Determination of the number of harvests to select elite sugarcane genotypes in North East Brazil

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Genet. Mol. Res. 17 (1): gmr16039869

Received December 14, 2017

Accepted January 8, 2018

Published January 20, 2018

DOI http://dx.doi.org/10.4238/gmr16039869

ABSTRACT. Sixty-eight sugarcane genotypes were evaluated to determine the number of harvests required to select new genotypes in the sugarcane belt in the state of Pernambuco, northeast Brazil. Using a random block design, the following parameters were evaluated: (i) polarizable sugars (POL) per hectare, in metric tons (TPH); (ii) culm productivity per hectare (TCH); (iii) fiber content (FIB); (iv) adjusted percent POL (PCC); (v) soluble solids (BRIX); (vi) total recoverable sugars (ATR); and (viii) metric tons of ATR per hectare (ATR t.ha-1). A variance analysis and genetic parameter estimation were carried out. Means were analyzed using the Scott and Knott test. The repeatability coefficient and the number of harvests were determined using analysis of variance, principal component analysis, and structured data analyses. The best cultivars were SP79-1011, RB952692, RB952675, RB813804, SP78-4764, RB952522, RB952511, RB953265, RB952754, RB952875, SP80-1816, RB763710, and RB892575. Two evaluations are enough to select elite genotypes in the early experimental stages, reducing the time-to-market of these cultivars by three years under the edaphic and climatic conditions in the sugarcane belt evaluated

Key words: Repeatability; Genetic breeding; *Saccharum* spp.

INTRODUCTION

Sugarcane holds considerable importance in Brazil's economy, accounting for approximately 2% of the country's gross domestic product (Biosev, 2013). Recent biotechnological breakthroughs have afforded to explore the biological potential of sugarcane more fully. For example, current research has shown that the plant species may be used to produce biodiesel, in a process based on a genetically modified yeast in a partnership between the company Amyris and the São Martinho Group (Única, 2013). Also, Coelho et al. (2001) described a microbiological process to produce a sugarcane biopolymer with interesting healing properties both for domestic animals and for humans with skin lesions or submitted to surgery. However, sugar and ethanol remain the core sugarcane products today due to the best return on interest they afford.

As with any industrial process, quality of sugarcane raw material is essential in the generation of energy as well as the production of sugar, ethanol, and any other item based on this plant species. In this sense, the quality of sugarcane cultivars is the starting point in estimating how successful an enterprise will be, and is the most important and least expensive technological variable from the producer's standpoint (Barbosa and Silveira, 2012).

Several factors determine sugarcane productivity when manufacturing sugar, ethanol, and other sugarcane-based products. These parameters include the management, planning, and implementation of up-to-date agricultural technologies, in addition to using agricultural inputs reasonably. In this sense, more productive and resistant cultivars with favorable traits developed by genetic improvement programs are central to obtain higher yields at lower costs and better quality. For Silva (2008), the ideal sugarcane cultivar is the one that affords high productivity even under harsh environmental conditions.

More specifically in Brazil, the state of Pernambuco (PE) stands out as the second largest sugarcane producer in the country's northeast region, with approximately 14.90 million metric tons produced to meet the demands of the sugar and energy industries (CONAB, 2013). The main hurdle to increasing productivity is the interaction genotype × environment, which is influenced by specific soil characteristics such as altitude, for instance, and more particularly so by irregular rainfall patterns marked by long droughts.

In their pioneering study, Koffler et al. (1986) characterized the sugarcane belt in PE. The authors systematically gathered a whole set of relevant environmental information with a view to widening the horizons of future genetic improvement research on sugarcane. With that in mind, they split the sugarcane belt in PE into five micro-regions, namely North Woodlands (NW), South Woodlands (SW), Mid Belt (MB), North Coast (NC), and South Coast (SC), and described the geology, geomorphology, climate, hydrology, natural plant cover, soils, and ecological zoning of each.

Subsequently, edaphic and climatic aspects of these micro-regions were investigated considering the suitability to grow sugarcane. It was found that the occurrence of distinctive environments is behind the specific limitations affecting the interaction of soil and climate factors with sugarcane productivity. In genetic improvement terms this means that the agro-industrial performance of a given sugarcane cultivar in a region may not match that in another, and that the environment may influence the expression of desired traits in plants. Interestingly, climate characteristics also vary across harvest seasons, and may shorten the lifespan of ratoons. As a result, sugarcane plantations require renewing at comparatively short intervals, increasing productivity losses.

For this reason, the samples used in cultivar assays at the final stages of an experiment are based on the means of three to four harvests (Koffler et al., 1986). These experiments compare the performance of new clones with that of cultivars more widely grown (Ferreira et al., 2005), identifying high-productivity and high-longevity cultivars in ratoons, as carried out by Melo et al. (2009). The authors assessed the agronomic performance of sugarcane genotypes in SC (PE) using both univariate and multivariate analysis of variance (ANOVA) of experiments and relevant genetic parameters, managing to characterize genotypes that performed better both in the field and in industrial processes. However, these analyses do not suffice to identify the genotypes with high longevity potential in ratoons.

The objective of genotype selection is to increase a genotype's agroindustry performance throughout its lifetime, and to make sure that the good performance of an individual plant in certain traits reflects the genetic potential of the cultivar as a whole (Cruz and Regazzi, 2001). More specifically in sugarcane, the expectation lies in more long-lived ratoons, that is, high productivity in the plant crop and the 1st, 2nd, and 3rd ratoon crops. In this context, a feasible alternative in the identification of more long-lived genotypes includes the use of the repeatability coefficient (r). The coefficient is useful to determine the number of harvests required to select the best genotypes, significantly reducing costs—since cultivar selection assays are costly and time-consuming. In addition, r also helps shorten the time-to-market of new cultivars from the 12 to 15 years on average required

today (Barbosa et al., 2005).

Currently, several methods are available to estimate *r*, such as ANOVA, principal component analysis (PCA) (Abeywardena, 1972) and structured data analysis (SA) (Mansour et al., 1981).

Ferreira et al. (2005) evaluated sugarcane genotypes grown in the production belts in the Brazilian states of São Paulo, Minas Gerais, and Goiás. Based on *r*, the authors discovered that three harvests are enough when selecting new genotypes with predictability degree above 80% of actual values. Santos et al. (2004) evaluated sugarcane genotypes in the state of Alagoas, Brazil, and concluded that the five harvests afford the selection of genotypes with predictability above 80% of actual values.

These studies are especially relevant in the context of sugarcane production in PE, Brazil, since no research covering the whole state's sugarcane belt has been published. So, the objectives of the present study were to evaluate the agro-industrial performance of 68 sugarcane genotypes and to determine the number of harvests needed to select elite genotypes for commercial growth of the plant species in the sugarcane belt in PE, Brazil.

MATERIALS AND METHODS

General description of the experiments

The experiments were conducted in plantations managed by the sugarcane mills participating in the Sugarcane Genetic Improvement Program, Federal Rural University of Pernambuco, Brazil, which is a affiliate of the Inter-university Network for the Development of the Sugar and Energy Sector (PMGCA/UFRPE/RIDESA): Usina São José, Usina Trapiche, Usina Central Olho d'Água, Usina Pumaty, and Usina Petribú. According to the classification system proposed by Koffler (1986), these mills are located in the sugarcane producer micro-regions North Woodlands (NW), South Woodlands (SW), Mid Belt (MB), North Coast (NC), and South Coast (SC), respectively, in the state of PE, Brazil.

A four-repeat randomized block design was used. A quadrat was defined as five 8-m lines 1 m apart with sugarcane grown using two culms placed next to each other, though the end of the first culm was next to the head of the second (Stolf, 1986). Soil pH adjustments and fertilization were carried out following the procedures used by the sugarcane mills cited above. The parameters evaluated were (i) polarizable sugars (POL) per hectare, in metric tons (TPH); (ii) culm productivity per hectare (TCH); (iii) fiber content (FIB); (iv) adjusted percent POL (PCC); (v) soluble solids (BRIX); (vi) total recoverable sugars (ATR); and (viii) metric tons of ATR per hectare (ATR $t.ha^{-1}$).

Productivity per area unit (TCH) was estimated weighing all culms of a quadrat (kg) according to the formula:

TCH = total sugarcane weight (kg) × 10/quadrat used area (m^2)

In turn, TPH was calculated using the formula: TCH × PCC/100

Also, ATR $t.ha^{-1}$ was calculated using:

ATR $t.ha^{-1}$ = TCH × ATR/1000.

BRIX was obtained using a refractometer and a homogenized sample of sugarcane juice obtained from 10 culms randomly collected in the quadrat. FIB, PCC, and ATR were calculated according to Fernandes (2003).

Genotypes evaluated and number of measurements

Four measurements were carried out (plant crop and the 1^{st}, 2^{nd}, and 3^{rd} ratoon crops) in micro-region NC using the genotypes RB72454, RB763710, RB813804, RB952517, RB952522, RB952571, RB952675, RB952681, RB952692, RB952749, RB952754, RB952796, RB952826, and SP7910-11. In micro-region SC, measurements were carried out using the genotypes RB813804, RB952517, RB952522, RB952692, RB952754, RB952796, SP79-1011, RB952511, RB952904, RB953002, RB953133, RB953265, and SP78-4764. In NW the genotypes used were RB72454, RB763710, RB813804, RB952517, CP851491, RB942898, RB952675, RB952514, RB952609, RB952875, RB952884, RB953155, and SP79-1011. In SW the genotypes used were RB952692, RB952597, RB952517, RB952522, RB952571, RB952675, RB952681, RB952609, RB952749, RB952754, SP79-1011, RB952511, SP78-4764, and SP80-1816. In micro-region MB, three measurements were carried out (plant crop and 1^{st} and 2^{nd} ratoon crops) using the genotypes IAC851491, RB763710, RB813804, RB892575, CP851491, RB953214, RB953270, RB953245, SP79-1011, RB953265, RB943339, and RB953206.

Genetic and statistical analyses

Multivariate ANOVA was carried out using the statistical model proposed by Cruz (2006a): $Y_{ijk} = \mu + (b/c)_{jk} + g_i + c_k + gc_{ik} + \varepsilon_{ijk}$

where $Y_{ijk} = i_{th}$ genotype evaluated in the j_{th} block in the k_{th} harvest

μ = overall mean value

$(b/c)_{jk}$ = effect of block j on the k harvest

g_i = effect of treatment (genotype) i

c_k = effect of harvest k

gc_{ik} = effect of the interaction genotype i and harvest k

ε_{ijk} = random error associated with the ijk value

So, means (μ) and genotype (g) were considered effect variables, while block (b), harvest (c), interaction genotype-harvest (gc), and experimental error (ε) were considered the random variables.

The results of the multivariate ANOVA of experiments were obtained using the formula shown in Table 1.

Table 1. Expected mean squares to obtain the results of the multivariate ANOVA of experiments conducted in the sugarcane belt in PE, Brazil, considering the interaction genotype-harvest (sugarcane harvest cycles).

SV	df	E(MS)	F
Blocks/Harvest	(r-1)c	$\hat{\sigma}^2 + g\hat{\sigma}^2_b$	
Harvests (H)	c – 1	$\hat{\sigma}^2 + g\hat{\sigma}^2_b + g\hat{\sigma}^2_c$	MSH/MSB
Genotypes (G)	g – 1	$\hat{\sigma}^2 + r\ell\, g\hat{\sigma}^2_{gc} + cr\varphi_g$	MSG/MSGH
Interaction (G × H)	(c – 1)(g –1)	$\hat{\sigma}^2 + r\ell\, \hat{\sigma}^2_{gc}$	MSGH/MSR
Residual	(g-1)(r – 1)c	$\hat{\sigma}^2$	
$\ell = g/(g-1)$			

Means were grouped using the Scott and Knott (1974) test at 5% probability. The genetic parameters were estimated according to Cruz (2006a):

Genetic variance component: $\hat{\varphi}_g^2 = \dfrac{QMG - QMGA}{cr}$

Genotype-harvest interaction variance component: $\sigma^2_{gc} = \dfrac{QMGC - QMR}{r}\dfrac{g-1}{g}$

Mean heritability: $h^2 = \frac{\hat{\varphi}_g}{(QMG/cr)}$

Genetic variance coefficient: $CV_g = \frac{(100\sqrt{\hat{\varphi}_g})}{m}$

b index: $CV_g/CV_e = \sqrt{\frac{\hat{\varphi}_g}{\sigma^2}}$

Hartley's F max was calculated before the multivariate ANOVA to evaluate the homogeneity of residuals and, according to Gomes (1990), all variables with a highest-to-lowest error variance ratio above 7 were adjusted for degrees of freedom of the mean residual error (n) and for the interaction between factors (n') of the multivariate analysis, as described by Cochran (1974).

The two-way ANOVA, the PCA (Abeywardena, 1972), and the SA methods (Mansour, 1981) were used to estimate *r*.

So, *r* was estimated based on ANOVA according to the statistical model described by Cruz and Regazzi (2001):

$Y_{ij} = \mu + g_i + a_j + \varepsilon_{ij}$

where

Y_{ij} = Estimated *r* for the i^{th} genotype in the j^{th} harvest (time or space)

μ = Overall mean

g_i = Effect of the i^{th} genotype under the influence of last harvest (i = 1, 2, …p)

a_j = Effect of the temporary harvest on the j^{th} measurement (j = 1, 2, … η)

ε_{ij} = experimental error based on the temporary effects on harvest in the j^{th} measurement of the i^{th} genotype. The ANOVA arrangement is shown in Table 2.

Table 2. Expected mean squares to obtain the results of estimated *r* values of experiments based on a two-way ANOVA in experiments conducted in the sugarcane belt in the state of Pernambuco, Brazil.

FV	df	E(MS)	F
Genotypes	p-1	MSG	$\hat{\sigma}^2 + \eta\sigma_g^2$
Harvests (H)	c-1	MSH	—
Residual	(p-1)(c-1)	MSR	$\hat{\sigma}^2$

After the ANOVA, *r* was obtained using the formula:

$$r = \frac{C\hat{o}v(Yij, Yij')}{\sqrt{\hat{V}(Yij)\hat{V}(Yij')}} = \frac{\hat{\sigma}^2_g}{\hat{\sigma}^2_y} = \frac{\hat{\sigma}^2_g}{\hat{\sigma}^2 + \hat{\sigma}^2_g}$$

Therefore, the number of repeats required to predict the real value of individuals was obtained using the formula:

$$\eta o = \frac{R^2(1-r)}{(1-R^2)r}$$

Next, *r* was estimated using PCA based on a phenotypic variance and multivariate matrix according to the statistical model introduced by Cruz and Regazzi (2001):

$Y_{ij} = \mu + g_i + a_j + \varepsilon_{ij}$

However, here the covariance matrix was obtained as:

$$r = \sigma^2_y = \begin{bmatrix} 1 & \rho & \ldots & \rho \\ \rho & 1 & \ldots & \rho \\ \ldots & \ldots & \ldots & \ldots \\ \rho & \rho & \ldots & 1 \end{bmatrix}$$

where

$$V(Yij) = V(Yij') = \hat{\sigma}^2_g + \sigma^2_y = \sigma^2_y$$

$$Cov(Yij, Yij') = ((\hat{\sigma}^2_g + \sigma^2)\ \rho = \rho\sigma^2_y$$

The main eigenvalue was obtained with:

$$\lambda_1 = \sigma^2_y[1 + (\eta - 1)\rho]$$

The corresponding eigenvalue was obtained using the formula:

$$\alpha'_1 = [1/\sqrt{\eta} \ldots 1/\sqrt{\eta}\ ]$$

The *r* estimator was obtained using:

$$r\hat{\rho} = \frac{\hat{\lambda}1 - \sigma^2_y}{\sigma^2_y(\eta - 1)}$$

In turn, the SA used to estimate *r* was based on the parametric matrix of correlations between genotypes in each analysis pair, and $\hat{R}$ was calculated using:

$$r = \frac{\alpha' R\hat{\alpha} - 1}{\eta - 1}$$

where

$$\alpha'_1 = \left[1/\sqrt{\eta} \ldots 1/\sqrt{\eta}\ \right]$$

However, here

$$\alpha'_1 \hat{R}\alpha = 1 + \frac{2}{\eta}\sum_j \sum_{<j'} rjj'$$

Therefore

$$r = \frac{2}{\eta(\eta - 1)}\sum_j \sum_{<j'} rjj'$$

This estimator of *r* is the arithmetic mean of the phenotypical correlations between genotypes considering each pair of measurements.

The determination coefficient was obtained using the formula:

$R^2 = \eta r/[1 + r(\eta - 1)]$

While the number of measurements required to predict the real individual value was:

$\eta 0 = R2(1 - r)/(1 - R2)r$.

All genetic and statistical analyses were carried out using the Genes (Cruz, 2006b) software.

RESULTS AND DISCUSSION

The multivariate ANOVA of experiments revealed significant differences in TPH, TCH, FIB, BRIX, and ATR t. ha^{-1} across all genotypes grown in the five sugarcane micro-regions in PE, Brazil (Table 3).

This indicates the existence of high genetic variability to be exploited between the genotypes analyzed concerning these traits, which are considered the most important factors in sugarcane production (Bastos et al., 2003). For PCC, statistically significant differences were observed in all regions, except SC, indicating that it is not possible to select genotypes with high sugar levels in this micro-region. The same finding was observed for the parameter ATR.

Table 3. Multivariate ANOVA in experiments conducted in the sugarcane belt in the state of Pernambuco, Brazil, considering the parameters polarizable sugars (POL) per hectare, in metric tons (TPH); culm productivity per hectare (TCH); fiber content (FIB); adjusted percent POL (PCC); soluble solids (BRIX); total recoverable sugars (ATR); and metric tons of ATR per hectare (ATR t. ha^{-1}).

Variables		**Mean squares**						
Environments	**Traits**	**Genotypes**	**Harvest**	**G × H**	**Residual**	**Mean**	**CV(%)**	**H**
	TPH	78.27**	332.7**	4.83**	1.22	11.00	10.07	2.22
	TCH	2413.4**	17883.5**	152.5**	27.27	74.71	6.98	2.62
	FIB	12.82**	33.10**	1.75**	1.03	14.05	7.24	2.08
NC	PCC	11.75**	24.42**	1.88*	1.09	14.71	7.09	3.61
	BRIX	14.64**	75.66**	2.08^{ns}	1.47	20.36	5.95	2.96
	ATR	1289.3**	2639.6**	224.0**	126.87	150.87	7.46	3.70
	ATR	82.33**	366.94**	5.28**	1.35	11.30	10.30	2.19
	TPH	72.00**	280.59**	5.58**	1.69	9.57	13.58	6.76
	TCH	2710.58**	12386.51**	167.6**	45.57	65.20	10.35	4.65
	FIB	3.44*	75.40**	1.46^{ns}	1.05	13.29	7.73	1.68
SC	PCC	3.50^{ns}	150.81**	2.19**	1.21	14.75	7.47	3.08
	BRIX	3.07*	119.60**	1.55*	0.99	20.37	4.87	2.50
	ATR	431.77^{ns}	17540.72**	262.0**	150.03	150.74	8.12	3.33
	ATR	76.50**	292.0**	7.98**	2.80	9.80	17.08	7.00
	TPH	128.48**	409.70**	5.21**	1.16	11.61	9.30	2.12
	TCH	5986.09**	10161.67**	224.0**	45.99	92.12	7.36	2.32
	FIB	30.92**	10.25**	2.63**	1.27	13.86	8.15	2.95
NW	PCC	10.96**	111.07**	1.70**	0.90	12.45	7.62	2.54
	BRIX	9.79**	184.02**	1.94**	1.10	17.56	5.98	2.15
	ATR	1170.11**	10697.89**	167.14*	97.86	127.76	7.74	2.42
	ATR	135.82**	411.57**	5.36**	1.26	11.95	9.40	2.27
	TPH	38.41**	648.77**	6.56**	0.90	9.10	10.47	5.77
	TCH	1640**	35908.43**	244.1**	32.04	64.18	8.81	4.13
	FIB	25.00**	90.14**	1.88*	1.27	14.86	7.60	3.93
SW	PCC	3.94**	17.04**	1.13*	0.72	14.25	5.97	4.00
	BRIX	5.37**	30.16**	0.71*	0.46	19.76	3.44	1.28
	ATR	452.11**	1622.93**	113.16*	69.67	147.17	5.67	2.40
	ATR	41.80**	694.0**	7.04**	0.95	9.42	10.38	5.79
	TPH	42.98**	253.00**	9.39**	0.72	7.85	10.68	3.99
	TCH	1974.43**	10565.58**	403.2**	44.23	61.83	10.75	8.09
	FIB	11.08*	2.94^{ns}	4.63**	0.99	14.50	6.88	1.54
MB	PCC	5.40*	68.99**	2.26**	0.55	12.54	5.93	1.96
	BRIX	6.51*	50.93**	2.87**	0.82	18.73	4.83	1.82
	ATR	525.73*	7509.30**	212.3**	56.16	127.00	5.90	1.64
	ATR	43.20**	254.10**	9.38**	0.73	7.96	10.68	4.41

NC: North Coast, SC: South Coast, NW: North Woodlands, SW: South Woodlands, MB: Mid Belt.

G × H: Interaction genotype – harvest, CV (%): Coefficient of experimental variation, H: Hartley's F max test

For the harvest cycles considered (plant crop and the 1st, 2nd, and 3rd ratoon crops, Table 3), significant differences were observed for all traits, except FIB in MB. For Rosse et al. (2002), these results indicate that harvest cycles represent environmental contrasts due to climate factors and therefore affect the traits evaluated in the present study. Silva (2008) investigated the interaction genotype-environment in sugarcane plantations in the state of São Paulo (SP), Brazil, and underline the fact that the higher mean square values based on site, as compared with other mean squares, signal the existence of considerable differences in yield potential of genotypes in the locations investigated. In the present study a large difference was observed in mean square values for harvest cycles in comparison with mean squares for genotype and the interaction genotype-harvest. Therefore, it may be said that genotypes differ as to yield potential in different harvest cycles, pointing to the need for continuous improvement in long-lived elite genetic material, that is, traits should remain essentially constant throughout harvest cycles.

The coefficients of variation varied from low to medium, according to the classification system proposed by Gomes (1990). Interestingly, in micro-region NW coefficient values were low (< 10) for all traits (Table 3).

The Scott and Knott test (Table 4) shows the emergence of elite genotypes throughout the sugarcane belt in PE, Brazil. In micro-region NC, for instance, genotypes SP79-1011, RB952692, and RB952675 stood out in terms of TPH and TCH. Genotypes RB813804, RB952749, RB952796, RB952754, RB952826, and RB952681 had interesting FIB values. Concerning PCC, except for RB952517 and RB952754, all other genotypes were classified into group 'a', with high potential for improvement in this richness trait. This was also valid for BRIX and ATR. For ATR t. ha^{-1}, genotypes SP79-1011, RB952692, RB952675, and RB813804 presented the best performance, forming an elite group.

Table 4. Groupings of mean values of the traits polarizable sugars (POL) per hectare, in metric tons (TPH); culm productivity per hectare (TCH); fiber content (FIB); adjusted percent POL (PCC); soluble solids (BRIX); total recoverable sugars (ATR); and metric tons of ATR per hectare (ATR t. ha^{-1}).

Variables		Parameters						
	Genotypes	TPH t.ha^{-1}	TCH t.ha^{-1}	FIB%	PCC%	BRIX%	ATR kg/t	ATR t.ha^{-1}
	SP79-1011	14.46a	95.62a	13.91b	15.15a	20.69a	155.97a	14.92a
	RB952692	13.44a	87.37a	12.54b	15.42a	20.64a	158.14a	13.81a
	RB952675	13.17a	89.43a	13.70b	14.83a	20.53a	151.52a	13.48a
	RB813804	12.74b	81.31b	14.55a	15.71a	21.39a	162.32a	13.18a
	RB763710	12.01b	83.81b	12.98b	14.51a	19.87a	148.27a	12.29b
	RB952571	11.64b	78.68b	14.09b	14.98a	21.07a	152.27a	11.87b
	RB952522	11.07c	73.31c	13.95b	15.14a	21.23a	154.21a	11.32c
	RB952749	10.64c	72.25c	15.18a	14.84a	20.95a	151.91a	10.90c
	RB952681	10.30c	68.62c	14.91a	15.07a	20.95a	154.95a	10.64c
	RB72454	10.23c	68.06c	12.85b	15.25a	20.37a	156.97a	10.55c
	RB952796	10.10c	67.68c	14.60a	14.90a	20.50a	153.60a	10.45c
	RB952826	10.09c	70.43c	15.10a	14.30a	20.04a	147.24a	10.44c
	RB952517	7.86d	59.62d	13.70b	13.59b	19.03b	137.84b	8.05d
NC	RB952754	6.12e	49.81e	15.12[a]	12.36b	17.81b	126.95b	6.33e
SC	RB813804	12.96a	83.12a	13.64a	15.72a	21.28a	161.90a	13.36a
	SP78-4764	11.77a	81.06a	13.77a	14.64a	20.48a	149.18a	12.02a
	RB962675	11.69a	76.81a	12.50a	15.19a	20.52a	155.28a	11.96a
	RB952522	10.53a	72.81b	13.14a	14.56a	20.35a	148.67a	10.74a
	RB952692	10.34a	71.15b	13.08a	14.68a	20.23a	149.94a	10.57a
	SP79-1011	10.32a	70.37b	13.22a	14.84a	20.33a	152.31a	10.61a
	RB952511	10.30a	68.81b	12.31a	15.00a	20.36a	152.99a	10.52a
	RB953265	10.23a	66.50b	13.60a	15.42a	21.08a	158.26a	10.50a
	RB952754	10.07a	69.50c	13.42a	14.63a	20.32a	149.29a	10.29a
	RB952796	8.75a	61.00c	13.60a	14.52a	20.20a	148.36a	8.97b
	RB952904	7.58a	52.43c	13.21a	14.64a	20.43a	149.04a	7.72b
	RB952517	7.36a	53.25c	12.98a	14.03a	19.60a	142.83a	7.52b
	RB953002	6.54a	46.93d	13.88a	14.02a	19.68a	143.09a	6.70b
	RB953133	5.60[a]	39.02d	13.66[a]	14.62a	20.38a	149.18a	5.72b
	RB952675	15.71a	117.31a	13.06b	13.44a	18.35a	138.01a	16.16a
	RB813804	14.60a	102.50b	13.97b	14.21a	19.46a	146.25a	15.03a
	RB952875	14.58a	108.68b	11.84b	13.38a	17.97a	137.18a	14.98a
	SP79-1011	13.47b	102.87b	13.31b	13.05a	18.10a	133.89a	13.84b
	RB763710	13.47b	108.87b	12.65b	12.31b	17.21a	125.81b	13.76b
	RB942898	12.52c	102.18b	13.80b	12.17b	17.10a	125.14b	12.89b
	RB953155	12.50c	105.68c	12.77b	11.72b	16.34a	120.70b	12.88b
	RB72454	11.47c	88.75c	12.78b	12.96b	17.75a	132.89b	11.77c
	RB952884	11.29c	92.50c	16.14a	12.19b	17.66a	125.60b	11.67c
	RB952514	10.24d	84.12c	15.33a	12.05b	17.65a	123.26b	10.49d
	RB952517	10.23d	86.31c	12.48b	11.72b	16.59a	119.83b	10.48d

	RB952609	89.59e	78.18d	16.00a	11.33b	17.26a	116.23b	9.20e
	RB953245	79.93e	66.56e	14.60a	11.70b	17.01a	120.90b	8.22e
NW	CP851491	55.13f	45.12f	15.24a	11.98b	17.39a	122.97b	5.67f
	SP78-4764	11.60a	82.37a	15.25b	13.92a	20.11a	145.24b	12.09a
	SP80-1816	10.64a	69.75b	14.99b	15.37a	21.01a	159.19a	11.03a
	RB952511	10.44a	76.50a	14.89b	13.74a	19.24b	141.33b	10.75a
	SP79-1011	10.23a	67.68b	14.46b	15.06a	20.47a	155.74a	10.62a
	RB952749	9.75b	68.62b	15.83a	14.26a	19.92b	147.42b	10.11b
	RB952692	9.73b	70.06b	12.71c	14.13a	18.89b	145.54b	10.04b
	RB952571	9.44b	67.12b	15.00b	14.17a	19.77b	145.84b	9.74b
	RB952681	9.20b	62.68b	15.01b	14.82a	20.29a	153.54a	9.55b
	RB952522	9.05b	64.18b	13.72c	14.19a	19.35b	146.09b	9.34b
	RB952675	8.69b	61.37b	14.52b	14.27a	19.58b	147.20b	9.01b
	RB952517	8.64b	61.75b	12.72c	14.13a	19.05b	145.01b	8.91b
	RB952609	6.93c	51.00c	17.37a	13.73a	19.86b	141.75b	7.17c
	RB952754	6.83c	50.37c	16.19a	13.79a	19.42b	142.67b	7.06c
SW	RB952597	6.21c	45.12c	15.42b	13.97a	19.64b	143.82b	6.41c
	RB813804	9.85a	71.33b	15.23b	13.46a	19.94[a]	136.25a	9.98a
	RB763710	9.82a	78.41a	13.31c	12.46b	18.37b	125.84b	9.91a
	RB892575	9.71a	76.83a	14.54b	12.42b	18.53b	126.16b	9.87a
	RB953265	9.51a	70.66b	14.16c	13.30a	19.92a	133.26a	9.54a
	SP79-1011	9.19a	68.58b	13.71c	13.21a	19.19a	133.65a	9.33a
	RB943365	8.02b	63.41c	14.93b	12.70a	18.92a	128.61a	8.13b
	RB953270	7.84b	62.83c	13.45b	12.45b	18.30b	125.86b	7.96b
	RB953206	7.64b	57.41c	14.66b	13.18a	19.33a	133.57a	7.76b
	IAC893143	7.42b	62.83c	13.60c	11.71b	17.62b	118.49b	7.51b
	RB953245	5.31c	47.75d	16.73a	11.21b	18.00b	113.75b	5.39c
MB	RB953214	5.05c	42.00d	14.64b	12.20b	18.20b	123.71b	5.15c
	CP851491	4.86c	39.91d	15.09b	12.31b	17.62b	124.79b	4.97c

NC: North Coast, SC: South Coast, NW: North Woodlands, SW: South Woodlands, MB: Mid Belt. Means followed by the same letter in a column indicate that values belong to the same group in the Scott and Knott test at 5% probability.

In micro-region SC, genotypes RB813804, SP78-4764, and RB962675 exhibited good TPH and TCH values. Concerning the traits FIB, PCC, BRIX, and ATR, genotypes exhibited essentially equivalent potential and were not classified into distinct groups. As for ATR t. ha^{-1}, RB813804, SP7847-64, RB952522, RB952692, SP-79-1011, RB952511, RB953265, and RB952754 exhibited high potential, and were classified into group 'a'.

In micro-region NW, genotypes RB952875, RB952675, and RB813804 presented the best performance, falling in group 'a' in the parameters TCH and ATR t. ha^{-1}. Therefore, improvement programs in NW should be focused on the commercial value of genotype RB952675, since the TPH value was significant. Similarly, important findings in terms of energy generation were observed for genotypes RB952884, RB952609, RB952514, and CP85-1491, which were classified into group 'a' concerning the trait FIB, with values over 15%. These values indicate that these genotypes should be exploited specifically in the generation of bioenergy. However, for BRIX, genotypes were not included in any specific group, showing that they present the same potential.

In micro-region SW, genotypes SP78-4764, SP80-1816, RB952511, and SP79-1011 presented excellent performance in TCH and ATR t. ha^{-1}, and were classified into group 'a'. Similarly, SP78-4764 and RB952511 had high TPH value and were also included in the same group. Genotype RB952609 stood out due to the very high level of FIB, which rendered it the best genotype to be included in improvement programs addressing biomass and bioenergy production. Concerning the parameter PCC, no elite genotype groups were formed. BRIX values of genotypes SP78-4764, SP80-1816, SP79-1011, and RB952681 were high and prompted inclusion in group 'a'. For ATR, SP79-1011, SP80-1816, and RB952681 also demonstrated superiority and were classified into group 'a'.

In micro-region MB, RB813804, RB763710, RB892575, RB953265, and SP7910-11 were included in group 'a', with high performance for TCH and ATR t. ha^{-1}. Genotypes RB763710 and RB892575 were included in group 'a' due to the good TPH values. Concerning FIB levels, genotype RB953245 exhibited the best performance. As for PCC and BRIX, genotypes RB813804, RB953265, SP79-1011, RB943365, and RB953206 were included in group 'a', and were superior to the other genotypes. In turn, genotypes RB813804, RB953265, SP79-1011, RB943365, and RB953206 presented the best performance and were included in group 'a'.

Of the genetic parameters evaluated (Table 5), TPH, TCH, and ATR t. ha^{-1} presented high genetic variance, superior to the variance of the interaction genotype-harvest in all micro-regions evaluated.

Table 5. Genetic parameters associated with the traits polarizable sugars (POL) per hectare, in metric tons (TPH); culm productivity per hectare (TCH); fiber content (FIB); adjusted percent POL (PCC); soluble solids (BRIX); total recoverable

Variables		Genetic parameters				
Environments	Traits	φ_g^2	$\hat{\sigma}_{gc}^2$	H^2	CVg	CVg / CVe
	TPH	4.59	0.83	94	19.48	2.0
	TCH	141.32	29.08	94	16.00	2.27
	FIB	0.69	0.16	86	5.92	0.82
NC	PCC	0.61	0.18	84	5.33	0.75
	BRIX	0.78	0.14	86	5.33	0.75
	ATR	68.0	23.0	82	5.40	0.72
	ATR $t.ha^{-1}$	4.82	0.91	94	19.40	1.88
	TPH	4.15	0.90	92	21.27	1.56
	TCH	158.94	28.33	94	19.33	1.86
	FIB	0.12	0.09	57	2.64	0.34
SC	PCC	0.08	0.23	38	1.94	0.26
	BRIX	0.09	0.13	50	1.51	0.31
	ATR	10.60	26.0	30	2.16	0.26
	ATR $t.ha^{-1}$	4.28	1.20	90	21.10	1.23
	TPH	7.70	0.94	95	23.89	2.57
	TCH	360.12	41.33	96	20.60	2.79
	FIB	1.76	0.31	91	9.59	1.17
NW	PCC	0.57	0.18	84	6.10	0.80
	BRIX	0.49	0.19	80	3.98	0.66
	ATR	62.68	16.08	85	6.19	0.80
	ATR $t.ha^{-1}$	8.15	0.95	96	23.92	2.54
	TPH	1.99	1.31	83	15.49	1.47
	TCH	87.24	49.24	85	14.55	1.65
	FIB	1.44	0.14	92	8.08	1.06
SW	PCC	0.17	0.09	71	2.93	0.49
	BRIX	0.29	0.05	86	2.73	0.79
	ATR	21.18	10.09	75	3.12	0.55
	ATR $t.ha^{-1}$	2.17	1.14	83	15.64	1.50
	TPH	2.79	1.98	78	21.29	1.96
	TCH	130.88	82.4	80	18.50	1.72
	FIB	0.53	0.83	58	5.05	0.73
MB	PCC	0.26	0.39	58	4.06	0.69
	BRIX	0.30	0.47	56	2.93	0.61
	ATR	26.11	35.79	56	4.02	0.68
	ATR $t.ha^{-1}$	2.81	1.98	78	21.08	1.97

NC: North Coast, SC: South Coast, NW: North Woodlands, SW: South Woodlands, MB: Mid Belt.

φ_g^2 : Genetic variance component.

$\hat{\sigma}_{gc}^2$: Interaction genotype-harvest variance component.

h^2: Genotypic determination at mean level.

CV_g: Genetic variance coefficient.

CVg / CVe: b index.

Such a result is highly desirable, since, according to Dutra Filho (2008a), it indicates that the expression of this important production aspect is mostly due to the genetic effects, suggesting the feasibility to select elite genotypes in the sugarcane belt in PE, Brazil. Concerning ATR $t.ha^{-1}$, it should be emphasized that the results obtained are highly significant, pointing to the possibility to increase sugarcane productivity significantly in PE and, therefore, to secure better return on investment, since sugarcane prices are defined based on ATR $t.ha^{-1}$ in Brazil.

For the traits PCC, BRIX, and ATR $t.ha^{-1}$, selecting elite genetic material is possible only in micro-regions NC, NW, and SW, where genetic variance was higher than the variance in the interaction genotype-harvest. Concerning FIB, only micro-region MB affords to select elite genotypes (Table 5).

The mean heritability coefficient values were high (> 75%) for TPH, THC, and ATR $t.ha^{-1}$ in all micro-regions (Table 5). For Falconer (1987), such a scenario is highly favorable in the selection of elite genotypes based on these traits, since it indicates the robustness of phenotypical value as an indicator of genotypic value. These

results confirm previous findings by Dutra Filho et al. (2008b), in a study that evaluated the progeny of sugarcane in NL at the early improvement stage, and endorse the results published by Melo et al. (2006), who assessed sugarcane genotypes from NW. We also observed that the mean heritability coefficient for TPH was higher than that obtained by Souza et al. (2012) in MB. According to Melo et al. (2009), these interesting heritability coefficients translate as an important aspect in genetic improvement programs, since they clearly show that it is possible to obtain significant genetic advantages in the selection of elite genotypes considering these traits. Since heritability is defined as the transferrable part of the total genetic heritability, Gonçalves et al. (2007) highlight the fact that it is possible to improve production using genotypes with higher performance in these traits obtained crossing the appropriate genetic materials. Mean heritability coefficients were also high for the traits FIB, PCC, BRIX, and ATR t.ha^{-1} considering the edaphic and climatic conditions in NC, NW, and SW in PE, Brazil. This indicates that elite genotypes should be exploited based on these traits in these micro-regions.

The selection of elite genotypes in the sugarcane belt in PE should be based on TPH, TCH, and ATR t.ha^{-1}. These traits presented the highest genetic variability, with genetic variation coefficients above 10% in all micro-regions (Table 5). According to Oliveira et al. (2008), genetic variation coefficients above 10% are considered high. The ratio of the genetic variation coefficient to the experimental variation coefficient (index b) were above 1 for the traits TPH, TCH, and ATR t.ha^{-1} (Table 5), showing that these traits are essential in the expression of genetic variability between the genotypes evaluated in the sugarcane belt in PE, Brazil, and lending strength to the hypothesis that selection may become more effective.

Also, *r* (Table 6) was higher than 0.5 for TPH, TCH, and ATR t.ha^{-1} across the sugarcane belt in PE, in the three methodologies used. However, in NC and SC, values of *r* were above 0.75. In NW, *r* values were considered excellent using the three methodologies, with values over 0.85. For Santos (2004), these results indicate superior genetic control in the expression of these traits in the genotypes evaluated. Consequently, these traits are more evenly expressed across the harvest cycles of sugarcane in the region, which increases ratoon longevity. Cruz and Regazzi (2011) also underline the fact that the higher the *r* value, the lower the number of measurements required to predict the actual value of genotypes.

Table 6. Repeatability coefficient (*r*) values for the traits polarizable sugars (POL) per hectare, in metric tons (TPH); culm productivity per hectare (TCH); fiber content (FIB); adjusted percent POL (PCC); soluble solids (BRIX); total recoverable sugars (ATR); and metric tons of ATR per hectare (ATR t.ha^{-1}) of sugarcane genotypes evaluated in experiments conducted in the sugarcane belt in the state of Pernambuco (PE), Brazil.

Variables		ANOVA		PCA		AS	
Environments	Traits	*r*	R^2	*r*	R^2	*r*	R^2
	TPH	0.79	94.00	0.82	95.00	0.80	94.34
	TCH	0.79	93.67	0.83	95.01	0.79	94.00
	FIB	0.61	86.34	0.63	87.00	0.62	87.00
NC	PCC	0.57	84.00	0.63	87.00	0.62	87.00
	BRIX	0.60	86.00	0.69	90.00	0.63	87.00
	ATR	0.54	82.00	0.58	84.00	0.56	84.00
	ATR t.ha^{-1}	0.78	94.00	0.81	95.00	0.80	94.00
	TPH	0.75	92.00	0.79	94.00	0.79	94.00
	TCH	0.79	94.00	0.81	95.00	0.82	95.00
	FIB	0.25	57.00	0.27	61.00	0.28	61.10
SC	PCC	0.13	38.00	0.18	48.00	0.14	39.00
	BRIX	0.19	49.00	0.28	61.00	0.18	47.00
	ATR	0.13	39.00	0.21	52.00	0.14	40.00
	ATR t.ha^{-1}	0.74	92.00	0.79	94.00	0.79	93.00
	TPH	0.85	96.00	0.86	96.00	0.86	96.00
	TCH	0.86	96.00	0.87	96.00	0.87	96.00
	FIB	0.73	91.00	0.75	92.00	0.74	92.00
NW	PCC	0.58	84.00	0.65	88.00	0.61	86.00
	BRIX	0.50	80.00	0.61	86.00	0.56	84.00
	ATR	0.60	86.00	0.65	88.00	0.63	87.00
	ATR t.ha^{-1}	0.86	96.00	0.87	96.00	0.87	96.00
	TPH	0.55	82.00	0.61	86.00	0.62	87.00
	TCH	0.59	85.00	0.62	87.00	0.65	88.00
	FIB	0.75	92.00	0.85	96.00	0.81	94.00
SW	PCC	0.38	71.00	0.40	72.00	0.43	76.00
	BRIX	0.62	87.00	0.72	91.00	0.62	87.00
	ATR	0.43	75.00	0.47	78.00	0.46	77.00
	ATR t.ha^{-1}	0.55	83.00	0.61	86.00	0.63	87.00
	TPH	0.54	78.00	0.93	97.00	0.59	78.00
	TCH	0.62	83.00	0.90	96.00	0.70	87.00
	FIB	0.31	58.00	0.40	67.00	0.36	63.00
MB	PCC	0.31	58.00	0.63	84.00	0.26	52.00
	BRIX	0.30	56.00	0.57	80.00	0.26	51.00

	ATR	0.33	60.00	0.64	84.00	0.27	53.00
	ATR t.ha^{-1}	0.55	78.00	0.93	97.00	0.60	78.00

NC: North Coast, SC: South Coast, NW: North Woodlands, SW: South Woodlands, MB: Mid Belt.
r: Repeatability coefficient
R^2: Determination coefficient

Similarly, the values of the traits FIB, PCC, BRIX, and ATR t.ha^{-1} were regularly repeated in the genotypes evaluated in NC and NW, PE using the three methodologies. In SW, FIB and BRIX also exhibited consistent repeatability, in the three methods. However, in MB only the traits PCC, BRIX, and ATR t.ha^{-1} were regularly repeated, in PCA.

The estimated number of repeated measurements required to select genotypes with 80%, 90%, and 95% predictability of actual values are shown in Table 7.

Table 7. Number of measurements required to select superior sugarcane genotypes considering the traits polarizable sugars (POL) per hectare, in metric tons (TPH); culm productivity per hectare (TCH); fiber content (FIB); adjusted percent POL (PCC); soluble solids (BRIX); total recoverable sugars (ATR); and metric tons of ATR per hectare (ATR t.ha^{-1}) of sugarcane genotypes evaluated in experiments conducted in the sugarcane belt in the state of Pernambuco (PE), Brazil.

Variables		ANOVA			PCA			SA		
	Traits	R^2=0.8	R^2=0.9	R^2=0.95	R^2=0.8	R^2=0.9	R^2=0.95	R^2=0.8	R^2=0.9	R^2=0.95
	TPH	1.05	2.36	5.0	0.87	1.97	4.1	0.96	2.15	4.5
	TCH	1.08	2.42	5.0	0.84	1.88	3.9	1.01	2.33	4.9
	FIB	2.53	5.69	12.0	2.39	5.39	11.39	2.51	5.62	11.88
NC	PCC	3.06	6.99	14.0	2.41	5.42	11.45	2.77	6.23	13.15
	BRIX	2.66	5.98	12.64	1.83	2.60	8.73	2.30	5.18	1.00
	ATR	3.36	7.57	16.00	2.78	6.26	13.21	3.12	7.02	14.83
	ATR t.ha^{-1}	1.10	2.46	5.20	0.90	2.04	4.31	0.99	2.24	4.73
	TPH	1.34	3.02	6.39	1.02	2.31	4.89	1.03	2.33	4.91
	TCH	1.05	2.37	5.01	0.88	1.98	4.18	0.88	1.99	4.20
	FIB	11.89	26.76	56.50	8.87	19.96	42.13	10.18	22.91	48.37
SC	PCC	26.61	59.18	126.41	17.39	39.14	82.00	24.79	55.79	117.78
	BRIX	16.32	36.72	77.52	10.10	22.73	48.00	17.67	39.77	84.00
	ATR	24.70	55.58	117.35	14.92	33.57	71.00	23.67	53.27	112.00
	ATR t.ha^{-1}	1.39	3.14	6.63	1.06	2.39	5.06	1.07	2.41	5.09
	TPH	0.68	1.52	3.21	0.63	1.42	3.01	0.63	1.43	3.01
	TCH	0.62	1.40	2.96	0.59	1.34	2.84	0.60	1.35	2.86
	FIB	1.48	3.34	7.06	1.32	2.97	6.26	1.40	3.16	6.69
NW	PCC	2.93	6.61	13.95	2.19	4.93	10.40	2.54	5.73	12.10
	BRIX	3.96	9.91	18.81	2.53	5.70	12.40	3.13	7.04	14.87
	ATR	2.66	6.00	12.66	2.10	2.97	9.98	2.34	5.27	11.26
	ATR t.ha^{-1}	0.65	1.48	3.12	0.60	1.37	2.88	0.60	1.36	2.89
	TPH	3.33	7.42	15.67	2.55	5.75	12.15	2.42	5.45	11.50
	TCH	2.79	6.29	13.29	2.14	4.81	10.16	2.19	4.93	10.41
	FIB	1.30	2.93	6.19	0.73	1.64	3.48	0.96	2.17	4.59
SW	PCC	6.46	14.54	30.70	3.43	8.87	18.76	5.15	11.60	24.48
	BRIX	2.46	5.54	11.70	1.58	3.57	7.54	2.46	5.54	11.70
	ATR	5.34	12.02	25.37	3.81	8.57	18.10	4.70	10.58	22.34
	ATR t.ha^{-1}	3.24	7.30	15.41	2.28	5.14	10.85	2.35	5.29	11.7
	TPH	3.35	7.55	15.94	0.32	0.72	1.53	2.74	6.16	13.02
	TCH	2.41	5.42	11.45	0.44	1.00	2.12	1.66	3.74	7.91
	FIB	8.63	19.42	41.00	5.97	13.43	28.36	7.09	15.95	33.68
MB	PCC	8.68	19.54	41.00	2.35	5.29	11.18	11.10	24.77	52.73
	BRIX	9.48	21.35	45.04	3.06	6.90	14.57	11.59	26.09	55.09
	ATR	8.13	18.29	38.62	2.27	5.12	10.82	10.85	24.42	51.55
	ATR t.ha^{-1}	3.33	7.49	15.81	0.32	0.72	1.53	2.65	5.97	12.60

NC: North Coast, SC: South Coast, NW: North Woodlands, SW: South Woodlands, MB: Mid Belt.
ANOVA: Analysis of variance; PCA: Principal component analysis; SA: Structured data analyses

Resende (2002) concluded that determination coefficients above 80% afford appropriate predictive power for the actual value of an individual and, consequently, the number of measurements required for selection. Therefore, it becomes clear that the traits TPH, TCH, and ATR t. ha^{-1} require no more than two evaluations to select elite genotypes intended for commercial sugarcane plantations in the sugarcane belt in PE, with predictability of 90% of actual values for each trait in NC and NW, using the three methodologies. Similarly, predictability above 80% was observed for SC and SW using the three methodologies, and for MB using PCA and SA.

Concerning the trait FIB, two assessments are enough to select elite genotypes with 80% predictability of actual values for growth in micro-regions NC, NW, and SW, using the three methodologies. In micro-regions SC and MB at least four evaluations, or four harvests, are required to select genotypes with the same 80% predictability level, which is economically unfeasible (Table 7).

For PCC, two evaluations are enough to select genotypes with 80% predictability of actual values using PCA and SA in NC and NW, respectively. For micro-region MB, two evaluations are required to select genotypes with 80% predictability of actual values in a PCA. For micro-region SC, more than four evaluations are necessary (Table 7).

In turn, for the trait BRIX, two evaluations suffice to select genotypes with 80% predictability of actual values in micro-regions NC and SW. For micro-regions NW and MB, two and three evaluations are required, respectively, to select genotypes with 80% predictability, using PCA (Table 7).

For ATR $t.ha^{-1}$, three evaluations are necessary to select genotypes with 80% predictability of actual values in micro-region NC, in the three methods used, while for micro-region NW two evaluations are required using the three methods. For SW, three evaluations should be carried out, using PCA. For MB, two assessments are necessary using the same method (Table 7).

In estimating the number of measurements, the PCA was more effective than ANOVA and SA to select elite genotypes considering PCC in micro-regions SW and MB. The same was observed for the trait BRIX in micro-regions NW and MB, and for ATR in SW and MB. For Cruz and Regazzi (2001), the experimental error component is more effectively eliminated in the PCA than in the ANOVA. Despite that, the number of assessments required to select superior genotypes with 80% predictability of the actual value in SC, in the three methodologies used, is much higher than four.

In this sense, it is important to evaluate the genotypic stabilization of materials evaluated under the edaphic and climatic conditions in micro-region SC (Table 8).

Table 8. Genotypic stabilization of sugarcane genotypes considering the traits polarizable sugars (POL) per hectare, in metric tons (TPH); culm productivity per hectare (TCH); fiber content (FIB); adjusted percent POL (PCC); soluble solids (BRIX); total recoverable sugars (ATR); and metric tons of ATR per hectare (ATR $t.ha^{-1}$) evaluated in experiments conducted in the sugarcane belt in the state of Pernambuco (PE), Brazil.

Trait	Correlation / No of assessments	ANOVA	R^2	CP	R^2
	1-2	0.82	89.91	0.88	93.47
	2-3	0.64	78.39	0.66	79.62
TPH	3-4	0.85	92.15	0.89	94.26
	1-3	0.72	88.41	0.75	89.97
	2-4	0.73	89.23	0.81	92.57
	1-4	0.75	92.24	0.80	93.95
	1-2	0.87	93.22	0.88	93.64
	2-3	0.72	83.92	0.73	84.11
TCH	3-4	0.84	91.23	0.88	93.77
	1-3	0.78	91.37	0.78	91.56
	2-4	0.78	91.35	0.83	93.42
	1-4	0.79	93.81	0.82	94.78
	1-2	-0.07	0	0.07	13.69
	2-3	0.26	41.00	0.26	41.38
FIB	3-4	0.34	51.20	0.35	51.74
	1-3	0.13	31.16	0.16	36.97
	2-4	0.27	52.60	0.28	54.20
	1-4	0.25	57.35	0.31	64.33
	1-2	0.16	27.72	0.16	2.77
	2-3	-0.08	0	0.08	1.40
PCC	3-4	0.04	7.58	0.04	7.71
	1-3	0.06	15.12	0.08	20.84
	2-4	0.10	23.96	0.18	39.62
	1-4	0.13	37.54	0.18	46.87
	1-2	0.20	32.91	0.20	3.29
	2-3	0.07	13.17	0.07	13.55
BRIX	3-4	0.02	3.71	0.02	3.75
	1-3	0.09	23.65	0.10	25.65
	2-4	0.23	46.57	0.27	52.23
	1-4	0.20	49.50	0.24	55.32
	1-2	0.22	35.65	0.22	35.74
	2-3	-0.09	0	0.09	17.08
ATR	3-4	0.00	0	0.00	0.07
	1-3	0.07	19.42	0.11	26.81
	2-4	0.09	22.87	0.20	42.99

	1-4	0.14	3.93	0.19	49.20
	1-2	0.81	89.34	0.87	93.28
	2-3	0.63	77.61	0.65	79.01
ATR t.ha^{-1}	3-4	0.85	91.72	0.88	93.69
	1-3	0.71	87.99	0.74	89.73
	2-4	0.73	88.87	0.80	92.29
	1-4	0.74	91.97	0.79	93.75

Genotypic stabilization is obtained based on the correlations between all measurements carried out. Concerning FIB, for instance, the correlation between the values obtained in plant crop and the 1st and 2nd harvests was negative in ANOVA and very low in PCA. This explains the low R^2 value, which was zero using ANOVA and only 13.69 using PCA. This explains the need for a significantly higher number of evaluations required to predict the actual value of genotypes. The poor correlation between the measurements the present study indicates the severe climatic variations between harvest years, which negatively influence the regularity of expression of these traits in micro-region SC. However, this was not observed for TPH, when the high correlations between measurements both in ANOVA and in PCA were high, increasing R^2 values and reducing the number of measurements required to predict the actual value of genotypes.

However, as previously demonstrated for the estimation of genetic traits the selection of superior genotypes in the commercial growth of sugarcane in the sugarcane belt in PE, Brazil should be carried out based on the traits TPH, TCH, and ATR t.ha^{-1}. Also, considering *r* values, the traits were regularly expressed in the genotypes evaluated, and two measurements are enough to select superior genotypes with 80% predictability of actual values. Pedroso et al. (2011) evaluated sugarcane families grown in the state of Minas Gerais, Brazil, and obtained high repeatability values, concluding that the selection of these families based on two harvests and of clones during the 2nd harvest may be an interesting option in improvement programs, increasing the efficiency in the production of cultivars. Therefore, the results of the present study afford to reduce the time-to-market of new cultivars by three years in the sugarcane belt in PE, Brazil.

CONCLUSION

The use of two evaluations in the beginning of experiments was enough to select superior genotypes in the sugarcane belt in PE, Brazil. It is possible to reduce the time-to-market of new sugarcane cultivars by three harvest years in the sugarcane belt in PE, Brazil, which affords to decrease labour costs significantly. The best cultivars in micro-region NC were SP79-1011, RB952692, RB952675, and RB813804. For micro-region SC, the best cultivars were RB813804, SP78-4764, RB952675, RB952522, RB952692, SP79-1011, RB952511, RB953265, and RB952754. In NW, the best cultivars were RB952675, RB813804, RB952875, and RB952675, while in SW the best cultivars were SP78-4764, SP80-1816, RB952511, and RB952675. For MB, the best cultivars were RB813804, RB763710, RB892975, RB953265, and SP79-1011.

CONFLICTS OF INTEREST

The authors declare that they have no conflicts of interest.

ACKNOWLEDGMENTS

CAPES - BRAZIL by grant of scholarship.

RIDESA - Interuniversity Network for the Development of the Sucroenergetic Sector for the granting of genotypes for research.

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