European Journal of Agronomy 130 (2021) 126371

Contents lists available at ScienceDirect

European Journal of Agronomy

journal homepage: www.elsevier.com/locate/eja

Global sensitivity and uncertainty analysis of a sugarcane model considering the trash blanket effect

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ARTICLE INFO

Keywords:
Correlated parameters
GLUE
PRCC
Stochastic

ABSTRACT

The deterministic approach in crop modeling simplifies uncertainty present in the environment using a unique parameter set. In practice, this uncertainty is seen in the variability of data collected in a field experiment. One way to exploit this uncertainty is to use the stochastic approach, by inserting the range of plausible variability into the simulation's parameters and inputs. This study aims to evaluate the ability of a process-based crop model to simulate the uncertainty of a sugarcane field. We employed the recently updated version of SAMUCA model to simulate the sugarcane growth and development in a 4-year field experiment, where the crop was grown under the effect of green cane trash blanket (GCTB) and bare soil (Bare). To analyze the effect of genotype and soil variability on output variables, a stochastic approach was applied to the corresponding parameters of the SAMUCA model. A global sensitivity analysis was utilized to prioritize and identify the most important parameters to explain the model uncertainty. Then, the uncertainty was analyzed in three different ways: uncertainty analysis only for genotype parameters (UG), uncertainty analysis only for soil parameters (US) and the analysis of both soil and genotype parameters (UGS). We quantified the variability of the stochastic simulation by the ratio between the average of the standard deviation of the simulations and the average of the standard deviation of the observed data. The variability observed in the field is not fully explained by the hydraulic parameters of the soil, possibly due to irrigation and good rainfall distribution in the area. Furthermore, the variability in US simulations were higher for GCTB than in Bare treatment, suggesting that the GCTB has a larger influence in SAMUCA's variability than for the hydraulic parameters in the conditions of this study. The UG and UGS had the same capacity to quantify the variability present in the environment for the treatments Bare and GCTB. In this case, sensitivity to soil parameters can simply be ignored and genotype parameters can be chosen as the only source of variability for practical applications. Our suggestion for future work is to explore environments without irrigation, different amounts of GCTB and other soil parameters present in the model.

1. Introduction

The use of modeling as a decision making tool is a common practice in several areas of science. In agriculture, process-based crop models (PBCM) represent the state-of-art in this area of science (Jones et al., 2017). When properly calibrated, they are commonly used to simulate the growth and development of crops in certain regions and test "what if " scenarios of managements and adaptation strategies(Faivre et al., 2009). Scientist and decision makers have used crop modeling as a tool to address issues related to the sugar and bioenergy sectors, including climate change (Jones et al., 2015; Singels et al., 2013), plant breeding (Hoffman et al., 2018), risk analysis (Everingham et al., 2002) and yield forecasting (Everingham et al., 2016).

Most of the aforementioned findings were achieved by using the deterministic approach, which meant that they considered a "best set" of parameters to characterize the simulated system and providing only one simulation path for the entire environment. This criterion implicitly means that such best value represents the state of the crop in the studied

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https://doi.org/10.1016/j.eja.2021.126371
Received 26 March 2021; Received in revised form 26 July 2021; Accepted 3 August 2021
Available online 14 August 2021

area, and that there are no sampling errors associated with the plant, microclimate or soil variability (Petersen, 1994). However, agricultural experimental data usually shows great dispersion (variance and deviation) caused by the environment and management (Brogi et al., 2020; Usowicz and Lipiec, 2017; van Bussel et al., 2016). This dispersion in the measured data is common in a biological system, where the reality of processes that occur in nature are not deterministic, but rather stochastic (Wilkinson, 2006), as it considers situations influenced by random effects to be a stochastic process (e.g. light scattering). In this way, a stochastic process can show the different possible pathways that a PBCM can take from varying a range of parameters (Wallach et al., 2018). This observed dispersion can be seen as uncertainty in the data collected and quantified in the PBCM simulation by the range of variation in the model's input parameters (He et al., 2009; Li et al., 2018).

A PBCM can take four different approaches to estimate uncertainty in its simulations: (i) comparison of hindcasts with observations; (ii) multimodel ensemble studies; (iii) propagating input and/or parameter uncertainty through the model; (iv) using simulations with multiple model structures, multiple input and multiple parameter vectors for each model (Wallach et al., 2016). The first two approaches provide a unique answer or explore the uncertainty present in the structure of each PBCM. However, for daily-practical problems, we are often not interested in a model with average parameters, as a simulated area may have different genotypes and variability associated with soil properties and microclimate conditions (Wallach et al., 2016; Wallach and Thorburn, 2017).

One of the challenges in crop modeling stochastic simulation is to accurately choose parameters distributions respecting the correlation between them, which is often neglected (Jones et al., 2011). To preserve the correlation between the parameters, a normal multivariate distribution must be generated (He et al., 2009), and the Generalized Likelihood Uncertainty Estimator (GLUE) combined with the Cholesky decomposition of the variance-covariance matrix is a robust option for generating a set of correlated parameters (Baigorria and Jones, 2010; Marin et al., 2017). Yet, the sensitivity of the parameters is relevant when using the stochastic approach in PBCM, as it can aid on selecting the set of parameters with largest influence in the targeted process or output (Wallach et al., 2018; Zhang et al., 2020).

In a previous attempt to include uncertainty in the sugarcane model Marin et al. (2017) used a previous version of the SAMUCA model (Marin and Jones, 2014) under a stochastic approach. In that study, the uncertainty of 13 genotype parameters were considered, taking into account their correlation among parameters of two genotypes grown in several environments of Brazil. However, those authors listed some important limitations in that study: (i) the structural uncertainty of the model, (ii) uncertainty in the data observed in the experiments, (iii) uncertainty present in the environment, mainly in relation to the soil parameters. Yet, Marin et al. (2017) only used data from plant cane, they neglected the sensitivity of model parameters, and they did not evaluated the model simulation skill to capture the effect of green cane trash blanket (GCTB) on the growth and development of sugarcane, an important component of Brazilian sugarcane cropping systems.

Being the sugarcane the main source of sugar and the second largest feedstock for bioenergy in the world (Goldemberg et al., 2008; Jaiswal et al., 2017; Marin et al., 2019) and to overcome the model and experimental limitations reported in Marin et al. (2017), we use a detailed 4-year experiment to evaluate model uncertainty under a stochastic approach together with a new version of SAMUCA (Vianna et al., 2020), which would allowed us to evaluate aspects related to soil variability, different crop stages (plant cane and ratoons) and the effect of GCTB on the crop growth and development. Thus, in this paper we aimed to evaluate a sugarcane crop model used under a stochastic approach to represent the existing variability in an experimental plot. Our specific objectives were: (i) analysis of global sensitivity in the genotype parameters to determine which are significant, and use them in the stochastic simulation with correlated parameters; (ii) explore the uncertainty in the soil-hydraulic and textural parameters (US), genotype (UG) and both of them together (UGS); (iii) to model the variability present in the field considering the presence or absence of the GCTB.

2. Material and methods

2.1. Brief history of the SAMUCA model

The SAMUCA model was created due to the argument of Sinclair and Seligman (1996), where they highlight the importance of developing the proper models for knowledge groups, allowing to deepen the mechanisms involved in the simulation process and the uncertainties inherent to the used models. In addition, the SAMUCA model also had the objective of exploring the uncertainty in genotype parameters, incorporating a calibration procedure based on the Generalized Likelihood Uncertainty Estimator (GLUE) to ensure a consistent and reliable adaptation of the model for applications in Brazil (Marin and Jones, 2014). The SAMUCA model was built with a database of different locations in Brazil, comprising of different climates, soils and managements which is also used to evaluate other widely used sugarcane dynamic models (Marin et al., 2015). Even with good results to simulate the growth and development of sugarcane, it was a first version with several limitations. Such limitations were primarily related to the oversimplified soil water balance and the non-inclusion of GCTB effect into the model routines as it is extremely important to represent the Brazilian sugarcane cropping systems.

Because of this, a new version of SAMUCA model was built by Vianna et al. (2020) to reduce the uncertainties around model structure, soil moisture and heat flow in comparison with its previous version. Soil moisture is simulated by the widely tested "tipping bucket" method, whereas heat flow is solved numerically according to Kroes et al. (2009). Both processes can also be simulated under the effect of GCTB, which has recently emerged as an important operational practice for Brazilian farmers (Carvalho et al., 2017). Further improvements were also made to the subroutines dedicated to the simulation of carbon partitioning at phytomer level, layered-canopy photosynthesis, tillering and root growth (Bezuidenhout et al., 2003; Laclau and Laclau, 2009; O'Leary, 2000). This new version of SAMUCA model is also included in the DSSAT platform v4.8.

2.2. Field experiment

We conducted a field experiment of approximately 2.5 ha of sugarcane in the College of Agriculture "Luiz de Queiroz", Piracicaba, São Paulo (Lat: 22°41′55″S, Lon: 47°38′34″W, Alt: 540 m) (Table 1). The sugarcane cultivar was the RB86−7515, a widely used genotype in Brazil (*ca.* 30 % of Brazil's planted area). It was planted on October 16, 2012 with a row spacing of 1.4 m and depth of 0.2 m. A bare soil treatment (Bare) was conducted during the four sequential years, whereas the GCTB treatment onset in the first ratoon (Oct-2013) and was carried out for 3 years. Agricultural practices were adopted to represent high yield farming systems and to ensure the crop was free from pests, diseases and nutritional stress. The climate is characterized by hot and humid summer with dry winter (Cwa – Koppen classification), and the soil classified as Typic Hapludox. The experiment was irrigated by a center-pivot, based on monitoring the soil moisture by Frequency Domain Reflectometry (FDR) and the evapotranspiration by Bowen Ratio Method (BRM) in both treatments (Nassif et al., 2014).

Crop growth was monitored by regular destructive sampling of biomass (stalk fresh and dry mass; SFM and SDM) throughout the sugarcane growing cycles. A total of 30 plants per treatment were collected every month at random locations and immediately transported to weigh fresh biomass. Biomass was then dried at 60 °C in an air circulation oven (TE-394/5-MP,Tecnal®, Piracicaba, São Paulo, Brazil) for four days before weighing as dry biomass parts with a precision balance (2098 PP, Mettler Toledo, Mississauga, Ontario, Canada). Crop development crop was monitored with non-destructive sampling in four sub-plots of 35 m^2

Table 1
Description of seasons, planting and harvesting dates, duration in days, treatments and measurements variables of the field experiment in Piracicaba, Brazil.

Season	Planting	Haverst	Duration	Variables	Treatments
Plant Cane	10/16/2012	10/15/2013	364	SDM,SFM,TIL,LAI *and* POL	Bare
1st Ratoon	10/15/2013	07/15/2014	273	SDM,SFM,TIL,LAI *and* POL	Bare and GCTB
2nd Ratton	07/15/2014	06/08/2015	328	SDM,SFM,TIL,LAI *and* POL	Bare and GCTB
3rd Ratton	06/08/2015	06/08/2016	365	SDM,SFM,TIL	Bare and GCTB

Green cane trash blanket (GCTB), stalk dry mass (SDM) and stalk fresh (SFM) of, leaf area index (LAI), sucrose concentration in fresh matter (POL) and tillering (TIL).

randomly positioned at the beginning of each season (total of 8 plots). The tiller population (TIL) was regularly counted in the non-destructive plots and scaled to 1.0 m^2. The Leaf Area Index (LAI) was regularly measured with an plant canopy analyzer (LAI-2000, LI−COR, Inc, Lincoln, Nebraska, USA) with eight repetitions for each treatment. During crop maturation, fifteen culms per treatment were randomly cut and immediately transported for milling where the fraction of fiber and sugars were determined by digital saccharimeter (SDA5900, Acatec, São Paulo, São Paulo, Brazil) and precision balance (Prix 110, Mettler Toledo, Mississauga, Ontario, Canada), so the sucrose concentration in fresh matter (POL) was determined.

2.3. Genotype parameters and global sensitivity analysis

The choice of genotype parameters for uncertainty analysis was based on a global sensitivity analysis (GSA) using the partial rank correlation coefficient (PRCC) method (Wallach et al., 2019). We employed this method as the arbitrary selection of parameters could not generate variations in the output of the model that would explain the variability in the real environment (Varella et al., 2010). The method consists of massive sampling of parameters using the Monte Carlo method, to assess the correlation between each parameter and model output. Therefore, we obtained the linear relationship between the genotype parameters and the model output with the PRCC method; where the positive PRCC values being a direct linear relationship while the negative PRCC values being an inverse linear relationship. The difference between the PRCC and its advantage over Person correlation coefficient and the partial correlation coefficient is that it can explore the non-linear relationships between inputs and outputs. The PRCC values range from -1 to 1, as does the Pearson correlation, taking a measure of the strength of a linear association between an input and an output. Mukaka (2012) presented different classes of interpretation for the PRCC correlation (Table 2). In the following analysis, we only considered the genotype parameters that were statistically significant at 1% for the output model components of sugarcane: SDM, SFM, TIL, LAI and POL.

2.4. Soil parameters

The hydraulic soil parameters (HSP) were obtained from samples taken in four random locations within the experimental area. At each location, three repetitions of undisturbed soil samples were taken at the depths of 5, 15, 30, 60 and 100 cm. The 60 undisturbed samples were used to obtain water retention curves (at the potentials of 10, 20, 60, 100, 330, 1,000, 3,000, and 15,000 kPa) for each depth, used to derive the permanent wilting point (WPp), field capacity (FCp), saturation point (STp) and saturated hydraulic conductivity (Ksat) required by the SAMUCA model. Thus, a retention curve was obtained for each depth and location, where maximum, minimum and average values of parameters were obtained for each depth (Table 3). We chose to work with the maximum and minimum values to generate an uniform distribution, regardless of the spatial position of the sample; that is, within the study area we considered that the soil parameters varied within these maximum and minimum values.

Table 2
Rules for interpreting the size of a correlation coefficient (Mukaka, 2012).

Size of Correlation	Interpretation
0.90 to 1.00 (-0.90 to -1.00)	Very high positive (negative) correlation
0.70 to 0.90 (-0.70 to -0.90)	High positive (negative) correlation
0.50 to 0.70 (-0.50 to -0.70)	Moderate positive (negative) correlation
0.30 to 0.50 (-0.30 to -0.50)	Low positive (negative) correlation
0.00 to 0.30 (-0.00 to -0.30)	Negligible correlation

The soil texture parameters (TSP) used were clay (Pclay), sand (Psand) and silt (Psilt) for the same depths as HSP. The TSP interval (Table 3) was obtained in the literature from two studies conducted in the same experimental area at different periods, such studies done at a depth of 60 cm and in this case we considered for the depth of 100 cm the same interval measured at a depth of 60 cm.

To determine which parameters would be inserted in the uncertainty and stochastic simulations, we performed a GSA by applying the same method as the parameters of the genotype, considering the parameters presented in Table 3 and their respective depths. If at least one of depths was significant, we assumed the other depths would have the uncertainty inserted, maintaining the correlation between them.

2.5. Generalized likelihood uncertainty estimation method

The generalized likelihood uncertainty estimation method (GLUE) was used to select the parameter set with the highest likelihood to reproduce the end-of-season observation; this set of parameters is hereafter called the *best parameter set*. Yet, GLUE was used to create the variance-covariance correlation matrix of model parameters, which in turn was used for generate the correlated parameter sets for stochastic simulations. It is a parameter estimation method that deals with problems associated with parameter interactions and non-linearity in the models response (Beven and Binley, 1992). Present in platforms such as DSSAT, it is widely used to estimate genotype parameters (He et al., 2010; Jones et al., 2011), especially those that cannot be measured directly in typical experiments; instead, they should be estimated based on data measured in experiments (Marin and Jones, 2014). The method is an approach based on the Monte Carlo application, which uses a set of parameters in massive simulation process to select a set of parameters in a uniform distribution within the sample space (Sreelash et al., 2012).

The GLUE procedure consists of five stages: (i) Develop prior parameter distributions, in this case, we assume uniform distributions from predefined range of variation for soil and genotype parameters (Marin et al., 2017); (ii) Generate random parameters sets from prior parameter distributions based on the Monte Carlo method, where the largest the number of simulations leads in more stable results. However, only a limited number of parameter sets had significant likelihood values that could be used to derive posterior distributions, even though 21,000 sets of parameters were generated in this study, considered a large sample (He et al., 2010); (iii) Run the model with the random parameters sets, where the model was run for each parameter set using developed R-scripts. The input files for the parameters were changed to simulate each random parameter set in sequence and for each parameter set the model outputs (SDM, SFM,TIL, LAI and POL) were tabulated for use in the GLUE likelihood calculations; (iv) Calculate the likelihood values to generated observations (O, three replicates each for each variables) were used along with the corresponding simulated outputs to compute the likelihood value, $L(\theta_i|O)$, for each of the N generated parameter vectors θ_i. Then, the probability p_i of each parameter set was

Table 3
Average (Avg), maximum (Max) and minimum (Min) for: soil depth (DP), wilting point (WPp), field capacity (FCp), saturation point (STp), saturated hydraulic conductivity (Ksat), content clay (Pclay), content silt (Psilt), content sand (Psand)[γ].

Hydraulic parameters												
DP	FCp (cm^3. cm^{-3})			K_{sat} (cm. h^{-1})			STp (cm^3. cm^{-3})			WPp (cm^3. cm^{-3})		
(cm)	Avg	Max	Min	Avg	Max	Min	Avg	Max	Min	Avg	Max	Min
5	0.285	0.305	0.255	1.7	2.51	1.03	0.38	0.413	0.34	0.216	0.23	0.191
15	0.303	0.325	0.287	1.01	1.2	0.85	0.352	0.396	0.334	0.24	0.245	0.224
30	0.347	0.414	0.305	0.95	1.02	0.14	0.39	0.448	0.36	0.278	0.357	0.231
60	0.394	0.406	0.346	0.62	1.02	0.14	0.428	0.474	0.392	0.307	0.35	0.273
100	0.393	0.434	0.357	0.21	0.4	0.1	0.456	0.486	0.422	0.253	0.304	0.198

Texture parameters									
DP	Pclay (g. g^{-1})			Psilt (g. g^{-1})			Psand (g. g^{-1})		
(cm)	Avg	Max	Min	Avg	Max	Min	Avg	Max	Min
5	0.544	0.624	0.464	0.234	0.296	0.172	0.222	0.240	0.204
15	0.544	0.624	0.464	0.234	0.296	0.172	0.222	0.240	0.204
30	0.596	0.694	0.498	0.215	0.292	0.138	0.189	0.210	0.167
60	0.633	0.689	0.576	0.200	0.264	0.136	0.168	0.160	0.175
100	0.633	0.689	0.576	0.200	0.264	0.136	0.168	0.160	0.175

[γ] values observed by Sousa et al. (2008) and Santos et al. (2017).

computed with the following Eq. (1) and likelihood function was:

$$L(\theta_i O) = \prod_{j=1}^{M} \frac{1}{\sqrt{2.\pi.\sigma_o^2}}.exp\left(-\frac{(O_j - f(\theta_i))^2}{2\sigma_o^2}\right) \quad (1)$$

$$p(\theta_i) = \frac{L(\theta_i|O)}{\sum_{j}^{N} L(\theta_i|O)} \quad (2)$$

$$L_{comb}\left[\theta_i\right] = \prod_{k=1}^{K} L_k(\theta_i|O_k) \quad (3)$$

where $p(\theta_i)$ is probability or likelihood weight of the *i*th parameter set θ_i; $L(\theta_i|O)$ is the likelihood value of parameter set θ_i; given observations O_j the *j*th observation of O. The *M* is the number of observation replicates; $f(\theta_i)$ is the model output referring to θ_i; *K* is the number of observation types; $L_{comb}[\theta_i]$ is the combined likelihood value of *i*th parameter set θ_i; σ_o^2 the variance model errors, assumed to be the variances of observations for this study.

(v) Construct posterior distribution and statistic. The pairs of parameter sets and pobabilities, $((\theta_i, p_i)$, i=1 , ...*N,* were used to construct emperical posterior distributions and to compute the means and variance of selected parameters using the following equations:

$$\hat{\mu} = \sum_{i=1}^{N} p(\theta_i)\theta_i \quad (4)$$

$$\hat{\sigma}^2 = \sum_{i=1}^{N} p(\theta_i)(\theta_i - \hat{\mu})^2 \quad (5)$$

where $\hat{\mu}$, $\hat{\sigma}^2$ they are the mean and variance of the posterior distribution of the set parameters; *N* (10,000*)* is the number of random parameter set.

To apply and evaluate the performance of the GLUE method, this study used the following measured data: dry (SDM) and fresh stalk mass (SFM), leaf area index (LAI), tillers population (TIL) and sucrose concentration on fresh sugarcane basis (POL). For the GLUE method, only the measured data of SDM, SFM, and TIL were used to estimate the optimal parameters (genotype and soil), since these were the only variables sampled continuously over the four years of the experiment. To evaluate the model performance and the stochastic simulations, we used SDM, SFM, TIL, LAI, and POL.

2.6. Simulation of correlated parameters

We applied the Toeplitz-Cholesky decomposition (Baigorria, 2014) from a correlation matrix obtained from the 10,000 sets of parameters generated by the GLUE method. From this correlation matrix, we then generate a new set of parameters, comprised of 10,000 combinations. This new set was used to run the stochastic simulations, respecting the correlation among parameters.

$$\mathbf{R} = \begin{Bmatrix} r_1^{\psi} = r_1 C_{1,1} + \ldots + r_n C_{1,n} \\ . \\ . \\ . \\ r_n^{\psi} = r_n C_{n,1} + \ldots + r_n C_{n,n} \end{Bmatrix} \quad (6)$$

The **R** matrix is multiplied by a square matrix containing the weghting values C_{ij} (*i* is the parameter and *j*th simulation), which are calculated based on the pairwise correlation values that form the correlation matrix **P** (Baigorria and Jones, 2010). As mentioned, the factorization matrix used here was the Toeplitz-Cholesky factorization matrix **C**:

$$\mathbf{C} = \mathbf{U}diag(\mathbf{U}^{\frac{1}{2}}) \quad (7)$$

where **U** is an upper triangular matrix with positive diagonal entries generated from a special case of the symmetric **LU** decomposition of the correlation matrix, with $\mathbf{L} = \mathbf{U}^{\mathbf{T}}$.

2.7. Parameter set analysis and model evaluation

From the 10,000 simulations with the correlated parameters sets we extracted the standard deviation of the simulations outputs to evaluate the model performance in replicating the variability observed in the field. This analysis was divided into three different sets to isolate the uncertainty of: (i) genotype parameters (UG); (ii) soil parameters (US); and (iii) both genotype and soil parameters (UGS). This means that only genotype parameters were considered for the GLUE method in the UG analysis, only soil parameters in the US, and both sets of parameters were considered for GLUE processing for the UGS analysis. When the GLUE method is not used for uncertainty analysis (e.g. soil parameters in UG), we assume the genotype and soil parameter values as reported by Vianna et al. (2020) (Table 4 and Table 3).

To evaluate the model performance in replicating the average condition of the experiment and its uncertainty, the statistical analysis was done in two different ways. Firstly, we compared the best set parameters

Table 4
Cultivar-specific parameters, descriptions, units, and range used for uniform distribution sampling and standard values assumed for initial simulations. In bold are the parameters used in GLUE.

Parameter	Description	Min	θ	Max	Reference
amax	Assimilation rate at light saturation point *(μmol. $m^{-2}.s^{-1}$)*	41.3	44.9	60.7	Sage et al. (2013)
chudec	Heat units for start of tiller abortion *(°C.d)*	1200	1600	1800	Liu et al. (1998)
chumat	Heat units for population establishment *(°C.d)*	1500	1600	2850	Zhou and Shoko (2011)/Marin and Jones (2014)
chupeak	Heat units for population peak *(°C.d)*	400	1400	1950	Coelho et al. (2020); Marin et al. (2017) Nassif et al., (2014)
chustk	Heat units for start culm elongation *(°C. d)*	404	650	1050	Marin et al. (2017); /Singels and Bezuidenhout (2002)
eff	Carboxylation efficiency *(μmol. $m^{-2}.s^{-1}$ / μmol. $m^{-2}.s^{-1}$)*	0.040	0.069	0.080	Sage et al. (2013)
end_tt_it_gro	Thermal time for completion of internode growth *(°C.d)*	600	1200	1400	Lingle (1999)
end_tt_lf_gro	Thermal time for completion of leaf growth *(°C.d)*	1100	1300	1500	Smit and Singels (2006)
init_lf_area	Initial leaf area of first appeared leaf *(cm^2)*	15	10	30	Zhou et al. (2003)
max_ini_la	Initial leaf area of leaves appeared after topr parts formation *(cm^2)*	80	120	180	Zhou et al. (2003)
max_it_dw	Maximum dry biomass of internodes *(g)*	18	28	35	Lingle (1999)
maxdgl	Maximum number of developed green leaf a tiller can hold *(#/tiller)*	6	6	12	Vianna et al. (2020)
maxgl	Maximum number of green leaf a tiller can hold (#/tiller)	10.0	12.0	12.0	Marin et al. (2015)
mid_tt_it_gro	Thermal time where internodes can achieve half of its maximum biomass	380	400	700	Lingle (1999)
mid_tt_lf_gro	Thermal time where leaves can achieve half of its maximum biomass	400	700	800	Smit and Singels (2006)
mla	**Maximum leaf area *(cm^2)***	**450**	**600**	**800**	**Marin et al. (2014)**
n_lf_it_from	**Number of leaves appeared before internode formation *(#/tiller)***	**3**	**3**	**8**	Vianna et al. (2020)
n_lf_stk_em	**Number of leaves appeared before stalks emerges at soil surface *(#/tiller)***	**3**	**4**	**8**	Vianna et al. (2020)
phyllochron	Phyllochron interval for leaf appearance *(°C.d)*	107	132	169	Marin et al. (2015)/ Inman-Bamber, 1994
plastochron	**Thermal time required for the appearance of phytometer *(°C.d)***	**107**	**132**	**169**	Marin et al. (2015)/ Inman-Bamber, 1994
popmat	Number of tillers on maturation *(tiller/m^2)*	8.0	9.5	12.0	Marin and Jones (2014)
poppeak	Maximum number of tillers *(tiller/ m^2)*	17.0	22.0	30.0	Marin et al. (2015)
sla	Specific leaf area *(cm^2. g^{-1})*	100.0	120.00	121.00	Ehara et al. (1994)
tillochron	**Thermal time required for emergence of new tiller *(°C. d)***	**48.1**	**69.0**	**134.8**	Bezuidenhout (2000); Zhou and Shoko (2011)

θ is the value calibrated by Vianna et al. (2020) for cultivar RB867515; Max and Min value are range used for random parameters uniform distribution.

obtained by GLUE with the average of the observed data. In this way, it was used the statistical indices root mean squared error (RMSE), determination index (R^2), Nash-Sutcliff modeling efficiency (EF) (Nash and Sutcliffe, 1970) bias index (Bias) and Wilmont accuracy index (d) (Willmott et al., 2012). Secondly, we compared the variability observed in the field experiment, by using the standard deviation $\sigma_{(\sigma obs)}$, with those from stochastic simulations using the standard deviation of the stochastic simulations $\sigma_{(\sigma sim)}$. We also calculated the ratio (ξ in %) between σ_{sim} and σ_{obs} in order to verify the model skill in representing the observed variability:

$$\xi = \left(\frac{\sigma_{sim}}{\sigma_{obs}}\right) * 100 \quad (8)$$

3. Results

3.1. Global sensitivity analysis for soil and genotype parameter

The GSA was performed for 24 genotype parameters (Table 5), and among those only five were statistically significant and had a monotonic response to the model outputs: n_lf_stk_emerg, n_lf_it_form, tillochron, mla, plastochron. Thus, these five genotype parameters were used to perform the stochastic simulations with correlated parameters in the UG and UGS analysis. The GSA analysis was performed considering the two treatments used in the experiment (GCTB and Bare), and no difference was found in terms of the correlation among parameters. For GCTB treatment, all output variables have at least one significant (0.01) parameter, being: two parameters for SDM (plastochron; n_lf_it_from)

Table 5
Value of the partial rank correlation coefficient (PRCC) for genotype parameters (PAR) for output variables stalk dry mass (SDM), stalk fresh mass (SFM), tillering (TIL), sucrose concentration (POL) and leaf area index (LAI). Parameters marked with * were statiscally significant at 1%.

PAR	GCTB treatment - PRCC					Bare treatment -PRCC				
	SDM	SFM	TIL	POL	LAI	SDM	SFM	TIL	POL	LAI
amax	0.00	0.01	−0.05	0.00	0.03	0.02	0.01	−0.21	0.02	0.06
chudec	−0.03	−0.03	0.05	0.01	−0.01	−0.03	−0.04	0.05	0.00	−0.03
chumat	0.03	0.04	−0.03	0.00	−0.05	0.03	0.05	−0.02	−0.04	−0.03
chupeak	−0.06	−0.07	0.03	0.00	−0.02	−0.07	−0.07	0.03	0.00	−0.02
chustk	0.05	0.04	−0.02	0.03	0.02	0.04	0.03	−0.07	0.03	0.02
eff	0.00	−0.01	0.04	0.07	0.08	0.10	0.08	0.00	0.04	0.17
end_tt_it_growth	−0.07	0.01	−0.02	−0.20	−0.01	−0.33	−0.19	−0.02	−0.34	0.07
end_tt_lf_growth	−0.02	−0.01	0.11	−0.10	−0.44	−0.02	−0.02	0.12	0.01	−0.40
init_leaf_area	−0.06	−0.06	−0.11	0.00	−0.03	−0.07	−0.05	−0.26	−0.02	−0.11
ma_ini_la	−0.03	−0.04	−0.12	0.02	−0.10	−0.08	−0.07	−0.41	0.01	0.21
max_it_dw	0.35	0.35	0.00	0.06	0.25	0.53	0.52	−0.27	−0.05	−0.26
maxdgl	0.01	0.02	−0.01	0.00	0.05	0.01	0.02	−0.02	0.00	0.03
maxgl	0.03	0.04	0.00	0.00	0.46	0.00	0.02	−0.02	0.02	0.50
mid_tt_it_growth	−0.54	−0.62	−0.01	0.34	0.01	−0.59	−0.73	0.00	0.64	0.07
mid_tt_lf_growth	0.04	0.06	0.69	0.00	−0.31	0.06	0.08	0.50	−0.02	0.01
mla	−0.11	−0.11	−0.65	0.02	0.92*	−0.15	−0.14	−0.50	0.02	0.91*
n_lf_it_form	−0.85*	−0.82*	−0.01	−0.50	0.11	−0.88*	−0.81*	0.00	−0.81*	0.25
n_lf_stk_eme	−0.85*	−0.83*	−0.14	−0.50	0.3	−0.79	−0.70	−0.40	−0.64	0.49
phyllochron	−0.07	−0.06	−0.03	−0.10	0.01	−0.07	−0.07	−0.06	−0.02	−0.01
plastochron	−0.85*	−0.83*	0.63	−0.40	−0.55	−0.87*	−0.82*	0.69	−0.68	−0.13
popmat	0.17	0.19	0.71	0.00	0.73	0.23	0.25	0.63	−0.02	0.65
poppeak	−0.01	0.00	0.04	0.00	−0.01	0.01	0.01	−0.01	0.00	−0.02
sla	0.02	0.02	0.04	0.06	−0.03	0.02	0.01	−0.02	0.01	−0.01
tillochron	−0.15	−0.16	−0.92*	0.00	−0.71	−0.29	−0.30	−0.91*	0.01	−0.77

Table 6
Absolute value of the partial rank correlation coefficient (PRCC) for soil parameters (PAR) for output variables stalk dry mass (SDM), stalk fresh mass (SFM), tillering (TIL), sucrose concentration (POL) and leaf area index (LAI). Parameters marked with * were statiscally siginificant at 1%.

PAR	Depth	GCTB treatment - PRCC					Bare treatment -PRCC				
	(cm)	SDM	SFM	LAI	POL	TIL	SDM	SFM	LAI	POL	TIL
	5	0.03	0.05	0.01	−0.07	0.00	−0.15	−0.11	−0.17	−0.06	−0.11
	15	0.01	0.02	−0.04	−0.03	−0.01	−0.06	−0.05	−0.06*	−0.02	0.06
FCp	30	0.17	0.25	−0.19	−0.34	0.00	−0.17	−0.08	−0.29*	−0.14	0.03
	60	0.06	0.09*	−0.04	−0.12*	0.00	0.08	0.12*	−0.03	−0.13*	0.05
	100	0.35	0.43*	0.07	−0.49*	−0.04	0.31	0.47*	0.01	−0.59*	0.03
	5	−0.01	−0.05	0.05	0.09	0.00	0.02	0.01	0.03	0.03	−0.09
	15	0.02	0.03	−0.02	−0.02	−0.04	−0.01	−0.03	0.00	0.03	−0.08
Ksat	30	−0.05	−0.09	0.10	0.17	−0.14	0.06	0.03	0.09	0.05	0.02
	60	0.07	0.06	0.12	−0.03	0.01	0.01	0.03	0.07	−0.01	−0.01
	100	0.06	0.07	0.05	−0.01	0.07	0.03	0.04	0.00	−0.03	−0.05
	5	0.00	0.02	0.03	−0.06	−0.03	−0.05	−0.03	0.03	−0.01	0.00
	15	0.04	0.03	0.08	0.00	0.02	0.06	0.05	0.09	−0.01	0.02
Pclay	30	0.02	0.02	0.05	0.00	0.00	0.06	0.04	0.08	0.01	−0.01
	60	−0.01	−0.01	−0.08	−0.02	−0.10	0.07	0.07	−0.03	−0.01	0.00
	100	−0.04	−0.03	−0.07	0.01	−0.06	−0.05	−0.03	−0.07	−0.02	−0.04
	5	−0.01	0.01	0.03	−0.04	−0.10	−0.04	0.00	0.02	−0.06	−0.02
	15	−0.01	−0.03	0.04	0.02	−0.04	0.00	−0.01	0.04	0.07	0.05
Psand	30	−0.02	−0.04	0.05	0.07	−0.10	0.03	0.03	0.05	−0.01	0.02
	60	−0.11	−0.06	−0.06	−0.07	−0.05	−0.06	−0.09	−0.01	0.09	−0.02
	100	0.07	0.07	0.00	−0.04	0.02	0.07	0.06	0.02	−0.03	0.04
	5	0.04	0.04	0.06	0.00	0.05	0.02	0.03	0.08	−0.04	0.04
	15	0.04	0.06	0.09	−0.09	−0.03	0.07	0.04	0.17	0.01	−0.06
Psilt	30	−0.06	−0.08	0.00	0.07	0.02	−0.02	−0.03	0.02	0.06	0.01
	60	−0.03	−0.05	−0.03	0.08	0.06	0.02	0.01	0.00	0.05	0.01
	100	0.00	0.04	0.00	−0.09	0.08	0.00	0.00	0.00	−0.06	0.00
	5	−0.16	−0.14	−0.35	0.04	0.10	−0.08	−0.07	−0.25	0.00	0.03
	15	−0.08	−0.08	−0.35	0.01	0.15	−0.05	−0.03	−0.23	−0.05	0.06
STp	30	−0.15	−0.17	−0.25	0.16	−0.02	−0.13	−0.11	−0.22	−0.02	−0.04
	60	0.04	0.04	0.17	0.01	−0.10	−0.03	−0.03	0.09	0.04	−0.05
	100	0.13	0.15	0.14	−0.14	−0.01	0.13	0.12	0.15	−0.03	0.09
	5	−0.05	−0.11	0.07	0.18	−0.02	0.14	0.07	0.12	0.13	0.05
	15	−0.07	−0.08	0.07	0.05	−0.02	0.04	0.02	0.09	0.05	0.00
WPp	30	−0.17	−0.24*	0.28*	0.32*	−0.02	0.24	0.13	0.44*	0.20	0.00
	60	−0.20*	−0.25*	−0.09	0.26*	0.00	0.00	−0.07	0.02	0.18*	0.02
	100	−0.60*	−0.67*	−0.30*	0.70*	0.02	−0.44*	−0.59*	−0.17	0.65*	0.00

and SFM (plastochron; n_lf_it_from) and only one for TIL (tillochron), POL (n_lf_it_from) and LAI (mla) (Table 5). For the Bare treatment, only POL variable does not have any significant parameter, while SDM (plastochron; n_lf_it_from; n_lf_stk_eme) and SFM (plastochron; n_lf_it_from; n_lf_stk_eme) showed three significant parameters, and LAI (mla) and TIL (tillochron) had only one significant parameter (Table 5). The correlation levels obtained from all parameters were classified as high or very high correlation levels, as described in Table 3. We observed that among the significant parameters analyzed, only mla showed positive correlation (PRCC = 0.92) for LAI. The remaining parameters have a strong negative correlation with other variables, such as tillochron for TIL (PRCC = -0.92), plastochron for SDM and SFM (PRCC = -0.85 and PRCC = -0.83, respectively), and n_lf_it_from for POL (PRCC = -0.81) (Table 5). We perfomerd the GSA considering the parameters for the different layers of the soil and found its significance depending on the layer. Unlike the GSA for genotype parameters, there was no parameter with a strong correlation with the model output variables. The highest correlations were WPp for POL (PRCC = -0.70 and -0.65) at a depth of 100 cm (Table 6). TIL was the only variable that did not present any significant soil parameterts in both treatments. The texture parameters in both treatments. The texture parameters Psand, Psilt and Pclay were not evaluted, as well as the hydraulic parameters Ksat and STp. Finally, only the FCp and WPp parameters were the significant soil parameters, so in the stochastic simulation we inserted the uncertainty in the five layers (5,153,060 and 100 cm) to maintain the correlation between them.

Table 7
Best set of parameter values considering four crop seasons (1 plant cane and 3 ratoons) for cultivar RB867515 based on the generalized likelihood uncertainty estimation method (GLUE) analyzing the uncertainty due to genotype parameters (UG), uncertainty due to soil parameters (US) and uncertainty due both genotype and soil parameters together (UGS).

§ Parameters		UG (μ ± σ)	US (μ ± σ)	UGS (μ ± σ)	Calibration by Vianna et al. (2020)
Genotype	n_lf_stk_eme	5 ± 1	#	5 ± 1	4
	n_lf_it_form	3 ± 1	#	3 ± 1	3
	tillochron	82 ± 20	#	82 ± 20	69
	mla	625 ± 82	#	627 ± 84	600
	plastochron	134 ± 15	#	135 ± 15	132
Soil	FCp (5 cm)	#	0.2800 ± 0.0144	0.2800 ± 0.0144	0.2850
	FCp (15 cm)	#	0.3060 ± 0.0055	0.3060 ± 0.0055	0.3030
	FCp (30 cm)	#	0.3590 ± 0.0316	0.3590 ± 0.0316	0.3470
	FCp (60 cm)	#	0.3760 ± 0.0175	0.3760 ± 0.0175	0.3940
	FCp (100 cm)	#	0.3900 ± 0.0209	0.3900 ± 0.0209	0.3930
	WPp(5 cm)	#	0.2110 ± 0.0112	0.2110 ± 0.0112	0.2160
	WPp(15 cm)	#	0.2340 ± 0.0061	0.2340 ± 0.0061	0.2400
	WPp(30 cm)	#	0.2950 ± 0.0361	0.2950 ± 0.0361	0.2780
	WPp(60 cm)	#	0.3110 ± 0.0222	0.3110 ± 0.0222	0.3070
	WPp(100 cm)	#	0.2661 ± 0.0283	0.2660 ± 0.0283	0.2530

§ For parameter definitions, see Table 2 and Table 3; # value used by calibration Vianna et al. (2020).
μ average calculated by Eq. 4 and σ standard deviation by Eq. 5.

3.2. Best parameters set obtained with GLUE

The values obtained from GLUE were compared with the values reported by Vianna et al. (2020), that used the BFGS technique (Broyden-Fletcher-Goldfarb-Shanno) to calibrate the genotype parameters of SAMUCA model for the same dataset. We noticed that there was a difference in tilochron and mla (Table 7). These two genotype parameters increased by 18 % for TIL and 4% for mla compared to the prior calibration. In the soil parameters the biggest difference was WPp at a depth of 30 cm, reaching 6%. The 5 and 15 cm layers did not exceed 2%. In the 60 and 100 cm layer, the variation was up to 5% for WPp compared with Vianna et al. (2020), that considered the average soil values for each soil layer.

To confirm there were differences in soil water storage from the parameters estimated by GLUE, we calculated the available water (AW) for sugarcane in each layer. Fig. 1 shows that the correlation of soil parameters resulted in almost constant available water (AW) to the crop within the 0−15 cm soil depth, whereas the AW significantly varied for deeper layers (30-to-100 cm). The total available water (TAW) was 90 mm from the GLUE and the TAW obtained from the data by Vianna et al. (2020) was 102 mm.

3.3. Uncertainty analysis considering the genotype parameters (UG)

In the GCTB treatment, variables that had better model efficiency were SDM (EF = 0.83), SFM (EF = 0.75), POL (EF = 0.56), TIL (EF = 0.32) and LAI (EF = 0.70), respectively. The σ_{sim} over time (gray area in Fig. 2A) was less or equal than the σ_{obs} for SFM (Fig. 2A), representing 106 % of the observed field variability (Table 8). The simulations for SFM (blue line) underestimated the observed data (Bias = -14.69 Mg ha^{-1}; Table 8), with an RMSE = 23.79 Mg ha^{-1} (Table 8). For SDM, the variability of the stochastic simulation was able to explain 64 % of the observed data (Table 8). The simulations was also underestimated (Bias = -2.80 Mg ha^{-1}; Table 8), and with an RMSE = 4.30 Mg ha^{-1}. The POL, TIL, and LAI variables were also underestimated in comparison with observed data, showing Bias = -0.50, -2.48, and -0.01, respectively. Unlike SFM, SDM, and TIL, for POL and LAI, the variability was overestimated by 23 % and 13 %, respectively. The simulated variability for TIL = 52 % of the observed one (Table 8).

For the Bare treatment, the SDM and SFM variables had EF = 0.83 and 0.87 (Table 8), followed by POL (EF = 0.58), TIL (EF = 0.53) and LAI (EF = 0.44) (Table 8). The variability of the stochastic simulation (gray area in Fig. 2B) was less or equal, over time than the standard deviation of the observed SFM data (Fig. 2B), explaining 85 % of the variability seen in the field (Table 8). The simulation for SFM (blue line) was underestimated about the observed data (Bias = -12.66 Mg ha^{-1}; Table 8), with an RMSE of 20.94 Mg ha^{-1} (Table 8). For SDM, the variability of the stochastic simulation was able to explain 56 % of the observed data (Table 8). The average of the simulations was also underestimated (Bias = -2.21 Mg ha^{-1}; Table 8), with an RMSE of 4.21 Mg ha^{-1}. The variables POL and TIL were also underestimated about the observed data, with Bias = -0.50, -2.48, respectively. Unlike SFM, SDM, and TIL, for the POL and LAI variables, the variability was overestimated by 21 % and 24 % (Table 8), respectively. The simulated variability in TIL was 68 % the observed variability (Table 8).

3.4. Uncertainty analysis considering the soil parameters (US)

Considering the data collected for the Bare treatment, the variability of the stochastic simulation did not well represent the variability observed in the observed data, considering all the variables analyzed (Fig. 3). The variance in US was almost zero (SDM = 0.001 %; SFM = 0.004 %; POL = 0.001 %; TIL = 0.0002 % and LAI = 0.002 %) for all variables (Table 8). The variables referring to mass, SFM and SDM, were well characterized over time by the best set parameters (blue line in Figs. 3 B and D), with EF = 0.87 for both SDM and SFM (Table 8). TIL

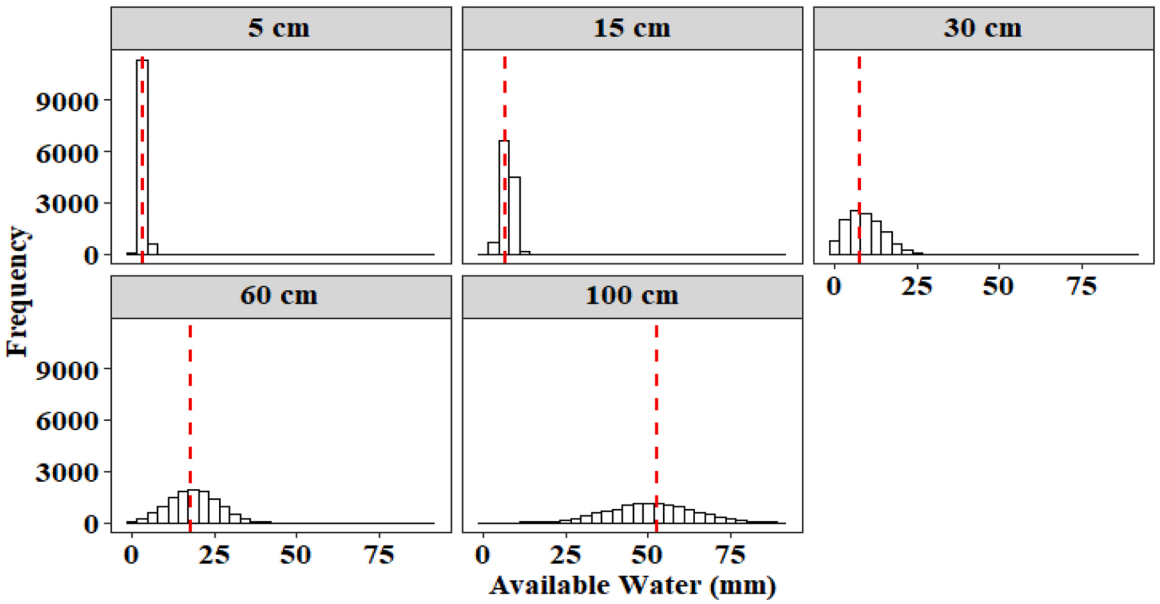

Fig. 1. Histogram of total available water (AW) for 5 layers. The red dashed lines are the AW averages.

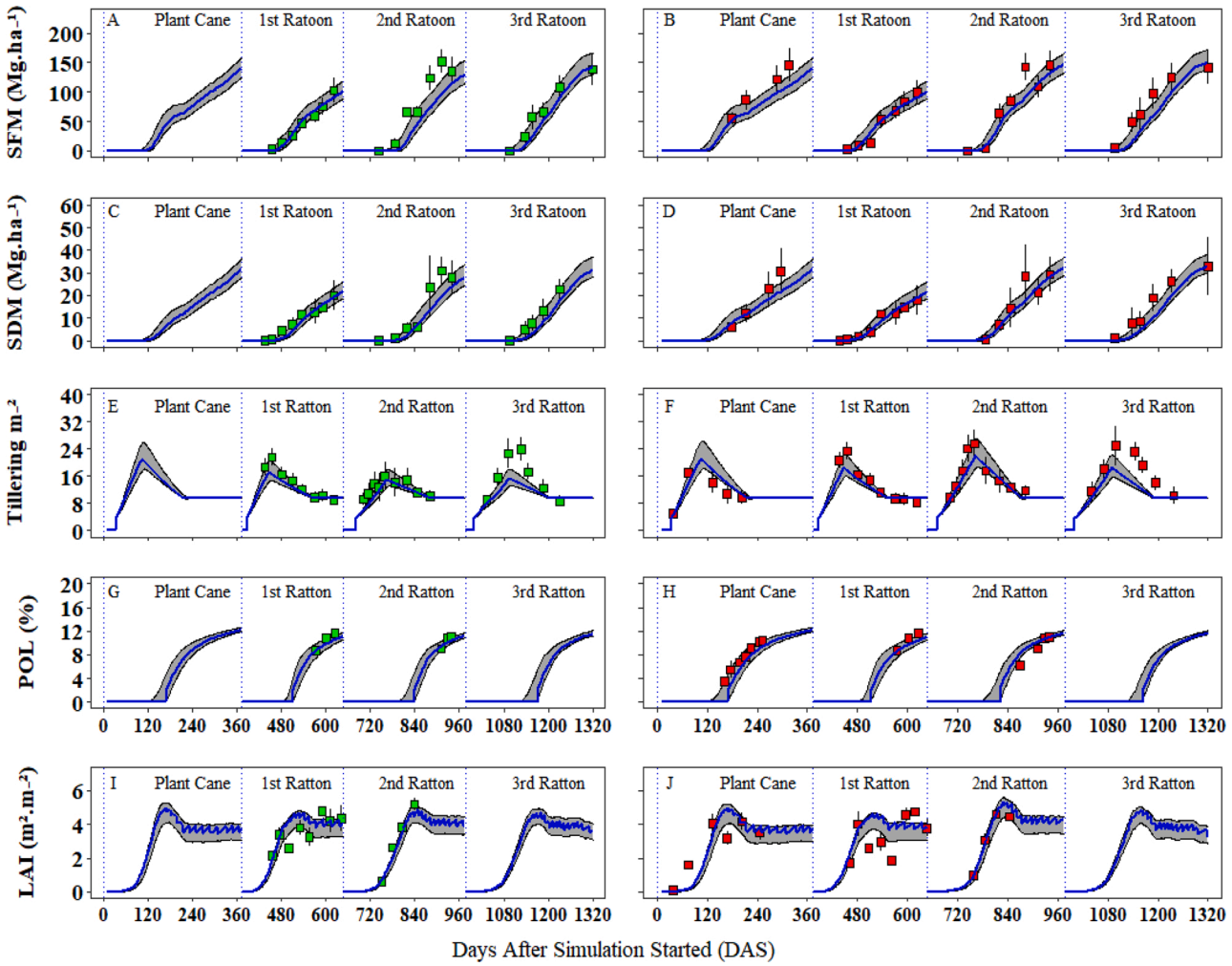

Fig. 2. Representation of the uncertainty due to genotype parameters (UG) in stalk fresh (SFM) and dry (SDM) mass, tillering, sucrose concentration of fresh matter (POL) and leaf area index (LAI), considering parameters stastisticaly significante in the global sensitivity analysis. Blue line simulation with best set parameters (Table 7); gray area is the standard deviation of the stochastic simulation; green and red square are the observed data with their respective error bar for treatments GCTB and Bare, respectively.

Table 8
Statistical indexes of performance of the SAMUCA model applied with best set of parameters. UG: Uncertainty analysis consdering only genotype parameters ; US: Uncertainty analysis considering only soil parameters; UGS: Uncertainty analysis considering both genotype and soil parameters.

Bare Treatment										
Variables	Uncertainty Analysis	Bias	RMSE	EF	R^2	d	σ_{obs}	σ_{sim}	Sample Size	ξ
Stalk	Uncertainty Analysis	−2.21	4.21	0.83	0.88	0.84		2.72	Sample Size	56 %
Dry Mass	US	−0.87	3.69	0.87	0.88	0.84	4.83	$5.0e^{-05}$	25	0.001 %
(Mg ha^{-1})	UGS	−2.37	4.24	0.83	0.89	0.84		2.71		56 %
Stalk	UG	−12.66	20.94	0.87	0.88	0.84		12.92		85 %
Fresh Mass	US	−5.24	17.41	0.87	0.89	0.84	15.18	$6.0e^{-04}$	24	0.004 %
(Mg ha^{-1})	UGS	−13.33	21.24	0.81	0.89	0.80		12.80		84 %
	UG	−0.77	1.52	0.58	0.83	0.68		1.15		221 %
POL	US	−0.14	1.00	0.82	0.84	0.80	0.52	$3.0e^{-06}$	14	0.001 %
(%[fresh])	UGS	−0.88	1.57	0.55	0.83	0.67		1.12		215 %
Tillering	UG	−2.02	3.76	0.53	0.68	0.69		1.71		72%
(# m^{-2})	US	−0.73	3.07	0.68	0.70	0.76	2.53	$4.5e^{-06}$	34	0.0002 %
	UGS	−1.97	3.89	0.49	0.63	0.68		1.67		70%
LAI	UG	0.19	0.99	0.44	0.58	0.65		0.42		124 %
(m^2. m^{-2})	US	0.03	0.95	0.48	0.58	0.66	0.34	$7.1e^{-06}$	23	0.002 %
	UGS	0.18	0.95	0.48	0.10	0.67		0.42		124 %
GCTB Treatment										
Stalk	UG	−2.80	4.30	0.83	0.92	0.87		2.59		64 %
Dry Mass	US	−1.32	3.27	0.90	0.92	0.87	4.02	0.11	21	3%
(Mg ha^{-1})	UGS	−3.20	4.69	0.79	0.90	0.81		2.59		64 %
Stalk	UG	−14.69	23.79	0.75	0.87	0.83		13.26		106 %
Fresh Mass	US	−6.83	18.87	0.84	0.87	0.83	12.53	0.77	20	6%
(Mg ha^{-1})	UGS	−16.63	25.61	0.71	0.83	0.77		13.28		106 %
POL	UG	−0.50	0.70	0.56	0.87	0.66		0.78		223 %
(%[fresh])	US	−0.23	0.57	0.71	0.94	0.71	0.35	0.08	6	23 %
	UGS	−0.72	0.87	0.33	0.88	0.60		0.77		220%
Tillering	UG	−2.48	3.28	0.32	0.70	0.63		1.30		52 %
(# m^{-2})	US	−1.49	2.73	0.61	0.74	0.74	2.52	0.07	24	3%
	UGS	−1.49	2.71	0.61	0.74	0.74		1.32		52 %
LAI	UG	−0.01	0.65	0.70	0.72	0.73		0.44		113 %
(m^2. m^{-2})	US	−0.09	0.70	0.66	0.68	0.69	0.39	0.06	12	15 %
	UGS	0.04	0.76	0.60	0.66	0.69		0.44		113 %

Bias: model bias index; RMSE: Root mean squared error; EF: Modeling efficiency; R^2: Determination index;
d: accuracy index of Wilmot; σ_{obs} is the average of the standard deviation of the observed data;
σ_{sim} is the average of the standard deviation of the simulated data; ξ is the ratio bet $\sigma_{sim}/\sigma_{obs}$ in percentage.

simulations well agreed with observed data (Table 8), with major discrepancies only for 3rd ratton (Fig. 3 F), for in which simulated TIL did not reach the observed peak of TIL and decreased faster than other ratooning cycles. For POL, EF = 0.82 and R^2 = 0.84, showing that model well simulated this output variable. For LAI, EF = 0.48 and R^2 = 0.58, and such weak results might be related to the great dispersion obseved in this variable, mainly for 1st ratton.

For GCTB treatment, the stochastic simulated variability for US was generally lower than that observed in the observed data (Table 8 and Fig. 3), representing only 3% for SDM, 6% for SFM, 23 % for POL, 3% for TIL and 15 % for LAI (Table 8). Still, the variables referring to crop mass, such as SDM and SFM, were well characterized over time by the best set parameters (blue line in Figs. 3A and B), with EF = 0.90 and 0.84 for SDM and SFM, respectively. For TIL, the simulations obtained good statistical indexes (Table 8), being negatively affected per 3rd ratton (Fig. 3 E), for which maximum value of TIL was not well simulated. The LAI data observed had less dispersion in the 1st Ratton in the Bare treatment, which resulted in better statistical indices in relation to the simulation with GCTB

3.5. Uncertainty analysis considering the combined effect of genotype and soil parameters (UGS)

For the Bare treatment, the UGS analysis had a similar performance than the UG in explaining both the variability and average of the observed data. The variables that had the best performance based on the coefficient of modeling efficiency (EF), were SDM (EF = 0.83), SFM (EF = 0.81), POL (EF = 0.55), TIL (EF = 0.49) and LAI (EF = 0.48). The variability of the stochastic simulation (gray area in Fig. 4B) was less or equal, over time than the standard deviation of the observed SFM data (Fig. 4B), explaining 84 % of the variability seen in the field (Table 8). The simulations for SFM (blue line) underestimated observed data (Bias = -13.33 Mg ha^{-1}; Table 8), with an RMSE = 21.24 Mg ha^{-1} (Table 8). For SDM, the variability of the stochastic simulation was able to explain 56 % of the observed data (Table 8). The simulation was also underestimated (Bias = -2.37 Mg ha^{-1}; Table 8), and with an RMSE = 4.24 Mg ha^{-1}. The TIL and POL variables were also underestimated about the observed data, with Bias = -1.97 and -0.88, respectively. Unlike SFM, SDM, and TIL, POL and LAI variables, the variability was overestimated by 115 % and 24 % (Table 8), respectively. The simulated variability for TIL was 66 % of the observed variability (Table 8).

The variability of the stochastic simulation was greater than the observed over time for GCTB treatment for all variables (Fig. 4). It was overestimatied by 6% for SFM, 120 % for POL, and 13 % for LAI (Table 8). In the GCTB treatment the output variables with better performance were SDM (EF = 0.79), SFM (EF = 0.71), TIL (EF = 0.61), LAI (EF = 0.60) and POL (EF = 0.33, and the simulations for SFM (blue line) underestimated the observed data (Bias = -16.63 Mg ha^{-1}; Table 8), with an RMSE = 25.61 Mg ha^{-1} (Table 8). The simulations also underestimated SDM (Bias = -3.20 Mg ha^{-1}; Table 8), and with and RMSE = 4.69 Mg ha^{-1}, as well as POL and TIL (Bias = -0.72 and -1.49, respectively).

4. Discussion

We observed that Bare and GCTB treatments influenced the GSA results, here used to select which genotype and soil parameters to use in the uncertainty analysis (Table 5 and 6). Therefore, using both

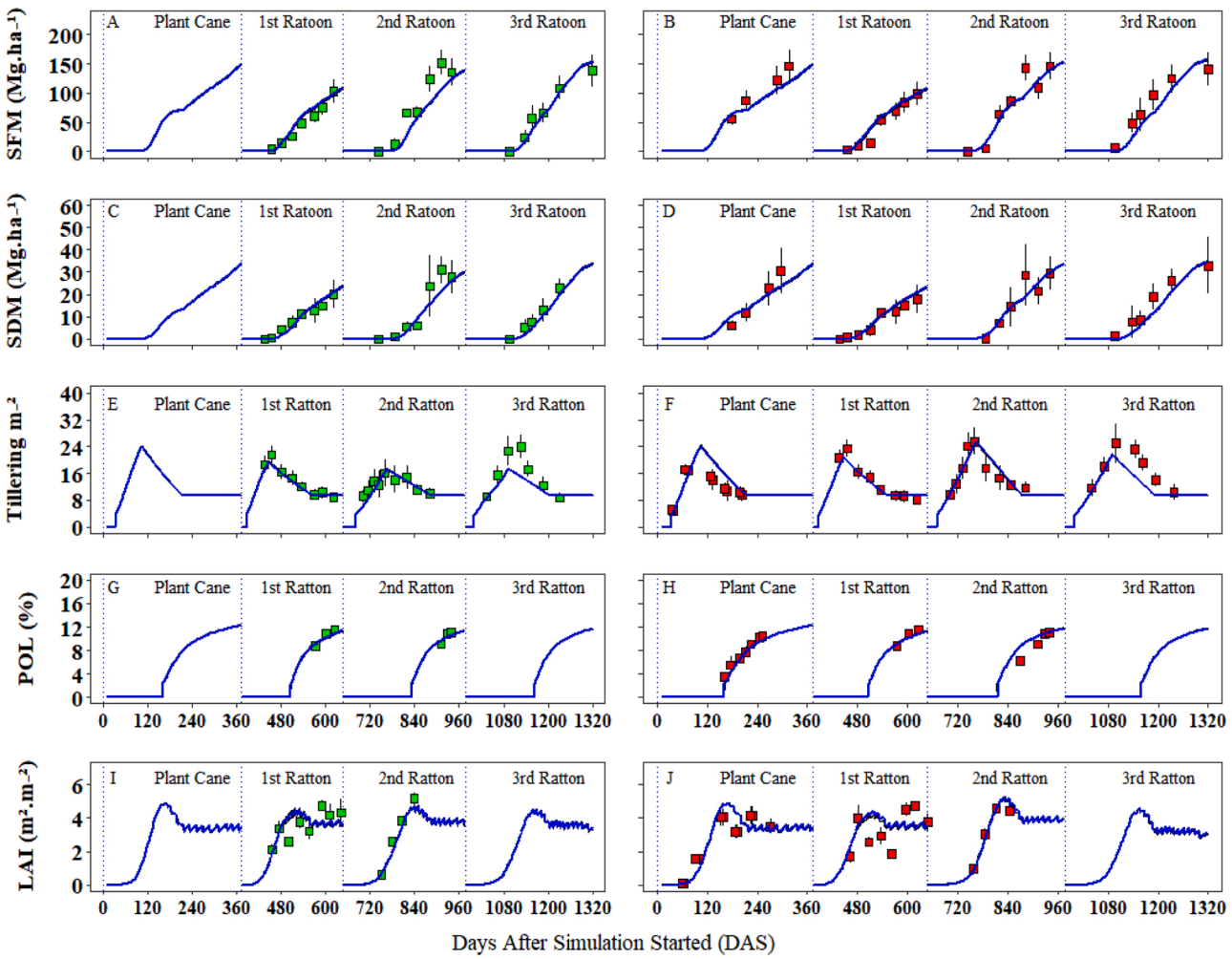

Fig. 3. Representation of the uncertainty due to soil parameters (US) in stalk fresh (SFM) and dry (SDM) mass and tillering, sucrose concentration of fresh matter (POL) and leaf area index (LAI), considering parameters stastisticaly significante in the global sensitivity analysis. Blue line simulation with best set parameters (Table 7); gray area is the standard deviation of the stochastic simulation; green and red square are the observed data with their respective error bar for treatments GCTB and Bare, respectively.

treatment was complemental for chosing the parameters sets that best represent the field variability. Results from the GSA shown that the most influencial parameters of SAMUCA to the main sugarcane growth components were the genotype parameters of plastochron, n_lf_when_eme, n_lf_it_from, tillochron, and mla; and the soil parameters of field capacity (FCp) and wilting point (WPp). We note the inclusion of the n_lf_when_eme parameter only for the GCTB treatment (SFM and SDM), whereas we didn't find any statistcally significant parameter for the POL output. In total, the new version of SAMUCA has 101 parameters that were divided to represent the species, ecotype and genotype characteristics of sugarcane, accordingly with the DSSAT framework (Jones et al., 2003; Vianna et al., 2020). In our study, we considered that only the genotype parameters would have an influence in the simulations uncertainty (Table 4), assuming that the species and ecotype parameters were well defined. Further, finding plausible ranges for all the species and ecotype parameters is challenging, and considering the full list of parameters would dramatically increase the computation requirements of this study (GSA, GLUE and stochastic).

The calibration obtained from GLUE to UG had a lower performance for all variables (Table 8), when compared to the simulation performed by Vianna et al. (2020). However, we must emphasize that we do not estimate all genotype parameters, only those significant that were obtained from the GSA. In future studies it would be interesting to evaluate the different calibration methods, such as GLUE and BFGS to the operational cost for the simulation and performance, while there's still no consensus on the choices of methods and decisions made by modelers during crop models calibrations (Wallach et al., 2020). Nevertheless, we observed that the application of GLUE to soil parameters (US) generated a performance similar to the results of Vianna et al. (2020) (Table 8).

The PRCC method provides answers to questions about how the result is affected if we increase (or decrease) a specific parameter (linearly discounting the effects on the other parameters) (Marino et al., 2008). Thus, the PRCC can be informative about which parameters to target if we are to achieve specific objectives. For example, one can identify the set of parameters that most likely can be used to determine how to increase biomass (SDM or SFM) with the PRCC results. The main limitation of this method is that it does not answer which parameters are responsible for the greatest variance in the model's output (Marino et al., 2008). Different simulation conditions such as the biophysical enviroment (Sexton et al., 2017), management (Zhang et al., 2020), and even GSA methods (Drouet et al., 2011; Marino et al., 2008) can generate divergent results obtained from GSA. Thus, for a more robust overview of the model's sensitivity to parameters, more than one GSA method and other experimental sets could be considered in future studies to confirm our findings.

Nevertheless, when one want to explore the variability in the environment through stochastic simulation, not necessarily the use of statisticaly significant parameters would produce the best results. In the

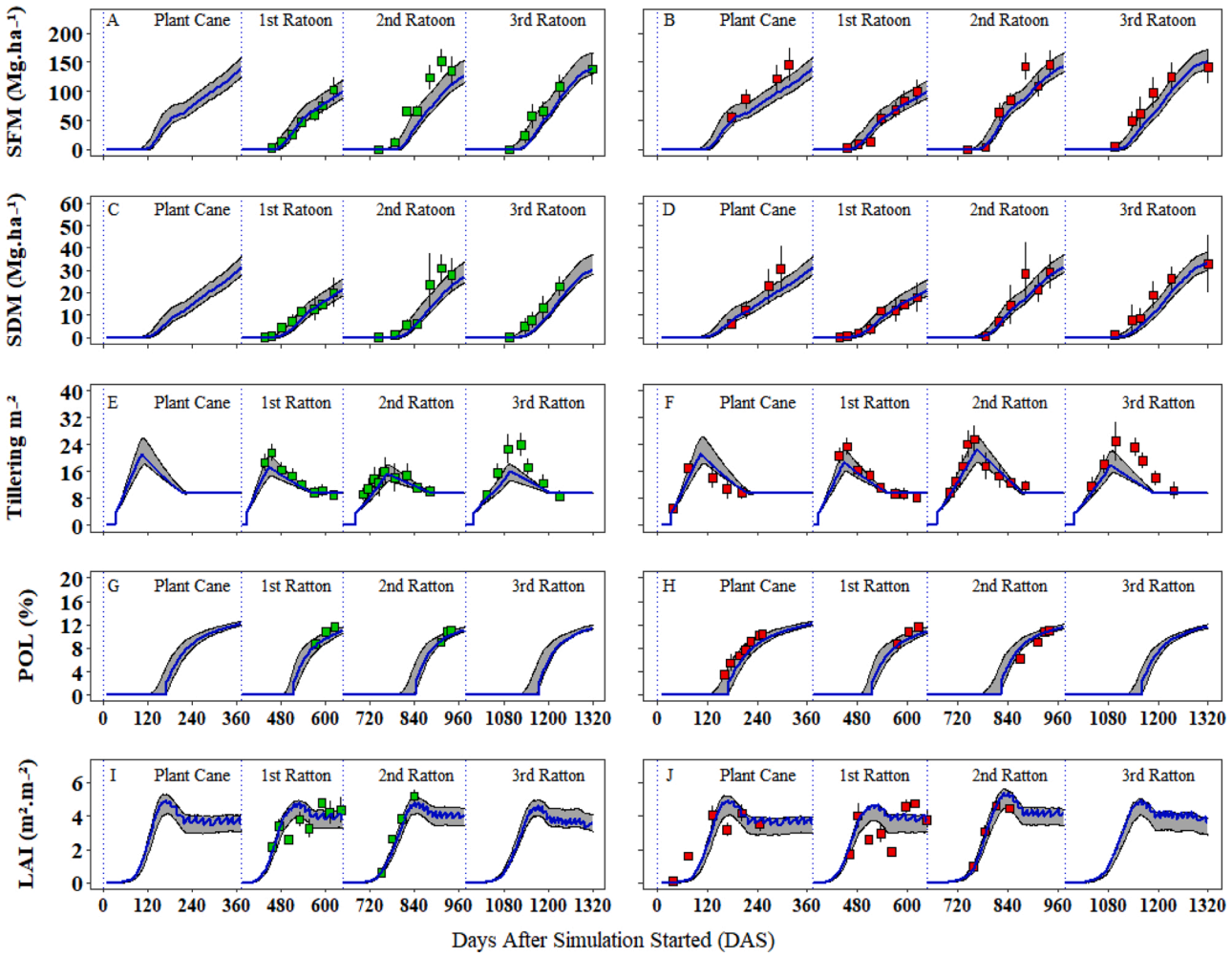

Fig. 4. Representation of the uncertainty due to genotype and soil parameters (UGS) in stalk fresh (SFM) and dry (SDM) mass and tillering, sucrose concentration of fresh matter (POL) and leaf area index (LAI)), considering parameters stastisticaly significante in the global sensitivity analysis. Blue line simulation with best set parameters (Table 7); gray area is the standard deviation of the stochastic simulation; green and red square are the observed data with their respective error bar for GCTB and Bare treatments, respectively.

present study, we show that by considering only the statisticaly significant parameters we were able to well simulate the mean of field observations. However, such procedure overestimated the variability of some model's outputs in comparison with that observed in the experimental field, as it was found for POL and LAI variables in Bare and SFM, POL, and LAI in GCTB (Table 8). We used the whole set of observed data in GLUE procedure, but a possible solution would be on implementing a filter in GLUE methodology to constrain the generated parameters within the observed variability.

The greatest variability in simulations for UG and UGS was due to the greater model sensitivity to genotype parameters. For the US, we found that the variability was less than the other two (UG and UGS). This result agreed with previous studies showing soil parameters with less influence on model behaviour likely as a result of irrigation in the experiment, which further reduced the model sensitivity to soil parameters (Attia et al., 2021; Dejonge et al., 2012; Zhang et al., 2020). We have not included the soil textural parameters because they did not have any significance in the GSA, nor were the physical characteristics of the mulch layer in our analysis of US and UGS. In addition, our field conditions were not limited (adequate inputs in clay soil) and the distribution of soil parameters showed small variation TAW, which can help explain why the soil parameters did not have a greater influence in the field variability.

The model performance under GCTB conditions was slightly better for the SDM, TIL and LAI in comparison with the Bare treatment, whereas the Bare simulations performed better in the SDM and POL simulation. The GCTB is interpreted in the SAMUCA model as an additional soil layer, with its respective saturation point and water content (Vianna et al., 2020). According to Ritchie (1998), the number of layers and their depth is an important factor to simulate the water balance more precisely. This is specifically important to guarantee water and heat fluxes in the soil medium (Harper et al., 2020). Furthermore, the SAMUCA is still not capable of capturing all the belowground processes affecting crop growth, such as soil compaction, nutrient uptake and microbiological processes (Vianna et al., 2020). These model limitations may explain the low capacity to simulate the variability seen in US. Finally, it leads to two possible causes for the low model responses to soil parameters found in the present study: (i) the low influence of the soil hydraulic parameters in a irrigated experiment; and (ii) that the observed variability in the field is not fully explained by the soil hydraulic process and parameters represented in the model.

5. Conclusion

The GSA was a useful tool for choosing parameters for stochastically simulating crop growth and development aiming to explore the genotype variability existing in the environment. The UG and UGS had the same capacity to quantify the variability present in the environment for

the treatments Bare and GCTB, and we did not find any influence of soil parameters in model variability that is likely because our data were collected in field experiments fully irrigated and with no nutritional limitation. In our case, because the water stress is the main reducing factor linked with soil that is accounted for in the SAMUCA model, the sensitivity to the soil parameters may be simply ignored and the genotype parameters can be chosen as the only source of variability for practical applications. Indeed, the simulated variability found in the US was caused by GCTB and not due to soil hydraulic parameters. Our suggestion for future work is to explore rainfed environments, different amounts of GCTB and other soil types.

Funding information

Research Foundation of the State of São Paulo (FAPESP 2017/20925-0, 2017/50445-0, 2021/00720-0), Brazilian Research Council (CNPq, 301424/2015-2, 300916/2018-3, 401662/2016-0 and 425174/2018-2), and Coordination for the Improvement of Higher Education Personnel (CAPES)- Ministry of Education of Brazil.

CRediT authorship contribution statement

Rodolfo Armando de Almeida Pereira: Conceptualization, Methodology, Software, Formal analysis, Writing - original draft, Writing - review & editing. **Murilo dos Santos Vianna:** Software, Data curation, Writing - review & editing, Investigation, Conceptualization. **Daniel Silveira Pinto Nassif:** Data curation, Writing - review & editing, Investigation, Conceptualization. **Kássio dos Santos Carvalho:** Data curation, Writing - review & editing, Investigation, Conceptualization. **Fábio Ricardo Marin:** Supervision, Conceptualization, Funding acquisition, Writing - review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

Attia, A., El-Hendawy, S., Al-Suhaibani, N., Tahir, M.U., Mubushar, M., Vianna, Mdos S., Ullah, H., Mansour, E., Datta, A., 2021. Sensitivity of the DSSAT model in simulating maize yield and soil carbon dynamics in arid Mediterranean climate: effect of soil, genotype and crop management. F. Crop. Res. 260, 107981 https://doi.org/10.1016/j.fcr.2020.107981.

Baigorria, G.A., 2014. Stochastic Models to Generate Geospatial-, Temporal-, and Cross-Correlated Daily Maximum and Minimum Temperatures. https://doi.org/10.1155/2014/365362.

Baigorria, G.A., Jones, J.W., 2010. GiST: a stochastic model for generating spatially and temporally correlated daily rainfall data. J. Clim. 23, 5990–6008. https://doi.org/10.1175/2010JCLI3537.1.

Beven, K., Binley, A., 1992. The future of distributed models: model calibration and uncertainty prediction. Hydrol. Process. 6, 279–298. https://doi.org/10.1002/hyp.3360060305.

Bezuidenhout, C., 2000. A Model Review and Proposed Mechanistic Tiller Model for the Canegro Sugarcane Crop Model. Undefined. Faculty of Engineering at Technikon Natal, Durban.

Bezuidenhout, C.N., O'Leary, G.J., Singels, A., Bajic, V.B., 2003. A process-based model to simulate changes in tiller density and light interception of sugarcane crops. Agric. Syst. 76, 589–599. https://doi.org/10.1016/S0308-521X(02)00076-8.

Brogi, C., Huisman, J.A., Herbst, M., Weihermüller, L., Klosterhalfen, A., Montzka, C., Reichenau, T.G., Vereecken, H., 2020. Simulation of spatial variability in crop leaf area index and yield using agroecosystem modeling and geophysics-based quantitative soil information. Vadose Zone J. 19 https://doi.org/10.1002/vzj2.20009.

Carvalho, J.L.N., Nogueirol, R.C., Menandro, L.M.S., Bordonal, R., de, O., Borges, C.D., Cantarella, H., Franco, H.C.J., 2017. Agronomic and environmental implications of sugarcane straw removal: a major review. Gcb Bioenergy 9, 1181–1195. https://doi.org/10.1111/gcbb.12410.

Coelho, A.P., Dalri, A.B., Fischer Filho, J.A., de Faria, R.T., Silva, L.S., Gomes, R.P., 2020. Calibration and evaluation of the DSSAT/Canegro model for sugarcane cultivars under irrigation managements. Rev. Bras. Eng. Agric. e Ambient. 24, 52–58. https://doi.org/10.1590/1807-1929/agriambi.v24n1p52-58.

Dejonge, K.C., Ascough Ii, J.C., Ahmadi, M., Andales, A.A., Arabi, M., 2012. Global sensitivity and uncertainty analysis of a dynamic agroecosystem model under different irrigation treatments. Ecol. Modell. 231, 113–125. https://doi.org/10.1016/j.ecolmodel.2012.01.024.

Drouet, J.L., Capian, N., Fiorelli, J.L., Blanfort, V., Capitaine, M., Duretz, S., Gabrielle, B., Martin, R., Lardy, R., Cellier, P., Soussana, J.F., 2011. Sensitivity analysis for models of greenhouse gas emissions at farm level. Case study of N 2O emissions simulated by the CERES-EGC model. Environ. Pollut. 159, 3156–3161. https://doi.org/10.1016/j.envpol.2011.01.019.

Ehara, H., Takamura, T., Tsuchiya, M., 1994. Growth and dry matter production of sugar cane in warm temperate zone of Japan. Japanese J. Trop. Agric. 38, 335–342.

Everingham, Y.L., Muchow, R.C., Stone, R.C., Inman-Bamber, N.G., Singels, A., Bezuidenhout, C.N., 2002. Enhanced risk management and decision-making capability across the sugarcane industry value chain based on seasonal climate forecasts. Agric. Syst. 74, 459–477. https://doi.org/10.1016/S0308-521X(02)00050-1.

Everingham, Y., Sexton, J., Skocaj, D., Inman-Bamber, G., 2016. Accurate prediction of sugarcane yield using a random forest algorithm. Agron. Sustain. Dev. 36 https://doi.org/10.1007/s13593-016-0364-z.

Faivre, R., Leenhardt, D., Voltz, M., Benoît, M., Papy, F., Dedieu, G., Wallach, D., 2009. Spatialising crop models BT - sustainable agriculture. In: Lichtfouse, E., Navarrete, M., Debaeke, P., Véronique, S., Alberola, C. (Eds.), Springer. Dordrecht, Netherlands, pp. 687–705. https://doi.org/10.1007/978-90-481-2666-8_42.

Goldemberg, J., Coelho, S.T., Guardabassi, P., 2008. The sustainability of ethanol production from sugarcane. Energy Policy 36, 2086–2097. https://doi.org/10.1016/j.enpol.2008.02.028.

Harper, A., Williams, K., McGuire, P., Duran Rojas, M.C., Hemming, D., Verhoef, A., Huntingford, C., Rowland, L., Marthews, T., Breder Eller, C., Mathison, C., Nobrega, R., Gedney, N., Vidale, P.L., Otu-Larbi, F., Pandey, D., Garrigues, S., Wright, A., Slevin, D., De Kauwe, M., Blyth, E., Ärdo, J., Black, A., Bonal, D., Buchmann, N., Burban, B., Fuchs, K., de Grandcourt, A., Mammarella, I., Merbold, L., Montagnani, L., Nouvellon, Y., Restrepo-Coupe, N., Wohlfahrt, G., 2020. Improvement of modelling plant responses to low soil moisture in JULESvn4.9 and evaluation against flux tower measurements. Geosci. Model Dev. Discuss. 1–42. https://doi.org/10.5194/gmd-2020-273.

He, J., Dukes, M.D., Jones, J.W., Graham, W.D., Judge, J., 2009. Applying GLUE for estimating CERES-Maize genetic and soil parameters for sweet corn production. Trans. ASABE 52, 1907–1921. https://doi.org/10.13031/2013.29218.

He, J., Jones, J.W., Graham, W.D., Dukes, M.D., 2010. Influence of likelihood function choice for estimating crop model parameters using the generalized likelihood uncertainty estimation method. Agric. Syst. 103, 256–264. https://doi.org/10.1016/j.agsy.2010.01.006.

Hoffman, N., Singels, A., Patton, A., Ramburan, S., 2018. Predicting genotypic differences in irrigated sugarcane yield using the Canegro model and independent trait parameter estimates. Eur. J. Agron. 96, 13–21. https://doi.org/10.1016/j.eja.2018.01.005.

Inman-Bamber, N.G., 1994. Temperature and seasonal effects on canopy development and light interception of sugarcane. F. Crop. Res. 36, 41–51. https://doi.org/10.1016/0378-4290(94)90051-5.

Jaiswal, D., De Souza, A.P., Larsen, S., Lebauer, D.S., Miguez, F.E., Sparovek, G., Bollero, G., Buckeridge, M.S., Long, S.P., 2017. Brazilian sugarcane ethanol as an expandable green alternative to crude oil use. Nat. Clim. Chang. 7, 788–792. https://doi.org/10.1038/nclimate3410.

Jones, J.W., Hoogenboom, G., Porter, C.H., Boote, K.J., Batchelor, W.D., Hunt, L.A., Wilkens, P.W., Singh, U., Gijsman, A.J., Ritchie, J.T., 2003. The DSSAT cropping system model. J. Agron. 18, 235–265.

Jones, J.W., He, J., Boote, K.J., Wilkens, P., Porter, C.H., Hu, Z., 2011. Estimating DSSAT cropping system cultivar-specific parameters using Bayesian techniques. Methods Introd. Syst. Model. into Agric. Res. 365–394. https://doi.org/10.2134/advagricsystmodel2.c13.

Jones, M.R., Singels, A., Ruane, A.C., 2015. Simulated impacts of climate change on water use and yield of irrigated sugarcane in South Africa. Agric. Syst. 139, 260–270. https://doi.org/10.1016/j.agsy.2015.07.007.

Jones, J.W., Antle, J.M., Basso, B., Boote, K.J., Conant, R.T., Foster, I., Godfray, H.C.J., Herrero, M., Howitt, R.E., Janssen, S., Keating, B.A., Munoz-Carpena, R., Porter, C. H., Rosenzweig, C., Wheeler, T.R., 2017. Brief history of agricultural systems modeling. Agric. Syst. 155, 240–254. https://doi.org/10.1016/J.AGSY.2016.05.014.

Laclau, P.B., Laclau, J.P., 2009. Growth of the whole root system for a plant crop of sugarcane under rainfed and irrigated environments in Brazil. F. Crop. Res. 114, 351–360. https://doi.org/10.1016/j.fcr.2009.09.004.

Li, Zhenhai, He, J., Xu, X., Jin, X., Huang, W., Clark, B., Yang, G., Li, Zhenhong, 2018. Estimating genetic parameters of DSSAT-CERES model with the GLUE method for winter wheat (Triticum aestivum L.) production. Comput. Electron. Agric. 154, 213–221. https://doi.org/10.1016/j.compag.2018.09.009.

Lingle, S.E., 1999. Sugar metabolism during growth and development in sugarcane internodes. Crop Sci. 39, 480–486. https://doi.org/10.2135/cropsci1999.0011183X0039000200030x.

Liu, D.L., Kingston, G., Bull, T.A., 1998. A new technique for determining the thermal parameters of phenological development in sugarcane, including suboptimum and supra-optimum temperature regimes. Agric. For. Meteorol. 90, 119–139. https://doi.org/10.1016/S0168-1923(97)00087-7.

Marin, F.R., Jones, J.W., 2014. Process-based simple model for simulating sugarcane growth and production. Sci. Agric. 71, 1–16. https://doi.org/10.1590/S0103-90162014000100001.

Marin, F.R., Thorburn, P.J., Nassif, D.S.P., Costa, L.G., 2015. Sugarcane model intercomparison: structural differences and uncertainties under current and

potential future climates. Environ. Model. Softw. 72, 372–386. https://doi.org/10.1016/j.envsoft.2015.02.019.
Marin, F.R., Jones, J.W., Boote, K.J., 2017. A stochastic method for crop models: including uncertainty in a sugarcane model. Agron. J. 109, 483–495. https://doi.org/10.2134/agronj2016.02.0103.
Marin, F.R., Rattalino Edreira, J.I., Andrade, J., Grassini, P., 2019. On-farm sugarcane yield and yield components as influenced by number of harvests. F. Crop. Res. 240, 134–142. https://doi.org/10.1016/j.fcr.2019.06.011.
Marino, S., Hogue, I.B., Ray, C.J., Kirschner, D.E., 2008. A methodology for performing global uncertainty and sensitivity analysis in systems biology. J. Theor. Biol. 254, 178–196. https://doi.org/10.1016/j.jtbi.2008.04.011.
Mukaka, M.M., 2012. Statistics corner: a guide to appropriate use of correlation coefficient in medical research. Malawi Med. J. 24, 69–71.
Nash, J.E., Sutcliffe, J.V., 1970. River flow forecasting through conceptual models part I — a discussion of principles. J. Hydrol. 10, 282–290. https://doi.org/10.1016/0022-1694(70)90255-6.
Nassif, D.S.P., Marin, F.R., Costa, L.G., 2014. Evapotranspiration and transpiration coupling to the atmosphere of sugarcane in Southern Brazil: scaling up from leaf to field. Sugar Tech 16, 250–254. https://doi.org/10.1007/s12355-013-0267-0.
O'Leary, G.J., 2000. A review of three sugarcane simulation models with respect to their prediction of sucrose yield. F. Crop. Res. 68, 97–111. https://doi.org/10.1016/S0378-4290(00)00112-X.
Petersen, R.G., 1994. . Agricultural Field Experiments: Design and Analysis.
Ritchie, J.T., 1998. Soil water balance and plant water stress. Understanding Options for Agricultural Production. Springer, pp. 41–54.
Sage, R.F., Peixoto, M.M., Sage, T.L., 2013. Photosynthesis in Sugarcane, Sugarcane: Physiology, Biochemistry, and Functional Biology. https://doi.org/10.1002/9781118771280.ch6.
Santos, O.N.A., Andrade, I.P., de, S., Lena, B.P., Folegatti, M.V., Diotto, A.V., Romanelli, T.L., 2017. Impact of irrigation and nitrogen fertilization on the energy balance and energy return on investment of jatropha production. Rev. Bras. Agric. Irrig. 11, 1738–1746. https://doi.org/10.7127/rbai.v11n500792.
Sexton, J., Everingham, Y.L., Inman-Bamber, G., 2017. A global sensitivity analysis of cultivar trait parameters in a sugarcane growth model for contrasting production environments in Queensland. Australia. Eur. J. Agron. 88, 96–105. https://doi.org/10.1016/j.eja.2015.11.009.
Sinclair, T.R., Seligman, N.G., 1996. Crop modeling: from infancy to maturity. Agron. J. 88, 698–704. https://doi.org/10.2134/agronj1996.00021962008800050004x.
Singels, A., Bezuidenhout, C.N., 2002. A new method of simulating dry matter partitioning in the Canegro sugarcane model. F. Crop. Res. 78, 151–164. https://doi.org/10.1016/S0378-4290(02)00118-1.
Singels, A., Jones, M., Marin, F., Ruane, A., Thorburn, P., 2013. Predicting climate change impacts on sugarcane production at sites in Australia, Brazil and South Africa using the canegro model. Sugar Tech 16, 347–355. https://doi.org/10.1007/s12355-013-0274-1.
Smit, M.A., Singels, A., 2006. The response of sugarcane canopy development to water stress. F. Crop. Res. 98, 91–97. https://doi.org/10.1016/j.fcr.2005.12.009.
Sousa, V.F., Foleggatti, M.V., Frizzone, J.A., Dias, T.J., Albuquerque, B.S., Batista, E.C., 2008. Effect of irrigation levels and potassium doses on nutrient content of yellow passion fruit leaves. Rev. Bras. Eng. Agric. e Ambient. 12, 41–46. https://doi.org/10.1590/S1415-43662008000100006.
Sreelash, K., Sekhar, M., Ruiz, L., Tomer, S.K., Guérif, M., Buis, S., Durand, P., Gascuel-Odoux, C., 2012. Parameter estimation of a two-horizon soil profile by combining crop canopy and surface soil moisture observations using GLUE. J. Hydrol. 456–457, 57–67. https://doi.org/10.1016/j.jhydrol.2012.06.012.
Usowicz, B., Lipiec, J., 2017. Spatial variability of soil properties and cereal yield in a cultivated field on sandy soil. Soil Tillage Res. 174, 241–250. https://doi.org/10.1016/j.still.2017.07.015.
van Bussel, L.G.J., Ewert, F., Zhao, G., Hoffmann, H., Enders, A., Wallach, D., Asseng, S., Baigorria, G.A., Basso, B., Biernath, C., Cammarano, D., Chryssanthacopoulos, J., Constantin, J., Elliott, J., Glotter, M., Heinlein, F., Kersebaum, K.C., Klein, C., Nendel, C., Priesack, E., Raynal, H., Romero, C.C., Rötter, R.P., Specka, X., Tao, F., 2016. Spatial sampling of weather data for regional crop yield simulations. Agric. For. Meteorol. 220, 101–115. https://doi.org/10.1016/j.agrformet.2016.01.014.
Varella, H., Guérif, M., Buis, S., 2010. Global sensitivity analysis measures the quality of parameter estimation: the case of soil parameters and a crop model. Environ. Model. Softw. 25, 310–319. https://doi.org/10.1016/j.envsoft.2009.09.012.
Vianna, Mdos S., Nassif, D.S.P., dos Santos Carvalho, K., Marin, F.R., 2020. Modelling the trash blanket effect on sugarcane growth and water use. Comput. Electron. Agric. 172, 105361 https://doi.org/10.1016/j.compag.2020.105361.
Wallach, D., Thorburn, P.J., 2017. Estimating uncertainty in crop model predictions: current situation and future prospects. Eur. J. Agron. 88, A1–A7. https://doi.org/10.1016/j.eja.2017.06.001.
Wallach, D., Thorburn, P., Asseng, S., Challinor, A.J., Ewert, F., Jones, J.W., Rotter, R., Ruane, A., 2016. Estimating model prediction error: should you treat predictions as fixed or random? Environ. Model. Softw. 84, 529–539. https://doi.org/10.1016/j.envsoft.2016.07.010.
Wallach, D., Makowski, D., Jones, J.W., Brun, F., 2018. Working With Dynamic Crop Models: Methods, Tools and Examples for Agriculture and Environment. Academic Press.
Wallach, D., Makowski, D., Jones, J.W., Brun, F., Wallach, D., Makowski, D., Jones, J.W., Brun, F., 2019. Data assimilation for dynamic models. Work. With dyn. Crop Model. 487–518. https://doi.org/10.1016/B978-0-12-811756-9.00014-9.
Wallach, D., Palosuo, T., Thorburn, P., Hochman, Z., Gourdain, E., Andrianasolo, F., Asseng, S., Basso, B., Buis, S., Crout, N., Dibari, C., Dumont, B., Ferrise, R., Gaiser, T., Garcia, C., Gayler, S., Ghahramani, A., Hiremath, S., Hoek, S., Horan, H., Hoogenboom, G., Huang, M., Jabloun, M., Jansson, P.E., Jing, Q., Justes, E., Kersebaum, K.C., Klosterhalfen, A., Launay, M., Lewan, E., Luo, Q., Maestrini, B., Mielenz, H., Moriondo, M., Nariman Zadeh, H., Padovan, G., Olesen, J.E., Poyda, A., Priesack, E., Pullens, J.W.M., Qian, B., Schütze, N., Shelia, V., Souissi, A., Specka, X., Srivastava, A.K., Stella, T., Streck, T., Trombi, G., Wallor, E., Wang, J., Weber, T.K.D., Weihermüller, L., de Wit, A., Wöhling, T., Xiao, L., Zhao, C., Zhu, Y., Seidel, S.J., 2020. The chaos in calibrating crop models. bioRxiv. https://doi.org/10.1101/2020.09.12.294744.
Wilkinson, D.J., 2006. Stochastic Modelling for Systems Biology. Chapman and Hall/CRC. https://doi.org/10.1201/9781420010664.
Willmott, C.J., Robeson, S.M., Matsuura, K., 2012. A refined index of model performance. Int. J. Climatol. 32, 2088–2094. https://doi.org/10.1002/joc.2419.
Zhang, Y., Arabi, M., Paustian, K., 2020. Analysis of parameter uncertainty in model simulations of irrigated and rainfed agroecosystems. Environ. Model. Softw. 126 https://doi.org/10.1016/j.envsoft.2020.104642.
Zhou, M.M., Shoko, M.D., 2011. Seasonal and varietal effects on tiller population development of sugarcane (Saccharum officinarum L.). S. Afr. J. Plant Soil 28, 11–16. https://doi.org/10.1080/02571862.2011.10640007.
Zhou, M., Singels, A., Savage, M.J., 2003. Physiological parameters for modelling differences in canopy development between sugarcane cultivars. Proc. South African Sugar Technol. Assoc. 77, 610–621.