SHORT NON-REFEREED PAPER

GENOTYPE BY ENVIRONMENT INTERACTION EFFECT ON GENOTYPE SELECTION AMONG REGIONAL VARIETY TRIALS IN SOUTH AFRICA

SHINGA N[1,2], ZHOU M[1,2,3] AND SIBIYA J[2]

[1]*South African Sugarcane Research Institute, P/BagX02, Mount Edgecombe, 4300, South Africa*
[2]*University of KwaZulu-Natal, P/Bag X01, Scotsville, 3209, South Africa*
[3]*University of Free State, PO box 339, Bloemfontein, 9300, South Africa*
Nomfundoshinga@sugar.org.za   Marvellous.Zhou@sugar.org.za

Introduction

Genotype x Environment interactions (GxE) influence differences in phenotype values of genotypes when exposed to a range of environments (Falconer and Mackay, 1996)) and confounds the selection of superior genotypes (Milligan *et al.,* 1990; Kimbeng *et al.*, 2002, 2009). In South Africa, sugarcane breeding programmes are established in four agro-ecological regions namely irrigated, midlands, coastal long and coastal short cycle with different growing conditions (Zhou., 2013). Irrigated region is characterised by low rainfall, and irrigation is used to optimise crop-growth. The coastal region has high temperatures, hilly topography, soil variability and summer rainfall, which is further divided into coastal short cycle characterised by early maturing cultivars (12-15 months) to escape yield loss from the stem borer *Eldana saccharina* Walker (Lepidoptera: Pyralidae) (eldana) infestation that occurs later in the region, and coastal long cycle characterised by late maturing cultivars (18 months) and high eldana predation. The midlands region has long and cold winters.

During the selection, magnitude and the source of GxE must be considered (Acquaah., 2009) as guides to selection of genotypes. The objectives of this study are to determine magnitudes of genotype by environment interaction effects among regional advanced variety trials and identify important components of genotype by environment interaction among regional variety trials.

Materials and Methods

Data from plant, first, second and/or third ratoon crops were collected from advanced variety trials series planted in 2010 at five to six locations in each of the regional breeding programmes. Irrigated data was collected from early and late planted trials, coastal long and short cycle from average and high potential sites while midlands was from humic and sandy soils. Genotypes in trials ranged from 25 to 34 genotypes and were different among breeding programmes. A randomised complete block design with three to six replications was used. Plots were 5 rows by 8 m, spaced 1.1 m (midlands), 1.2 m (coastal) and 1.5 m (irrigated).

At harvest, the stalks in each plot were hand cut. Twelve stalks were randomly chosen, bundled and sent to the sucrose laboratory for cane quality using the standard protocol of Shoonees-Muir et al. (2009). The millable stalks in each plot were weighed using a digital scale mounted on a tractor operated hydraulic boom and converted to tons cane per hectare. Data were analysed using the linear mixed model of the Statistical Analysis System (SAS):

$$Y_{ijkl} = \mu + L_l + R(L)_{kl} + G_i + GL_{il} + GR(L)_{ikl} + C_j + LC_{jl} + GC_{ij} + GLC_{ijl} + E_{ijkl} \quad \text{Equation 1}$$

where, Y_{ijkl} = the observation for genotype i (i = 1,2,3….g) in C_j = crop year j (j = 1,2,3....c), at L_l = location l (l = 1,2,3…l), in R_k = replication k (k = 1,2,3), L_l = the fixed effect of the lth location, $R(L)_{kl}$ = the random effect of kth replication nested within lth location, G_i = the fixed effect of the ith genotype, GL_{il} = the fixed interaction effect between the ith genotype in the *l*th

location, *GR(L)ikl* = the random interaction effect between the *ith* genotype and the *kth* replication nested with the *lth* location, *Cj* = the fixed effect of the jth crop-year; *LCjl* = the fixed interaction effect between the *lth* location and *jth* crop, *GCij* = the fixed interaction effect between the *ith* genotype and the *jth* crop year; *LGClij* = fixed interaction effect between the *lth* location and the *ith* genotype and the *jth* crop year, and *Eijkl* = residual error.

Results and Discussion

Location, genotype and crop year F-values were highly significant (P<0.001) for all breeding programmes for all traits (Table 1), indicating differences in trait values among locations, crop-years and genotypes. Genotype by location interaction (GL) for cane and sugar yield was significant (P<0.01) across irrigated, coastal long and midlands trials and significant (P<0.05) for ERC% cane across all regions, suggesting genotype locations influenced genotype ERC% cane. Location by crop year (LC) interaction effect was highly significant across all traits and regions, indicating that at each location, trait values were different among crop years. Genotype by crop-year interaction (GC) for cane and sugar yield was significant across regions, suggesting ratooning of genotypes was different. The GC for ERC was significant for irrigated, coastal long and midlands regions. Genotype by location by crop year interaction (GLC) for cane yield was significant for irrigated, coastal short and midlands indicating the ratooning of genotypes could be location specific. GLC for ERC% cane was significant across irrigated, coastal long and midlands, while that for sugar yield was significant across irrigated and midlands.

Location differences for cane yield were largest among irrigated and midlands, suggesting correct siting compared to coastal regions. Genotype differences for cane yield were highest for irrigated and midlands compared to coastal regions. Crop year and GC effects were highest among coastal long and midlands (18-24 months cutting cycles) than irrigated and coastal short (12 month cutting cycles). GL effects were largest for irrigated (confounding of seasonal effect) compared to midlands and coastal regions. LC effects were largest for irrigated compared to coastal and midlands. For ERC% cane, location effects were highest for coastal short cycle (breeding for early maturity) and lowest for coastal long cycle while genotype effects were highest for coastal short and midlands compared to irrigated and coastal long cycle. For sugar yield, genotype differences were highest for irrigated and midlands compared to coastal regions while GL was largest for irrigated compared to other regions, probably due to confounding seasonal effects. GC was highest for midlands compared to other regions.

The coefficient of variation was highest for coastal compared to irrigated midlands due to the high field variability at Gingindlovu research station.

Conclusion

GL effects were largest for irrigated compared to other regions in all traits due to confounding of seasonal effect. Crop year and GC effects were highest among coastal long and midlands where ratooning ability is expected to be more important. Location effects for ERC% cane were highest for coastal short cycle where breeding for early maturity is a major objective and lowest for coastal long cycle, while genotype effects were highest for coastal short and midlands compared to irrigated and coastal long. For sugar yield, genotypes differences were highest for irrigated and midlands, while GL was largest for irrigated compared to other regions probably due to confounding seasonal effects. GC was highest for midlands compared to other regions.

REFERENCES

Falconer DS and Mackay TFC (1996). Introduction to Quantitative Genetics. 4th Edition, Longmans Group Ltd, England.

Kimbeng CA, Rattey AR and Hetherington M (2002). Interpretation and implications of genotype by environment interactions in advanced stage sugarcane selection trials in central Queensland. *Australian Journal of Agricultural Research* 53: 1035-1045.

Kimbeng CA, Zhou MM and Da Silva JA (2009). Genotype x environment interactions and resource allocation in sugarcane yield trials in the Rio Grande valley region of Texas. *Journal of the American Society of Sugar Cane Technologists* 29: 11-24.

Milligan SB, Gravois KA, Bischoff KP and Martin FA (1990). Crop effects on broad-sense heritabilities and genetic variances of sugarcane yield components. *Crop science* 30: 344-349.

Shoonees-Muir B, Ronaldson M, Naidoo G, and Schorn P (2009). SASTA laboratory manual including the official methods. South African Sugarcane Technologists Association Publication, Durban

Zhou M (2013). Conventional sugarcane breeding in South Africa: Progress and future prospects. *American Journal of Plant Sciences* 4: 189.

Table 1. The F-values and P-values for cane yield, sugar yield and ERC % cane traits for advanced variety trials for irrigated, coastal short cycle, coastal long cycle and midlands regions.

Effect	Irrigated	Coastal short cycle	Coastal long cycle	Midlands
Cane yield (t/ha)				
L	126.5***	73.88***	61.49***	127.56***
G	9.99***	5.67***	5.15***	12.07***
GL	2.23***	1.14ns	1.5**	1.5**
C	237.35***	189.6***	1283.32***	2587.01***
LC	119.65***	45.27***	55.77***	39.53***
GC	1.79***	1.65***	3.2***	5.27***
GLC	1.17*	1.27*	1.27ns	1.24*
R^2	0.92	0.83	0.94	0.95
CV	10.78	27.70	16.51	13.33
Mean±SD	119.93±12.93	61.96±17.16	80.82±13.34	99.20±13.22
R(L)	13.52±7.22*	-	10.10±7.13ns	9.39±5.44*
R*G(L)	44.88±6.99***	102.06±15.86***	84.93±16.17***	51.11±9.42***
Residual	167.13±7.23***	289.98±15.90***	178.03±14.54***	176.24±9.75***
ERC % cane				
L	274.71***	769.1***	56.22***	268.75***
G	19.89***	30.46***	18.44***	30.25***
GL	2.71***	2.29***	2.03***	1.34*
C	90,41***	115.34***	910.4***	1292.95***
LC	82.84***	76.84***	391.87***	92.13***
GC	1.67***	1.15ns	1.74*	3.51***
GLC	1.24**	1.09ns	1.37*	1.30**
R^2	0.91	0.94	0.93	0.92
CV	9.54	7.28	8.22	5.64
Mean±SD	12.33±1.18	11.31±0.82	11.32±0.93	12.76±0.72
R(L)	0.05±0.03*	0.01±0.01ns	0.01±0.01ns	0.00±0.00ns
R*G(L)	0.10±0.04**	0.01±0.02ns	0	0.05±0.02**
Residual	1.38±0.06***	0.67±0.04***	0.86±0.05***	0.52±0.03***
Sugar yield (t/ha)				
L	74.35***	133.33***	97.53***	60.97***
G	7.59***	3.49***	4.06***	7.12***
GL	2.87***	1.24ns	1.91***	1.58***
C	256.58***	183.09***	392.06***	3234.06***
LC	107.50***	33.74***	164.8***	40.87***
GC	2.52***	1.44*	2.37***	5.22***
GLC	1.35***	1.17ns	1.16ns	1.34**
R^2	0.87	0.84	0.93	0.95
CV	13.51	33.44	20.03	14.68
Mean±SD	14.41±1.95	7.10±2.37	9.11±1.82	12.67±1.86
R(L)	0.17±0.10*	-	0.12±0.09ns	0.17±0.10*
R*G(L)	0.80±0.14***	1.72±0.29***	0.86±0.25***	0.93±0.18***
Residual	3.80±0.16***	5.53±0.30***	3.33±0.27***	3.49±0.19***

*** P<0.001 **P<0.01 *P<0.05, ns=non-significant, L=location, G=genotype, GL=genotype by location interaction, GC=genotype by crop-year interaction, GLC=genotype by location by crop year interaction, R^2=coefficient of determination, CV=coefficient of variation