Original Research Article

Genotype x Harvest Cycles Interaction in Sugarcane on the South Coast of Pernambuco

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ABSTRACT

Aims: To quantify the magnitude of the genotype x harvest cycle interaction (GxC) of sugarcane during three harvest cycles and to select superior clones for cultivation on the Coast of the Southern Forest of Pernambuco. **Study design:** The experiment was conducted in a randomized complete block design. **Place and Duration of Study:** Evaluated during the 2010/2011, 2011/2012 and 2012/2013 harvest years in the agricultural area of the Cucaú Plant, located in the Municipality of Rio Formoso (8º39' 49" S and 35º09'31" W, altitude of 5m), Microregion of the Southern Forest of Pernambuco. **Methodology:** 11 genotypes Republic of Brazil of the RB 2004 series and three RB cultivars were evaluated. Each plot was represented by five grooves of 8.0 m in length, spaced in 1.0 m, totaling 40 m^2. The crops were harvested 15 months after planting (MAP) for the first crop cycle and 12 MAP during the two subsequent cycles were evaluated tons of sugarcane per hectare (TCH), tons of pol per hectare (TPH) and total recoverable sugar (ATR). The variance analyses, the Scott and Knott clustering test, the estimative of the simple and complex parts of the G x C interaction and the Pearson correlation coefficient were processed in the Genes program. **Results:** The genotypes showed a significant reduction of TCH from the first to the second cycle and that only the genotype UFRPE11 showed a significant decrease for the third. The genotypes UFRPE10, UFRPE6, UFRPE11, UFRPE7, UFRPE2, UFRPE9 and UFRPE1 exceeded all commercial varieties in TPH. It was observed for the variable ATR that there were no significant differences between the genotypes in the third cycle. The simple fraction of the interaction G x C were predominant between cycles C1 and C2 for TCH (67.91%) and TPH (69.35%), while for ATR (56.42%) the complex fraction was predominant. For the pair C2 x C3, the simple fraction of the interaction G x C predominated only in the TCH (62.85%) and TPH (62.41%) variables, but was not significant for the variable ATR. It is worth mentioning that the C1 x C3 cycle pair presented predominantly complex type interactions for all variables TCH (50.42%), TPH (52.20%) and ATR (59.66%). **Conclusion:** The simple fraction of the genotype x harvest cycles (G x C) interaction provides genetic gain for yield of sugarcane and sugar in selection in subsequent pairs of harvest cycles, year by year. The complex fraction of G x C interaction reduces the predictability of genetic gain, making it difficult to select new cultivars. Local selection favors expressive genetic gain in a few selection cycles. However, it does not favor the selection of genotypes with high adaptability and phenotypic stability, requiring tests in several environments. The UFRPE06 and UFRPE10 clones can be selected to continue the selection cycles for the southern coastal conditions of the Mata de Pernambuco.

***Keywords**: Saccharum spp., genotype x harvest cycles interaction, genetic gain.*

1. INTRODUCTION

The verticalization of sugarcane production in Brazil occurs due to the development and implementation of new agricultural production technologies, among which are the new cultivars developed by the breeding programs [1, 2]. According to Barbosa et al. [3], the cultivars are the basis of the productive chain and their continuous replacement by other more productive ones represents significant economic gain for the sugar-energy sector.

The main characteristics used as parameters for the selection of superior cultivars are: agroindustrial productivity, tolerance to water stress, resistance to pests and diseases, adaptability and phenotypic stability [4,5,6]. To better explore the genetic variability of sugarcane, the selection should be based on the main components for agricultural and industrial productivity, the most important variables being tons of sugarcane per hectare (TCH), tons of pol. per hectare (TPH) and total recoverable sugars (ATR).

The selection of cultivars that present favorable alleles for these characteristics, as well as the recommendation of these cultivars for the different production environments, are the main challenges for sugarcane breeding programs, especially in the Northeast region of Brazil. This is because the region presents high variation of soils and topography, besides a great oscillation of the climatic conditions between the years [7].

Such environmental variations are determinant for genotype expression, which can cause significant variations in the performance of the cultivars when evaluated in different locations and in different agricultural years, hindering the selection and recommendation of cultivars [8,9,10,11,12].

Several studies aimed at quantifying the genotype x environment interaction (GxC), have been carried out in sugarcane, which helps to recommend the most appropriate varietal management and to determine strategies for exploring genetic variability to optimize the selection gain [13,14; 15,16,17,18].

The GxC interactions can be provided by the existence of great variability between the genotypes in the environments, called the simple part, or associated with the lack of correlation between the genotypes, called the complex part. Complex-type interactions hinder selection in breeding, as they indicate that genotype superiority does not occur due to the inheritable portion of the genetic variance, but rather due to environmental factors [19].

The present work aimed to quantify the magnitude of the genotype x harvest cycle interaction (GxC) of sugarcane during three harvest cycles and to select superior clones for cultivation on the Coast of the Southern Forest of Pernambuco.

2. MATERIALS AND METHODS

Fourteen genotypes of the Sugarcane Genetic Improvement Program (PMGCA) of the Interuniversity Network for the Development of the Sugarcane Sector (RIDESA), Republic of Brazil (RB), were evaluated, being eleven clones of the RB 2004 series, developed by the Sugarcane Experimental Station of Carpina (EECAC), belonging to the Federal Rural University of Pernambuco (UFRPE), and three commercial RB varieties.

The experiment was conducted under a randomized complete block design (RDBC), with four replications, and evaluated during the 2010/2011, 2011/2012 and 2012/2013 agricultural years in the agricultural area of the Cucaú Plant, located in the Municipality of Rio Formoso (8º39' 49" S and 35º09'31" W, altitude of 5m), Microregion of the Southern Forest of Pernambuco. The experimental unit was represented by five grooves of 8.0 m in length, spaced in 1.0 m, totaling 40 m².

Planting was carried out on a dystrophic Yellow Red Latosol in July 2010. The crops were harvested 15 months after planting (MAP) for the first crop cycle and 12 MAP during the two subsequent cycles.

During the experiment, pluviometric precipitations of 3178.00 mm, 1147.00 mm and 1947.20 mm respectively were recorded in the agricultural years 2010/2011, 2011/2012 and 2012/2013, as shown in figure 1.

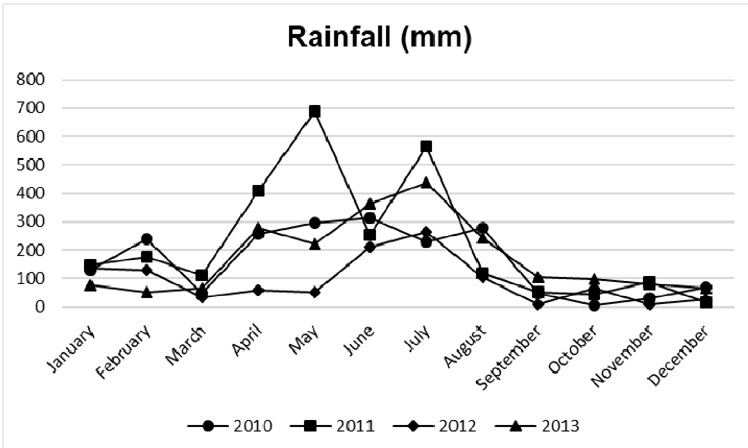

Figure 1. Rainfall (mm) observed in the agricultural years 2010/2011, 2011/2012 and 2012/2013.

Were evaluated tonnes of sugarcane per hectare (TCH), tons of pol per hectare (TPH) and total recoverable sugar (ATR), calculated according to the methodology presented by Fernandes [20].

To verify the homogeneity between the mean squares of the residual variances (QMR), the Hartley maximum F test was applied. Subsequently, the analysis of variance was performed using the statistical model $y_{ijk} = \mu + G_i + \frac{\beta}{C_{jk}} + C_j + GC_{ij} + \varepsilon_{ijk}$, where: y_{ijk} is the i-th genotype in the j-th block within the k-th harvest cycle; µis the overall mean of the test; G_i is the effect of the i-th genotype; C_j is the effect of the j-th block within harvest cycles; $\frac{\beta}{C_{jk}}$ is the effect of the j-th block within the k-th harvest cycle; GC_{ij} is the effect of the interaction of the i-th genotype with k-th harvest cycle and ε_{ijk} is the effect of experimental error.

The effects of genotypes (G) were determined as fixed, while the effects of harvest cycles (C) were randomized. The test F (P<0.01 e P<0.05) was applied and the means were grouped by the Scott and Knott test [21].

Unfolding of the components of variance of the G x C interaction were made, being split into simple and complex parts by the method of Cruz and Castoldi [19]. Finally, the Pearson correlation coefficient was applied between the pairs of crop cycles evaluated. All of the Genetic-statistical analyzes were processed in the Genes program [22].

3. RESULTS AND DISCUSSION

It was verified that the relation between the highest and the lowest value of the QMR was 1.93, 1.56 and 2.32 respectively for the variables TCH, TPH and ATR. According to Pimentel-Gomes [23], it can be affirmed that there is homogeneity among the residual variances, which allows the accomplishment of the analysis of joint variance, according to Table 1.

Table 1. Summary of the joint variance analysis for the variables tons of sugarcane per hectare (TCH), tons of pol. Per hectare (TCH) and total recoverable sugar (ATR).

FV	GL	QM		
		TCH	**TPH**	**ATR**
Genotype (G)	13	1602.94**	36.40**	226.30^{ns}
harvest cycle (C)	2	20646.29**	329.09**	1364.51**
G X C	26	172.01**	5.29**	115.59**
Média		68.37	9.84	140.69
CV_e (%)		12.35	13.35	4.21
>(QMR)/<(QMR)		1.93	1.56	2.32

(**) significant at 1% probability by the F test; (ns) not significant.

The coefficients of variation (CV) were 12.35%, 13.35%, and 4.21%, respectively for TCH, TPH and ATR, indicating adequate experimental accuracy [23] (Table 1).

The source of variation genotypes (G) showed significant differences at the 1% probability level by the F test for the TPH and TCH variables, indicate the existence of a high degree of genetic variability among the evaluated sugarcane genotypes. The existence of wide genetic variability among sugarcane genotypes was also observed by Fernandes Júnior [24] and by Souza et al. [25], who found significant differences at 1% probability for the TCH and TPH variables in experiments in the Northern Pernambuco Forest, and also by Bressiani [26] and Silva et al. [27] in studies of families of sugarcane (Table 1).

Significant differences (P<0.01) were observed between harvest cycles (C) for the three variables analyzed (Table 1). These differences occur due to the polygenic nature of the TPH, TCH and ATR variables, being their genotypic expressions were strongly influenced by oscillations of the meteorological variables, such as the precipitations verified during the conduction of the tests (Figure 1).

There were significant differences (P<0.01) for the G x C interaction. The differentiated behavior of the genotypes in the various harvest cycles corroborates that the genotypic expression of the polygenic characters TCH, TPH and ATR are strongly influenced by the environment (Table 1). These findings were also verified by Melo et al. [14], studying RB clones of sugarcane from the 94 series in four harvest cycles in the state of Pernambuco and by Silva [16], which verified a highly significant effect of the genotype x environment interaction for the TCH and TPH variables.

The result of the Scott and Knott [21] test (P<0.05), from the interaction of G x C, for the TCH variable showed that, in the first cycle, the means of the genotypes were grouped into four distinct groups, while in the subsequent cycles, they were grouped into three groups. It is also observed that most of the genotypes showed a significant reduction of productivity from the first to the second cycle and that only the genotype UFRPE11 showed a significant decrease for the third. The above observations occur due to genetic factors, as well as to non-controllable environmental factors, such as variation of intensity and distribution of rainfall in the three cycles considered, 3178.00 mm, 1147.00 mm and 1947.20 mm respectively.

Table 2. Mean values of tons of sugarcane per hectare (TCH) obtained in sugarcane genotypes in the first, second and third harvesting cycles, in the coast south of Pernambuco, Usina Cucaú, in the years 2010/2011, 2011/2012 and 2012/2013.

Genotypes	**TCH**			**Averages**
	First	**Second**	**Third**	
UFRPE10	116.50aA	78.13aB	69.06aB	87.90
UFRPE8	106.31aA	67.50aB	62.81aB	78.88
UFRPE6	97.25bA	66.88aB	71.88aB	78.67
UFRPE11	92.75bA	72.19aB	58.13aC	74.35
RB863129*	104.75aA	61.25aB	50.63bB	72.21
UFRPE2	93.25bA	61.25aB	61.25aB	71.92
UFRPE7	84.50cA	66.25aB	61.88aB	70.88
UFRPE9	95.75bA	57.81aB	56.25aB	69.94
UFRPE1	84.75cA	60.00aB	61.25aB	68.67
RB867515*	93.25bA	52.81bB	51.25bB	65.77
RB92579*	94.00bA	54.06bB	45.63bB	64.56
UFRPE5	80.75cA	50.31bB	51.88bB	60.98
UFRPE3	59.00dA	39.06cB	49.06bA	49.04
UFRPE4	64.00dA	35.00cB	31.56cB	43.52

(*) Commercial varieties (standards); Averages followed by the same lowercase letters at the vertically and by the same uppercase letters at the horizontally constitute a statistically homogeneous group by the Scott and Knott [21] clustering test (P<0.05).

Among the genotypes evaluated, the UFRPE10, UFRPE06 clones and the cultivar RB863129 stood out in the first harvest cycle, which presented the following averages 116.50, 106.31 and 104.75 tons of sugarcane per hectare, respectively. In the second cycle, the genotypes UFRPE10, UFRPE11, UFRPE8, UFRPE6, UFRPE7, RB863129, UFRPE2, UFRPE1 and UFRPE9 showed the highest means, but statistically equal. Finally, in the third harvest cycle, UFRPE6, UFRPE10, UFRPE8, UFRPE7, UFRPE2, UFRPE1, UFRPE11 and UFRPE9 clones exceeded all commercial varieties, demonstrating that the available genetic variability favored statistically significant selection gain (Table 2).

For the variable tones of pol per hectare (TPH), one can observe the formation of five distinct groups for the first harvest cycle and three different groups for the second and third harvest cycles. These results confirm that this character is influenced by the harvest cycles and that the variations presented are due to the different genotypic characteristics of the clones under study, according to Table 3. Similar data were found by Arantes [28] in the State of São Paulo, which states that the TPH variable is dependent on the environmental factor.

Table 3. Mean values of tons of pol. per hectare (TPH) obtained in sugarcane genotypes in the first, second and third harvesting cycles, in the coast south of Pernambuco, Usina Cucaú, in the years 2010/2011, 2011/2012 and 2012/2013.

Genotypes	TPH			Averages
	First	Second	Third	
UFRPE10	17.50aA	11.26aB	10.30aB	13.02
UFRPE6	14.95bA	10.48aB	10.86aB	12.10
UFRPE11	13.16cA	10.01aB	8.93aB	10.70
UFRPE8	13.10cA	9.56bB	8.88aB	10.51
UFRPE7	11.80dA	9.74aB	9.64aB	10.39
UFRPE2	13.37cA	8.95aB	8.58aB	10.30
RB863129*	14.71bA	8.83aB	7.33bB	10.29
UFRPE9	13.18cA	8.07aB	8.74aB	9.99
RB92579*	14.68bA	8.07bB	6.96bB	9.90
RB867515*	12.53cA	7.58bB	7.77bB	9.29
UFRPE1	10.15dA	8.72aA	8.95aA	9.27
UFRPE5	11.31dA	7.81aB	7.47bB	8.86
UFRPE3	7.73eA	5.57cB	7.36bA	6.89
UFRPE4	8.89eA	5.54bB	4.71cB	6.38

(*) Commercial varieties (standards); Averages followed by the same lowercase letters at the vertically and by the same uppercase letters at the horizontally constitute a statistically homogeneous group by the Scott and Knott [21] clustering test (P<0.05).

In the first harvest cycle, clone UFRPE10 presented an average of 17.50 tons of pol per hectare, which was statistically superior to all other genotypes evaluated in the experiment. According to Khan et al. [29], the selection of sugarcane genotypes can be emphasized based on the factors of production that contribute to the recovery of sugar in percentage and to the maximum sugar yield. In the second cycle, the genotypes UFRPE10, UFRPE6, UFRPE11, UFRPE7, UFRPE2, RB863129, UFRPE9, UFRPE1 and UFRPE5 stood out, which presented the highest and statistically similar averages. Finally, in the third cycle, the genotypes UFRPE10, UFRPE6, UFRPE11, UFRPE7, UFRPE2, UFRPE9 and UFRPE1 exceeded all commercial varieties, demonstrating that the available genetic variability favored statistically significant selection gain for the evaluated character (Table 3).

Regarding the variable total recoverable sugar (ATR), in the first harvest cycle, four groups were statistically different. The genotypes RB92579, UFRPE6 and UFRPE10 presented the highest averages, respectively 149,06, 146,67 and 143,22 kilograms of sugar per tons of sugarcane, according to Table 4. Differentiated ATR values among sugarcane genotypes in the first harvest cycle were also observed by Silva et al. [30], which studied the productive potential of sugarcane under irrigation in the State of São Paulo. Similar results were also observed by Souza et al. [25] when evaluating sugarcane genotypes for the beginning of the harvest in the northern forest area of Pernambuco.

Table 4. Mean values of total recoverable sugar (ATR) obtained in sugarcane genotypes in the first, second and third harvesting cycles, in the coast south of Pernambuco, Usina Cucaú, in the years 2010/2011, 2011/2012 and 2012/2013.

Genotypes	ATR			Média
	First	Second	Third	
UFRPE6	146.67aA	151.51aA	145.94aA	148.04
RB92579*	149.06aA	145.52aA	146.80aA	147.12
UFRPE4	137.43bB	151.38aA	143.02aB	143.94
UFRPE7	134.54bB	142.56bB	151.66aA	142.92
UFRPE10	143.22aA	141.15bA	144.37aA	142.91
UFRPE5	136.26bB	148.46aA	140.18aB	141.63
UFRPE11	137.94bB	136.45bB	149.02aA	141.13
UFRPE9	134.86bB	135.93bB	149.68aA	140.16
RB863129*	135.49bA	140.50bA	142.84aA	139.61
UFRPE2	138.63bA	140.43bA	138.56aA	139.20
RB867515*	130.26cB	140.80bA	145.91aA	138.99
UFRPE3	127.26cB	139.04bA	145.20aA	137.17
UFRPE1	119.99dB	140.70bA	142.93aA	134.54
UFRPE8	120.58dB	137.20bA	138.95aA	132.24

(*) Commercial varieties (standards); Averages followed by the same lowercase letters at the vertically and by the same uppercase letters at the horizontally constitute a statistically homogeneous group by the Scott and Knott [21] clustering test (P<0.05).

In the second harvest cycle, the formation of two distinct groups was observed. The genotypes UFRPE6, UFRPE4, UFRPE5 and RB92579 showed the highest averages, respectively 151.51, 151.38, 148.46 and 145.52 kilograms of sugar per ton of sugarcane. It is also observed that in the third cycle there were no significant differences between the genotypes.

Estimates of the simple and complex fractions of the interaction genotypes x harvest cycles showed that the simple type fraction between cycles C1 and C2 for TCH (67.91%) and TPH (69.35%) variables was predominant, while for the ATR variable, 56.42% of the interactions resulted of the complex type fraction being predominant, according to Table 5.

Table 5. Estimates of the simple (% FS) and complex (% FC) fractions of the interaction genotypes x harvest cycles and correlation (r) between pairs of harvest cycles for tons of sugarcane per hectare (TCH), tons of pol. per hectare TPH) and total recoverable sugar (ATR).

Pairs of harvest cycles	TCH			TPH			ATR		
	%FS	%FC	r	%FS	%FC	r	%FS	%FC	r
C1 x C2	67.91	32.99	0.49**	69.35	30.65	0.44*	43.58	56.42	0.79*
C1 x C3	49.58	50.42	0.98*	47.79	52.20	0.91*	40.33	59.66	0.67*
C2 x C3	62.85	37.15	0.59*	62.41	37.59	0.60*	00.00	100.00	0.03^{ns}

(**; *) significant at 1% and 5% of probability by the F test, respectively; (ns) not significant.

It is observed in Table 5 that, for the pair C2 x C3, the simple fraction of the interaction G x C predominated only in the TCH (62.85%) and TPH (62.41%) variables, but was not significant for the variable ATR. These results indicate that most of the evaluated genotypes presented differentiated responses of low intensity as a function of the variation between subsequent agricultural years. This statement corroborates the results of the average test between cycles C1 x C2 and C2 x C3 presented previously in Table 4.

It is worth mentioning that the C1 x C3 cycle pair, the variables TCH (50.42%), TPH (52.20%) and ATR (59.66%) presented predominantly complex type interactions, indicating the need for more robust test applications to better understand the magnitude of G x C interaction as adaptability and stability models, as well as repeatability parameters to aid selection and recommendation of cultivars.

The Pearson correlation coefficient was significant by the t-test for all pairs of harvest cycles for the variables TCH (r = 0.49, 0.98 and 0.59, respectively) and TPH (r = 0,44, 0.91 and 0.60 respectively), confirming that the observed interactions are due to the strong influence of the environment on the expression of the polygenic characters evaluated, confirming the positive association between the harvest cycles (Table 5).

The ATR presented significant ($P<0.05$) for the pairs of cycles C1 x C2 (r = 0.79) and C1 x C3 (r = 0.67), with no significance for the pair of harvest cycles C2 x C3. This character presented G x C interaction predominantly attributed to the complex fraction, indicating large differences between environments (Table 5).

4. CONCLUSION

The simple fraction of the genotype x harvest cycles (G x C) interaction provides genetic gain for yield of sugarcane and sugar in selection in subsequent pairs of harvest cycles, year by year.

The complex fraction of G x C interaction reduces the predictability of genetic gain, making it difficult to select new cultivars.

Local selection favors expressive genetic gain in a few selection cycles. However, it does not favor the selection of genotypes with high adaptability and phenotypic stability, requiring tests in several environments.

The UFRPE06 and UFRPE10 clones can be selected to continue the selection cycles for the southern coastal conditions of the Mata de Pernambuco.

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