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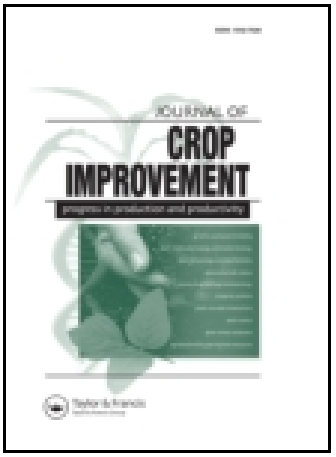

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Modeling Spatial Correlation Structure in Sugarcane (Saccharum spp.) Multi-Environment Trials

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Published online: 09 Jan 2015.

To cite this article: S. Ostengo, M. I. Cuenya & M. Balzarini (2015) Modeling Spatial Correlation Structure in Sugarcane (Saccharum spp.) Multi-Environment Trials, Journal of Crop Improvement, 29:1, 53-64, DOI: 10.1080/15427528.2014.965861

To link to this article: http://dx.doi.org/10.1080/15427528.2014.965861

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Journal of Crop Improvement, 29:53–64, 2015
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ISSN: 1542-7528 print/1542-7536 online
DOI: 10.1080/15427528.2014.965861

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Modeling Spatial Correlation Structure in Sugarcane (*Saccharum* spp.) Multi-Environment Trials

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Comparative multi-environment trials (METs) of sugarcane genotypes are frequently conducted using a randomized complete-block design (RCBD) within environments. However, blocking does not always ensure spatial variation control because of differential competition for resources among neighboring genotypes. Heterogeneity within trials may also cause between-trial heterocedasticity. This work aims to evaluate different linear mixed models (LMMs) that enable the analysis of spatial correlation and residual heterogeneity among trials for both tons of cane per hectare (TCH) and sucrose content (SC%) in three series of multi-environmental trials conducted to evaluate advanced sugarcane clones. A total of 16 sugarcane trials conducted at different sites and in different crop cycles (age) were analyzed. Individual (age×site combination) and multi-environment analyses were performed. For SC%, the classic RCBD analysis within trial was adequate. For TCH, the anisotropic autoregressive model of order 1 (AR1×AR1) was the best to compare genotype means in most trials, allowing gain in information equivalent, on average, to the addition of 1.6 replicates to the original design. In the case of multi-environment analysis, the AR1×AR1 within-trial with among-trial heteroscedasticity was the best model to compare variety means, both for TCH and SC%. The results showed how a

Received 3 June 2014; accepted 11 September 2014.
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more appropriate mixed model would help avoid commission of judgment errors in sugarcane variety recommendations.

KEYWORDS anisotropic-autoregressive spatial models, efficiency, experimental design, linear mixed model, yield trials

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INTRODUCTION

Traditional sugarcane breeding programs consist mainly of three stages: i) selection of progenitors from a germplasm collection, ii) hybridization, and iii) selection of progeny following successive clonal multiplication (Berding et al. 2004; Ming et al. 2006). At the last stage, in advanced selection stages, METs are very important for variety evaluation because of the presence of genotype-environment interactions. In METs, a set of genotypes is compared at different sites to recommend cultivars for the target production area. Trials are frequently planted in rectangular arrangements in a randomized complete-block design (RCBD). The RCBD principle assumes heterogeneity among blocks and homogeneity within blocks. However, the plot-data within a block may sometimes be correlated because of small-scale irregularities. Spatial analysis is recommended when the RCBD and/or the traditional linear models have failed to detect genotypic differences caused by large unknown variation/error terms (Smith et al. 2001). They are usually used in poor light soils where there are a lot of leaching, dry spells, weeds, and pests. However, they may also be needed to analyze plant population aspects.

The RCBD does not always guarantee control of the underlying spatial variation in sugarcane trials (Mariotti et al. 1997) because of the differential competition for resources among neighboring genotypes. Uncontrolled spatial variation adds to the residual variation affecting the standard error used in comparing variety means, and consequently this can lead to errors in varietal recommendations.

For within-trial analysis, adjusting for the variances to be used for comparing genotype means is necessary to take into account the spatial correlation among plots. Currently, the statistical analysis of geo-referenced data can be carried out under the theoretical approach of LMMs (West et al. 2007). In contrast to the linear models traditionally used, LMMs are highly flexible in modeling experimental data. The spatial analysis in the LMMs context allows consideration of possible correlations among observations from neighboring plots through the modeling of the model variance-covariance structure. An LMM allows estimation of error correlation functions that depend on distance among plots. To perform the analysis, considering spatial variation, it is necessary to define the plot location using a coordinate system, which in rectangular arrangements, such as the RCBD, is usually specified in two

dimensions: row and column position of the experimental plot or latitude and longitude from the center of the plot.

Among the various correlation functions used to model the spatial structure in rectangular arrangements of field trials, one of the most used ones is the function indicating that correlation between plot data decay with increasing distance between plots, which is designated as autoregressive of order 1 model (AR1) (Schabenberger and Pierce 2002). The model is a reparameterization of the exponential function, where spatial dependence among plots diminishes exponentially as distance among them increases. However, these spatial correlation functions may be isotropic or anisotropic, depending on whether correlations between plots are independent of the direction in which distance between them are calculated or may change according to direction. The anisotropic autoregressive of order 1 model, which calculates plot correlations in two directions (AR1xAR1), has been recommended for variety trials (Gilmour et al. 1997; Smith et al. 2001). Therefore, the isotropic autoregressive of order 1 model (AR1) depends on only one parameter (ρ) and characterizes the correlation between data from two different plots as ρ^{d}, where d is the Euclidean distance between plots. By contrast, the anisotropic power correlation model (AR1xAR1) depends on two parameters, where one of them represents correlation among data from plots on the same row (ρ_r) and the other reflects correlation among data from plots on the same column (ρ_c).

Experience from sugarcane trials has shown that LMMs that include autoregressive spatial correlation are efficient in identifying best genotypes at early selection stages (Stringer and Cullis 2002; Edmé et al. 2007). Other studies have also selected this model type for multi-environment evaluations (Smith et al. 2007). However, most of these studies considered the genotype effect as random and also introduced potential genetic correlations among varieties.

The precision with which a trial is conducted in a particular environment is reflected in the magnitude of the residual variance. Heteroscedasticity in residual variance among trials in different environments is common, making it difficult to draw conclusions from multi-environment data. The heteroscedasticity can also be considered by using LMMs (Kang et al. 2004; Casanoves et al. 2005).

In the sugarcane breeding program of Estación Experimental Agroindustrial "Obispo Colombres" (SCBP-EEAOC) in Tucumán, Argentina, multi-environment trials are used in the final selection stage during consecutive crop cycles for each variety series. In these trials, a small number of outstanding genotypes are compared with one another and with commercial varieties. A comparison of genotype means is performed with classical fixed linear models for RCBD, even when there might be heterogeneity within blocks. In addition, by-environment analyses are performed independently. At this stage of selection, to avoid the commission of errors of judgment

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in recommending varieties, it is necessary to apply statistical approaches for assessing, more efficiently and accurately, the productive performance of the evaluated clones.

This work aims to evaluate, in a wide range of sugarcane multi-environment trials, the goodness of fit of alternative LMMs that allow for spatial correlation and heterocedasticity when analyzing both tons of cane per hectare (TCH) and sucrose content (SC%) at the beginning of harvest; both TCH and SC% are components of sugar yield, which is the main breeding criteria for the development of new sugarcane varieties.

MATERIALS AND METHODS

Data

We used three MET series (2005, 2006, and 2007) from the SCBP-EEAOC. For each series, different genotypes and crop ages were evaluated in six sites representing contrasting environments typical of the sugarcane plantation area in Tucumán (Table 1). Codes used for each environment are: FRO (Fronterita), ING (Ingas), LAB (La Banda), LCO (Los Córdoba), MER (Mercedes), and PAL (Palá-Palá). The environmental data of each locality are reported in Table 2.

Trials in each environment were planted according to a randomized complete-block design (RCBD) with three replicates. Each plot of three 10-meter-long rows served as an experimental unit. In each series, 20 to 22 highly selected genotypes were compared. Data were obtained and analyzed for the following variables: crop yield as TCH and SC%.

Statistical Analyses

Two different types of analyses were performed using TCH and SC% data from all trials. In the first one, 48 independent analyses, for each environment and crop age, were performed, 20 of which combined five sites and four crop ages: plant cane (P), ratoon 1 (R1), ratoon 2 (R2), and ratoon 3 (R3) for the

TABLE 1 Series, number of genotypes, crop cycles (ages), and sites used in sugarcane multi-environment trials

Series	Number of genotypes	Ages[†]	Sites[‡]
2005	20	P - R1 - R2 - R3	FRO, ING, LAB, LCO, and MER
2006	20	P - R1 - R2	FRO, ING, LAB, LCO, MER, and PAL
2007	22	P - R1	ING, LAB, LCO, MER, and PAL

[†](P) Plant-cane; (R1) Ratoon 1; (R2) Ratoon 2; (R3) Ratoon 3.
[‡](FRO) Fronterita; (ING) Ingas; (LBA) La Banda; (LCO) Los Córdoba; (MER) Mercedes; (PAL) Palá Palá.

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TABLE 2 Sites, geographic coordinates, and environmental characteristics of the sugarcane multi-environment trials

Sites	Geographic coordinates (latitude and longitude)	Average annual rainfall (mm)†	Soil characteristics (texture, organic matter and drainage)‡
Fronterita (FRO)	26°00′37″S 65°27′31″W	1453	Sandy loam, high and well drained
Ingas (ING)	27°26′46″S 65°21′24″W	700	Loam – Sandy loam, medium-low and somewhat poorly drained
La Banda (LAB)	26°59′58″S 65°23′04″W	1325	Clay loam, high and somewhat poorly drained
Los Córdoba (LCO)	27°29′29″S 65°36′35″W	1194	Sandy loam, medium and well drained
Mercedes (MER)	26°56′38″S 65°19′27″W	1142	Loany sand, medium and somewhat excessively drained
Palá-Palá (PAL)	27°02′41″S 65°13′11″W	929	Silt loam, medium-low and somewhat poorly drained

†Average of 50 years.
‡Classification according the Soil Survey Manual (Soil Survey Staff 1951).

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2005 series. Eighteen data sets came from six sites and three crop ages (P, R1, and R2) for the 2006 series, and 10 data sets were obtained from five sites and two crop ages (P and R1) for the 2007 series. In these analyses, three linear models were adjusted in turn: i) a classical linear model [LM] for RCBD, with the variety effect as fixed and block as a random effect, without considering spatial variation, i.e., assuming independence among the error terms; ii) an isotropic autoregressive of order one (AR1) spatial correlation model; iii) an anisotropic autoregressive of order one (AR1xAR1) model. In the last two models, as in the LM, variety effect was treated as fixed and block effect was treated as random.

Finally, an analysis under a multi-environment trial model for each series and crop age was performed using two different models: i) a classical linear model [LMMET] considering independent errors (with no spatial variation) and homogeneous residual variances among environments, and ii) a model with AR1xAR1 spatial correlation structure in error terms for plots of the same site, which also considered heterogeneous residual variances among sites [AR1xAR1(H)]. The basic model equation for both strategies was as follows:

$$y_{ijk} = \mu + G_i + S_j + B(S)_{k(j)} + GS_{(ij)} + \varepsilon_{ijk}$$

where y_{ijk} is yield of genotype i at site j, block k; μ is general mean; G_i is genotype i fixed effect with $I = 1, \ldots, g$; S_j is site j random effect with $j = 1, \ldots, s$; $B(S)_{k(j)}$ is block k random effect at site j with $k = 1, \ldots, n$; $GS_{(ij)}$ is

the random effect of genotype $i \times$ site j interaction, and ϵ_{ijk} is the error term associated with observation y_{ijk}.

Models were adjusted using PROC MIXED of SAS, Version 9.1 (SAS Institute 2003). Model comparison was based on Akaike information criterion (AIC). Models with lower AIC values are considered superior with regard to adjustment. The AIC was calculated as follows:

$$\mathrm{AIC} = -2\left(L - p\right)$$

where L is the residual log-likelihood and p is the number of parameters of the model.

Additionally, residual maximum likelihood ratio test (LRT) was also used for evaluation. The LRT statistic was calculated as follows:

$$-2\left(L_0 - L_1\right),$$

where L_0 and L_1 are the residual log-likelihood for models 0 and 1, respectively, model 0 being a model with a reduced number of parameters in comparison with model 1. This statistic is distributed as Chi-square with $p_1 - p_0$ degrees of freedom, where p_0 and p_1 are the numbers of parameters estimated for models 0 and 1, respectively. When the p-value associated with the LRT was ≤ 0.05, model 1 was identified as the best model.

Efficiency of either model was assessed by means of relative efficiency (RE), which was computed as follows:

$$\mathrm{RE} = \left[\mathrm{SED\ (LM)}\ /\mathrm{SED\ (SP)}\right]^2,$$

where SED (LM) is the average standard error of the difference among genotypes after adjusting the classical randomized complete-block design linear model; SED (SP) is the average standard error of the difference among genotypes obtained with an autoregressive spatial model.

RESULTS AND DISCUSSION

By-Environment Analyses

The AIC values (Table 3) for TCH showed that the first-order autoregressive model, particularly the anisotropic one (AR1xAR1), was better than the classical model in 75% of the cases. As for plant cane, autoregressive models were superior to the classical one in >80% of cases, whereas these models were superior to the classical one in 62% cases involving first ratoon crop. This comparison is particularly interesting because the dynamics and characteristics of the plant-cane bud sprouting and growth are different from the ratoon crop (Romero et al. 2005). Heterogeneity recorded among plots may

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TABLE 3 Akaike information criteria (AIC) of alternative linear models for tons of cane per hectare (TCH) in three series (plantation dates) of sugarcane multi-environment trials. (Analyses per site and crop age. Lower values of AIC for each combination of series and crop age indicate the best model [underlined].)

		2005 series			2006 series			2007 series		
		Models §								
Site †	Age ‡	LM	AR1	AR1xAR1	LM	AR1	AR1xAR1	LM	AR1	AR1xAR1
FRO	P	269.1	268.7	270.5	305.1	291.6	284.4			
	R1	279.6	274.9	271.2	286.5	288.2	289.2			
	R2	297.4	298.1	292.3	294.5	292.8	289.2			
	R3	288.1	290.1	292.0						
ING	P	317.8	316.5	314.1	339.8	327.6	329.4	335.9	333.0	335.8
	R1	293.4	294.4	295.4	322.1	314.9	317.1	283.2	285.1	286.8
	R2	342.9	344.9	339.9	307.7	304.7	299.0			
	R3	343.9	343.7	343.0						
LAB	P	278.3	(¶)	(¶)	316.1	318.1	319.2	294.3	291.0	290.5
	R1	333.9	335.7	335.5	323.1	322.4	323.9	347.3	345.4	344.7
	R2	289.4	291.0	283.1	343.3	345.2	337.1			
	R3	283.8	285.8	286.6						
LCO	P	321.9	304.0	299.0	325.7	319.5	321.1	354.7	336.8	338.4
	R1	333.1	328.5	323.2	332.7	315.0	320.6	330.1	332.1	333.0
	R2	318.4	320.4	306.9	297.3	299.0	299.2			
	R3	322.4	313.0	306.2						
MER	P	302.1	299.3	300.5	355.1	347.7	347.9	330.8	330.4	331.3
	R1	305.2	299.0	300.9	329.3	327.7	323.9	291.2	292.3	289.2
	R2	264.1	262.0	261.9	294.0	291.4	291.8			
	R3	279.2	280.1	281.8						
PAL	P				300.4	302.0	303.9	339.3	339.9	337.4
	R1				333.0	333.0	334.9	326.5	328.4	325.4
	R2				353.6	353.6	355.6			

† (FRO) Fronterita; (ING) Ingas; (LBA) La Banda; (LCO) Los Córdoba; (MER) Mercedes; (PAL) Palá Palá.
‡ (P) Plant-cane; (R1) Ratoon 1; (R2) Ratoon 2; (R3) Ratoon 3.
§ (LM) classical linear model; (AR1) first-order autoregressive model; (AR1xAR1) anisotropic first-order autoregressive model.
(¶) Convergence problems during the estimation process. Underlined numbers indicate AIC minimum values (best model) within each site, series, and crop age.

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affect cultivar comparison more in the plant cane than in the ratoon crop. In comparing models according to the LRT (data not shown), models that take into account the spatial correlation (first-order autoregressive models) were also better fitted in most cases.

Relative efficiency of AR1xAR1 with respect to the classical linear model for TCH is shown in Table 4. The choice of this model provides gain in information equivalent to the addition of 1 to 8 additional replicates to the original trial design (RCBD).

The AIC values for SC% (Table 5) indicated that the classical model could be better adjusted than those modeling error spatial correlations through autoregressive functions (AR1 and AR1xAR1) in most cases. Based on AIC

TABLE 4 Comparative relative efficiency (RE) and replicate number (N° Rep) as necessary to model tons of cane per hectare (TCH) in a classical linear model with a randomized complete block design model (LM) to obtain the same efficiency level as with an anisotropic autoregressive model (AR1xAR1)

		2005 series		2006 series		2007 series	
Site †	Age ‡	RE §	N° Rep	RE	N° Rep	RE	N° Rep
FRO	P	1.040	3	3.762	11		
	R1	1.822	5	1.220	4		
	R2	1.552	5	1.404	5		
	R3	1.009	3				
ING	P	1.768	5	1.901	6	1.214	4
	R1	1.001	3	1.404	4	1.042	3
	R2	1.632	5	1.523	5		
	R3	1.439	4				
LAB	P	1.007	3	1.039	3	1.534	5
	R1	1.020	3	1.122	3	1.307	4
	R2	1.697	5	1.354	4		
	R3	1.080	3				
LCO	P	3.810	11	1.502	5	2.840	9
	R1	1.876	6	1.737	5	1.072	3
	R2	2.136	6	1.011	3		
	R3	2.483	7				
MER	P	1.610	5	1.877	6	1.213	4
	R1	1.654	5	1.635	5	1.232	4
	R2	1.451	4	1.357	4		
	R3	1.164	3				
PAL	P			1.020	3	1.322	4
	R1			1.008	3	1.232	4
	R2			1.001	3		
	R3						

† (FRO) Fronterita; (ING) Ingas; (LBA) La Banda; (LCO) Los Córdoba; (MER) Mercedes; (PAL) Palá Palá.
‡ (P) Plant-cane; (R1) Ratoon 1; (R2) Ratoon 2; (R3) Ratoon 3.
§ Relative efficiency (RE=[SED(LM)/SED(AR1xAR1)]2. SED(LM) and SED(AR1xAR1) are average standard errors of the difference of genotype means for LM and AR1xAR1 models, respectively.

values, this was true for 64% of the cases. This suggested that sugar content was a more stable variable than TCH when spatial heterogeneity existed in the trial.

Multi-Environment Analyses

Among multi-environment models for TCH, the model that takes into account anisotropic autoregressive spatial correlations of order one and heterogeneity of residual variances among sites [AR1xAR1(H)] showed better adjustment than the classical linear model, which was based on the assumption of independence of error terms among data from different blocks within each trial and constant residual variances at all sites (LMMET). This applied to all

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TABLE 5 Akaike information criteria (AIC) of alternative linear models for sucrose content at the beginning of harvest (SC%) in three series (plantation dates) of sugarcane multi-environment trials. (Analyses per site and crop age. Lower values of AIC for each combination of series and crop age indicate the best model [underlined].)

		2005 series			2006 series			2007 series		
		Models §								
Site †	Age ‡	LM	AR1	AR1xAR1	LM	AR1	AR1xAR1	LM	AR1	AR1xAR1
FRO	P	107.7	109.6	110.5	122.3	120.5	120.8			
	R1	126.8	128.8	128.8	104.4	106.2	108.0			
	R2	124.1	123.8	124.7	109.5	110.8	112.8			
	R3	110.5	112.2	112.2						
ING	P	109.0	109.1	107.2	112.0	112.7	115.3	143.6	142.5	144.5
	R1	104.6	106.5	105.7	119.1	119.8	120.6	142.0	142.9	144.0
	R2	132.0	133.6	133.8	116.3	117.5	118.8			
	R3	118.6	120.1	119.7						
LAB	P	119.1	121.1	122.2	68.5	(¶)	(¶)	110.5	112.5	112.5
	R1	79.8	78.4	78.5	94.4	95.8	94.5	122.0	123.8	126.0
	R2	93.8	95.8	95.7	114.5	116.5	116			
	R3	100.7	102.5	104.1						
LCO	P	103.2	105.2	103	104.0	103.0	106.9	133.0	130.3	131.7
	R1	97.1	86.0	89.1	108.2	104.2	103.8	134.2	135.9	135.8
	R2	121.3	122	115.8	135.3	136.2	136.7			
	R3	113.7	114.6	114.7						
MER	P	137.2	139.0	139.1	132.3	134.2	136.0	114.7	114.4	116.6
	R1	118.5	120.3	120.5	119.4	121.3	121.3	79.9	78.5	80.8
	R2	95.8	95.0	94.7	96.9	98.9	93.8			
	R3	93.6	95.6	95.3						
PAL	P				121.9	120.2	123.9	128.6	130.6	132.1
	R1				144.7	146.4	147.0	129.1	128.7	128.5
	R2				120.7	122.6	124.4			

† (FRO) Fronterita; (ING) Ingas; (LBA) La Banda; (LCO) Los Córdoba; (MER) Mercedes; (PAL) Palá Palá.
‡ (P) Plant-cane; (R1) Ratoon 1; (R2) Ratoon 2; (R3) Ratoon 3.
§ (LM) classical linear model; (AR1) first-order autoregressive model; (AR1xAR1) anisotropic first-order autoregressive model.
(¶) Convergence problems during the estimation process. Underlined numbers indicate AIC minimum values (best model) for each site, series, and crop age.

MET series and crop ages, according to AIC values and LRT (Table 6). The AR1xAR1(H) model was judged to be better than heteroscedastic AR1 model.

For SC%, AIC values and LRT (Table 7) showed that the AR1xAR1(H) model was superior to the classical linear model in most of the cases for multi-environment trials. The AR1xAR1(H) was regarded as better than the heteroscedastic AR1 model (data not shown). However, because of the results of spatial analysis for each trial taken individually, where no important spatial correlation were found for SC%, the AR1xAR1(H) model was also compared with the multi-environment linear model that did not consider autoregressive spatial correlation but heterogeneity residual variance through environments. In five of the seven cases, where AR1xAR1 was judged to be

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TABLE 6 Akaike information criterion (AIC) and residual maximum likelihood ratio test (LRT) of heteroscedastic anisotropic first-order autoregressive model as compared with the classical linear model for multi-environment analysis. (Tons of cane per hectare (TCH) variable in three series (plantation dates) and crop ages.)

				LRT ‡		
		AIC		LMMET	AR1xAR1(H)	
Series	Age †	LMMET	AR1xAR1(H)	$-2\,L$	$-2\,L$	p
2005	P	2075.9	2018.6	2067.9	1986.6	<0.0001
	R1	2166.2	2096.8	2158.2	2066.8	<0.0001
	R2	2109.6	2064.2	2101.6	2034.2	<0.0001
	R3	2101.1	2064.0	2093.1	2030.0	<0.0001
2006	P	2731.5	2639.0	2723.5	1986.6	<0.0001
	R1	2687.2	2671.5	2679.2	2066.8	<0.0001
	R2	2684.4	2630.0	2676.4	2034.2	<0.0001
2007	P	2324.2	2267.6	2316.2	2231.6	<0.0001
	R1	2209.2	2189.4	2201.2	2157.4	<0.0001

† (P) Plant-cane; (R1) Ratoon 1; (R2) Ratoon 2; (R3) Ratoon 3.
‡ (LMMET) classical model; AR1xAR1(H) = heteroscedastic anisotropic first-order autoregressive model; $-2\,L = -2$ residual log-likelihood; p = probability value in relation to LMMET. Underlined numbers indicate AIC lower values and thus better adjustment.

TABLE 7 Akaike information criterion (AIC) and residual maximum likelihood ratio test (LRT) of heteroscedastic anisotropic first-order autoregressive model as compared with the classical linear model for multi-environment trials. (Sucrose content at the beginning of harvest [SC%] variable in three series [plantation dates] and crop ages.)

				LRT ‡		
		AIC		LMMET	AR1xAR1(H)	
Series	Age †	LMMET	AR1xAR1(H)	$-2\,L$	$-2\,L$	p
2005	P	793.3	780.0	785.3	748.0	0.0007
	R1	686.9	653.0	678.9	621.0	< 0.0001
	R2	745.5	732.5	739.5	704.5	0.0015
	R3	708.8	723.4	702.8	693.4	0.8046
2006	P	904.3	891.9	896.3	857.9	0.0022
	R1	926.1	921.8	918.1	883.8	0.0077
	R2	924.7	924.6	916.7	888.6	0.0438
2007	P	820.0	824.2	812.0	790.2	0.0828
	R1	819.7	792.9	811.7	762.9	< 0.0001

† (P) Plant-cane; (R1) Ratoon 1; (R2) Ratoon 2; (R3) Ratoon 3.
‡ (LMMET) classical model; AR1xAR1(H) = heteroscedastic anisotropic first-order autoregressive model; $-2\,L = -2$ residual log-likelihood; p = probability value in relation to LMMET. Underlined numbers indicate AIC lower values and thus better adjustment.

better than LMMET, the modeling of the heterogeneity residual variance was sufficient.

The implementation of spatial models in a multi-environment analysis not only provided a better fit for the data but also increased the number of

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TABLE 8 Statistical significant differences between pairs of genotypes regarding tons of cane per hectare (TCH) according to Fisher's LSD test (5%) in sugarcane multi-environment trials (series 2005, 2006, and 2007; two crop ages)

Series	Age †	Number of genotype evaluated	Number of possible comparisons	Number of comparisons with statistical significant differences	
				LMMET ‡	AR1xAR1(H)
2005	P	20	190	55	59
	R1			38	55
2006	P	20	190	68	72
	R1			91	101
2007	P	22	231	34	47
	R1			77	85

† (P) Plant cane; (R1) Ratoon1.
‡ (LMMET) classical model; AR1xAR1(H) = heteroscedastic anisotropic first-order autoregressive.

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comparisons with statistically significant differences between pairs of genotypes when a Fisher's LSD test ($\alpha = 5\%$) was applied for TCH (Table 8). In addition, the spatial model produced changes in genotype ranking according to predicted values across locations. For plant cane, under the spatial model, rank orders of 10, 12, and 12 genotypes changed in the 2005, 2006, and 2007 series, respectively, whereas for first ratoon, this situation occurred for 10, 14, and 13 genotypes in the 2005, 2006, and 2007 series, respectively.

CONCLUSIONS

For by-environment analyses, the anisotropic autoregressive models of order 1 would favor the comparisons of sugarcane cultivars for TCH, obtaining the same efficiency level as a classical linear model with a randomized complete block design but with a lower replicate number. However, for the by-environment comparisons it is not advisable to use spatial correlation models for SC% data. For a series of trials following a multi-environment model for TCH, the best alternative was the anisotropic first-order autoregressive model, with heterogeneity residual variances across environments. However, for SC%, the best model was that with heterogeneous residual variances without the need to model spatial correlation. The implementation of appropriate mixed models in the analysis of data would help avoid judgment errors while recommending sugarcane varieties for production.

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