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Modelling framework for scaling up genetic processes to predict tomato fruit yield and quality

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Background

Models for predicting fruit yield rarely incorporate information at scales below plant organ level. Recent research on tomato genomics elucidates the genetic basis of fruit growth and quality, but the mechanistics of the genotype x phenotype interactions are largely unknown.

Objectives

- to predict yield and quality of tomato fruit by up scaling (sub)cellular processes affected by genes and environment
- to explain fruit growth by incorporating genomic information into a mechanistic model on cell and tissue physiology

Methods

- Experiments on cells and fruits have been carried out to estimate parameter values of the model (Fig. 1);
- The processes of gene-regulated cell cycling are related to environmental factors and incorporated into an existing module for cell division;
- The simulated cell number is incorporated into a cell expansion model that uses turgor driven growth combined with sugar dynamics (Fig. 1);
- The expansion model is aggregated to fruit level and coupled to an existing crop growth model to receive data on assimilate supply per fruit.

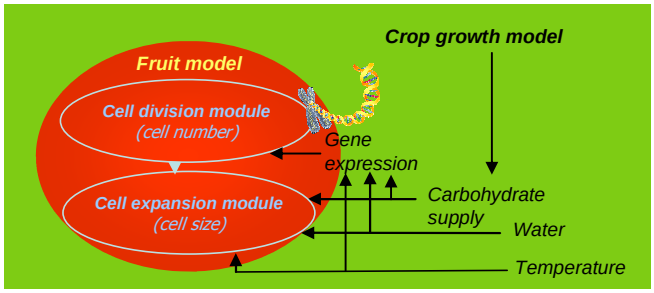

Figure 1. Modelling approach that considers different scales.

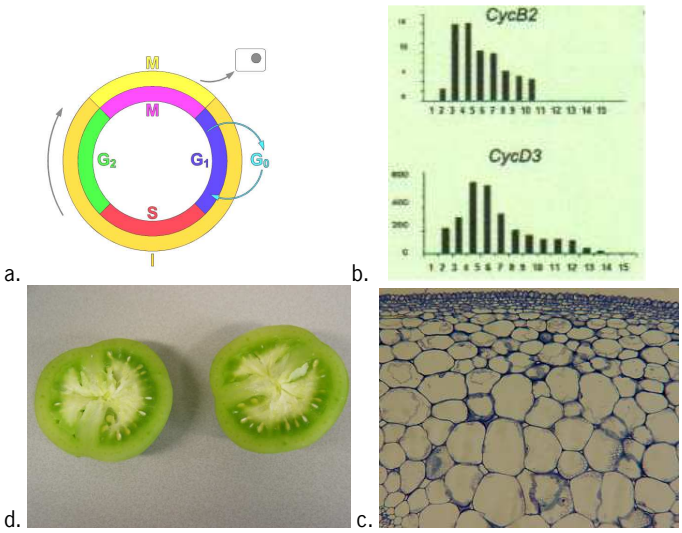

Figure 2. Illustration of (a) the cell cycle, (b) measurements of expression of the cell cycle regulators during fruit development, (c) simultaneous measurement of cell division and expansion, and (d) a specific fruit phenotype.

Results

Experiments

Fruit growth response to fruit load differed significantly between isogenic lines (Table 1). This will be linked to gene expression levels in the different growth stages.

Genotype *Fruit load*	Genotype1 *low/high*	Genotype2 *low/high*	Genotype3 *low/high*
Size (mm)	51/44	63/56	68/57
Mass (g)	50.5/35.0	104.6/72.3	108.4/78.2

Table 1. Genotypes with small-sized (Genotype 1), medium-sized (Genotype 2) or large-sized (Genotype 3) fruits have a different growth response to two different fruit loads, showing a significant GxE interaction.

Modelling

Differential equations on cell cycling have been programmed in Matlab and are now being linked to growth processes at tissue and organ scales.

Prospects

A novel and challenging approach is used that scales up sub cellular, gene related processes to organ level. This will show the quantitative effects of gene x environment interactions on fruit growth and quality.

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