

SUGARCANE TRAIT MODELLING WORKSHOP  
to be held on 26 and 27 June 2017 at Mount Edgecombe

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## RECENT ADVANCES IN GENETIC TRAIT MODELING IN DSSAT

Gerrit Hoogenboom

Institute for Sustainable Food Systems & Department of Agricultural and Biological Engineering  
University of Florida, Gainesville, Florida, U.S.A.

[gerrit@ufl.edu](mailto:gerrit@ufl.edu); [www.GerritHoogenboom.com](http://www.GerritHoogenboom.com)

The application of crop growth simulation to enhance plant breeding so far has been limited. One of the most challenging aspects of crop modeling for these and other applications is to obtain the values of the genetic coefficients or Genotype-Specific Parameters (GSPs), especially for new breeding lines or varieties. In crop models, the GSPs define the physiological responses and morphological characteristics of a species and allow the model to differentiate among the traits of a cultivar, variety or hybrids. Crop models range in complexity with respect to these GSPs. This includes “generic models with no reference to species (1), a species-specific model with no reference to cultivars (2), genetic differences presented by cultivar-specific coefficients (3), genetic differences represented by specific alleles, with gene-action represented through linear effects on model parameters (4), and genetic differences represented by genotypes with gene action explicitly simulated based on knowledge of gene expression and effects of gene products (5)” (Hoogenboom et al., 2004). In the Cropping System Model (CSM) of the Decision Support System for Agrotechnology Transfer (DSSAT; Jones et al, 2003; Hoogenboom et al., 2015) most of the modules that allow for the simulation of growth, development and yield of a crop include species, ecotype and cultivar-specific genetic coefficients, representing level 3 as presented by Hoogenboom et al. (2004). White and Hoogenboom (1996; 2003) were the first to develop a gene-based crop simulation model at level 4. GeneGro was implemented using the BEANGRO model of DSSAT for common bean as a framework (Hoogenboom et al., 1994) and included seven genes that affect the physiological processes of common bean. Messina et al. (2006) developed CSM-GeneGro-Soybean that incorporated the effects of six loci from for 48 near-isogenic soybean lines, while White et al. (2008) introduced two loci for simulating the effect on flowering in wheat. Since then, not much progress has been made in further advancing this technology, partially because of a lack of communication and interest among the biotechnology, plant breeding, and crop modeling communities. Technow et al (2015) recently reported on advances with the integration of crop modeling in plant breeding in the private sector. The most recent work with respect to DSSAT has been the development of simple vegetative and reproductive development models using genetic marker information (QTL) based on Recombinant Inbred Lines (RIL) of common bean generated from a cross between Jamapa and Calima (Hwang et al., 2017). The underlying idea of this approach is to develop simple modules that can be inserted into the existing CSM-CROPGRO-Dry bean model and to use QTL information for each unique line as input for the prediction of flowering and node appearance, replacing the GSPs. This approach is promising but still limiting, as it only applies to the RILs and cannot be extracted to other lines unless their QTL information is available. It also requires very detailed data collection for a diverse range of environments in order to be able to develop these simple models. Despite these limitation this might be the future for integrating detailed genetics into dynamic crop simulation models.

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## NEW FEATURES OF THE APSIM SUGAR MODEL FOR SIMULATING TRAITS FOR YIELD IMPROVEMENT OF SUGARCANE IN WATER LIMITED ENVIRONMENTS

G. Inman-Bamber, P. Jackson, C. Stokes, S. Verrall, P. Lakshmanan, J. Basnayake

Australian sugar production relies on irrigation to a greater or lesser extent for about 60% of the area under sugarcane. Alleviation of water stress through better irrigation or plant improvement could raise yields by 15% amounting to about \$250 M in revenue each year. Initial modelling with the APSIM Sugar model showed that some traits could lead to substantially higher yields in water limited conditions. A field research program was funded for about seven years in search of traits that would help to improve yield in such conditions. Vigour traits including canopy and yield components were measured in over 100 clones at three locations. Leaf conductance was measured frequently in all clones, transpiration efficiency (TE) in 18 clones and root water uptake in 10 clones. These data were used to define canopy traits, radiation use efficiency (RUE), hydraulic conductance and root function traits in the APSIM model in an attempt to explain the observed variation in crop biomass at two sites with different levels of irrigation. The modelling was restricted to the 40 clones that were common to the two sites. Environment (climate, soil and management) had an overwhelming effect on crop biomass. Varietal traits in the model accounted for only 3% additional variation in yield. However with individual environments, up to 87% of the yield variation was explained when all traits were simulated (for only 10 clones). RUE and canopy traits alone accounted for significant variation in yield of 40 clones in 10 out of 12 environments.

At this point it was clear that the APSIM model required improvement particularly for simulation of TE. Four key features were added to enable genetic variation in TE traits and root water supply (RWS) known to exist, to be modelled and assessed for predicted impact. These features were 1) the response of TE to water stress, 2) the midday flattening of hourly transpiration when plants are stressed, 3) conductance limits to hourly transpiration, which can apply even without stress and 4) the separation of soil hydraulic conductivity (k) and root length density (l) rather than the use of combined kl for determining RWS. A dataset of 182 observations of above ground biomass from 13 field experiments of sugarcane were used to check firstly that the new sugarcane module did not affect the simulation results when all the new features were disabled (model stability), secondly to check that the new features did not greatly reduce model performance, and thirdly, to determine the response or sensitivity of yields to the new features. Variation in parameter settings for the new features were based on the best evidence available for genetic variation in these traits, and were set before any testing against observations were made. With these features enabled in partial factorial combinations, the accuracy of the simulation of observed biomass, changed only to a minor extent compared to when no features were enabled. Separating k and l had the most consistent effect on improving model performance.

Three additional published experiments with varying levels of imposed water stress were also simulated, with and without the new features. The simulation of biomass yield from two of the experiments was remarkably accurate regardless of which features were used in the simulation. Dry stalk yields reported for the third experiment were simulated accurately when no features were enabled and when midday flattening of transpiration was enabled and separate k and l enabled, one at a time. When a limit was placed on hourly transpiration, simulated TE and yield increased substantially when water was limiting but not in well-watered conditions; where yield was reduced.

The new APSIM-Sugar features address the limitations of the original module (developed in 1999) for assessing water use related traits, including TE component traits and root growth. Effects of conductance on TE can now be simulated by limiting maximum hourly transpiration at the leaf level or k and specific root length at the root level. The new sugar module will also allow for better discrimination between sugarcane cultivars, now that vigour traits such leaf area development and radiation use efficiency are linked to root water uptake.

## COMBINING CALIBRATION TECHNIQUES IMPROVES THE QUALITY AND USEFULNESS OF SUGARCANE MODEL PREDICTIONS

Fabio R Marin

Dept. of Biosystems Engineering, College of Agriculture “Luiz de Queiroz” (ESALQ), University of São Paulo, Brazil

The usefulness of a crop model depends on how well the model is calibrated. Therefore, the calibration procedure must be conducted carefully to maximize the reliability of the model. In general, manual procedures for calibration can be time consuming and this might be a factor inhibiting the widespread use of models, in special for beginners. Unsupervised methods for calibration, in the other hand, can result in undesired parameter values and unrealistic crop model behavior. Here we describe the GLUE method for automatic calibration and compare it with the classical eye-fitting calibration based on our previous experience for sugarcane crops models, both for academic (Marin et al., 2015) and applied use of sugarcane crop models. Recently, System TEMPOCAMPO ([www.tempocampo.org](http://www.tempocampo.org)) was developed at University of Sao Paulo-ESALQ to be an on-time supporting system for helping sugarcane growers, companies and government to take better decisions and understand how current weather variability can influence the sugarcane crop along the main producing regions in Brazil and generates future yield scenarios for the current/next season to give some advice for agronomic and trade planning. Finally, we show how GLUE method can be used for improving the use of crop models including the quantification of uncertainties of crop yield prediction (Marin et al., 2016). To do so, we have developed a method for considering uncertainty in a crop model using a simple sugarcane (*Saccharum* spp.) model as a case study. A Bayesian Monte Carlo approach (generalized likelihood uncertainty estimation) was used to estimate model parameters, their uncertainties, and correlations among them

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## SUGARCANE TRAIT MODELLING AT SASRI

A. Singels, M. Jones and N. Hoffman

South African Sugarcane Research institute, Mount Edgecombe, South Africa

Crop models can be used to predict the impacts of genetically determined physiological traits on crop performance for different environments. This could indicate the desirability of traits in target environments and thus aid the formulation of ideotypes (breeding targets). This presentation will review the progress made at SASRI regarding the development and application of crop models for gaining a better understanding and prediction of genetic trait impacts on genotype response to environmental factors.

Initial research on a small mapping population of genotypes showed that leaf-level photosynthetic capacity was highly heritable and can be phenotyped conveniently using chlorophyll fluorescence. Stable genetic markers (QTLs) were identified for leaf size and photosynthetic capacity, suggesting that trait values could be estimated from genomic information (Singels et al., 2010).

The Canegro model has been used to explore the desirability of early stomatal closure in low and high potential rainfed environments (Singels et al., 2016a, Jones & Singels, 2017). Results suggest early stomatal closure reduces yield for most agro-climatic zones in South Africa under a current and future climate (Jones & Singels, 2017). The research indicated that although trait impact modelling could produce useful information that may benefit sugarcane breeding programs, it also pointed to shortcomings in the Canegro model that needed attention. The disconnect between the carbon balance and organ development routines were addressed with the development of the GTP-Canegro variant by relating structural growth to carbon availability and partitioning carbon to different pools according to the strength of the different sinks (Jones et al., 2011).

Manual phenotyping procedures have been developed to estimate trait parameter values for selected SASRI cultivars (Hoffman et al., 2016). Parameter values have also been estimated using a combination of experimental data and subjective expert ratings (Singels et al., 2016b). Preliminary results showed that genotypic differences in yield of irrigated sugarcane were predicted successfully using independently derived trait parameter values. A sensitivity analysis showed that maximum radiation use efficiency, stalk fraction and duration of canopy formation were the most impactful traits.

Trait modelling research at SASRI has demonstrated the potential value to breeding and has highlighted areas where further research and development are needed, namely further model improvement and the development of rapid phenotyping for impactful traits.

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## TRAIT PARAMETER ESTIMATION AND IDEOTYPING WITH CANEGRO

N. Hoffman, A. Singels, A. Patton, M. Jones and S. Ramburan

South African Sugarcane Research Institute, Mount Edgecombe, South Africa

The Canegro sugarcane model (Inman-Bamber 1991; Singels *et al.* 2016) has the potential to support plant breeding by identifying desirable genetic traits for improved crop performance. The suitability of Canegro for this application has not been tested because genetic trait parameter (TP) values for many genotypes are lacking, and appropriate phenotyping methods for obtaining these data have not been developed. This presentation will review the findings of an M.Sc study which evaluated the ability of Canegro to (1) simulate genetic differences in crop growth and yield observed in field trials using TP values estimated from pot trial data (phenotyping), and (2) identify a set of ideal TP values for a target environment (ideotyping) (Hoffman, 2016).

Phenotyping was conducted in a well-watered pot trial at Mount Edgecombe comprising 14 genotypes. TP values were estimated from monthly measurements of leaf and stalk development, leaf gas exchange measured on two occasions, and destructive sampling of biomass components at harvest. TP values for the different genotypes were determined directly from phenotypic data where possible, or through normalization with respect to the reference genotype (NCo376), for which statistically calibrated TP values were already available.

The study estimated the values of 10 TPs, and phenotyping procedures were developed for generating data required for TP estimation. Reference stalk elongation rate (SERo) showed the greatest genetic variation (range of 78% of the mean), followed by maximum leaf area (MXLFAREA, 73%), the leaf number at which MXLFAREA occurs (MXLFARNO, 63%) and phyllochron interval 2 (PI2, 52%). Maximum PAR conversion efficiency (PARCEmax) also showed significant variation with a range of 47% of the mean. Phyllochron interval 1 (PI1, 24%), maximum number of green leaves (LFMAX, 23%) and maximum sucrose content (SUCA, 15%) showed less variation, although these were still significant. A range of 17% for the maximum stalk partitioning fraction (STKPFMAX) was not statistically significant. The range for thermal time required to the start of stalk elongation (CHUPIBASE) was 30%, although this could not be tested for significance.

The model showed some potential for simulating genetic differences observed in field trials using TP values estimated from pot trial data. It predicted the genotype rankings for stalk dry mass (SDM) observed for an irrigated field trial in Pongola well ( $r=0.75^*$ ). There were no significant genotype differences in observed SDM in three other field trials at Komatipoort and Mount Edgecombe, and model simulations also showed small differences in SDM for these. The model was unable to predict genotype differences in canopy development observed in field trials.

A trait impact study identified three traits (PARCEmax, STKPFMAX and CHUPIBASE) which were most impactful on simulated SDM. Combining optimal values for these three traits in a single genotype could result in a SDM increase of 12 t ha<sup>-1</sup> when compared to the mean SDM value of genotypes with single optimal values only. Results suggest that these could be candidate traits for screening in early plant breeding stages.

The Canegro model in its present form is not suitable for exploring trait impacts on canopy development, a key process in sugarcane yield formation, as discussed by Jones *et al.* (2011). The knowledge generated in this study will be useful for improving the suitability of the Canegro model for supporting sugarcane breeding, and for developing procedures for screening sugarcane populations for desirable traits using high-throughput phenotyping (HTP). The procedures identified, particularly for measuring stomatal conductance, will be used to ground-truth HTP data in screening for drought tolerant genotypes in a follow-on Ph.D. project at SASRI.

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## SELECTING SUGARCANE WITH HIGHER TRANSPIRATION EFFICIENCY

P. Jackson

Commonwealth Scientific and Industrial Research Organisation, Townsville, Australia

In the past four years we have been conducting research to examine and better understand genetic variation in transpiration efficiency in sugarcane (TE, defined as growth per unit of water used) in Australia and China, with an ultimate aim to develop better ways to select sugarcane for water stress environments.

TE measured in a wide range of (100) sugarcane clones was found to vary about  $\pm 20\%$  around the mean. Crop growth simulation modelling indicated a 1% variation in TE translated to about 0.5 to 1.5% variation in final cane yield in commercial production environments in Australia, highlighting the potential value of this trait.

Physiological mechanisms underlying genetic variation in TE were examined. This highlighted a complication in selecting for high TE in that genetic variation in TE was found to be driven in part by genetic variation in mean stomatal conductance levels: such that genotypes with lowest conductance having higher TE on average. However, genetic variation in photosynthesis capacity at mean operating levels of conductance were also found, indicating that improvements in TE are possible in sugarcane without necessarily compromising growth rates. However, the significant contribution of conductance in affecting TE means that selecting for high TE alone (and without regard to growth rates) may in many cases act to reduce overall growth rates and therefore yield. This prediction is consistent with papers reporting results from strong selection pressure for TE in other crops such as wheat.

From a theoretical point of view it is argued that the use of well established (but arguably under-utilized) selection index theory could be used to help address these complications in practice. It is shown how combining measurements of yield and TE in optimal selection indices could in many situations provide greater realised selection gains for yield for water limited environments compared with customary approaches in breeding programs using direct selection for yield alone. This prediction has been supported by early empirical results in field trials (in China) which have shown that a combination of high yield and low leaf conductance or high leaf temperature (both of which may be related to reduced rates of water use), all measured under non-stress, was predictive of yield under the limited water treatments, with prediction levels better than either yield or leaf based measurements alone. This is suggestive of a potentially valuable role for this combination of measurements in optimal selection indices in early stages of selection in sugarcane breeding programs.

A practical problem in using measurements at leaf level for screening clones in commercial breeding programs was found to be high sampling error variance. This means measurements at a leaf level are too costly for screening large numbers of clones. However advances in aerial image capture and analysis technologies means that it may be possible to relatively cheaply and accurately screen clones in field trials for relative rates of canopy conductance. This approach is now being explored in follow up research to this project, and this is required to deliver practical impact on breeding programs and industry outcomes. Results from this project, including the predicted benefits of improving TE in different environments, should be used to guide this further research.

In separate experiments we have also shown that increasing CO<sub>2</sub> levels increased TE but genotypes ranked similarly for TE at different CO<sub>2</sub> levels, indicating selection at current atmospheric CO<sub>2</sub> levels will likely translate to improvements, and be amplified, in future years when CO<sub>2</sub> is higher.

## THE ICSM GENOTYPE GROWTH ANALYSIS DATASET

A. Singels<sup>1</sup>, A. Patton<sup>1</sup>, S. Chinorumba<sup>2</sup>, J. Shine<sup>3</sup>, C. Poser<sup>4</sup>

<sup>1</sup>South African Sugarcane Research institute, Mount Edgecombe, South Africa

<sup>2</sup>Zimbabwe Sugar Association Experiment Station, Chiredzi, Zimbabwe

<sup>3</sup>Sugarcane Industry Research Committee, Florida, U.S.A

<sup>4</sup>Centre De Coopération Internationale En Recherche Agronomique Pour Le Développement, Reunion Island, France

The ICSM is conducting a collaborative project to gain a better understanding of the physiological mechanisms underlying the genetic variation in sugarcane response to environmental factors by monitoring key plant processes contributing to yield in a common set of diverse cultivars grown in diverse environments from around the world. This presentation reports on the status of the field experiments and processing of data collected so far, and will highlight emerging trends.

Field experiments were planted in Pongola, South Africa; Chiredzi, Zimbabwe; La Mare, Reunion Island and Belle Glade, Florida using cultivars N41, R570, CP88-1762, HoCP96-540 and ZN7. In some cases NCo376 and Q183 were also planted.

Crop growth and development were monitored on a regular basis in irrigated plant and first ratoon crops. Non-destructive measurements included shoot emergence, tiller population and height, leaf number and dimensions, leaf area index and fractional interception of photosynthetically active radiation. Aboveground biomass components were destructively sampled on three or four occasions and stalk composition was sampled at harvest. Associated daily weather data, soil chemical and physical data and management data were also recorded. Other ad hoc measurements included leaf N and chlorophyll content, stomatal conductance, soil water content, leaf angle, and canopy reflectance. Data have been entered into customized data storage files with a common, standardised template.

The diverse climate of the different environments are illustrated by the differences in seasonal thermal time (2040 °Cd at Pongola vs. 3200 °Cd at La Mare) and seasonal ranges in temperature maxima (19.5 - 48.2 °C at Chiredzi vs. 21.4 - 32.8 °C at La Mare) and minima (-0.9 – 24.1 °C at Belle Glade vs. 14.5 - 26.7 °C at La Mare) recorded in the plant crop. Preliminary analyses of the plant and ratoon crop results reveal that:

- N41 generally produced the highest stalk population, and R570 the lowest,
- Q183 often developed canopy cover the quickest,
- cultivars often produced the highest cane yield in the environment that they were selected for (N41 in Pongola, CP88-1762 in Belle Glade and ZN7 in Chiredzi)
- yield ranking of cultivars at Pongola and Chiredzi, differed from that at Belle Glade and La Mare.

Each project participant will have an opportunity to highlight important aspects of their respective experiments. The presentation will conclude with a comparative overview of climate, canopy formation and cane yields.

## OTHER GENOTYPE GROWTH ANALYSIS DATASETS TO COMPLEMENT THE ICSM PROJECT

Sanesh Ramburan

South African Sugarcane Research Institute, Mount Edgecombe, South Africa  
[Sanesh.Ramburan@sugar.org.za](mailto:Sanesh.Ramburan@sugar.org.za)

SASRI is currently conducting a project to identify genetic traits associated with good ratooning ability (RA) in sugarcane. Twelve contrasting SASRI varieties have been planted in replicated field trials in each of the three major production regions of the industry (coastal, irrigated, midlands). Trials have been planted as three series (2011, 2012 and 2013 planting years) i.e. repeated three times at each site to eliminate confounding year effects when identifying traits associated with good RA.

A range of morpho-phenological characteristics have been measured from these trials at approximate two-week intervals, together with biomass component estimates at 3, 5, 7, 9, and 12 months of age. Measurements were used to derive traits that could be linked to RA and that could be easily implemented in a breeding program. Some of the traits are also embedded in sugarcane crop models as genetic coefficients. However, coefficient values are currently limited to one variety only. Therefore, this dataset presented an opportunity to assess the realistic range values of genetic coefficients (traits) for a more diverse set of genotypes. Additionally, information on genetic principles associated with the traits were lacking at SASRI.

A sub-study was therefore initiated at the MSc. level to evaluate the G x E effects associated with the traits, evaluate their stability across crops and sites, and estimate heritability. This presentation will briefly describe the traits derived from the above dataset, illustrate the nature and reliability of the data collected thus far, and outline plans for further analyses of the available data. The presentation will also highlight some key considerations for the use of crop model traits in a functional breeding program. Opportunities for this dataset to complement the ICSM project will also be discussed.

## SIMULATING GENOTYPE PERFORMANCE WITH DSSAT-CANEGRO

*M.R. Jones*

South African Sugarcane Research Institute, Mount Edgecombe, South Africa

This presentation deals with the evaluation of the DSSAT-Canegro model for simulating the development and growth of three contrasting sugarcane cultivars (N41, R570, CP88-1762) at four sites in South Africa (Pongola), Zimbabwe (Chiredzi), Florida USA (Belle Glade) and Reunion Island (La Mare). The objectives were to (1) gain an understanding of the capability of the model for simulating observed interactions between genotype and environment in canopy development and cane yield, and (2) to evaluate the suitability of the experimental data and the DSSAT software for model parametrization, development and evaluation.

The model was set up to reflect the management and environmental conditions as accurately as possible for each of the sites for plant and first ratoon crops. Trait parameters for each cultivar were calibrated manually across all sites, per plant process, focussing first on crop phenology and development processes, and then biomass accumulation and partitioning processes. Crop phenology/development parameters examined, in order, were: TTPLTNEM and TTRATNEM (thermal time to shoot emergence),  $TAR_0$  (tiller appearance rate per unit thermal time), POPTT16 (final stalk population), PI1 and PI2 (leaf phyllocron intervals), LFMAX (maximum number of green leaves), CHUIBASE (thermal time to start of stalk elongation), and MXLFAREA (maximum leaf area per leaf). Biomass accumulation and partitioning parameters investigated included MaxPARCE (maximum photosynthetic conversion efficiency), STKPFMAX (maximum stalk partitioning fraction), and SUCA (maximum stalk sucrose concentration).

Time series graphs of simulated and observed values, as well as statistical measures of model performance (RMSE and  $R^2$ ) will be presented. Comparisons of simulated and observed cultivar rankings for different crop variables will also be shown.

A number of difficulties were encountered in this model calibration process. Subtle differences in the definitions (units and measurement methods) of observed variables, along with differences in naming conventions, required manual intervention to prepare consistent observation datasets. Some of the green leaf area index data seemed unrealistically low for several of the experiments. The DSSAT GenCalc automatic calibration tool does not support for the use of time-series observations when used in conjunction with DSSAT-Canegro model. Finally, the Belle Glade site presented some unique modelling challenges: the water-table irrigation system could not be simulated by DSSAT; estimating soil water-holding characteristics from a 'soil' with > 80% organic matter was beyond the capabilities of the DSSAT SBuild software, and observations of drained upper limit, lower limit etc were not provided; and damage caused by very cold conditions is not simulated by the DSSAT-Canegro model.

It is hoped that the outcomes of this work will include improved data templates and data capture/verification protocols. It is clear that a robust automatic calibration tool will need to be developed for the DSSAT-Canegro model.

## SIMULATING GENOTYPE PERFORMANCE WITH MOSICAS

M. Christina, C. Poser, J-F. Martine

Centre De Coopération Internationale En Recherche Agronomique Pour Le Développement, France

The Mosicas model (Martine & Todoroff, 2004) is one of the growth simulation models under consideration for the ICSM project on “Modelling worldwide GxE interaction”. The presentation will focus on the simulations of different genotype of sugarcane based on datasets from Reunion Island and Pongola. The model has been calibrated on 7 cultivars, three common between Reunion Islands and Pongola (R570, N41 & CP881762), and four cultivars specific to Reunion Island experiments (NCo376 & Q183) or Pongola experiments (ZN7 & HoCP96). For each genotype, simulations will be presented for both crop plants and ratoon plants. Simulations and calibrations were performed on different processes:

- The green leaf area index and the light interception efficiency dynamics over growth
- The processes driving the production of:
  - The total dry mass of aboveground biomass including trash and dead stalks
  - The dry mass of millable stalks,
  - The sucrose production

Model performances will be compared based on RMSE and normalized RMSE depending on the considered processes, the genotype (e.i. variety), the environment (Reunion is. & Pongola) as well as the crop stage (plant or ratoon). Model performance differed depending on the processes (e.g. dry mass production RMSE < sucrose production RMSE), the genotype (e.g. CP881762 RMSE > R570 RMSE) as well as the environment (Reunion is. RMSE < Pongola RMSE).

These preliminary results highlighted the need to choose a common calibration approach between models, as well as specific recommendations (ex zero observed values required at the beginning of the growth for calibration). A better understanding of environmental data in both Reunion is. and Pongola are also required to understand the discrepancy of model performance depending on the environment.

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## SIMULATING GENOTYPE PERFORMANCE WITH APSIM-SUGAR

Fábio R Marin, Leandro G Costa

Dept. of Biosystems Engineering, College of Agriculture “Luiz de Queiroz” (ESALQ), University of São Paulo, Brazil

Crop models are increasingly being used for different purposes, including for assisting the understanding of genotype by environment (GXE) interaction and its underlying physiological mechanisms (Hammer & Jordan, 2007). One of the sugarcane models available for end-users is the APSIM-Sugar (AS) (Keating et al., 1999) which interacts with weather data and soil (Probert et al., 1998) and crop residue (Thorburn et al., 2001) models to mechanistically simulate soil–crop growth and development.

The main goal of the paper was to determine model trait parameters (genetic coefficients) for five cultivars (N41, ZN7, R570, CP88-1762, HoCP96) growing at the South African Sugarcane Research Institute (SASRI) research farm in Pongola, South Africa, derived from development, growth and water use measurements. To do so, the AS model was calibrated and its predictions evaluated using observed data from a crops planted in Pongola, South Africa.

Hydraulic soil parameters were measured at the experimental site and a weather station was installed near to the field trial. Model parameters were manually adjusted by eye-fitting with focus in the measured data of LAI, stalk and aerial dry mass, being predictions statistically evaluated. Exception was the cultivar R570, which had already been calibrated for APSIM and no change in parameters was required. AS simulated genotype responses to weather variation well, with performance comparable with that found in other sugarcane models. Predictions were best for above ground dry mass, stalk dry mass and leaf area index.

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## PROCESS-LEVEL COMPARISON OF APPROACHES TO SIMULATING ENVIRONMENTAL AND GENETIC EFFECTS

M.R. Jones<sup>1</sup>, M. Christina<sup>2</sup>, J-F. Martine<sup>2</sup>, F. Marin<sup>3</sup>, A. Singels<sup>1</sup>

<sup>1</sup> South African Sugarcane Research institute, Mount Edgecombe

<sup>2</sup> Centre De Coopération Internationale En Recherche Agronomique Pour Le Développement

<sup>3</sup>Dept. of Biosystems Engineering, ESALQ, University of São Paulo, Brazil

Several sugarcane growth simulation models are under consideration for the ICSM project on “Modelling worldwide GxE interaction”: DSSAT-Canegro (Jones & Singels, 2017; Singels et al., 2008; Inman-Bamber, 1991), APSIM-Sugar (Keating et al., 1999), Mosaicas (Martine & Todoroff, 2004), CASUPRO (F. Royce, pers.comm.) and Canesim (Singels & Paraskevopoulos, 2017). In order to understand model differences in the simulation outcomes, it is necessary to have some understanding of how each of the models simulates major plant processes, and how these are driven by environmental (E) factors, and controlled by genetic (G) effects.

Major plant processes considered are: bud sprouting (germination) and shoot emergence; canopy development (including leaf and tiller dynamics, development of leaf area and fractional interception of photosynthetically active radiation (FiPAR)); root development and growth; biomass accumulation (photosynthesis and respiration) and its partitioning between various plant organs; water and nitrogen uptake and estimation of water contents of plant components.

Similarities are apparent between models in the simulation of certain processes. For example, most models use some concept of thermal time to determine the timing of phenological events and temperature-related process rates. In the simulation of some other processes, however, a much greater degree of variation is evident. For example, Canesim uses a simple method for simulating canopy development and FiPAR directly as a function of thermal time (modified by a water stress factor). Mosaicas simulates green leaf area index (LAI) as a function of thermal time, and then converts this to FiPAR via a radiation extinction coefficient. DSSAT-Canegro is the most complex, and simulates the appearance, senescence and growth of individual leaves on individual tiller cohorts from which LAI is derived and FiPAR determined via a radiation extinction coefficient which increases with the number of leaves appeared. Other differences include: (1) presence or absence of simulating maintenance respiration, (2) simulating biomass partitions through allometry or dynamic source-sink interactions, and (3) simulation of water uptake.

Different modelling approaches lead to different ways in which genetic effects are accounted for. All model use trait parameters (“genetic coefficients”) to capture genotypic differences but the type and number of genetic trait parameters, how they are organized (e.g. species vs cultivar), how their values can be determined, may differ. This will be elaborated in the presentation and the availability of estimates of parameter values for germplasm will be explored.

The modelling approaches for each of the key simulated processes will be presented in detail for the DSSAT-Canegro, Mosaicas and APSIM-Sugar models. Highlights and unique approaches from other models will also be discussed.

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