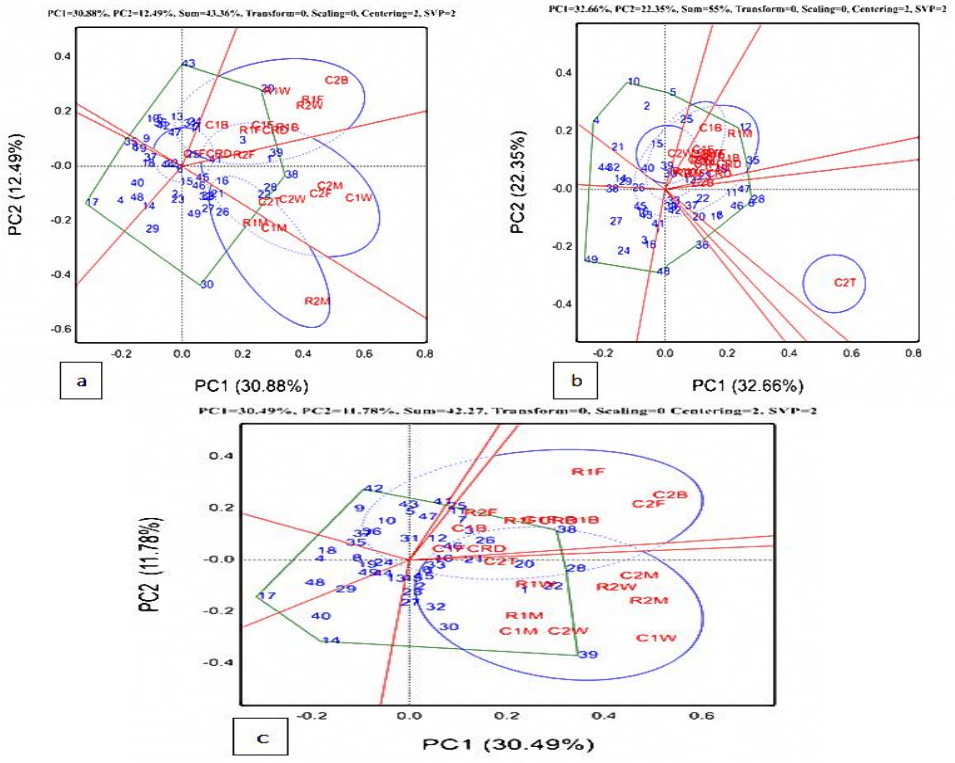


Fig. 1. The "which-won-where" View of GGE bi-plot based on Genotype x Environment two-way Table for (a) cane yield (b) recoverable sucrose% (c) sugar yield; Environments were represented by environmental alphabet and number codes (Table 1) and genotypes were represented by genotype code numbers (1-49) (Table 2).

Unlike to the cane yield, the GGE bi-plot (Fig. 1 b) constructed based on the recoverable sucrose data divided into ten sectors where the environments reside in only of the two sectors. One mega environment was formed where most of environments were closely clustered and genotype 12 was the best. Environment C2T (location Tendaho) solely and substantially separated in another mega environment where genotype 28 won. The GGE bi-plot for sugar yield (Fig. 1 c) was divided into seven sectors but the environments found in two sectors and two major mega environments were formed. Most of the trials from locations Belles and Finchaa classified in one mega environment where genotype 38 was at the corner of the sector, while crop trials from locations Wonji, Metahara and Tendaho formed the second mega environment where both genotypes 39 and 28 are the winners.

3.5. Relationships, discriminating power and representativeness of test environments

The GGE bi-plots for cane yield, recoverable sucrose% and sugar yield successfully displayed the environments that had discriminating power and representative (Fig. 2 a, b & c). The large angle among between plant cane and ratoon crops of the same location for cane yield (Fig. 2 a) thereby indicating their dissimilarity. Unlike to cane yield, plant cane crops in the same location made small angles, indicating their similarity in discriminating sugarcane genotypes based on yield performance of recoverable sucrose% (Fig. 2 b) and sugar yield (Fig. 2 c). As described by Yan and Kang (2003) and Jin et al. (2015), the AEC line that connected the origin to the average of all environments and an ideal environment is located on this line and an average environment is located near the AEC. In the present study, AEC line (blue arrow) that connected the origin to the average of all environments and an ideal environment is located on this line (blue arrow) and an average environment is located near the AEC (red circle).

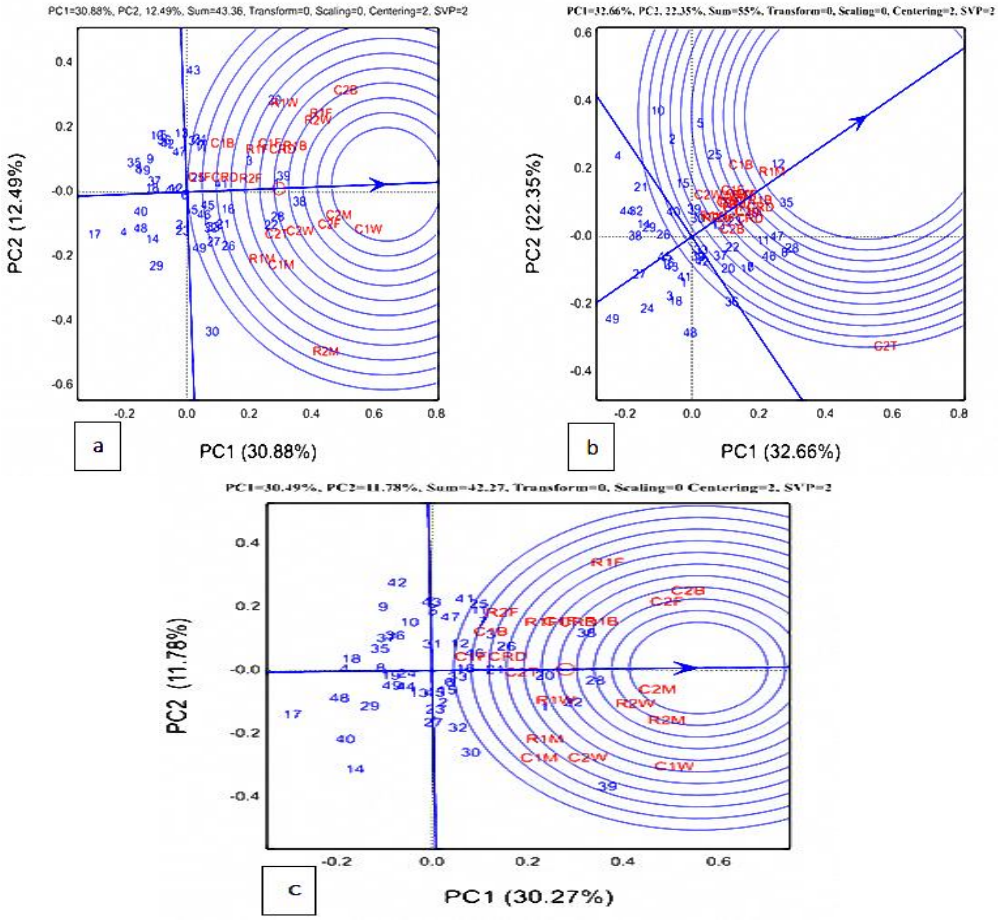


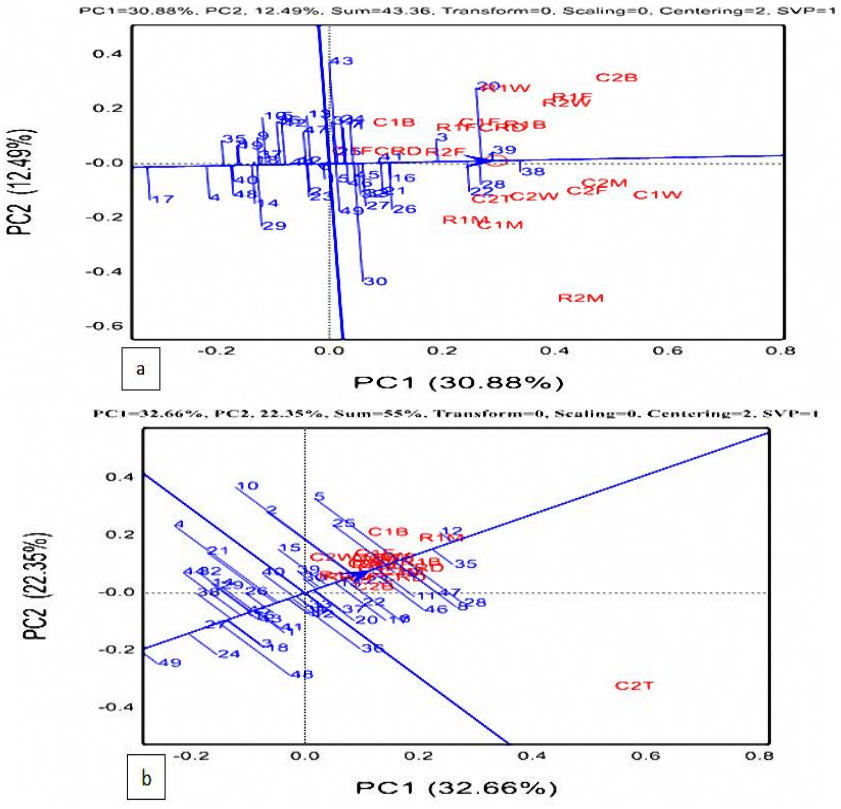
Fig. 2. GGE bi-plots displaying the discriminating power and representativeness of environments based on Genotype x Environment two-way able for (a) cane yield (b) recoverable sucrose% (c) sugar yield; Environments are represented by environmental alphabet and number codes (Table 1) and genotypes are represented by genotype code numbers (1-49) (Table 2).

Accordingly, the GGE bi-plot for cane yield (Fig. 2 a) indicated environments R2F, C1F, R1B, C1FCRD, C2W and C2T relatively located near the average environment (red circle) and are average environment where stable genotypes can be selected. Moreover, C2M located near the AEC line (blue arrow) and is relatively ideal environments while C2B, R1F, R2W, R1W and R2M had long vector from the origin and showed higher discriminating power.

Crop trials from location Wonji (C1W, C2W and R1W) located on the average environment and were more representative for selection of stable genotypes for recoverable sucrose% while R1M located near the ideal environment (Fig. 2 b). On the contrary, C2T located far from the origin with the longest vector from the origin and had higher discriminating power. It suggested it had high discriminating power and was less representative test environment for selection of superior genotypes in recoverable sucrose%. For sugar yield (Fig. 2 c), C2M located near the ideal environment while C2T located on the average environment. On the contrary, C2B, R1F, R2F, C1W, C2W, C1M, R1M and R1B had long vector from the origin and showed higher discriminating power as the discrimination power of an environment is proportional to the length of the environmental vector (Vargas et al., 2013).

3.6. Ranking of genotypes based on yield performance and stability

Based on the principles suggested by Yan (2012), the yield stability of the genotypes displayed on the GGE bi-plots (Fig. 3 a, b & c) can be measured by the projection of their markers on the derived axis (AEC ordinate) that is perpendicular to the abscissa AEC (blue single headed arrow) which points to the higher mean yield performance. Generally, those genotypes located in the right side of the ordinate yielded above average, while those genotypes located on the left side of the ordinate yielded below average. Genotypes located in the far right side of the ordinate are high yielder while those genotypes located far left of the ordinate line are poor performed. Moreover, on Fig. 4 a, b & c, an "ideal" genotype (the center of the concentric circles) to be a point on the AEA ("absolutely stable") in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of AEA ("highest mean performance"). Accordingly, genotypes FG04 187 (38), TCP93 4245 (12), and FG03 418 (28) located on the center of concentric circles and are ideal genotypes for cane yield, recoverable sucrose% and sugar yield, respectively.



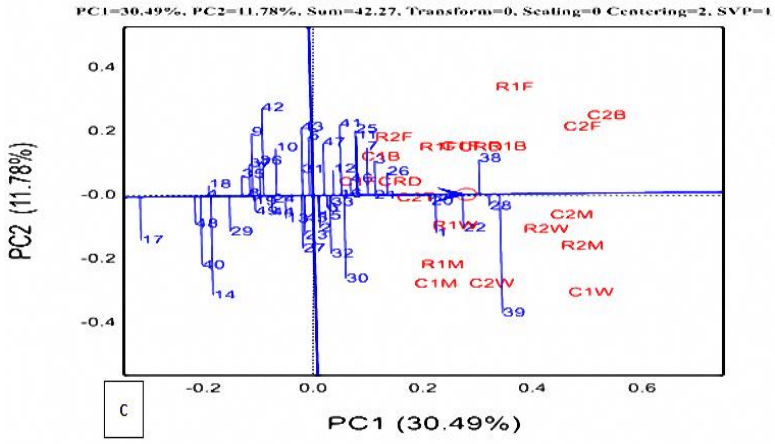


Fig. 3. The GGE bi-plot for ranking of genotypes based on yield performance using two ways GxE Means for (a) Cane yield (b) recoverable sucrose% (c) sugar yield; Environments are represented by environmental alphabet and number codes (Table 1) and genotypes are represented by genotype code numbers (1-49) (Table 2).

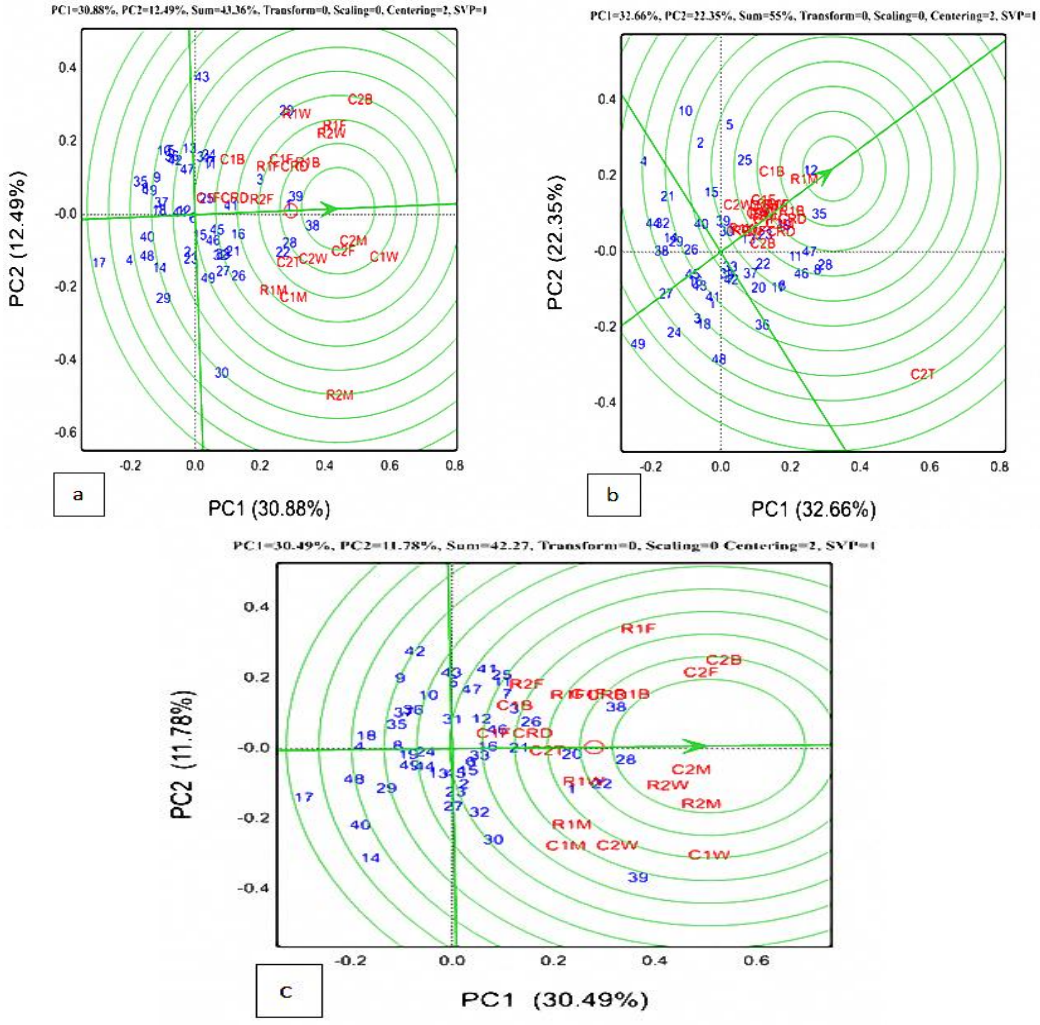


Fig. 4. The GGE bi-plot for ranking of genotypes based on yield performance and stability using two ways GxE Means for (a) Cane yield (b) recoverable sucrose% (c) sugar yield; Environments are represented by environmental alphabet and number codes (Table 1) and genotypes are represented by genotype code numbers (1-49) (Table 2).

Results from the analysis of variance (Table 3) indicated the significant effect ($p<0.05$) of location and crop years for most of the traits suggests the locations and crop years were diverse in nature highlighting the necessity of test trials across locations and over years. On the other hand, significant effect of location x crop year effect suggests the effect of crop year effect was strongly controlled by location. Our result is consistent with findings reported by Mulema et al. (2008) in which sugarcane yield quality traits were less affected by location effects (more of genetically controlled). The highly significant effect of genotype for all yield traits considered indicated strong genotypic effects in the total variability. Moreover, most of the cane yield components such as milleable stalk number, and milleable stalk height, stalk diameters and cane yield are highly influenced by crop year and location effects. These results were consistent with the findings reported by Tahir et al. (2014). The highly significant genotype effect for all yield traits suggested the availability of substantial genetic variability among genotypes for the traits considered.

As far as the significances of each component of genotype x environments interaction is concerned, the G x L interaction was significant for cane yield and its components, thereby suggesting quantitative yield traits were more affected by genotype x location interaction and increasing number of location benefited more selection gains. The G x L x C interaction was highly significant for all traits. It suggested demonstrated that the genotype x environments interaction was complex with high probability of cross over interaction which limits selection progress. These results were consistent with results reported by Rea and De Sousa-Vieira (2001) and Kimbeng et al. (2009) in which genotype by location (G x L) and genotype x location x crop year (G x L x C) interaction affects cane yield and its components of sugarcane. Based on the GE model of the same dataset, results from ANOVA revealed substantial genetic variability existed among genotypes, diverse nature of environments and significance of genotype x environment interaction (Table 3). The significances of effects were different when the same dataset was modeled based on GLC and GE models where more most of the traits studied were significant in the later model. It indicated the existence of an inflation of f-values when GE model was used which leads to overestimation in the importance of effects.

Regarding to the relative importance of each effect, the G x L x C and G x L interaction effects were more important than G x C, further indicated that testing across locations was more important than testing across crop cycles. The large and significant G x L x C interaction in cane yield, recoverable sucrose% and sugar yield demonstrated the difficulty of selecting superior genotypes based on yield traits because of crossover interaction. This is because yield traits are controlled by many quantitative genes that have small additive effects and thus, the effect of environment is cumulatively larger on yield traits resulting complex GEI. For recoverable sucrose%, the percent of the total sum of squares accounted for genotype was larger than the variation accounted by G x L x C interaction. It indicated that the genotypic effect was relatively stronger and the quality traits were genetically controlled. These results were in close agreement with the results reported by Mulema et al. (2008) and Barry and Kang (2008). The highly significant effect of the GE interaction for all yields (when the data was modeled based on the GE model) suggested the importance of GEI which is similar to reports of Alarmelu et al. (2015) and Luo et al. (2015). Moreover, the higher variation accounted by GEI effect, as compared to the genotypic effect, suggested the possibility of finding different mega environments within the sugarcane production environments in Ethiopia. Similar results were reported by Ramburan (2012), Luo et al. (2014) and Luo et al. (2015) but opposite to findings of Sandhu et al. (2014) in which the genotypic effect accounted for the largest variation in sucrose% and commercial cane sugar% as compared to the GEI. The variation accounted by the genotypic effect was extremely decreased in recoverable sucrose% when the data was analyzed based on the GE model thereby suggesting the inappropriate estimating of the genetic variability.

The classification of ratoon crops into different complex mega environments based on cane yield (Fig. 1 a) suggested seasonal climatic conditions and management practices were influential in separating ratoon crops from the specific plant cane crops. Ramburan (2012) reported similar trend to this result. In this classification the two mega environments are overlapped for the plant cane crop trial of Tendaho (C2T). Except under Belles and Finchaa conditions, the genotype x location interaction was non-repeatable over crop years for cane yield, indicating the mega environment classification was complex and non-repeatable. In other words, the performance of some genotypes across years in the same location was inconsistent thereby suggesting that G and GE must be considered together to make meaningful selection decisions rather than G alone. Such situations could happen as a result of non-repeatable G x L x C interaction (crossover GE interactions).

Even though most of the trials were closely grouped for sucrose% (Fig. 1 b), vectors length of the environments from the origin were variable thereby suggesting genotypes responses in accumulating sucrose were

variable over crop years. This could be attributed to the substantial influence of genotyes x crop year interaction for recoverable sucrose, which is consistent with results reported by Zou et al. (2011). Genotyes x crop year interactions are expected to be caused more by seasonal covariates. Moreover, the substantial separation of location Tendaho (C2T) from other locations for recoverable sucrose% could be attributed to the lower altitude and higher climatic conditions observed in this location (Table 1). Furthermore, Ftwi et al. (2017) reported similar findings where significant correlation between seasonal covariates and environmental IPCA scores of recoverable sucrose% were observed under Ethiopian agro-ecological conditions. The classification of the test environments in to different mega environments in sugar yield indicated the importance of breeding strategy for specific adaptation. A repeatable genotype x location over years was observed for recoverable sucrose% and sugar yield where two distinct mega environments were identified. The identified mega environments for sugar yield were based on geographical zoning which disagreed with results reported by Ramburan and Zhou (2011).

As suggested by different workers (Yan and Tinker, 2005; Yan et al., 2011; Yan, 2010), environments that made small angle have similarities. The large angle between Plant cane and ratoon crops of the same location for cane yield (Fig. 2 a) indicated selection over crop years in all location is beneficial to select genotypes with higher tonnage. On the contrary, the similarity among plant cane and ratoon crop trials of the same location for recoverable sucrose% (Fig. 2 b) and sugar yield (Fig. 2 c) suggested the repeatability of genotype x environment interaction for plant cane crops and less selection gain had been achieved from selection of sugarcane genotypes over successive plant cane crops for high sugar yield and should have been avoided to save resources. In other words, where GxC interaction had little impact while genotype x location played a major effect on yield traits for sugar cane trials. The result was consistent with reports of Lou et al. (2015), Ramburan (2014) and Zhou (2015).

From the product diversification point of view, the genotypes were recommended based of their performance in each yield traits studied (Fig. 3 a, b & c). Genotypes are discussed with both names and number codes (in brackets). Genotypes FG04 187 (38), FG03 372 (39), PSR97 092 (1), FG03 520 (20), FG03 418 (28), FG04 466 (22) and DB66 113 (3) located far right side of the ordinate and showed little projection onto this line. Theses genotypes produced higher biomass production (cane yield) in all environments (Fig. 3 a) and could be recommended for commercial purpose aimed at higher biomass production, and can be cultivated for wide range of environments. Genotypes TCP93 4245 (12), FG03 526 (23) and FG04 705 (35) located showed better yield quality and stability for recoverable sucrose% (Fig. 3 b) coupled with higher tonnage (Fig. 3 a); can be recommended for commercial purpose aimed higher alcohol production in wide range of environments. FG03 418 (28), FG06 729 (5), FG04 829 (10), DB70047 (2), FG03 396 (25), C90-501 (47) and FG03 425 (18) showed accumulated higher sucrose in certain environments and have specific adaptations. For sugar yield, genotypes FG03 418 (28), FG03 520 (20), FG04 466 (22), PSR97 092 (1) and FG04 754 (21) located far right side of the ordinate line with relatively little projection on to the line (Fig. 3 c). It suggested those genotypes showed better sugar yield performance and stability and are recommended for wide range of environments (Fig. 4 c). On the contrary, genotypes FG03 372 (39), FG03 204 (30), C86-56 (41), FG03 396 (25), FG03 103 (32) and DB71 060 (11) located far right of the ordinate line but with higher projection on to this line; are unstable genotypes, and recommended for specific environments. Based on sugar yield, FG03 372 (39) and FG03 204 (30) are specifically adaptable to locations Metahara and Wonji while FG04 187 (38) is specifically adaptable to Belles and Finchaa conditions.

Apart from the yield performance and stability, the genotypes were also evaluated from product diversification point of view. Those genotypes better performed in tillering capacity (FG04 705 and VMC95 212) suggested their potential for better ratoonability while those genotypes which showed better performance in milleable stalk height (FG03-520), milleable stalk diameter (B71 060, SR97 092, PSR97 087, C132-81, B78-505 and FG04 466) and milleable stalk population (HO 95988) than the commercial variety can be top growers' preferences (Table not presented). Regarding to yield and milling quality, FG04 705 followed by TCP93 4245, PSR97 051, FG04 829, FG03 418, FG04, 708, CP99 1894, FG06 700, FG03 396, PSR97 087, FG06 729, DB70047, HO95 988, C86-12, FG03 526, DB71 060 and C90-501 showed excellent performance in brix and pol% than CO449. While genotypes FGO5 408, HO95 988 and TCP93 4245 showed better purity%. These genotypes can greatly increase the limited number of alternative varieties for yield and milling quality in factory.

4. Conclusion

Results of the present study indicated the diverse nature of environments and substantial genetic variability among genotypes tested while the genotype x environment interaction was complex. When the data was analyzed

using the GE model, the f-values were inflated and the genetic variation was under estimated. Thus, for data obtained from yield trials conducted across locations and over seasons, the GLC model is appropriate. The significances of GLC interaction demonstrated the importance of conducting yield trials across locations and over crop years (plant cane + successive ratoon crops); evaluation across locations being more important than over crop years in case resource is limiting. The GGE bi-plots successfully generated substantial information about the mega environment classifications, environment and genotype evaluations. For cane and sugar yields, the sugarcane production environments in Ethiopia grouped into different mega environments. The genotype x location interaction was non-repeatable for cane yield over crop years while it was repeatable for recoverable sucrose% and sugar yield.

Genotypes FG04 187, PSR97 092, FG03 520, FG03 418, FG04 466 and DB66 113 produced higher biomass production (cane yield) in all environments and could be recommended for commercial purpose aimed at higher biomass production in wide range of environments. Genotypes TCP93 4245, FG03 526 and FG04 705 located showed better yield quality coupled with higher tonnage; can be recommended for commercial purpose aimed higher alcohol production in wide range of environments. For sugar yield, genotypes FG03 418, FG03 520, FG04 466, PSR97 092 and FG04 754 showed better sugar yield performance and stability and are recommended for wide range of environments. On the contrary, genotypes FG03 372, FG03 204, FG03 396, FG03 103 and DB71 060 are unstable genotypes and are recommended for specific environments. Moreover, FG03 372 and FG03 204 are specifically adaptable to locations Metahara and Wonji while FG04 187 is specifically adaptable to Belles and Finchaa conditions. Hence, a breeding strategy which focused on specific adaptation is recommended in future sugarcane breeding program. Generally, most of the introduced genotypes performed better than the commercial varieties for all yield traits and indicated the appropriateness of our variety introduction strategy. The inclusion of such alternative varieties for commercial use is a big opportunity to improve the productivity of the sugar industry in the country.

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Contribution of authors

Mebarahtom Ftwi contributed to research design, conducting and supervision of the experiment, data analyses and writing of the manuscript. Firew Mekibib contributed to initial designing and supervision of the experiments, and paper writing while Eyasu Abraha contributed to initial designing and supervision of the experiments. All authors have reviewed and approved the final manuscript. And at the end, the authors declare that they have no competing interests.

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