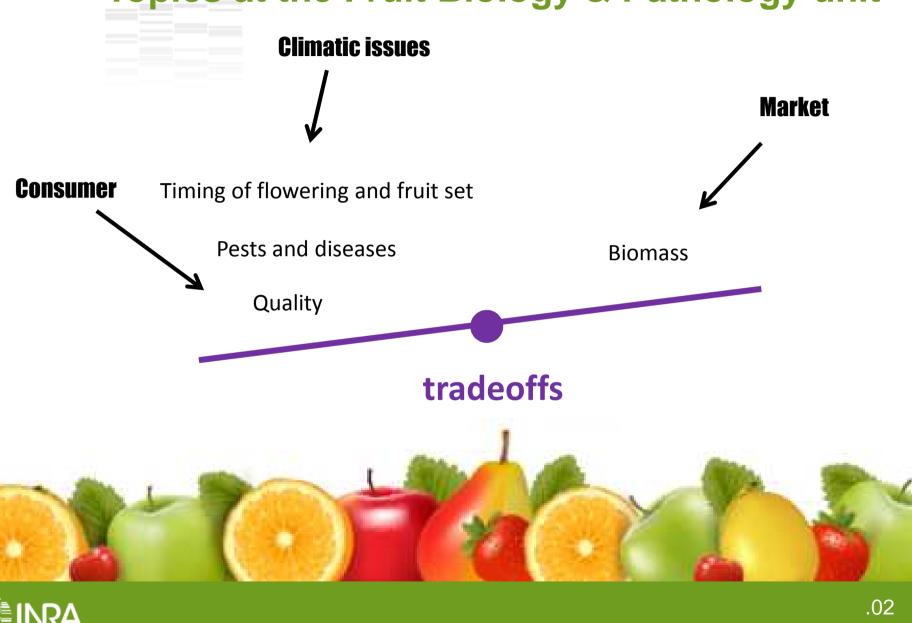


Topics at the Fruit Biology & Pathology unit



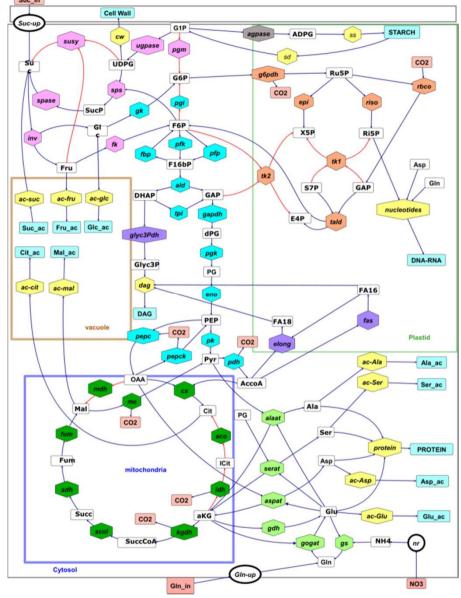


The engine that provides building blocks and energy to growth

- o biomass production and quality
- o stress resistance
- o signalling

■ Where are we?

- o topology getting well known
- knowledge about individual steps improving
- o Very little known at the network level





Manipulating enzymes in order to enhance fruit production or quality?

Table III.

Role of carbohydrate genes in tomato fruit derived from transgenic manipulation.

Enzyme	Manipulation ¹	Fruit phenotype	Reference	
Apoplastic invertase	RNAi², CaMV³	\uparrow sucrose, \downarrow hexose, reduced fertility, fruit set and fruit size	Zanor et al. [25]	
Acid invertase ⁴	Antisense ² , CaMV	\uparrow sucrose, \downarrow hexoses and fruit size	Ohyama <i>et al.</i> [24]; Klann <i>et al.</i> [17]	
Sucrose synthase 15	Antisense, CaMV	\downarrow sucrose unloading at 7 days after anthesis, \downarrow fruit set	D'Aoust et al. [101]	
Sucrose synthase 15	Antisense, 2A11 ⁶	No detectable change in starch or sucrose levels	Chengappa et al. [102]	
Hexokinase 1	Ectopic <i>AtHK</i> ⁷ , <i>CaMV</i>	\downarrow fruit size, seed dry weight, starch content, total soluble solids at breaker stage and red ripe stage	Menu <i>et al.</i> [22]	
Fructokinase 1	Antisense, CaMV	Delayed flowering, ↑ fruit sucrose	Odanaka et al. [23]	
Fructokinase 2	Antisense, CaMV	\downarrow seed number, flower and fruit set, \uparrow fruit sucrose	Odanaka et al. [23]	
Vacuolar H+-ATPase	Antisense, 2A11	\downarrow fruit weight, seed number, \uparrow sucrose	Amemiya et al. [103]	

¹ Transgenic manipulation and gene promoter used.

Beckles et al (2012) Fruits 67: 49-64

Transgenesis and yield: what are our targets?

Helen L. Jenner

Sainsbury Laboratory, John Innes Centre, Colney Lane, Norwich NR4 7UH, UK

Attempts to increase

yield of some agronomically important crops using this approach have highlighted the inherent complexities of modulating plant metabolism.



² RNAi and antisense methods are used to repress gene expression.

 $^{^{3}}$ Cauliflower Mosaic Virus 35S gene promoter.

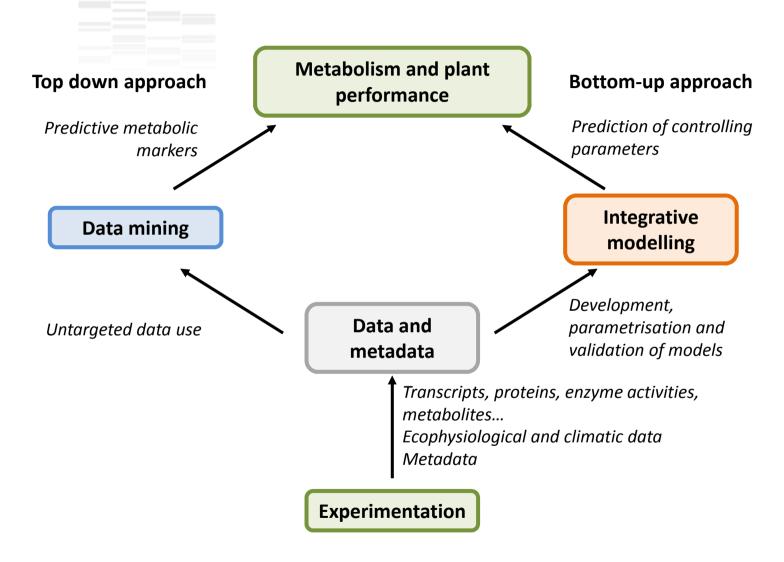
⁴ Both apoplastic and vacuolar acid invertase.

⁵ Isoform designation from Goren et al. [104].

 $^{^{\}rm 6}$ Fruit-specific gene from to mato ("2A11") promoter.

 $^{^{7}}$ Ectopic overexpression of ${\it Arabidopsis}$ hexokinase 1.

Scientific strategy







The top down approach

From metabolic traits to plant performance to genes



Metabolic traits as powerful biomarkers in maize

genetics

Genomic and metabolic prediction of complex heterotic traits in hybrid maize

Christian Riedelsheimer¹, Angelika Czedik-Eysenberg², Christoph Grieder¹, Jan Lisec², Frank Technow¹, Ronan Sulpice², Thomas Altmann³, Mark Stitt², Lothar Willmitzer^{2,4} & Albrecht E Melchinger¹

Table 1 Summary of whole-genome and metabolic prediction

			SNPs			Metabolites		
GCA	$h_{\rm GCA}^2$	$w_{\rm M}^2$	$r_{(\hat{y},y)}$	$r_{(\hat{g},g)}$	s.d.	$r_{(\hat{y},y)}$	$r_{(\hat{g},g)}$	s.d.
Dry matter yield	0.89	0.73	0.74	0.78	0.07	0.48	0.60	0.11
Plant height	0.95	0.72	0.70	0.72	0.06	0.52	0.63	0.10
Dry matter concentration	0.96	0.72	0.78	0.80	0.07	0.66	0.79	0.06
Female flowering	0.98	0.71	0.80	0.81	0.06	0.67	0.80	0.07
Starch content	0.93	0.73	0.70	0.73	0.07	0.59	0.71	0.07
Sugar content	0.94	0.74	0.69	0.72	0.06	0.55	0.67	0.09
Lignin content	0.82	0.73	0.72	0.80	0.05	0.50	0.64	0.10

Predictive abilities $r_{(i,y)}$ and prediction accuracies $r_{(i,p)}$ averaged over all cross-validation runs and their s.d. are shown for models using either SNPs or metabolites. Heritabilities of the predicted traits (h_{GCA}^2) are given as well as the repeatabilities of the used metabolic profile (w_W^2) calculated as the weighted sum of the repeatabilities of the individual metabolities (see Online Methods).

- 285 x 2 hybrids grown in several fields
- 130 metabolites measured at an early vegetative stage
- 56k SNPs
- Both groups provide prediction accuracies of up to 80% for agronomical traits using ridge regression—best linear unbiased predictions (RR-BLUP)
- Single metabolites correlate only weakly
- Predictions were made within an experiment



Can we predict agronomical traits using metabolic phenotyping?



Maize hybrids grown at Phenoarch in Montpellier
-> Leaf samples -> Metabolomics





Same genotypes evaluated in the field -> Yield









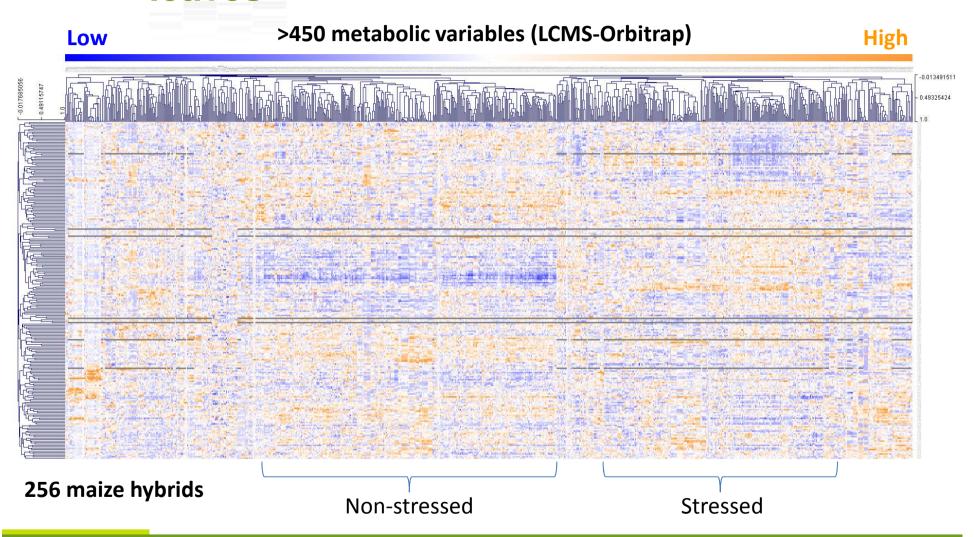






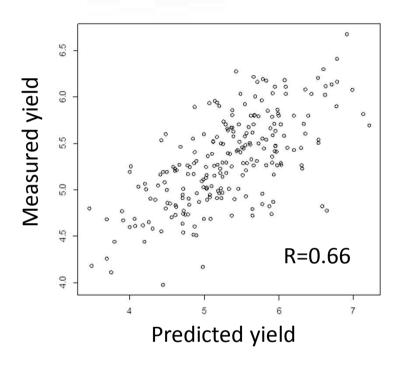


Untargeted metabolic profiling in maize leaves





Metabolomics-based yield prediction



Partial least squares regression:

- 256 maize hybrids
- Input: 230 metabolic variables measured in leaf samples collected in the greenhouse
- Output: average yield under optimal conditions (14 field experiments)

- **▶** Predict yield for various growth scenarios
- ► Use linear models in order to select the best biomarkers
- Search for QTLs





The bottom-up approach

From modelling to parameters to plant performance



Systems Biology

- Stoichiometric
- Kinetic
- Ecophysiological
- Statistical analysis

Parameterisation

Validation

Models

Data prediction

Data production

Experiments

Questions

Knowledge Targets for improvement

Fruit as the model system

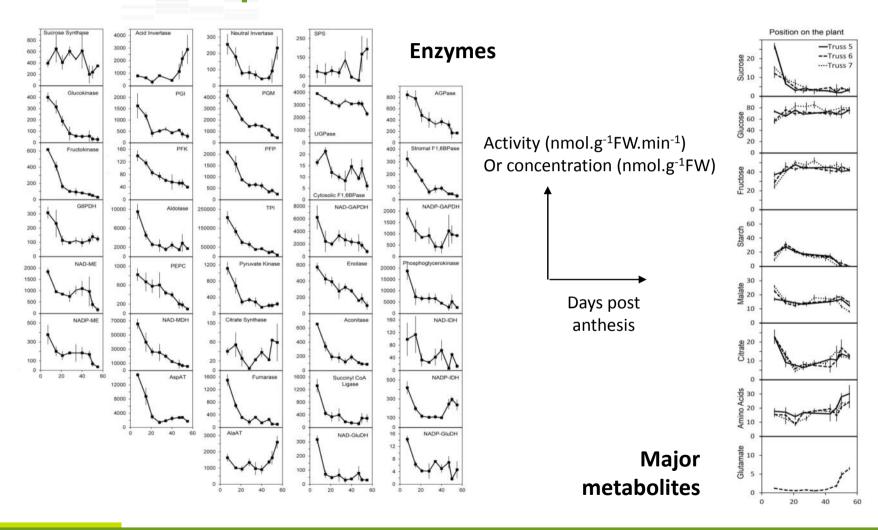
- Parameters (enzyme activities...)
 Internal variables (metabolic
 Plant :
- Internal variables (metabolic intermediates...)
- External variables (biomass composition)

- Plant and fruit growth
- Climatic and ecophysiological data
- Collection of fruit samples



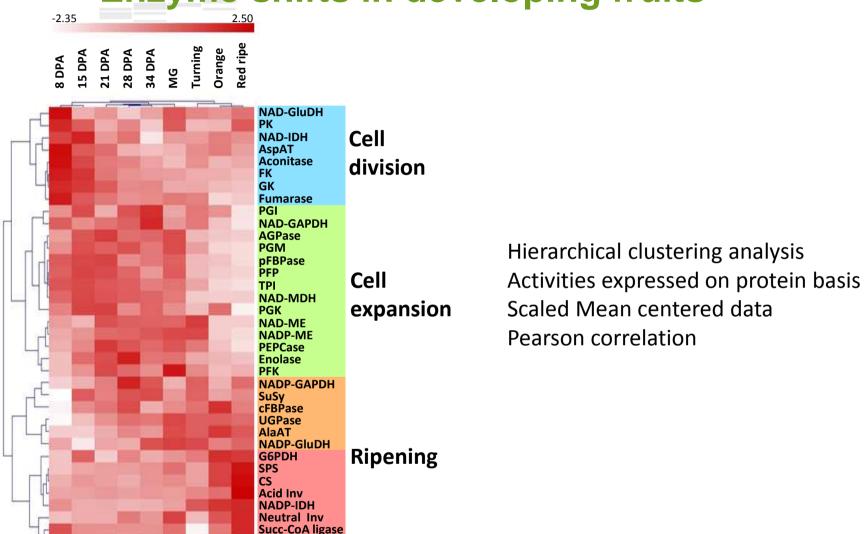


Metabolic profiles throughout fruit development



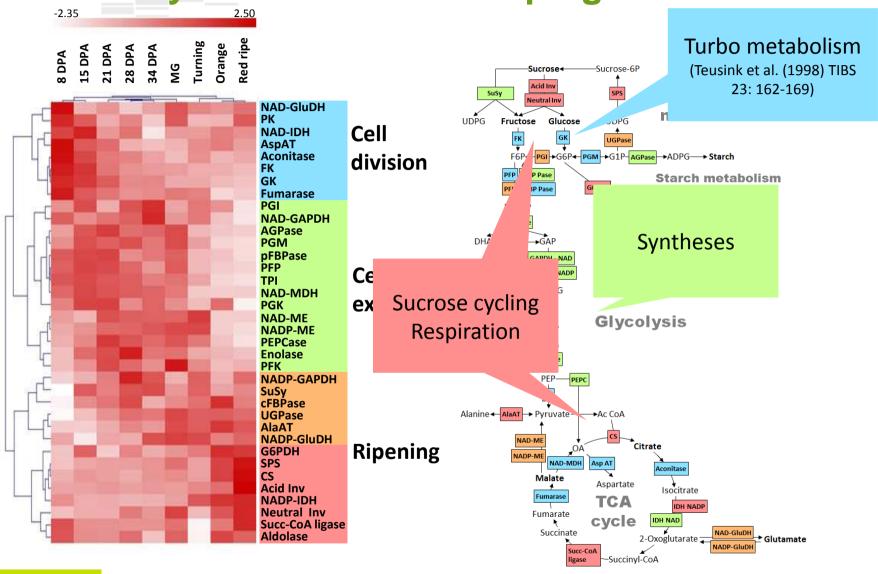


Enzyme shifts in developing fruits



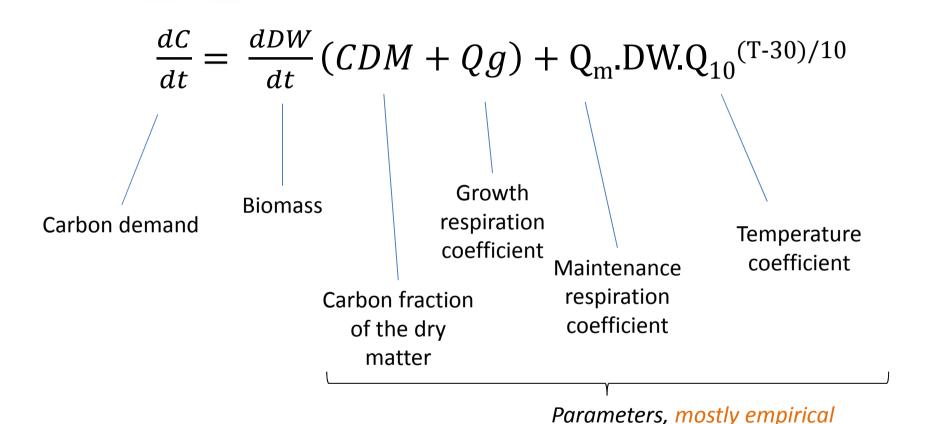


Enzyme shifts in developing fruits





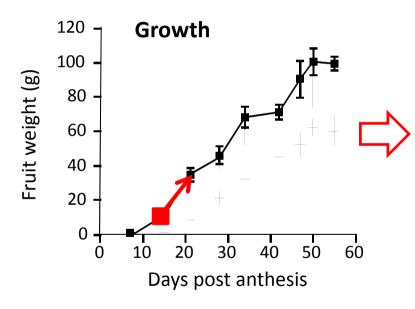
Ecophysiological modelling to link carbon demand and growth using TOMGRO

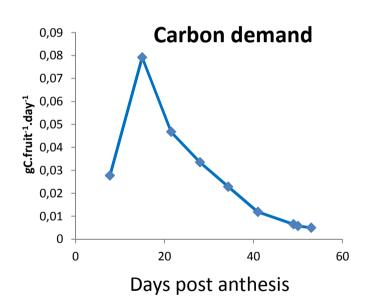




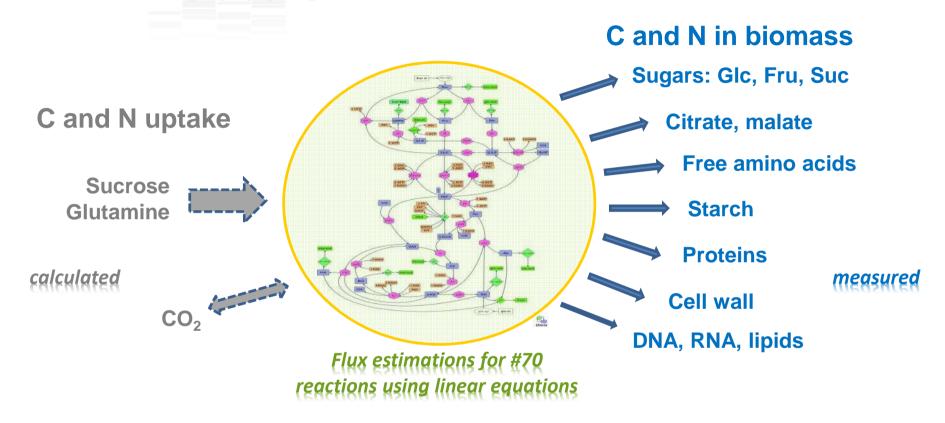
Ecophysiological modelling to link carbon demand and growth Climatic data

 $\frac{dC}{dt} = \frac{dDW}{dt}(CDM + Qg) + Q_{m}.DW.Q_{10}^{(T-30)/10}$





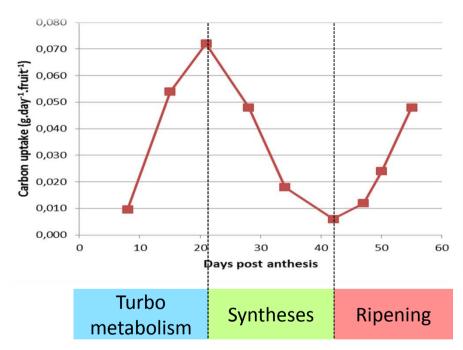
Stoichiometric model of fruit central metabolism



- All cells similar, pericarp homogenous
- **Assumptions:**
- Steady state at each of the 9 stages of development
- Objective function= Principle of flux minimization (Holzhütter 2004)

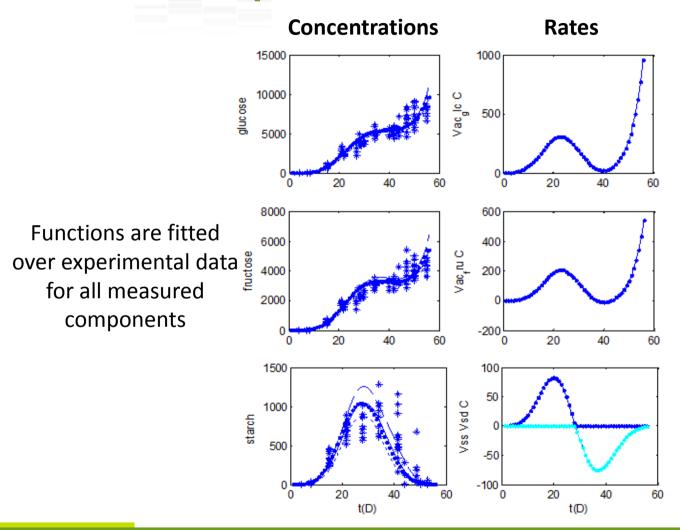


Estimation of the carbon demand



Prediction matches interpretation of enzyme profiles

Calculating fluxes at any time during fruit development

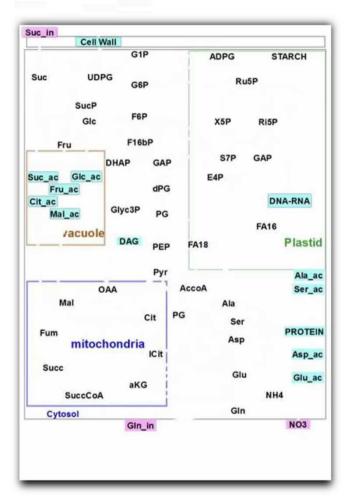


This enables the calculation of the corresponding fluxes at any time during fruit development

A time course can be considered as a succession of steady-states



Flux map throughout fruit development



Cell division: import of sugars and organic acids into the vacuole

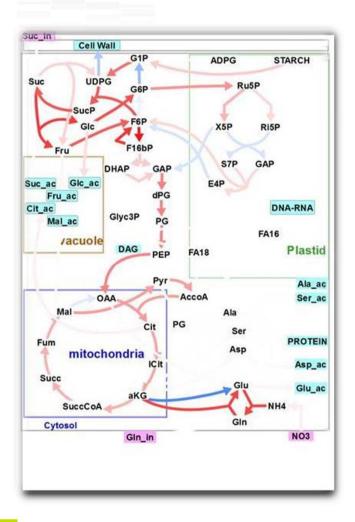
Cell expansion: slowing down of most fluxes, accumulation of starch

Breaker stage: a sudden metabolic burst following starch degradation

Ripening: reactivation of sugar and citrate import into the vacuole

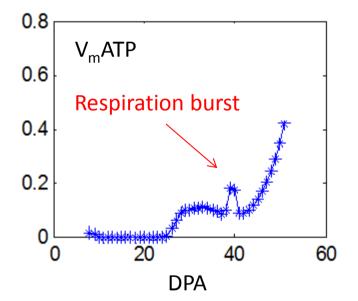


Respiration climacteric as an emergent property of the modelled system



ATP used for maintenance:

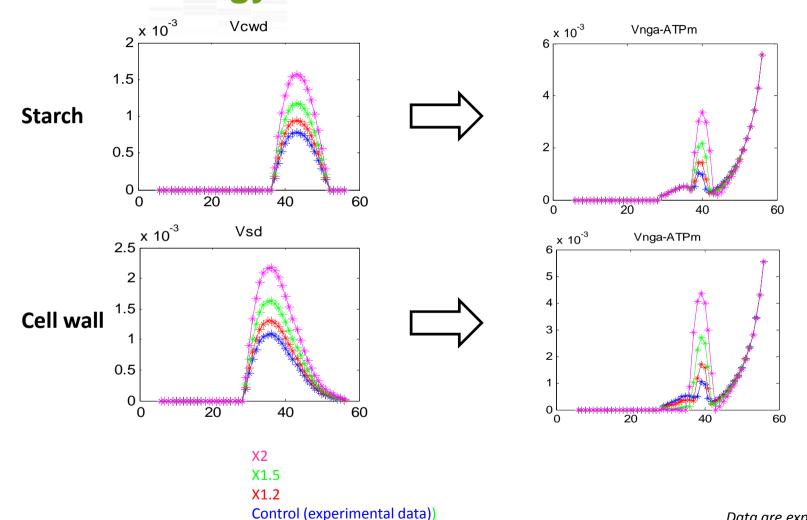
$$V_{m}ATP = V_{total}ATP - V_{biomass}ATP - V_{metab}ATP$$



ATP is known to increase at early ripening stages in various fruits (Brady 1987)

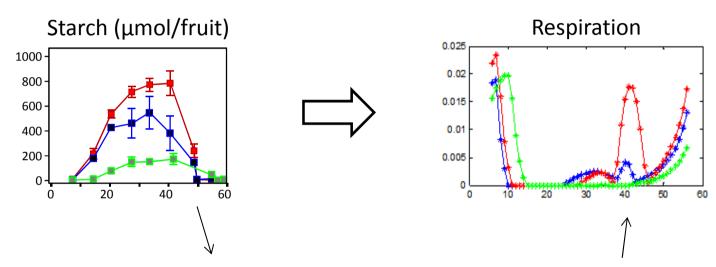


Starch and cell wall degradation feed the energy burst





The respiration climacteric buffers energy



Starch is degraded very quickly, leading to a massive energy boost

- Total protein increases and central metabolism is reprogrammed
- But there is no more growth
- Energy in excess probably needs to be dissipated...

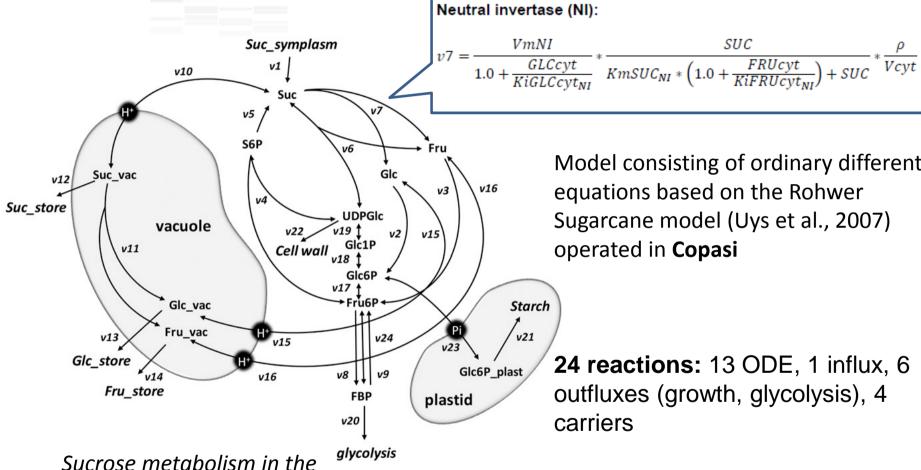
Water stress (50% decrease in irrigation)

Control (optimal conditions)

Shading (60% decrease in photosynthetically active radiation)



Kinetic modelling of metabolism



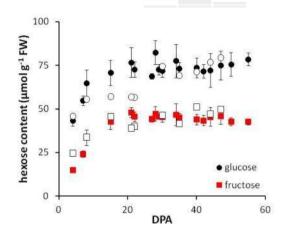
Model consisting of ordinary differential equations based on the Rohwer Sugarcane model (Uys et al., 2007) operated in Copasi

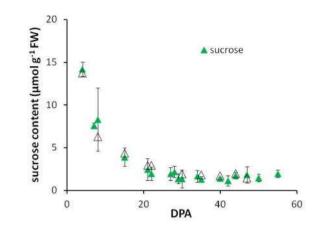
24 reactions: 13 ODE, 1 influx, 6 outfluxes (growth, glycolysis), 4 carriers

103 parameters

pericarp of tomato fruits

Model optimisation



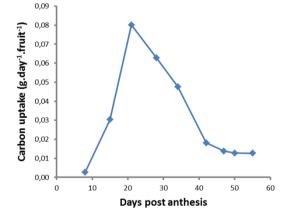


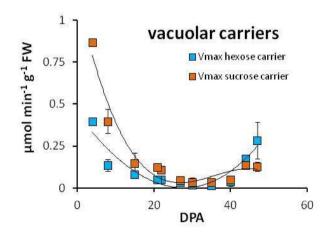
Variables

Open symbols represent predicted data

At each developmental stage, the 3 unknown parameters (C_uptake and sugar transport capacities) were optimized using a random search algorithm to fit the measured sugar content of the pericarp

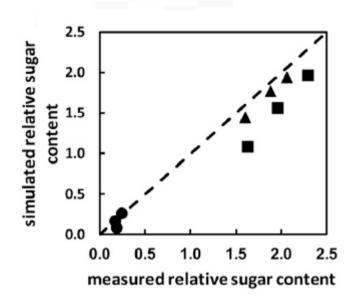








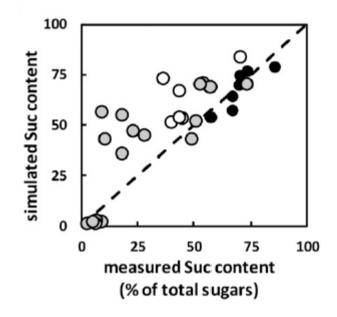
Model prediction: vacuolar invertase





- Glucose
- ▲ Fructose

Data from Steinhauser *et al.* (2010) and Carrari *et al.* (2006); 4 stages of fruit development

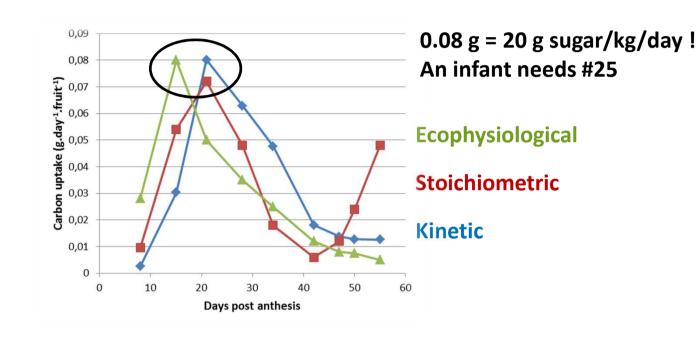


- Acid invertase antisense *S. Lycopersicum*
- O Solanum chmielewskii
- S. Chimielewskii x S. Lycopersicum introgression lines

Data from Klann et al. (1996) and Yelle et al. (1988, 1991)



Model cross-validation





Fruit abortion

"young tomatoes that fall before they ripen"

Message d'origine

Stephanie C (91) 01/08/2011 à 22:40

0 iQ 0 iQ

Good evening, I spoke with a colleague who has a serious problem with his tomato plants, they make beautiful clusters of flowers, small tomatoes grow then and they fall one after the other. As a result, he has very few tomatoes this year. Does it come from watering, weather? Have you ever encountered this problem? Thanks for your help.



A net intercepting 60% of the light (PAR) was installed during fruit growth:

- Nearly 100% of fruits at cell division stage aborted
- About 100% of fruits at cell expansion stage survived
- ► Improve yield by removing sinks of low value



Blossom end rot

- Non-pathogenic necrosis appearing at the bottom of growing fruits that provokes up to 50% losses
- Calcium often incriminated but probably multifactorial: drought, high temperatures, nutrient deficiencies...
- Turbo metabolism could be involved
- ► Control temperature as well as water and nutrient supply
- ► Breed for varieties having growing fruits with high levels of antioxidants











Acknowledgements

Metabolism Group Fruit Biology & Pathology Unit



Plant growth & ecophysiological measurements: Whole group

Metabolomics: Olivier Fernandez, Thierry Berton, Annick Moing, Dominique Rolin, Stéphane Bernillon, Mickaël Maucourt, Catherine Deborde, Daniel Jacob, Cécile Cabasson, Léa Roch

Enzyme profiling: Benoit Biais, Guillaume Ménard, Patricia Ballias, Mickaël Maucourt, Cédric Cassan

Subcellular compartmentation: Martine Dieuaide, Marie-Hélène Andrieu

Modelling: Sophie Colombié, Bertrand Beauvoit, Martine Dieuaide, Isma Belouah, Alice Destailleur

Collaborators

Maize: François Tardieu, Claude Welcker & colleagues (INRA-Montpellier), Fruit Tomato: Invenio, Jean-Pierre Mazat & Christine Nazaret (Bordeaux University)

This work was supported by INRA, EU DROPS, ANR Amaizing, Erasysbio+ FRIM, ANR FRIMOUSS

