

## **Partitioning of Genotype-Environment Interaction in Sugarcane (*Saccharum* spp.): Variance Component Analysis**

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### **ABSTRACT**

Genotype-environment (GE) interaction in sugarcane (*Saccharum* spp.) is very important under Ethiopian agro-ecological and climatic conditions. However, yield trials conducted in Ethiopia are customarily handled using fixed models which consider the crop year and location effects as fixed. The study was conducted to partition and compare the relative importance of the components GE interaction and estimate the repeatability of yield trials using both fixed and mixed models. Forty-three genotypes along with the six commercial varieties were evaluated over four crop years and across five locations using simple lattice design. Data of yield, yield components and yield qualities were collected and subjected to analysis of variance (ANOVA) and variance component analysis. Variance component analysis indicated large and highly significant estimates of genotypic and Genotype-Location-Crop year (GLC) interaction effects for all yield traits thereby suggesting strong genotypic effect and excess crossover interaction, respectively. Regarding to the relative importance of the components of the genotype-environment (GE) interaction, genotype effect was more important for cane yield components and yield quality traits than others while GLC interaction was more important for cane and sugar yields than other components. Generally, the variance component and broad sense heritability estimates revealed the effect of GLC interaction was prevalent. It implicated a substantial selection gain could be attained from conducting variety trials across locations and over crop years under Ethiopian agro-climatic conditions. Moreover, the heritability estimates obtained from GLC and GE models indicated better repeatability of the experiments in which the later model showed overestimation of broad sense heritability values. Thus, we recommend the use of GLC model in sugarcane METs conducted across locations and repeated over crop years.

**Keywords:** Fixed model, Multi environment, Random model, Repeatability, Standard error, Variance component

**Abbreviations:** GC-Genotype: Crop Year Interaction; GE-Genotype: Environment Interaction; GLC-Genotype: Location-Crop Year Interaction; GLY-Genotype: Location-Year Interaction; GL-Genotype: Location Interaction; METs: Multi Environment Trials

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### **INTRODUCTION**

Genotype Environment (GE) interaction is customarily taken as a critical factor during selection of superior genotypes in crop breeding programs. Many workers agreed that development of a cultivar to a particular location and production systems is beneficial. However, modern cultivars developed by seed companies, international researcher centers and large national breeding programs exhibit wide geographical adaptations, as well as broad adaptations to different management practices and the range climatic variations that affect the individual sites over crop years [1]. According to Atlin et al. [1], the use of GE model could be misleading in METs because it confounds the genotype x year, genotype x year x location effects in undifferentiated 'genotype-environment effect', resulting in great loss of information and frequent over estimation of the importance of location effects. The importance of the GE interaction caused by a

fixed environmental effect, relative to the importance of within target environment population (TEP) noise caused by random and unexplainable variation among genotypic effects across locations is easily accessed by incorporating a fixed factor in to the model for the combining analysis of MET trials. On the contrary, the GLY model is a realistic and complete model for METs as compared with the GE model as it can partitioned the E term in to year (Y) and location (L) effects and their interaction ( $L \times Y$ ). Similarly, it can partition the GE term in to GY, GL and GLY interaction components.

In the GE model, if the trials are conducted in more than one year (for sugarcane, over crop cycles), estimates of the genotypic effects are not confounded by GE interaction effects, and genotypic variances estimates are unbiased by the interaction variances. However, as the GL, GY and GLY interaction effects and variances are not estimated separately by the GE model; it is impossible to determine if the GE interaction is caused by random noises (GY and GLY interaction effects) or fixed adaption to specific location or sub regions [1]. As a result the very large size of the GLY interaction effects, which are truly random, relative to the GL interaction effects that may in some cases be considered to be fixed attributes of particular environments, is a potential source of misinterpretation in the analysis of METs using the GE model [2]. This is particularly true when analyses are conducted based on fixed effects models such as AMMI and GGE [3,4]. Yang et al. [5] showed that treating random GE interaction as fixed causes lack of repeatability and over interpretation of the which won where patterns observed in the AMMI and GGE Biplots. For this reason the inclusion of GLY model in ANAOVA variance and variance components analysis is very important in METs conducted across locations and over crop years.

In Ethiopia, significant and complex Genotype  $\times$  environment interaction is reported in sugarcane. Moreover, most of the commercial varieties and newly released varieties in Ethiopia have narrow adaptation [6]. Author reported the significances of components of GE interaction (G, GL, GC and GLC interactions) in sugarcane, especially for cane and sugar yields. The knowledge on relative importance of the GE components is helpful to determine relative selection gains obtained from selections across locations, over crop years and both across locations and over crop years. Under Ethiopian agro-ecological and climatic conditions, both the temporal and spatial covariates affected the nature of the GE interaction [7]. However, studies on the relative importance of the GE interaction components with regard to these covariates are very limited. Therefore, the objectives of this investigation were to partition and compare the relative importance of the components of GE interaction for yield, yield components and yield qualities, estimate the repeatability of GE interaction and relating its implications to the future sugarcane selection program in Ethiopia.

## MATERIALS AND METHODS

### Description of test environments and genotypes

Multi-environment trials (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) during 2013-2014, 2014-2015 and 2015-2016 crop seasons for both plant cane crops and ratoon crop trials). The trials are briefly described using site and seasonal covariates. Detail descriptions of the trials are presented in Table 1.

In this study, forty-three (43) introduced sugarcane genotypes along with six commercial varieties were included (Table S1).

### Experimental design and data collection

The experimental design was a  $7 \times 7$  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<sup>2</sup>) and total experimental area of used for each location was 0.78 hectare. At planting, thirty sets (two-budded) were used for each row of 6 m length and 1.45 m width while the spacing between two adjacent rows was 1 m. data for cane yield components, Cane yield (tons ha<sup>-1</sup>m<sup>-1</sup>), recoverable sucrose% and sugar yield (tons ha<sup>-1</sup>m<sup>-1</sup>) were obtained from thirteen trials of PhD Project and five additional ratoon crop trials were used. First and second ratoon crops were collected in the same plot as first plant cane crops. As the ratoon and the plant cane crops were harvested at 14 and 17 months age of cane respectively, data for cane and sugar yield were converted to tons ha<sup>-1</sup>m<sup>-1</sup> (tons per hectares per month) to bring the crops types to the same productivity unit.

### Data analysis

A mixed model was used as genotype and location effects were considered as fixed while crop year effect was considered

**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				
			Soil type	Latitude (m.a.s.l)	Altitude (m)	Pan n (mm)	Temperature (°C)		Relative humidity (%)		Pan (mm)		Temperature (°C)		Relative humidity (%)
Location (L)	Crop Year (C)	CODE				AEP	Min	Max.	Max.	Min.	AEP	Min	Max.	Max.	Min.
Wonji (W)	PC1	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
	PC2	C2W									6.31	28.8	9.6	83.6	65.15
	R1	R1W									7.5	29.1	6.58	77.5	60.8
	R2	R2W									6.71	28.73	9.29	82.40	64.27
Finchaa (F)	PC1	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
	PC2	C2F									5.05	31	13.64	85.5	63
	R1	R1F									5.65	31.5	13.25	84.5	57.37
	R2	R2F									5.09	30.97	13.84	85.43	61.19
	PC1	C1FCIRAD									NA				
	R1	R1FCIRAD									NA				
Metahara (M)	PC1	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
	PC2	C2M									6.8	32.37	17.3	81.3	75
	R1	R1M									6.97	31.8	17.95	84.4	80
	R2	R2M									6.82	32.48	17.28	83.33	70.38
Belles (B)	PC1	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
	PC2	C2B									7.23	31.88	13.79	78.33	61.27
	R1	R1B									12.2	34.6	16	69.44	54.44
Tendaho (T)	PC2	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; R2: Second 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

as random. For analysis of variance components, the same model was used but genotype effect was considered as random. The GLY model was as  $Y_{ijklnc} = \mu + Rr_{(ij)} + Bk_{(ijc)} + Cc + L_i + Gn + L * G(in) + G * C_{(nc)} + C * L(ci) + G * C * L(nci) + \epsilon_{jklinc}$ , where,  $Y_{ijklnc}$  is the average yield of genotype n in location i over crop years c, replication r nested in location and crop years, block k nested in replication, location and crop year,  $\mu$  is the grand mean,  $Rr_{(ij)}$  is the random effect of j<sup>th</sup> replication nested in location i and crop years c,  $B_{k(ij)}$  is the random effect of k<sup>th</sup> block nested in the j<sup>th</sup> replication, i<sup>th</sup> location and c<sup>th</sup> crop year and was the experimental error for testing the random effect of j<sup>th</sup> replication nested in location i and crop year with some adjustments, Cc = the random effect of c<sup>th</sup> crop year,  $L_i$  = random effect of i<sup>th</sup> Location, Gn = the fixed effect of genotype,  $L * G_{(in)}$  = the fixed effect of genotype × Location (interaction),  $G * C_{(nc)}$  = random effect of crop year × genotype interaction,  $C * L_{(hi)}$  = random effect of crop year × location interaction,  $G * C * L_{(nci)}$  = random effect of crop year × genotype × location interaction;  $\epsilon_{jklinc}$  = residual (Error). Alternatively, GE Model was used as  $Y_{ibjkl} = \mu + E_i + R(E)_{j(i)} + B_{(RE)b(ij)} + G_k + GE_{ik} + e_{ijkl}$  where  $Y_{ibjkl}$  = the measurement on plot l, in environment i, replication j, block b, containing genotypes k,  $\mu$  = the overall mean of all plots in all environments;  $E_i$  = the effect of environment (trial), i,  $R(E)_{j(i)}$  = the effect of replication j within environment i,  $B_{(RE)b(ij)}$  = the effect of block b within replication j and environment i,  $G_k$  = the effect of genotype k,  $GE_{ik}$  = the interaction of environment i with genotype k,  $e_{ijkl}$  = the plot residual. As mixed model was used, genotypic means were adjusted using PROC MIXED of SAS, Version 9.2 (SAS institute, 2009). As suggested by Atlin et al. [1], the broad sense heritability ( $H_B$ ) was estimated for two models.

$$H_B \text{ for GE model was estimated as } H_B = \frac{\sigma^2 G}{\sigma^2 G + \sigma^2 G \times L / l + \sigma^2 e / lr} \tag{1}$$

$$\text{For the GLY model, it was estimated as } H_B = \frac{\sigma^2 G}{\sigma^2 G + \sigma^2 G \times L / l + \sigma^2 G \times Y / y + \sigma^2 G \times L \times Y / ly + \sigma^2 e / l yr} \tag{2}$$

Variance components, standard errors and broad sense heritability ( $H_B$ ) were estimated using Proc Varcomp SAS syntax of Version 9.2 (SAS institute, 2009).

## RESULTS

## Analysis of variance

Means squares obtained from analysis of variances for yield, yield components and qualities (Table 2) 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 LC interaction effects were highly significant for all traits. Regarding to the components of genotype  $\times$  environment interaction, the GL interaction was significant ( $p < 0.05$ ) for number of tillers, milleable stalk height, milleable stalk population, cane yield, brix% and sugar yield while the GC 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 GLC interaction was highly significant ( $p < 0.01$ ) for all traits.

Moreover, results from the analysis of variance conducted based on the GE model indicated that the environment, genotype and the interaction effects were all highly significant ( $p < 0.01$ ) for all traits studied (Table 2).

## Partitioning of genotype-environment interaction using variance components: The random model GLY vs. fixed GE model

The variance components (variance  $\pm$  standard error) for crop year (C), location (L), location  $\times$  crop year interaction (LC), components of GE interaction (G, GL, GC and GLC) and error were estimated and tested for yield, yield components and yield qualities (Table 3). Moreover, broad sense heritability was estimated for G, GL, GC and GLC interactions were estimated and tested for their significances. Results showed most of the components of the genotype-environment interaction were significant for all traits studied while GC was significant only for number of tillers, milleable stalk diameter and brix%. Strong and significant effect of G for cane yield components (number of tillers, milleable stalk diameter, milleable stalk height and milleable stalk population) yield quality traits (brix%, pol%, purity% and recoverable sucrose%). On the contrary, the effect of GLC interaction was strongest and highly significant ( $p < 0.01$ ) for cane and sugar yields. On the contrary, the magnitude of GC was relatively weak in most of

**Table 2:** Means squares of 49 sugarcane genotypes (G) evaluated across locations (L) and over crop years (C) for yield (tons ha<sup>-1</sup>m<sup>-1</sup>), yield components and yield qualities (The GLY and GE Models)

Sources of variation	DF	Random GLY (GLC) model									
		NT (ha <sup>-1</sup> )	MSD (cm)	MSH (m)	MSP (ha <sup>-1</sup> )	Cane yield (t ha <sup>-1</sup> m <sup>-1</sup> )	Brix in juice	Pol% in juice	Purity %	RS %	Sugar yield
Crop year (C)	3	1.44 $\times$ 10 <sup>12*</sup>	1.88 <sup>ns</sup>	8.83*	3.74 $\times$ 10 <sup>10ns</sup>	928.06*	18.22 <sup>ns</sup>	1.65 <sup>ns</sup>	100.83 <sup>ns</sup>	1.54 <sup>ns</sup>	0.66*
Locations (L)	4	1.09 $\times$ 10 <sup>11ns</sup>	5.63*	81.31*	2.51 $\times$ 10 <sup>10ns</sup>	1731.41*	214.76 <sup>ns</sup>	103 <sup>ns</sup>	933.65*	35.55 <sup>ns</sup>	20.19**
L $\times$ C	7	1.4 $\times$ 10 <sup>11**</sup>	0.67 <sup>ns</sup>	3.97**	1.37 $\times$ 10 <sup>10**</sup>	155.09*	48.87 <sup>ns</sup>	34.31**	110.40**	27.55**	2.88**
Replication	15	5.16 $\times$ 10 <sup>9**</sup>	0.62**	0.61**	6.06 $\times$ 10 <sup>8ns</sup>	13.12*	2.79 <sup>ns</sup>	8.32 <sup>ns</sup>	17.90*	3.12 <sup>ns</sup>	0.22*
Block(adj)	180	1.3 $\times$ 10 <sup>9*</sup>	0.05**	0.09 <sup>ns</sup>	4.42 $\times$ 10 <sup>8*</sup>	4.03 <sup>ns</sup>	1.52*	3.39*	5.08*	1.22**	0.08 <sup>ns</sup>
Genotypes (adj)	48	2.16 $\times$ 10 <sup>10**</sup>	0.59**	1.29**	2.98 $\times$ 10 <sup>9**</sup>	37.20**	9.13**	11.65**	22.75**	8.70**	0.38**
G $\times$ L	192	2.03 $\times$ 10 <sup>9*</sup>	0.06*	0.16**	6.04 $\times$ 10 <sup>8**</sup>	5.89**	2.10**	3.36 <sup>ns</sup>	6.09 <sup>ns</sup>	1.30 <sup>ns</sup>	0.10*
G $\times$ C	144	4.4 $\times$ 10 <sup>9**</sup>	0.07**	0.13 <sup>ns</sup>	3.26 $\times$ 10 <sup>8ns</sup>	4.63*	1.86 <sup>ns</sup>	3.65 <sup>ns</sup>	5.36 <sup>ns</sup>	1.36 <sup>ns</sup>	0.08 <sup>ns</sup>
G $\times$ L $\times$ C	336	1.5 $\times$ 10 <sup>9**</sup>	0.04 <sup>ns</sup>	0.10**	2.76 $\times$ 10 <sup>8**</sup>	4.44*	1.49**	3.21**	4.37 <sup>ns</sup>	1.16**	0.09**
Error	834	8.93 $\times$ 10 <sup>8</sup>	0.14	0.08	2.19 $\times$ 10 <sup>8</sup>	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
Fixed GE model											
Environment	17	3.7 $\times$ 10 <sup>11**</sup>	2.41**	26.**	2.1 $\times$ 10 <sup>10**</sup>	713.87**	79.4**	48.2**	319**	145.9**	7.20**
Replication	18	5.16 $\times$ 10 <sup>9**</sup>	0.62**	0.61**	6.06 $\times$ 10 <sup>8*</sup>	11.88**	2.79**	7.97**	10.86*	2.9*	0.22*
Block(adj)	216	1.3 $\times$ 10 <sup>9*</sup>	0.05**	0.09 <sup>ns</sup>	4.4 $\times$ 10 <sup>8**</sup>	3.80 <sup>ns</sup>	0.44 <sup>ns</sup>	03.45*	4.96*	1.52*	0.08 <sup>ns</sup>
Genotypes	48	2.16 $\times$ 10 <sup>10**</sup>	10.6**	1.3**	2.98 $\times$ 10 <sup>9**</sup>	51.39**	9.54**	12.8**	22.6**	8.99**	0.38**
GE	816	2.18 $\times$ 10 <sup>9*</sup>	0.05**	0.13**	3.75 $\times$ 10 <sup>8**</sup>	4.78**	1.55**	3.16**	5.02**	1.7**	0.097*
Error	648	8.93 $\times$ 10 <sup>8</sup>	0.036	0.08	2.19 $\times$ 10 <sup>8</sup>	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  $< 0.05$ ; <sup>ns</sup>: non-significant; E: Environment; R: Replication; Blk: Block; adj: adjusted; NT: Numbers of Tillers; MSD: Milleable Stalk Diameter; MSH: Milleable Stalk Height; MSP: Milleable Stalk Population

**Table 3:** Components of genotype x environment interaction and variance components (Variance estimate+Standard Error) for Yield (tons ha<sup>-1</sup>m<sup>-1</sup>), yield components and yield qualities (%) (GLY model)

Variance Component	Cane Yield and Yield Components (Variance estimate+Standard Error)				
	NT (ha <sup>-1</sup> )	MSD (cm)	MSH (m)	MSP (ha <sup>-1</sup> )	Cane yield (t ha <sup>-1</sup> m <sup>-1</sup> )
Crop year (C)	3.3 × 10 <sup>9</sup> ± 3.96 × 10 <sup>9ns</sup>	0.0054 ± 0.007 <sup>ns</sup>	0.01 ± 0.023 <sup>ns</sup>	6.03 × 10 <sup>7</sup> ± 9.7 × 10 <sup>7ns</sup>	0
Location (L)	0	0.017 ± 0.016 <sup>ns</sup>	0.27 ± 0.23 <sup>ns</sup>	3.76 × 10 <sup>7</sup> ± 7.5 × 10 <sup>7ns</sup>	3.87 ± 3.81 <sup>ns</sup>
L × C	1.3 × 10 <sup>9</sup> ± 6.25 × 10 <sup>8*</sup>	0.0004 ± 0.005 <sup>ns</sup>	0.04 ± 0.024 <sup>ns</sup>	1.33 × 10 <sup>8</sup> ± 8.08 × 10 <sup>7*</sup>	2.09 ± 1.15*
G	8.5 × 10 <sup>8</sup> ± 2.3 × 10 <sup>7*</sup>	0.025 ± 0.003**	0.05 ± 0.0006**	8.8 × 10 <sup>7</sup> ± 1.2 × 10 <sup>6*</sup>	0.91 ± 0.21**
G × L	1.13 × 10 <sup>8</sup> ± 5.07 × 10 <sup>7*</sup>	0.002 ± 0.0013*	0.01 ± 0.004**	5.8 × 10 <sup>7</sup> ± 1.3 × 10 <sup>6**</sup>	0.24 ± 0.17**
G × C	4.42 × 10 <sup>8</sup> ± 9.5 × 10 <sup>7*</sup>	0.004 ± 0.0014**	0.003 ± 0.003 <sup>ns</sup>	8.9 × 10 <sup>6</sup> ± 7.5 × 10 <sup>6ns</sup>	0.019 ± 0.005 <sup>ns</sup>
G × L × C	3.34 × 10 <sup>8</sup> ± 6.7 × 10 <sup>7**</sup>	0.003 ± 0.0021 <sup>ns</sup>	0.02 ± 0.006**	2.91 × 10 <sup>7</sup> ± 1.2 × 10 <sup>7**</sup>	0.96 ± 0.21**
Error	9.05 × 10 <sup>8</sup> ± 0.00**	0.037 ± 0.002**	0.07 ± 0.005**	2.24 × 10 <sup>8</sup> ± 0.00	3.8 ± 0.23**
HB (GLY)	0.81	0.89	0.88	0.79	0.77
Sugar yield and quality traits (Variance estimate+Standard Error)					
	Brix in juice (%)	Pol% in juice (%)	Purity (%)	RS (%)	Sugar yield (t ha <sup>-1</sup> m <sup>-1</sup> )
Crop year (C)	0	0	0	0	0
	0.26 ± 0.29 <sup>ns</sup>	0.41 ± 0.47 <sup>ns</sup>	2.53 ± 2.4 <sup>ns</sup>	0.08 ± 0.12 <sup>ns</sup>	0.06 ± 0.056 <sup>ns</sup>
L × C	0.45 ± 0.24*	0.19 ± 0.14 <sup>ns</sup>	1.07 ± 0.6*	0.16 ± 0.10*	0.021 ± 0.01*
G	0.45 ± 0.07**	0.66 ± 0.12**	1.4 ± 0.2**	0.35 ± 0.05**	0.013 ± 0.0005**
G × L	0.157 ± 0.05**	0.25 ± 0.09**	0.56 ± 0.17**	0.076 ± 0.033*	0.004 ± 0.0028*
G × C	0.08 ± 0.038*	0.097 ± 0.07 <sup>ns</sup>	0	0.036 ± 0.027 <sup>ns</sup>	0.0027 ± 0.0025 <sup>ns</sup>
G × L × C	0.18 ± 0.061**	0.11 ± 0.14 <sup>ns</sup>	0.36 ± 0.21*	0.15 ± 0.05**	0.017 ± 0.0046**
Error	0.87 ± 0.057**	2.42 ± 0.15**	3.71 ± 0.23**	0.67 ± 0.044**	0.063 ± 0.004**
HB (GLY)	0.83	0.80	0.84	0.82	0.72

\*\*= highly significant at p<0.01; significant at p<0.05; Rep: Replications; SS: Sum Squares; Blk: Block; G: Genotypes; GxL: Genotype × Location interaction; G × C: Genotype × Crop year interaction; G × L × C=Genotype × Location × Crop year interaction; H2B: Broad Sense Heritability (Repeatability); G: Genotypes; G × L: Genotype × Location interaction; G × C=Genotype × Crop Cycle interaction; G × L × C: Genotype × Location × Crop Cycle interaction; H2B: Broad Sense Heritability (Repeatability); \*NT: Numbers of Tillers; MSD: Milleable Stalk Diameter; MSH: Milleable Stalk Height; MSP: Milleable Stalk Population

**Table 4:** Components of genotype × environment interaction and variance components (Variance estimate+Standard Error) for yield (tons ha<sup>-1</sup>m<sup>-1</sup>), yield components and yield qualities (%) (Fixed GE Model)

Component	Cane Yield and Yield Components (Variance estimate+Standard Error)				
	NT (ha <sup>-1</sup> )	MSD (cm)	MSH (m)	MSP (ha <sup>-1</sup> )	Cane yield (t ha <sup>-1</sup> m <sup>-1</sup> )
Environment (E)	3.7 × 10 <sup>9*</sup>	0.023**	0.26**	2.08 × 10 <sup>8**</sup>	5.35**
Genotype (G)	9.7 × 10 <sup>8**</sup>	0.027**	0.055**	1.06 × 10 <sup>8*</sup>	1.065**
GxE	7.5 × 10 <sup>8*</sup>	0.007*	0.03*	9.2 × 10 <sup>7**</sup>	1.28**
Error	8.9 × 10 <sup>8**</sup>	0.037**	0.074**	2.07 × 10 <sup>8*</sup>	3.69**
SE	9944	0.004	0.002	1.5 × 10 <sup>8</sup>	0.23
HB (GE)	0.93	0.95	0.94	0.90	0.78
Sugar yield and quality traits (Variance estimate+Standard Error)					
	Brix in juice (%)	Pol% in juice (%)	Purity (%)	RS (%)	Sugar yield (t ha <sup>-1</sup> m <sup>-1</sup> )
Environment (E)	0.79*	0.44**	3.18**	1.51**	0.07*
Genotype (G)	0.39**	0.46**	0.80**	0.23**	0.013**
GxE	0.38**	0.42**	0.84**	0.47 <sup>ns</sup>	0.022**
Error	0.86**	2.37 <sup>ns</sup>	3.67 <sup>ns</sup>	0.84**	0.063**
SE	0.06	0.14	0.21	0.06	0.001
HB (GE)	0.89	0.84	0.85	0.83	0.82

\*\*= highly significant at p<0.01; significant at p<0.05; Rep: Replications; SS: Sum Squares; Blk: Block; G: Genotypes; G × L: Genotype × Location Interaction; G × C: Genotype × Crop Year Interaction; G × L × C: Genotype × Location × Crop Year Interaction; H<sup>2</sup><sub>B</sub>: Broad Sense Heritability (Repeatability); G: Genotypes; G × L: Genotype × Location Interaction; G × C: Genotype × Crop Cycle Interaction; G × L × C: Genotype × Location × Crop Cycle Interaction; H<sup>2</sup><sub>B</sub>: Broad Sense Heritability (Repeatability); \*NT: Numbers of Tillers; MSD: Milleable Stalk Diameter; MSH: Milleable Stalk Height; MSP: Milleable Stalk Population

the traits. Based on the fixed GE model, variance components were estimated and tested for G, GE and error (Table 4). The same trend was observed as in the GLC model where the variance component for G was highest and significant

for yield components and quality traits. Moreover, the variance component of GLC interaction was still dominant for yield (cane and sugar yields). Furthermore, the standard errors were computed based on the residual all traits. Using the GLY (GLC) model, standard errors of  $2.3 \times 10^7$ , 0.0051, 0.006,  $1.2 \times 10^6$ , 0.24, 0.07, 0.16, 0.22, 0.008 and 0.005 genotype means were computed for number of tillers, milleable stalk diameter, milleable stalk height, milleable stalk population, cane yield, brix%, pol%, purity%, recoverable sucrose% and sugar yield, respectively. while using GE model on the same dataset, values of the standard errors were changed to 2035800, 0.004, 0.002, 586327, 0.23, 0.06, 0.14, 0.21, 0.06 and 0.004 for number of tillers, milleable stalk diameter, milleable stalk height, milleable stalk population, cane yield, brix%, pol%, purity%, recoverable sucrose% and sugar yield, respectively.

#### **Broad sense heritability ( $H_b$ ) (repeatability): GLY vs. GE model**

Based on the GLY model, the broad sense heritability estimates (repeatability) of 0.81, 0.89, 0.88, 0.79, 0.77, 0.83, 0.80, 0.84, 0.82 and 0.72 were recorded for number of tillers, milleable stalk diameter, milleable stalk height, milleable stalk population, cane yield, brix%, pol%, purity%, recoverable sucrose% and sugar yield, respectively (Table 3). Moreover, the broad sense heritability estimates for number of tillers, milleable stalk diameter, milleable stalk height, milleable stalk population, cane yield, brix%, pol%, purity%, recoverable sucrose % and sugar yield were 0.93, 0.0.95, 0.94, 0.90, 0.82, 0.89,84, 0.85, 0.83 and 0.82, respectively (Table 4).

### **DISCUSSION**

Results of analysis of variance (Table 2) indicated the location and crop year effects were significant effect ( $p < 0.05$ ) for most of the traits. It suggested the locations and crop years were diverse in nature highlighting the necessity of conducting variety trials across locations and over crop years. On the other hand, the significance of location  $\times$  crop year effect suggests crop year effect was strongly controlled by location. Our result is consistent with findings reported by Mulema et al. [8] 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. [9]. 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  $\times$  environments interaction is concerned, the GL interaction was significant for cane yield and its components thereby suggesting quantitative yield traits were more affected by genotype-location interaction and increasing number of location benefited more selection gains. The GLC interaction was highly significant for all traits. It suggested demonstrated that the GE 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 [10] and Kimbeng et al. [11] in which genotype-location (GL) and genotype-location-crop year (GLC) interactions affects cane yield and its components of sugarcane. The non-significant smallest and variance estimate of GC interaction in cane yield, sugar yield and recoverable sucrose% suggested yield traits of genotypes were least affected by genotype-crop year interaction thereby suggesting relatively less selection gain could be obtained from selection of genotypes over crops years.

Furthermore, GLC and GL interaction effects were more important than GC interaction, further indicated that testing across locations was more important than testing across crop cycles. The large and significant GLC interaction, especially for recoverable sucrose %, indicated that complexity of selecting for yield traits. 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 GE interaction. The variance component analysis for the yield quality traits revealed that larger and highly significant variance was estimated for genotype; a strong genotypic effect controls the quality traits in sugarcane which was greater than the GLC variance estimates. Most of the time, the genotype site or location is generally regarded as being repeatable (predictable), as it involves genotype interactions with relatively stable site characteristics such as soil type, latitude, altitude, etc. In the present study, the first and second ratoon crops were raised from the first plant cane crop and the ratoon crop would impose the confounding effect and probably contribute to the complexity of the GE as the GLC was larger than the GL. Result of the present study was in close agreement with reports of Ramburan et al. [12] and Zhou et al. [13].

Pooled analysis of variance based on the GE model also indicated the environment, genotype and GE interaction effects were all highly significant ( $P \leq 0.01$ ) for all traits studied. The result suggested that the environments were diverse while marked variability existed among the genotypes evaluated. The highly significant effect of the GE

interaction suggested the genotypes showed significant rank changes in performance across environments. Similar results were reported in which environment, genotype and GE interaction effects were all highly significant yield, cane yield components and yield quality traits. In the fixed GE model (Table 2), all of the sources of variations were significant for all traits studied as compared to the GLY model which could be due to inflation of errors as a result of using inappropriate model (the fixed model).

Results of variance component analysis revealed the larger and highly significance of G and GLC effects (Table 3). The large variance component of G indicated there was strong genotypic effect in controlling the variability. The large and significant GLC interaction indicated that complexity of selecting for yield traits, thereby suggesting the importance of testing across locations and over crop year. 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 GE interaction. Generally, the order of the importance was G>GLC>GL>GC for cane yield components and quality traits. The significance and dominance of the G effect in all traits demonstrated high level of genetic stability within the genotypes introduced from different geographical origins. This is ideal for making progress from selection of superior genotypes for high yield. In this case, our result is consistent with the findings reported by Zou et al. [14]. For yield traits (cane and sugar yields), GLC interaction was more important than the other components of GE interaction. The relatively strong and high significance level of GLC interaction for yield suggested the possibility of the non-repeatable GE interaction under Ethiopian agro-ecological condition. In the present investigation, the inclusion of random GLY model helped us efficient partitioning of the GE interaction in to its components. Results of similar studies carried out by Yang [5] indicated ignoring GLC interaction resulted in the declaration of excess crossover interactions and misinterpretations of results. In GLC model, the magnitude of the error term was the largest variance component as compared with the components of GE interactions (Table 4). It suggested the models used were not sufficient enough to account the variability and the use of appropriate experimental design and optimum numbers of replications could solve such problems.

The heritability estimates based on both GLY (Table 3) and fixed GE (Table 4) models indicated better repeatability (0.72-0.95) of the experiments over crop years and across locations. For comparison purposes, the broad sense heritability and standard errors were estimated for both models. It also suggested that the overestimation of heritability values by the fixed GE model. The repeatability of the experiments or trials were overestimated by 12.9, 6.32, 6.38, 12.22, 6.74, 4.76, 1.18, 1.2 and 11.20% in number of tillers, milleable stalk diameter, milleable stalk height, milleable stalk population, cane yield, brix%, pol%, purity%, recoverable sucrose % and sugar yield, respectively when the GE fixed model was used. The changes of inflations were more prevalent in yield components than in yield qualities thereby suggesting yield components were more subjected to spatial and temporal variations as compared to yield quality traits. Our result suggested such repeatability could be attained by conducting trial over a minimum of three crop years and across four locations for the traits studied. It also indicated that the cross over interaction existed does not significantly limit our selection progress. Result of the present study was in agreement with reports of Atlin et al. [1].

Compared to the cane yield components and yield qualities, the heritability estimates for cane and sugar yields were relatively lower in both models. This could be attributed to the higher variance component of crossover interaction (GLC interaction) observed in cane and sugar yields. Generally, the changes in variance component estimates observed as a result of using different models dictates the future decisions made on the alternative use of these models over time and across locations determines strengthens of future sugarcane breeding program in Ethiopia.

## CONCLUSION AND RECOMMENDATIONS

Results of the present investigation indicated the existence of complex genotype x environment interaction which necessitates testing of genotypes across locations and over crop years. In both random and fixed models, variance component estimates revealed strong genotypic and GLC interaction effects for all yield traits. Regarding to the relative importance of the components of the genotype-environment interaction, genotypic effect was more important for cane yield components and yield quality traits than the other components while GLC interaction was relatively more important for cane and sugar yields. The larger and significant variance component of the GLC interaction indicated the existence of cross over interaction where the crop year effect was highly controlled by location effect. Heritability estimates of traits studied under both models indicated better repeatability of the experiments. Compared to the GLC model, the fixed GE model showed overestimation of heritability values. Thus, we recommend including random GLC model in sugarcane METs analysis conducted over crop years and across locations under Ethiopian agro ecological conditions.

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