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Predicting genotypic differences in irrigated sugarcane yield using the Canegro model and independent trait parameter estimates

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ABSTRACT

Crop models have the potential to support plant breeding by predicting genotype response to environmental factors, and identifying desirable genetic traits for improved crop performance.

The study tested whether the Canegro sugarcane model can predict genotypic differences in stalk dry mass (SDM) yields observed in field trials using independently derived genetic trait information. Other objectives included the estimation of three trait parameters (TP) for selected genotypes, and assessing their role in determining genotypic differences in SDM yields.

Phenotyping was conducted in a well-watered pot trial at Mount Edgecombe, South Africa comprising 14 genotypes. Gross photosynthate produced per unit of intercepted photosynthetically active radiation under ideal conditions (PARCEo) was estimated from leaf level photosynthetic efficiency (A) and stomatal conductance (g_s). Thermal time from shoot emergence to the start of stalk elongation (CHUPIBASE) was estimated from measurements of leaf number. Maximum fraction of aerial dry biomass growth partitioned to stalks (STKPFMAX) was estimated from the measured stalk fraction of aerial biomass at harvest.

Values of PARCEo (A) and PARCEo (g_s) differed significantly between genotypes with a range of 47% and 67% of the mean, respectively. CHUPIBASE values also differed significantly between genotypes and showed a range of 23% of the mean. STKPFMAX values did not differ significantly between genotypes and showed the least variation with a range of 17% of the mean.

The Canegro model predicted SDM yields and rankings well ($r = 0.90^{**}$) for nine genotypes grown in well-watered field trials at Pongola, South Africa, using these independent estimates of PARCEo (A), CHUPIBASE and STKPFMAX values. The overestimation of the observed genotypic range in SDM yields were corrected by dynamically scaling leaf level photosynthetic efficiency using fractional sunlit leaf area. The reliable prediction of genotype performance was mostly ascribed to the impact of PARCEo. The extent of genetic variation in PARCEo found in the relatively small number of genotypes for well-watered crops, suggest that sugarcane improvement could be enhanced by screening breeding populations for high values of this trait.

The study provided proof of concept that realistic sugarcane models could be used for identifying key traits (in this case PARCEo) and their ideal values (in this case as high as possible), and therefore could be used to assist in defining sugarcane breeding targets.

1. Introduction

Sugarcane is a major agricultural crop grown world-wide in tropical and subtropical regions (Chandel et al., 2012) under rainfed and irrigated conditions. Globally 1.9 billion tons of cane were produced in 2014 from 27 million ha (FAO, 2017). The most important products from sugarcane are sugar, an important source of food energy, renewable energy in the form of bio-ethanol and electricity, and other by-products such as molasses. There is need to maximise yields due to an increasing demand for food and energy with a growing population amidst a limited (or declining) supply of suitable land and irrigation water for cultivation.

Breeding high yielding sugarcane cultivars is a resource-intensive and time-consuming process. The typical duration of the breeding cycle from crossing of the parents to release of a cultivar is between 11 and 20 years (Skinner et al., 1987; Zhou, 2013). Conventional sugarcane breeding consists of repeated cycles of selection of clones from very large populations grown in trials conducted in the main agro-climatic

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zones. Selection criteria are based on the family values for yield, growth vigour and disease resistance (early stages) and average yield data across sites and years (late stages). The use of physiological knowledge about desirable traits for high yields in breeding programs is rare (Skinner et al., 1987; Ghannoum, 2016; Jackson et al., 2016) because traits are often complex, difficult to measure, subject to genotype by environment interactions and not well characterized (genetic variability and heritability). This knowledge can potentially enhance breeding by identifying genotypes with high yield potential early in the breeding program when selection for yield is biased by inter-plot competition effects (Jackson and McRae, 2001). The prediction of phenotype from genetic (G) information could be hugely valuable, but is difficult because of the confounding influence of environmental (E) and management (M) factors. Process-based crop simulation models predict crop growth and development by simulating the dynamic responses of plant processes to E and M factors, as driven by G characteristics. This technology could be used to assist plant breeding by gaining a better understanding of GxExM interactions, and for identifying key traits for improved crop performance in target ExM scenarios. This modelling application is referred to as “trait impact modelling”.

Examples of sugarcane models include APSIM-sugarcane (Keating et al., 1999; Inman-Bamber et al., 2016), QCANE (Liu and Bull, 2001), DSSAT-Canegro (Inman-Bamber, 1991; Singels and Bezuidenhout, 2002; Singels et al., 2008) and Mosicas (Martiné and Todoroff, 2004). Although these models may use different algorithms and inputs to simulate specific processes, they use a similar simulation framework that consists of: (1) the formation of a crop canopy that intercepts solar radiation, (2) the conversion of intercepted radiation to biomass growth, and (3) the partitioning of biomass growth to different plant organs depending on the developmental stage. These processes respond to environmental input factors (e.g. solar radiation, temperature and soil water) and are controlled by the genetic characteristics of the given genotype. Genetic characteristics are represented in models by “genetic coefficients” or genetic trait parameters. Sugarcane development and canopy formation, in the absence of soil water and nutritional limitations, are generally controlled by thermal time requirements and allometric parameters, biomass growth by photosynthetic efficiency, and partitioning of biomass to stalks by a partitioning fraction that depends on the developmental stage.

Trait impact modelling studies have been carried out in a number of crops (e.g. Boote and Jones, 1986; Aggarwal et al., 1997; Boote et al., 2001; Suriharn et al., 2011; Khan, 2012; Casadebaig et al., 2016). Very limited work has been done for sugarcane. Inman-Bamber et al. (2012) used APSIM-sugarcane to identify desirable traits for water limited environments. The study found that increased rooting depth, reduced plant hydraulic conductance and increased transpiration efficiency leads to increased yields, while accelerated leaf and stalk senescence did not. Sexton et al. (2017) found that radiation use efficiency, number of green leaves and plant hydraulic conductance had the most influence on APSIM-sugarcane simulated yields. Both studies found that trait impacts depended on soil and climate conditions.

Two main issues have prevented the successful application of sugarcane models to support sugarcane crop improvement. The first is that models have not been thoroughly evaluated for their ability to accurately predict genetic trait impacts on yield. The theoretical studies by Inman-Bamber et al. (2012) and Sexton et al. (2017) with APSIM-sugarcane provided useful information, but also highlighted weaknesses. The second challenge is the lack of reliable trait parameter values and lack of knowledge regarding the extent of genetic variation. Sexton et al. (2016) pointed out that only 14 sugarcane cultivars were defined in APSIM, and many of these are no longer grown commercially. Jones and Singels (2008) provide Canegro trait parameter values for seven cultivars. Apart from the reference cultivar NCo376, the values for other cultivars are based on very limited data. More recently Marin et al. (2011) calibrated the Canegro model for two Brazilian cultivars, while Marin et al. (2015) calibrated the APSIM and Canegro models for a more recently released Brazilian cultivar. The lack of characterised cultivars can be ascribed to the difficult nature of reliably estimating trait parameter values from limited experimental data. Some of these parameters cannot be measured directly and can only be derived through indirect statistical calibration on associated data, while direct measurements are often extremely cumbersome and time consuming.

This problem could be addressed by (1) estimating values of appropriately defined genetic trait parameters using appropriate phenotyping procedures; and (2) evaluating and improving model capabilities for simulating observed genotypic differences in crop growth and yield.

The aim of this study was to test the hypothesis that an existing process-based sugarcane model (Canegro) can reliably predict genotypic differences in stalk dry mass yields observed in well-watered field trials using independently derived genetic trait information.

The specific objectives were to:

- estimate values of three key trait parameters for selected (14) genotypes from phenotypic data collected in a pot trial,
- compare simulated and observed SDM yield for a subset (9) of the same genotypes in four well-watered field experiments, and
- assess the role of the three traits in determining genetic differences in SDM yields

Achieving these objectives will be a first step in demonstrating the potential of crop models and physiological trait information to enhance sugarcane breeding.

2. Materials and methods

2.1. The model

The Canegro sugarcane model (Inman-Bamber, 1991; Singels et al., 2008; Jones and Singels, 2018) is a well-established sugarcane crop simulation model which forms part of the Decision Support System for Agrotechnology Transfer (DSSAT) crop modelling software package (Jones et al., 2003). Improvements have been made to the simulation of biomass accumulation and partitioning (Singels and Bezuidenhout, 2002; Singels et al., 2005; Jones and Singels, 2018), and atmospheric CO_2 and high temperature impacts (Jones and Singels, 2018). A comprehensive scientific documentation of the model can be found in Jones and Singels (2018), while Singels (2014) provides an overview of approaches to simulate the main development and growth processes.

2.2. Phenotyping

2.2.1. Experimental details

The study was conducted in the South African Sugarcane Research Institute (SASRI) rainshelter facility (29°42′40″S; 31°02′0″E) at Mount Edgecombe, South Africa. Fourteen genotypes were selected based on the availability of suitable field trial data, as well as to represent widespread diversity in field performance traits and genetic makeup. Genotypes N12 and N19 share NCo376 as the female parent, while N25 has N14 as the male parent. None of the other genotypes shared common parents. Single-budded setts were sprouted in a synthetic medium of river sand, sugarcane filter press and vermiculite (4:2:1) under controlled conditions with the average daily temperature of 30 °C. Thereafter, four setts were transplanted into each experimental pot (80 l capacity; internal diameter of 0.44 m and height of 0.64 m) containing the same synthetic growth medium on 3 October 2014. The trial design consisted of a randomised complete block design of five replications of 14 genotypes (70 pots in total), with guard pots placed around the perimeter to minimise edge effects. The trial was well-watered, with drip irrigation applied up to three times daily, with amounts ranging from 335 ml to 1000 ml per application, as determined by monitoring of soil water status in selected pots. Pots were fertilised to