

## Development of the Generic APSIM Cereal Template to Enhance Functionality of Whole-Plant Modelling

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### Abstract

The utility of crop growth and development models for investigating emergent behaviour of complex gene-to-phenotype interactions is limited if such models rely on algorithms that describe key aspects of crop growth and development too simply. While this approach has proven adequate for predicting crop responses to agronomic management and some major genetic factors (e.g. physiological maturity), attempts at connecting these frameworks with drivers of genetics that underpin complex traits have had little success or impact on crop improvement. In further development of the generic APSIM Cereal model we have introduced aspects of physiological development at a more detailed level so that complex phenotypic responses become emergent properties of the model dynamics. At the same time, we intend to retain model simplicity by dealing with crop growth and development processes at a mostly similar level (organ-plant-canopy) to that used in conventional agronomic models. However, we argue that more biologically-grounded quantification of the underpinning processes will provide more robust avenues to link plant response to molecular genetics. There is some evidence for this from a range of studies on adaptation of crops to drought stress, where the generic APSIM cereal template has been employed. In this paper, we present an outline of the template framework and detail the approach to modelling nitrogen dynamics (uptake, allocation, retranslocation) in sorghum. This provides an example of how genetic variation linked to specific attributes of the plant (e.g. height) can generate emergent phenotypic differences in leaf area retention associated with nitrogen. We consider that the generic APSIM Cereal template provides a good framework to develop and enhance the functionality of whole-plant modelling required to help bridge the gene-to-phenotype gap.

### Key Words

Plant model, genotype-to-phenotype, prediction, emergent properties, crop physiology, APSIM

### Introduction

Progress in crop improvement and particularly molecular approaches to plant breeding are limited by our ability to predict plant phenotype based on its genotype, especially for complex traits like water productivity. This genotype-to-phenotype (G-to-P) prediction problem is one of the major roadblocks to effective use of advances in molecular technologies and remains one of the fundamental challenges in biology (Cooper et al., 2002). Robust explanatory plant models have the potential to underpin G-to-P prediction by linking their coefficients with the genomic regions known to be associated with complex multi-genic traits. However, to be effective in discriminating the linkage of these traits to model coefficients, it is necessary to reduce (or remove) the environmental and genetic context dependencies related to the phenotypic trait(s) that they generate (Hammer et al., 2008, these proceedings).

Crop models have been used successfully to facilitate decision making by crop managers (Carberry, 2001; Nelson et al., 2002), but Hammer et al. (2002) suggested that greater explanatory power was required for their effective application in both understanding and advancing genetic regulation of plant performance and plant improvement. Agronomic models contain a mix of descriptive and empirical approaches that suffices for their application in decision/discussion support for crop management. Adequate prediction of resource use, crop growth and yield can be obtained with algorithms that describe aspects of crop growth, such as nitrogen responses. However, a physiological framework that introduces

greater explanatory power to models, while not introducing undue complexity, is required for effective use in molecular plant breeding so that phenotypic attributes emerge as consequences of the model dynamics.

In this paper we present the concepts, structure and status of the generic APSIM cereal template, which has been designed to facilitate the G-to-P modelling required for crop improvement applications, while retaining capacity for agronomic applications. The concept of simulating complex genotypic traits as emergent phenotypes of model dynamics is demonstrated via an example showing how gene effects for height impact on nitrogen dynamics in sorghum.

### APSIM Cereal Template

The APSIM cereal model template has been developed to provide a platform to easily integrate knowledge from current research into a validated model using modern programming techniques in an efficient way. The APSIM generic crop model (Wang *et al.* 2002; Keating *et al.* 2003) was used as a basis for the development of the APSIM cereal model template. The sorghum module, which was written in Fortran and based on the fusion of earlier models and concepts (Birch *et al.*, 1990; Chapman *et al.*, 1993; Hammer *et al.*, 1994), was redesigned in an object-oriented format (Figure 1). Plant parts and processes are simulated as classes, and each class performs a function, independent of the parent class or other classes. The template is focused at organ scale and uses concepts of (1) potential organ growth to define demand for resources and (2) resource capture to define potential supply. There is scope to operate at individual organ scale (e.g. individual leaf, grain, etc) by breaking down organ pools into cohorts. Allocation among organs within the plant is handled via an arbitrator, which contains rules and priorities that are dependent on plant status.

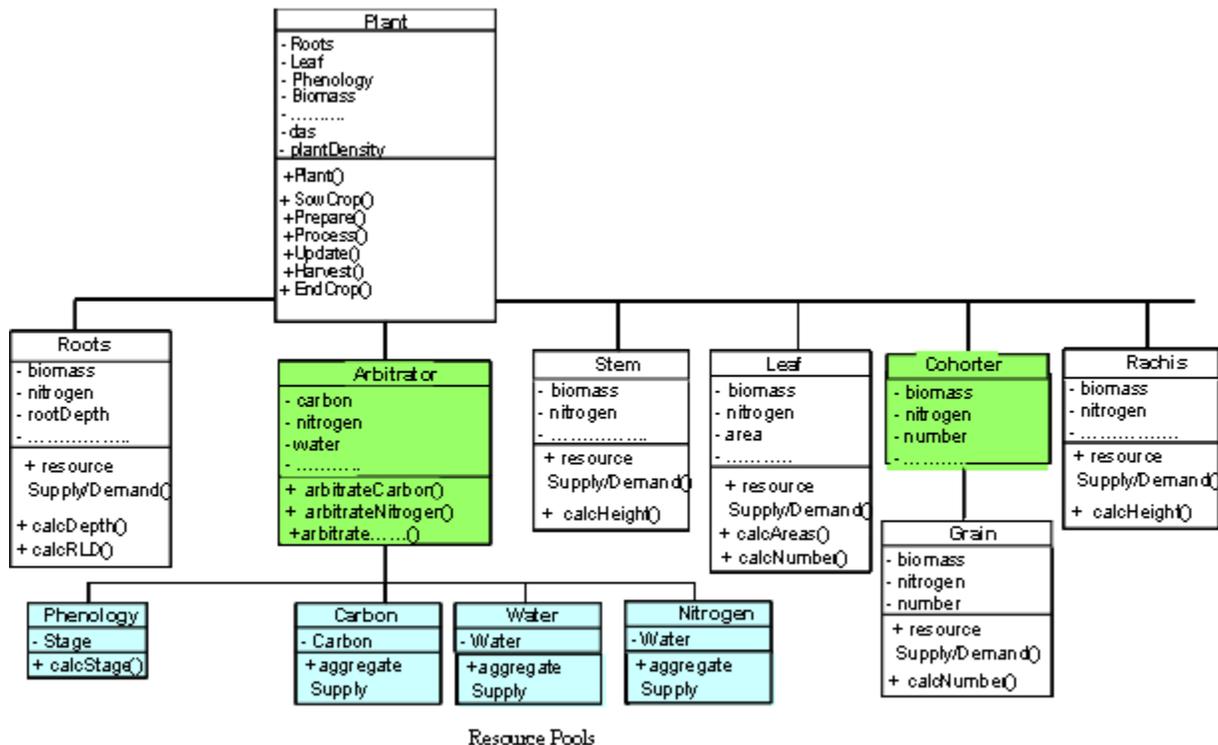


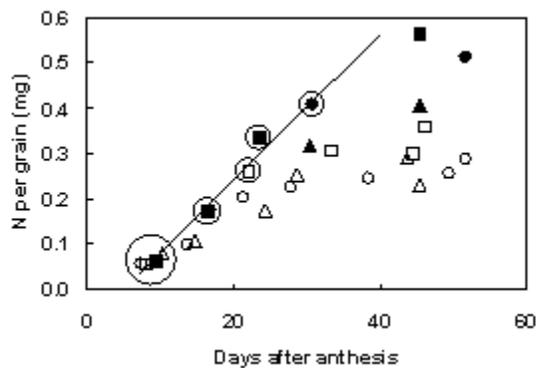
Figure 1. The object-oriented structure of the APSIM cereal model template.

The cereal template provides a platform to allow the study of an individual process while not unintentionally affecting the operation of others. It is then possible to examine effects of variation in the parameters of the trait processes, which might reflect genetic differences, on the overall performance of the crop under differing management or environmental scenarios. Further, the objects and sub-processes can be inter-changed to test the effectiveness of alternate approaches to modelling specific processes. This facilitates pursuing a more explanatory approach to modelling the underlying physiology. For example, in order to better explore connections with genetic effects, Chenu *et al.* (2008) replaced the conventional approach to modelling of plant leaf area development in maize based on a function describing the final leaf size distribution, by a method using expansion rate of individual leaves, which was dependent on a combination of genotype and environment. In this way the leaf size distribution was generated as an emergent consequence of the model dynamics.

## Height and N Dynamics in Sorghum

### *Crop N-dynamics module*

Originally, the descriptive approach used to model nitrogen demand relied on ‘telling’ the model the expected range of nitrogen concentration for each plant part at each phenological stage. As this was based on experimental observations, accurate predictions resulted. In the APSIM cereal template, this is replaced by a more detailed explanatory algorithm driven by an approach based on specific leaf nitrogen (SLN), which relates more directly to the photosynthetic capacity of a canopy. In this approach, pre-anthesis N-demand of individual organs is calculated by the demand process in the individual plant part object on a daily time step. Minimum structural N for stem and rachis is first calculated from their growth and minimum [N]. The N demand of new leaves is simulated via a target SLN and leaf area growth, independent of stage of development (van Oosterom *et al.*, in press a). Any N available beyond these amounts is then allocated to leaves and stems. N-uptake from the soil is a two part process; first mass flow is calculated as a passive uptake with the transpiration stream; second, diffusion then provides an active uptake proportional to the demand of the plant. A maximum N uptake rate, which is based on experimental observations and depends on soil N content, is used to limit active uptake. Timing of cessation of N uptake during grain filling is a genotype specific variable in accord with experimental observations. Post-anthesis grain N demand depends on grain number, which is estimated via a function of crop growth rate around anthesis. In the first part of grain filling, N uptake rate per grain is fixed (Figure 2) as this relates to the accumulation of metabolic proteins. Subsequently, grain N demand is a fraction of C-uptake rate per grain to model accumulation of storage proteins. Based on analysis of experimental data (van Oosterom *et al.*, in press b), N-translocation from vegetative plant parts to supply grain N is first obtained from the stem, and then from the leaves in a source-driven first order kinetic reaction that represents enzyme activity.



**Figure 2. N uptake rate per grain during grain filling for three hybrids ( $\Delta$  $\square$  $\circ$ ) under high (closed) and low (open) N supply. The regression line represents maximum N uptake rate per grain.**

## The effect of height genes on N-dynamics in sorghum

Studies on sorghum hybrids differing in height genes have shown that a tall, single dwarf sorghum has a higher radiation use efficiency (RUE) and greater carbon partitioning to the stem than a short, triple dwarf sorghum, but total shoot N uptake is the same (unpublished data). Hence, there is no direct association of height with N. How do height genes affect crop N-dynamics?

To simulate the overall effect of plant height genes in sorghum on N-dynamics via the effects on RUE and dry matter allocation, three hypothetical hybrids were parameterised:

**Hybrid 1:** standard short hybrid (low RUE (1.25 g/MJ), low partitioning to the stem)

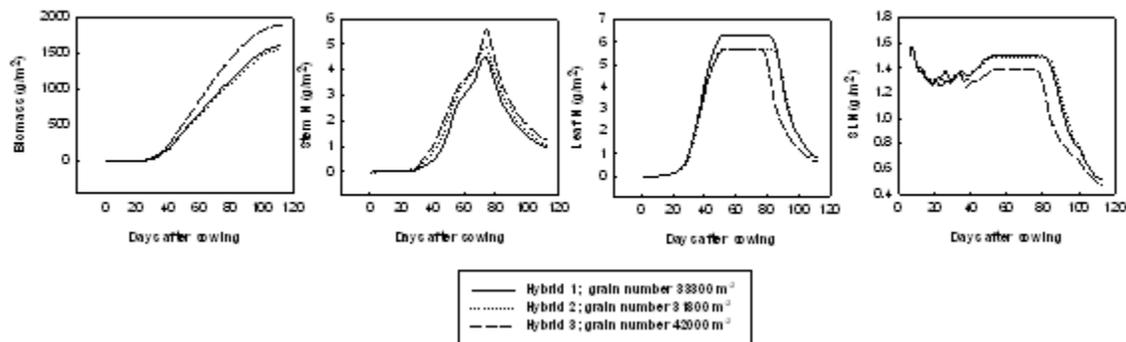
**Hybrid 2:** short hybrid (low RUE), with the higher partitioning of a tall hybrid.

**Hybrid 3:** tall hybrid (high RUE (1.60g/MJ) and high dry matter partitioning to the stem)

The simulated crop was sown on 15 Dec 1995 at Dalby with soil N of 25 kg N/ha, and three applications of 50 kg N/ha (sowing, initiation, anthesis). Simulated crops did not experience any drought stress.

The model dynamics generated emergent consequences of the height genes on the timing of leaf N retranslocation and hence, leaf senescence (i.e. staygreen), during grain filling (Figure 3). By firstly adding only the enhanced partitioning to stem (hybrid 2 vs. hybrid 1), the simulated higher stem mass required more N. This caused reduced leaf N and SLN, which generated slightly reduced growth and hence, grain number (Fig. 3). As a consequence the stem N was able to meet grain N demand for longer resulting in delayed onset of leaf N translocation (2 days). By next adding the higher RUE of the tall type (hybrid 3 vs. hybrid 2), the higher growth rate generated higher grain number, so that the increased N demand caused earlier onset of leaf N translocation (6 days, Fig. 3). Hence, the overall effect of removing the dwarfing genes generated lower SLN and earlier onset of leaf senescence, both of which were observed experimentally (van Oosterom et al., in press b).

The example highlights the point that modelling genetic variation linked to specific attributes of the plant (e.g. height) can generate emergent phenotypic differences in other crop attributes (e.g. leaf area retention associated with nitrogen) **if** the underpinning process connections are incorporated realistically. This functionality can be incorporated into any appropriate modelling platform, but it would have been impossible to generate the emergent properties of this functional whole plant modelling with the original descriptive approach. The model used retains a simplicity not far removed from the original.



**Figure 3. Simulated biomass, stem N content, leaf N content and SLN for the 3 contrasting hypothetical hybrids.**

## Concluding Remarks

It is possible to satisfy needs for both understanding and prediction in crop modelling while retaining simplicity. The generic APSIM cereal template has been designed to facilitate this. It is a suitable

approach to advance the G-to-P modelling required for crop improvement applications while retaining capacity for agronomic applications.

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