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 indicate superior clones for cultivation on the Coast of the Southern Forest of Pernambuco.**Study design:**The experiment was conducted under a randomized design.**Place and Duration of Study:**Evaluated during the 2011/2012, 2012/2013 and 2013/2014 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 seriesand three RB cultivars. 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 (CUL). The crops were harvested 15 months after planting (MAP) for the first crop cycle and 12 MAP during the two subsequent cyclesWere evaluated tonnes of sugarcane per hectare (TCH), tons of pol.per hectare (TPH) and total recoverable sugar (ATR).**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 to the TPH. It was observed for the variable total recoverable sugar (ATR) that there were no significant differences between the genotypes in the third cycle.**Conclusion:**The simple fraction of the interaction G x C provides genetic gains 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 gains, making it difficult to select new cultivars.Local selection favors expressive genetic gains 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. Harvest cycle. Decomposition of the interaction genotype x harvest cycles.*

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 gains 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].

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 gains (13,14; 15,16,17,18).

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

2. MATERIAL AND METHODS

Fourteen genotypes Republic of Brazil (RB) of the Sugarcane Genetic Improvement Program (PMGCA) of the Interuniversity Network for the Development of the Sugarcane Sector (RIDESA) 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 block design (DBC), with four replications, and evaluated during the 2011/2012, 2012/2013 and 2013/2014 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 (CUL) 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 1,943.10 mm, 2,663.20 mm and 1,105.30 mm respectively were recorded in the years 2011/2012, 2012/2013 and 2013/2014, as shown in figure 1.

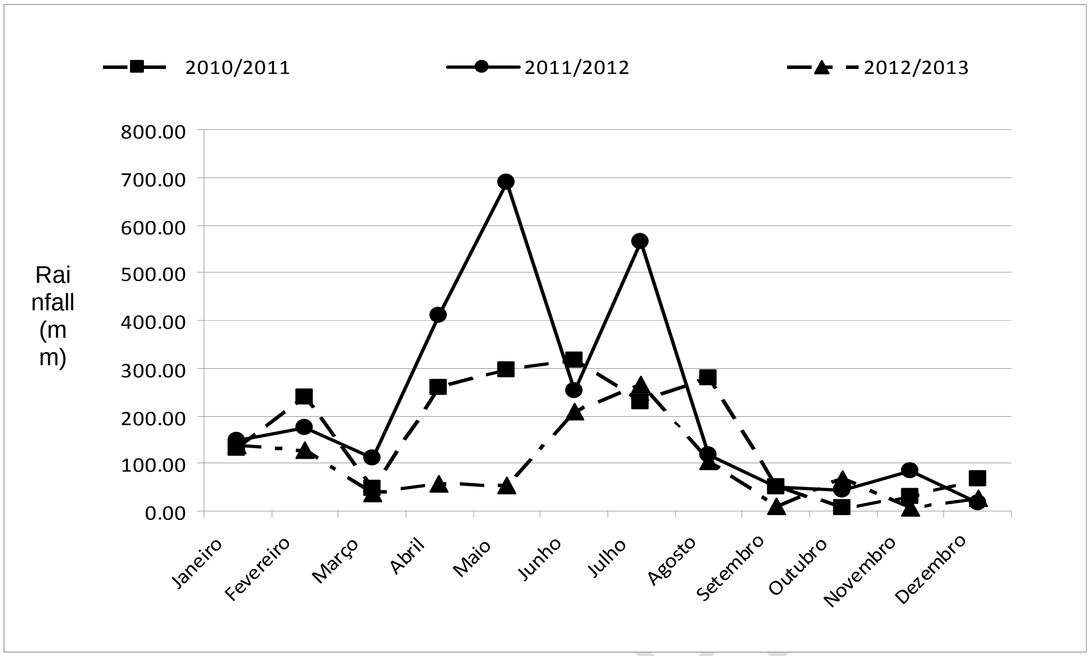

Figure 1. Rainfall (mm) observed in the agricultural years 2010/2011, 2011/2012 and 2012/2013

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 [19].

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 [20] (P<0.05).

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 [21]. 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 crops of the crop corroborates that the genotypic expression of the polygenic characters TCH, TPH and ATR is 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 [20] 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 cycles considered.

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 [20] 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, UFRPE8, UFRPE6, UFRPE11, RB863129, UFRPE2, UFRPE7, UFRPE9 and UFRPE1 showed the highest means, but statistically equal. Finally, in the third harvest cycle, UFRPE10, UFRPE6, UFRPE11, UFRPE2, UFRPE2, UFRPE7, UFRPE9 and UFRPE1 clones exceeded all commercial varieties, demonstrating that the available genetic variability favored statistically significant selection gains (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 cycle. 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 [20] 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 gains 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 UFRPE6, RB92579 and UFRPE10 presented the highest averages, respectively 146,67, 149,06 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	Soca	First	
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 [20] clustering test (P<0.05).

In the second harvest cycle, the formation of two distinct groups was observed. The genotypes UFRPE6, RB92579, UFRPE4 and UFRPE5 showed the highest averages, respectively 151.51, 145.52, 151.38 and 148.46 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, 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 tonnes of sugarcane per hectare (TCH), tonnes 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, being 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 is reinforced by the results of the average test between cycles C1 x C2 and C2 x C3 presented previously in table 4.

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).

It is worth mentioning that the C1 x C3 cycle pair, for all variables, presented 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.

4. CONCLUSION

The simple fraction of the interaction G x C provides genetic gains 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 gains, making it difficult to select new cultivars.

Local selection favors expressive genetic gains 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.

5. REFERENCES

1. Scortecci KC et. al. Challenges, opportunities and recent advances in sugarcane breeding. In: Abdurakhmonov IY editor. Plant breeding. London: IntechOpen Limited; 2012.

2. Nyko D, Valente MS, Milanez AY, Tanaka AKR, Rodrigues AVP. The evolution of agricultural technologies in the sugar-energy sector: temporary stagnation or structural crisis? Rio de Janeiro: BNDES Sectorial / Bioenergy; 2013.

3. Barbosa MHP, Resende MDV, Dias LAS, Barbosa GVS, Oliveira RA, Peternelli LA, Daros E. Genetic improvement of sugar cane for bioenergy: the Brazilian experience in network research with RIDESA. Crop Breeding and Applied Biotechnology. 2012; 12 (S2): 87-98.

4. Rosse LN, Vencovsky R, Ferreira A. Comparison of regression methods to evaluate phenotypic stability in sugarcane. Pesquisa Agropecuária Brasileira. 2002; 37 (1): 25-32.

5. Andrade JSCO, Oliveira FJ, Annunciation Son CJ, Melo LJOT, Ov Kings. Evaluation of progenies in RB families in the initial phase of genetic improvement in sugarcane. Brazilian Journal of Agricultural Sciences. 2011; 6 (4): 609-616.

6. Souza AER, Oliveira FJ, Annunciation Son CJ da; Melo Filho PA, Melo LJOT, Tabosa JN. Selection of RB families aiming at high productivity and precocity in maturation in sugarcane. Bragantia. 2011; 70 (4): 788-795.

7. Koffler NF, Lima JFWF, De Lacerda MF, Santana JF, Silva MA. Soil-climatic characterization of the Sugarcane Regions of Brazil: Pernambuco. Piracicaba: IAA / Planalsucar; 1986.

8. Garbuglio DG, Gerage AC, Araujo PM, Juniro NSF, Shioga PS. Factor analysis and bissegmented regression in studies of environmental stratification and adaptability in maize. Pesquisa Agropecuária Brasileira. 2007; 42 (2): 183-191.

9. Cancellier LL, Afférri FS, Carvalho EV, Dotto MA, Leo FF. Efficiency in nitrogen use and phenotypic correlation in tropical corn populations in Tocantins. Agronomic Science Journal. 2011; 42 (1): 139-148.

10. Ribeiro JZ, Almeida MIM. Environmental stratification by the analysis of genotype x environment interaction in maize. Pesquisa Agropecuária Brasileira. 2011; 46 (8): 875-883.

11. Peluzio JM, Gerominni G, Silva JPA, Afférri FS, Vendruscolo JBG. Stratification and environmental dissimilarity for evaluation of soybean cultivars in the state of Tocantins. Bioscience Journal; 2012; 28 (3): 332-337.

12. Mattos PHC, Oliveira RA, Bespalhok Filho JC, Daros E, Veríssimo MAA. Evaluation of sugarcane genotypes and production environments in Paraná by GGE biplot and AMMI analysis. Crop Breeding and Applied Biotechnology. 2013;1(13):83-90.

13. Raizer AJ, Vencovsky R. Phenotypic stability of new varieties of sugarcane for the State of São Paulo. Pesquisa Agropecuária Brasileira, Brasília. 1999; 34 (12): 2241-2246.

14. Melo LJOT, Oliveira FJ, Bastos GQ, Annunciation Son CJ da, Ov Kings. Genotype interaction x sugarcane harvest cycles of the Zona Norte Mata de Pernambuco. Bragantia. 2006; 65 (2): 197-205.

15. Bastos IT, Barbosa MHP, Resende MDV, Peternelli LA, Silveira LCI., Donda LR, Fortunato AA, Costa PMA, Figueiredo ICR. Evaluation of the interaction genotype x

environment in sugarcane via mixed models. Tropical Agriculture Research. 2007; 4 (37): 195-203.

16. Silva MA. Genotype x environment interaction and phenotypic stability of sugarcane in the sugarcane cycle. Bragantia. 2008; 67 (1): 107-117.

17. Verissimo MAA, Anjos e Silva SD, Aires RF, Daros E, Panziera W. Adaptability and stability of early genotypes of sugarcane in Rio Grande do Sul. Brazilian Agricultural Research. 2012; 47 (4): 561-568.

18. Silva GC, Oliveira FJ, Melo LJOT. Selection of sugarcane genotypes through interaction x crop cycles in the Zona da Mata de Pernambuco. Brazilian Journal of Agricultural Sciences. 2015; 10 (2): 184-188.

19. Fernandes AC. Calculations in the sugarcane agroindustry. Piracicaba: STAB; 2011.

20. Scott AJ, Knott MA. The cluster analysis method for grouping means in the analysis of variance. Biometrics. 1974; 3 (30): 507-512.

21. Cross CD, Castoldi F. Decomposition of interaction genotypes x environments in simple and complex parts. Ceres Journal. 1991; 38 (219): 422-430.

22. Cross CD. Genes program: computational application in genetics and statistics version 7.0. Viçosa: UFV; 2009.

23. Pimentel-Gomes F. Experimental Statistics Course.Piracicaba: FEALQ; 2009.

24. Fernandes Júnior AR, Andrade JAC, Santos PC, Hoffmann HP, Chapola RG, Carneiro MS, Cursi DE. Adaptability and stability of sugarcane clones. Bragantia.2013; 72 (3): 208-216.

25. Souza PHN de, Bastos GQ, Annunciation Filho CJ da, Dutra Filho JA, Machado PR. Evaluation of sugarcane genotypes for beginning of harvest in the Central Microregion of Pernambuco.Revista Ceres. 2012; 59 (5): 677-683.

26. Bressiani JA. Sequential selection in sugarcane. Doctoral thesis. Luiz de Queiroz College of Agriculture-University of São Paulo. 2001; 104.

27. Silva MA, Landell MGA, Gonçalves PS, Martins ALM. Yield components in sugarcane families at four locations in the state of São Paulo, Brazil. Crop Breeding and Applied Biotechnology. 2002b; 2 (1): 97-106.

28. Arantes FC. Genotype x environment interaction, adaptability and stability in sugarcane genotypes. Doctoral thesis. Faculty of Agrarian and Veterinary Sciences of Jaboticabal-Paulista State University. 2013; 94.

29. Khan IA, Seema N, Race S, Yasmine S, Bibi, S. Environmental Interactions of Sugarcane Genotypes and Yield Stability Analysis of Sugarcane. Pakistan Journal of Botany. 2013; 45 (5): 1617-1622.

30. Silva MA, Arantes MT, Rhein AF de L, Gava GJC, Kolln OT. Productive potential of sugarcane under drip irrigation due to varieties and cycles. Brazilian Journal of Agricultural and Environmental Engineering.2014; 18 (3): 241-249.