

SHORT NON-REFEREED PAPER

THE INFLUENCE OF GENOTYPE BY ENVIRONMENT INTERACTION ON YIELD, QUALITY AND AGRONOMIC TRAITS FOR THE COASTAL SHORT CYCLE BREEDING PROGRAMME

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Abstract

Breeding programme decisions commonly rely on knowledge of the underlying genetic structure of the population and an understanding of genotype by environment (GE) interaction. GE is known to confound selection decisions by altering the genotype performance across locations. The Coastal Short Cycle (CSC) average potential represents environments where sugarcane is harvested at 12 months to reduce *Eldana saccharina* Walker (Lepidoptera: Pyralidae) (eldana) damage. The objective of this study was to evaluate the influence of GE trends on yield, quality and agronomic traits for the CSC programme. Yield, quality and agronomic data were collected from plant, first and second ratoon crops of the on-station (UV) and off-station (U1V) variety trials at Gingindlovu research station. Data were analysed using the mixed procedure of SAS. The genotype effect produced the highest F-values (4.14 to 15.14); these were highly significant ($P < 0.001$) for all trial series and traits, indicating high genotype variability. Genotype by location effect was not significant ($p > 0.05$) for fibre, purity and length, indicating that these traits were stable across locations. Significant ($p < 0.01$) GE effects were however, observed for all the other traits, indicating that genotypes perform differently in different locations and site specific evaluation is required. There were significant ($p < 0.01$) genotype x crop interaction effects for all traits except purity, indicating the importance of ratooning ability. A non-significant ($p > 0.05$) location by genotype by crop interaction was observed for length and diameter, indicating the stability of these traits. It can be concluded that GE interaction has a significant influence on the performance of genotypes.

Keywords: genotype-environment interaction, yield components, quality, ratooning

Introduction

Several studies have shown the importance of genotype by environment (GE) interactions in sugarcane affect the selection process (Jackson and Hogarth, 1992; Mirzawan *et al.*, 1993; Jackson *et al.*, 1995). GE effects confound the genotype selection.

The Coastal Short Cycle (CSC) average potential represents environments where sugarcane is harvested at 12 months crop age to reduce *Eldana saccharina* Walker (Lepidoptera: Pyralidae) (eldana) damage by an escape mechanism. Studies are required to identify key selection variables that determine adaptation to CSC and would enhance selection gains. The objective of this study was to evaluate the influence of GE trends on yield, quality and agronomic traits for the CSC programme and their implications on variety development for the CSC.

Materials and Methods

Data from plant, first and second ratoon crops were collected from four advanced variety trial series planted in 2005 to 2009 at Gingindlovu on and off-station sites. A randomised complete block design was used, with 30 genotypes, 3 replications, and plot sizes of 5 rows by 8 m, spaced at 1.2 m apart. At harvest, all millable stalks in the plots were hand cut, counted and weighed. A sample of 12 stalks was randomly chosen from each plot for the estimation of quality traits, stalk height and stalk diameter. Data were analysed using the Statistical Analysis System (SAS Institute, 2009) using the linear mixed model:

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

where, Y_{ijkl} = the observation for genotype i ($i = 1, 2, 3, \dots, g$) in C_j = crop year j ($j = 1, 2, 3, \dots, c$), L_l = the fixed effect of the l th location; $R(L)_{kl}$ = the random effect of k th replication nested within l th location; G_i = the fixed effect of the i th genotype; GL_{il} = the fixed interaction effect between the i th genotype in the l th location; $GR(L)_{ikl}$ = the random interaction effect between the i th genotype and the k th replication nested with the l th location; C_j = the fixed effect of the j th crop-year; LC_{jl} = the fixed interaction effect between the l th location and j th crop; $CR(L)_{jkl}$ = random interaction effect between the j th crop year and the k th replication nested within the l th location; GC_{ij} = the fixed interaction effect between the i th genotype and the j th crop year; LGC_{lij} = fixed interaction effect between the l th location and the i th genotype and the j th crop year; and E_{ijk} = residual error.

Results and Discussion

Only the G, GL, GC and GLC components of Gx E were interpreted because they influence genotype selection. The genotype effect had the largest and most highly significant ($P < 0.0001$) F-values for all quality compared to GE effects (Table 1). The order of magnitude of the effects was $G > GL > GC > GLC$, indicating that the most complex Gx E was least important. GLC was largely non-significant for the 2005 and 2007 trial series, while GL and GC were significant ($P < 0.05$) for most quality traits across series. The results suggest selection of genotypes for quality traits would be effective. The results also suggest the location effects (GL) were important, indicating that genotypes adapted to specific locations can be identified. The significant GC effects suggest that selecting for ratooning ability is required. The largely non-significant GLC effects suggest that ratooning ability of genotypes was not location specific. The order of magnitude of G effects for traits was dry matter (DM) % cane > Fibre % cane > Brix % cane > Pol % cane > ERC % cane > Purity %. Brix % cane, Pol % cane and ERC % cane had largely similar values, indicating the similarity of the traits. These traits largely reference sucrose content. Large R^2 values indicated that the statistical model adequately represented the data. ERC % cane, a derived variable, had the largest CV% while DM % cane and Purity % had the lowest.

For yield traits (Table 2), the G effect had the largest and most significant ($P < 0.0001$) F-values for all effects across trial series. The order of magnitude of the components of Gx E was $G > GL > GC > LGC$. The large G effect indicates genotypes can be accurately selected for yield traits. The significant GL and GC indicate location specific adaptation of genotypes and genotype differences in ratooning ability, respectively. GLC was largely non-significant ($P > 0.05$), or the least significant of the GE components for most traits. However, GLC was largest and most significant for tons cane/ha (TCH) and tons sugar/ ha (TSH), indicating the

complex GE for these traits. This result means that the ratooning of genotypes for traits, TCH and TSH was location specific. Generally, TCH and TSH are known to be controlled by several genes with additive and dominance effects. Diameter had non-significant GLC indicating that genotype values were not influenced by location and ratooning and that the ratooning was not location specific. Stalk height had largely non-significant GL but significant GC, indicating no genotype differences across locations but that height showed significant genotype differences across ratoon crops. Stalk height, stalk diameter and stalk population had larger F values than TCH and TSH indicating the reduced precision of selecting for yield compared to selecting for the yield components. The results suggest that selecting for yield via the components may be more efficient (Zhou *et al.*, 2013).

Quality traits produced larger F-values for G effects than yield traits indicating the lower efficiency associated with detecting genotype differences for yield traits. The yield traits also had lower R^2 and larger CV% than quality traits, further highlighting the lower precision associated with yield traits. The GLC component was largely more significant for yield than quality traits, indicating the complexity of identifying genotypic differences for yield rather than quality.

Conclusions

The genotype effects were the largest for all traits, indicating that superior genotypes can be identified. The study showed that yield traits were controlled by more complex GE effects. Further studies should quantify whether the GE effects result in rank changes.

Table 1. The F-values and their P-values for quality traits for trial series planted in 2005, 2006, 2007 and 2009.

Trait	Effect	2005	2006	2007	2009
DM % cane	L	284.53**	236.47**	116.88*	164.66*
	G	21.88**	20.06**	13.60**	19.42**
	LG	2.33*	1.64*	1.39ns	2.26*
	C	311.64**	1024.14**	1193.01**	1085.19**
	LC	214.50**	16.08**	334.74**	409.91**
	GC	1.98**	1.69*	1.62*	2.70**
	LGC	1.13ns	1.58*	1.46ns	1.46*
	R ²	0.91	0.94	0.96	0.95
	CV%	3.56	3.92	3.59	3.24
Fibre % cane	L	5.74ns	46.57*	0.30ns	41.91*
	G	14.35**	14.10**	9.47**	21.17**
	LG	1.35ns	0.95ns	1.03ns	1.63*
	C	368.10**	642.30**	370.81**	82.96**
	LC	98.55**	199.08**	39.43**	36.61**
	GC	1.79*	2.52**	1.82*	1.66*
	LGC	1.09ns	1.89*	1.11ns	1.24ns
	R ²	0.87	0.93	0.90	0.86
	CV%	7.04	6.39	6.73	6.38
Brix % cane	L	112.988	90.81*	337.39**	322.21**
	G	11.90**	12.85**	12.15**	8.01**
	LG	3.48**	3.40**	2.81**	1.36ns
	C	501.93**	430.72**	980.32**	1736.64**
	LC	60.46**	254.02**	419.17**	598.38**
	GC	1.88*	1.88*	1.28ns	2.64**
	LGC	1.21ns	2.01**	1.27ns	1.97*
	R ²	0.89	0.91	0.95	0.97
	CV%	4.77	5.32	4.28	3.56
Purity %	L	211.51**	56.03*	46.17*	847.14**
	G	6.02**	4.03**	6.12**	5.44**
	LG	1.95*	1.32ns	1.14ns	4.48**
	C	451.06**	345.37**	372.92**	302.25**
	LC	34.21**	77.32**	16.38**	411.92**
	GC	1.57*	1.42*	2.16**	2.28*
	LGC	1.07ns	1.33ns	0.88ns	2.45**
	R ²	0.87	0.85	0.89	0.92
	CV%	3.09	3.40	2.47	2.56
Pol % cane	L	174.92*	106.96*	311.05**	538.41**
	G	11.50**	10.31**	11.31**	7.97**
	LG	3.37**	2.70**	2.27*	2.27*
	C	240.44**	499.83**	886.55**	1483.35**
	LC	39.87**	207.19**	311.54**	739.43**
	GC	1.90*	1.81*	1.53*	2.61**
	LGC	1.12ns	1.83*	1.25ns	1.75*
	R ²	0.87	0.91	0.95	0.97
	CV%	6.86	7.44	5.88	5.03
ERC % cane	L	194.01*	100.17*	265.35**	653.77**
	G	10.50**	8.78**	10.31**	7.60**
	LG	3.10**	2.37*	1.98*	2.75**
	C	212.29**	485.76**	779.75**	1231.40**
	LC	31.36**	181.55**	246.11**	713.20**
	GC	1.86*	1.76*	1.67*	2.55**
	LGC	1.09ns	1.71*	1.17ns	1.75*
	R ²	0.86	0.90	0.94	0.96
	CV%	8.91	9.42	7.31	6.51

*= P<0.05, **= P<0.001; ns= P>0.05; CV= coefficient of variance; L= location effects; G = genotypic effect; LG = location by genotype effect; C = crop effect; LC = location by crop effect; GC = genotype by crop effect; LGC = location by genotype by crop effect.

Table 2. The F-values and their P-values for quality traits for trial series planted in 2005, 2006, 2007 and 2009.

Trait	Effect	2005	2006	2007	2009
TCH	L	54.47*	13.52*	26.00*	0.30ns
	G	4.14**	5.81**	4.70**	4.51**
	LG	2.31*	1.96*	3.08**	2.32*
	C	135.08**	204.70**	11.29**	27.65**
	LC	39.92**	215.74**	145.05**	85.73**
	GC	2.00**	4.13**	1.97*	2.93**
	LGC	1.65*	2.49**	1.82*	1.70*
	R ²	0.87	0.93	0.91	0.88
	CV%	14.29	12.78	12.57	10.45
TSH	L	5.25ns	23.62*	0.25ns	81.90*
	G	5.67**	4.35**	5.25**	4.17**
	LG	2.32*	2.46**	3.03**	2.32*
	C	138.27**	10.46**	106.16**	196.22**
	LC	61.16**	329.56**	18.95**	319.66**
	GC	1.77*	3.61**	1.65*	2.43**
	LGC	1.50*	2.63**	1.50ns	1.39*
	R ²	0.83	0.92	0.88	0.92
	CV%	18.16	15.97	14.97	13.34
Stalk Height	L	25.24*	8.91*	9.86*	5.52ns
	G	7.72**	5.51**	5.59**	7.38**
	LG	0.91ns	1.34ns	1.61*	1.09ns
	C	290.95*	62.44**	163.47**	10.62**
	LC	7.32*	18.37**	0.78ns	47.63**
	GC	1.73*	2.15**	2.18**	2.07**
	LGC	1.43*	1.82*	1.45ns	1.25ns
	R ²	0.88	0.85	0.84	0.86
	CV%	10.10	11.41	10.55	9.71
Diameter	L	21.27*	0.03ns	24.41*	5.83ns
	G	10.05**	10.55**	6.68**	13.62**
	LG	2.54*	1.56*	2.41*	2.01*
	C	58.08**	57.52**	76.88**	31.43**
	LC	36.06**	49.56**	36.16**	71.85**
	GC	2.05**	1.3ns	1.41*	1.85*
	LGC	1.21ns	1.31ns	1.46ns	1.08ns
	R ²	0.79	0.79	0.82	0.82
	CV%	13.65	15.39	13.66	14.91
Stalk population	L	9.84*	481.32**	38.25*	122.81*
	G	8.48**	3.57**	7.11**	15.14**
	LG	2.16*	1.97*	1.14ns	1.52ns
	C	27.04**	592.76**	37.29**	5439.66**
	LC	0.97ns	1501.52**	20.33**	131.57**
	GC	1.76*	1.49*	1.63*	5.38**
	LGC	0.64ns	1.75*	0.75ns	1.71*
	R ²	0.79	0.96	0.77	0.98
	CV%	17.22	16.33	15.27	13.63

*= P<0.05, **= P<0.001; ns= P>0.05; CV= coefficient of variation; L= location effects; G = genotypic effect; LG = location by genotype effect; C = crop effect; LC = location by crop effect; GC = genotype by crop effect; LGC = location by genotype by crop effect.

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