

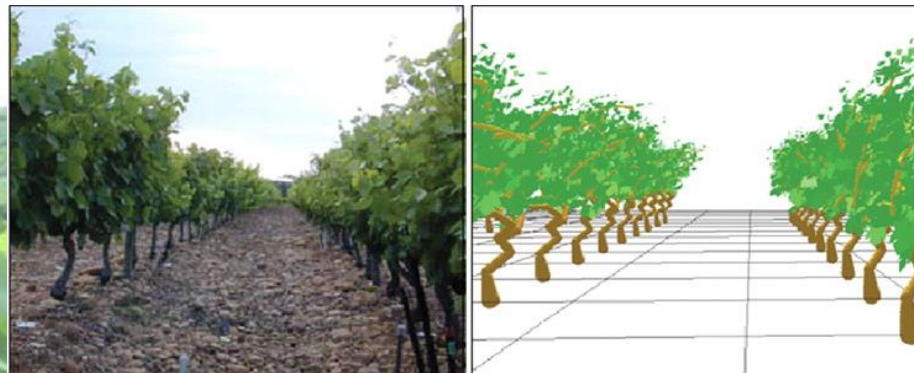
CLIMWINE International Symposium – April 10>13, 2016 – Bordeaux

# Process-based models for analysing grapevine genotype adaptation to climate changes: issues and challenges

**Philippe Vivin**

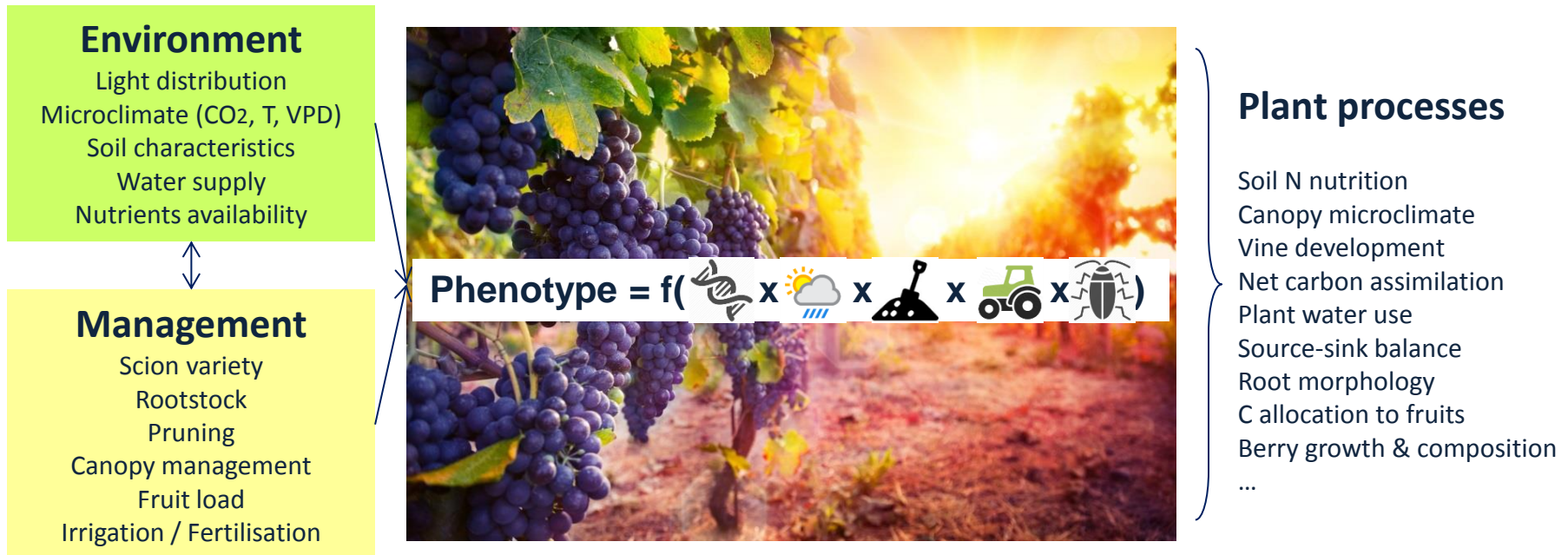
[vivin@bordeaux.inra.fr](mailto:vivin@bordeaux.inra.fr)

E. Lebon, Z. Dai, E. Duchêne, I. Garcia-Cortazar-Atauri, E. Marguerit, A. Coupel-Ledru, A. Parker, A. Peccoux, J. Zhu, P. Pieri, T. Simonneau, C. van Leeuwen, S. Delrot, N. Ollat



# Climate change context

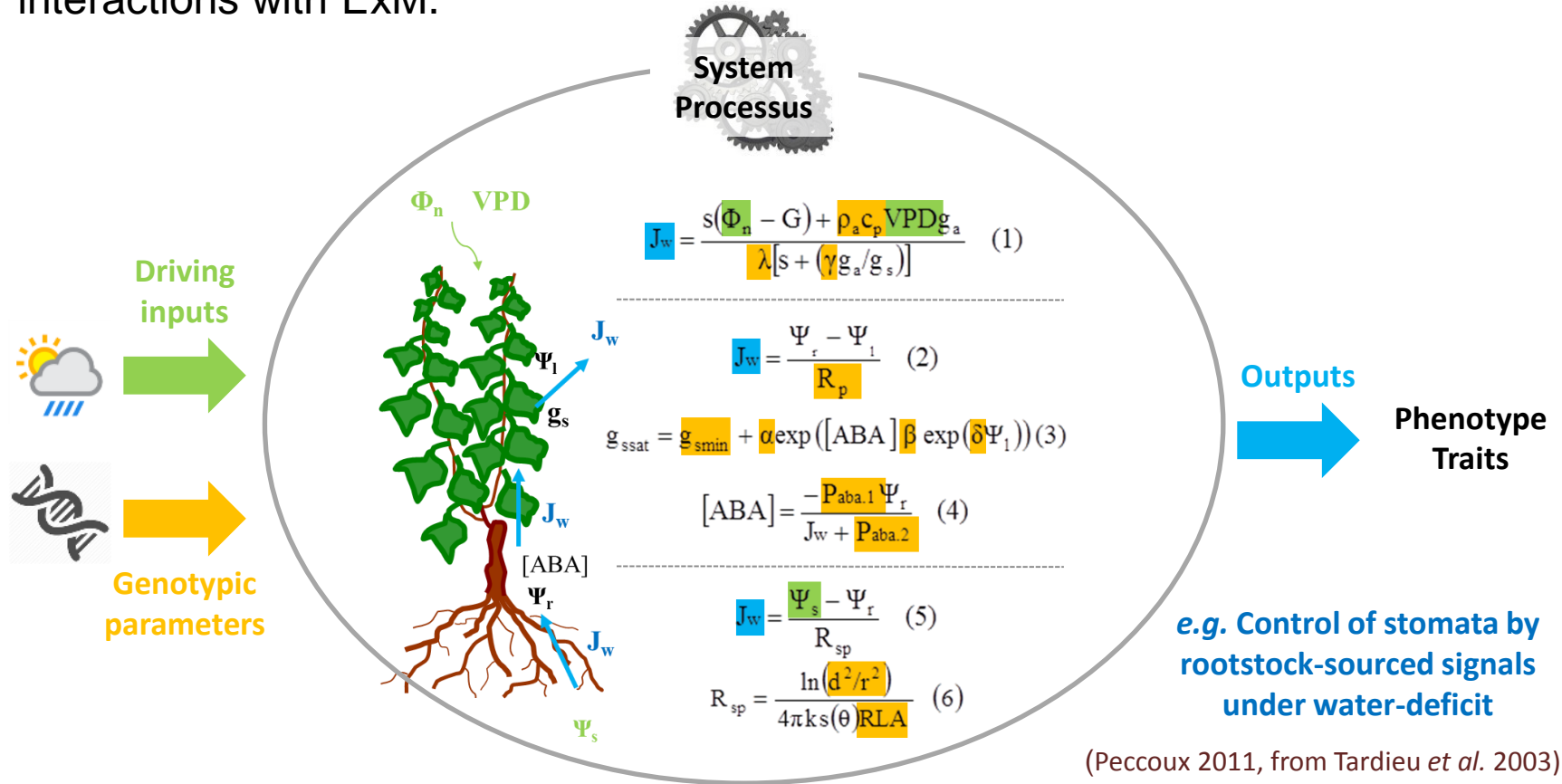
- ✿ Designing **genotypes better adapted** to future climate is a promising way to sustain high qualitative viticulture.
- ✿ Target traits for genetic improvement are complex with many interactions and **trade-offs among processes** and are **environment-dependent**.



- ✿ Need for a **holistic approach** to tackle phenotypic traits of interest.

# Process-based ecophysiological models (PBM) ?

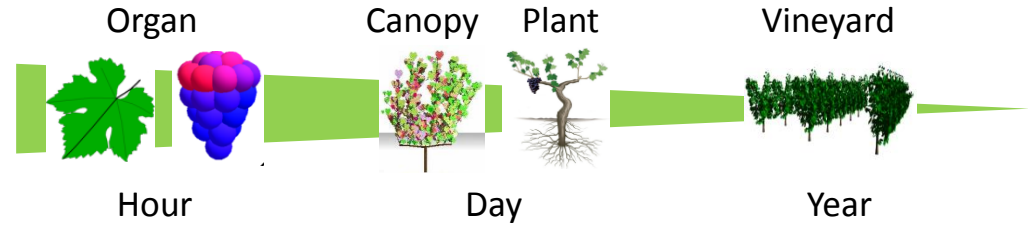
- ✿ A tool for quantifying plant behaviour within a mathematical framework.
- ✿ PBMs describe temporal variations of processes involved in final traits, and interactions with ExM.



- ✿ Predicting the **impacts of climate change** for a given G and assessing **virtual phenotyping** across many contrasting E.

# Grapevine PBM: where are we ?

A large diversity of PBMs :



1 scientific question = 1 model

frontiers in PLANT SCIENCE ORIGINAL RESEARCH ARTICLE published: 02 November 2013 doi: 10.3389/fpls.2013.00437

Using plant growth modeling to analyze C source–sink relations under drought: inter- and intraspecific comparison

Benoit Pallas<sup>1</sup>, Anne Clément-Vidal<sup>2</sup>, Maria-Camila Rebolledo<sup>2</sup>, Jean-Christophe Soulié<sup>2</sup> and Delphine Luquet<sup>2\*</sup>

J. AMER. SOC. HORT. SCI. 131(2):273–283. 2006.

Calibration and Evaluation of a STELLA Software-based Daily CO<sub>2</sub> Balance Model in *Vitis vinifera* L.

Stefano Poni<sup>1</sup>  
Istituto di Frutti-Viticultura, Università Cattolica del Sacro Cuore, Via Emilia Parmense 84, 29100 Piacenza, Italy

Plant, Cell & Environment

Plant, Cell and Environment (2012) 35, 1313–1328 doi: 10.1111/j.1365-3040.2012.02491.x

A leaf gas exchange model that accounts for intra-canopy variability by considering leaf nitrogen content and local acclimation to radiation in grapevine (*Vitis vinifera* L.)

JORGE A. PRIETO<sup>1</sup>, GAËTAN LOUARN<sup>2</sup>, JORGE PEREZ PEÑA<sup>3</sup>, HERNÁN OJEDA<sup>4</sup>, THIERRY SIMONNEAU<sup>1</sup> & ERIC LEBON<sup>1</sup>

Model-based analysis of sugar accumulation in response to source–sink ratio and water supply in grape (*Vitis vinifera*) berries

Zhan Wu Dai<sup>A</sup>, Philippe Vivin<sup>A,D</sup>, Thierry Robert<sup>A</sup>, Sylvie Milin<sup>A</sup>, Shao Hua Li<sup>C</sup> and Michel Génard<sup>B</sup>

Yield ?

Roots ?

General phenological model to characterise the timing of flowering and veraison of *Vitis vinifera* L.

A.K. PARKER<sup>1\*</sup>, I.G. DE CORTÁZAR-ATAURI<sup>2</sup>, C. VAN LEEUWEN<sup>1</sup> and I. CHUINE<sup>2</sup>

Vitis 36 (2), 73–76 (1997)

A simple model for simulation of growth and development in grapevine (*Vitis vinifera* L.). II. Model validation

by M. BINDI<sup>1</sup>, F. MIGLIETTA<sup>2</sup>, B. GOZZINI<sup>3</sup>, S. ORLANDINI<sup>4</sup> and L. SEGRÈ<sup>5</sup>

Contents lists available at ScienceDirect

Agricultural and Forest Meteorology

journal homepage: www.elsevier.com/locate/agrformet

Description and testing of a weather-based model for predicting phenology, canopy development and source–sink balance in *Vitis vinifera* L. cv. Barbera

Gabriele Cola<sup>1,2\*</sup>, Luigi Mariani<sup>3</sup>, Francesca Salinari<sup>3</sup>, Silvia Cvardi<sup>4</sup>, Fabio Bernizzoni<sup>4</sup>, Matteo Gatti<sup>1</sup>, Stefano Poni<sup>1,2\*</sup>

Multi-stress (CO<sub>2</sub> x T x W) ?



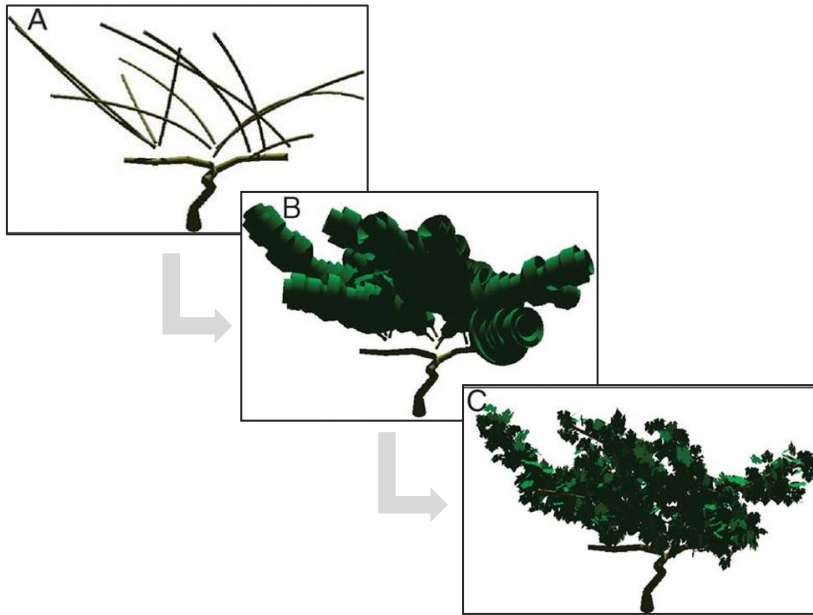
Choice of which processes and level of detail is :

- limited by scientific knowledge and available datasets
- governed by research focus and intended model use.

# Where are we ? Example 1/3



TOPVINE: a 3D reconstruction of grapevine canopy structure from probabilistic rules.



1

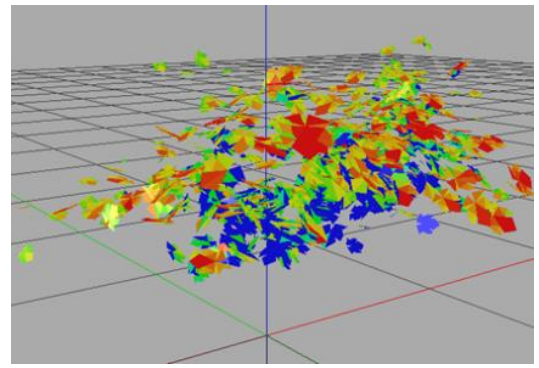
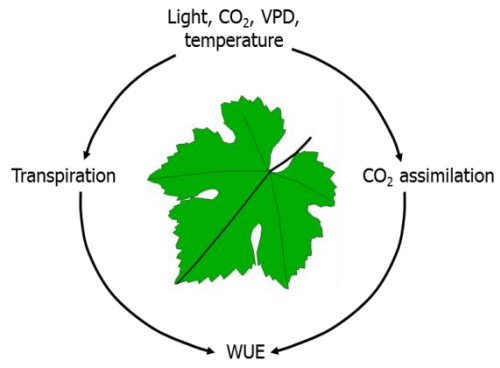
VSP 2W	Syrah		
	Grenache		
	Syrah		
BFC	Grenache		

**Variability between cultivar x training system**

(Louarn et al. 2008)

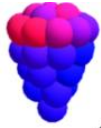
2

**Modelling distribution of leaf gas exchange within the canopy**

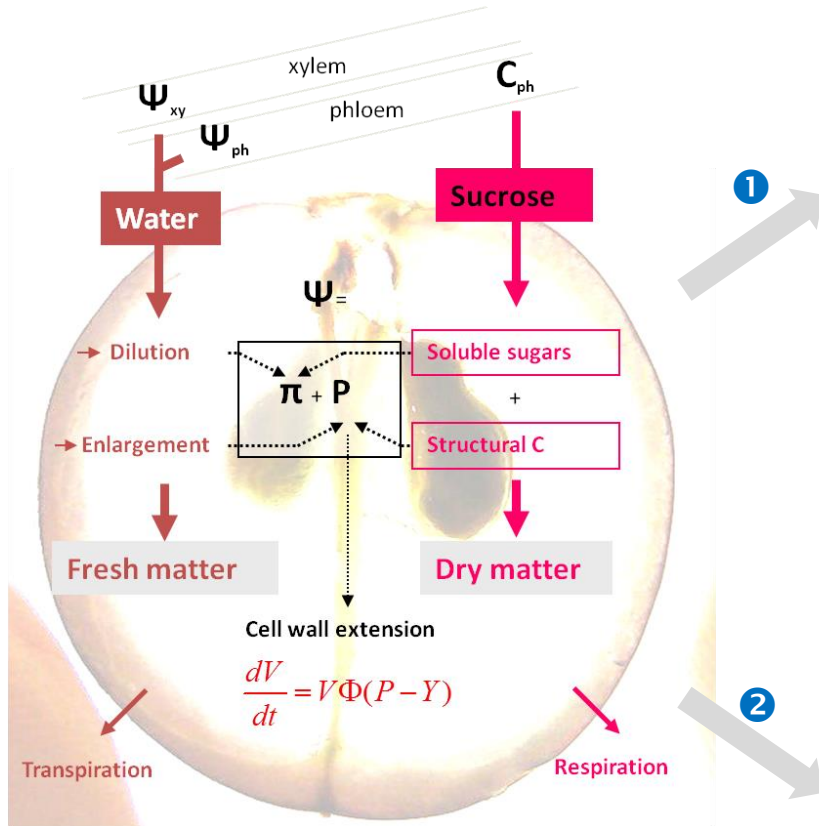


(Prieto et al. 2012)  
(Albasha et al., poster)

# Where are we ? Example 2/3



A biophysical fruit model to simulate post-veraison dynamics of berry mass.



(Dai et al. 2009)

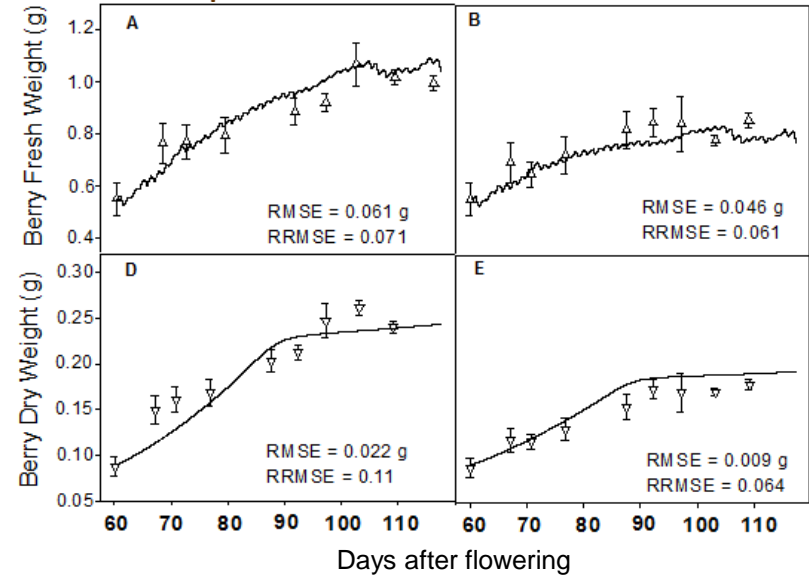
## Effect of leaf-to-fruit ratio (M)



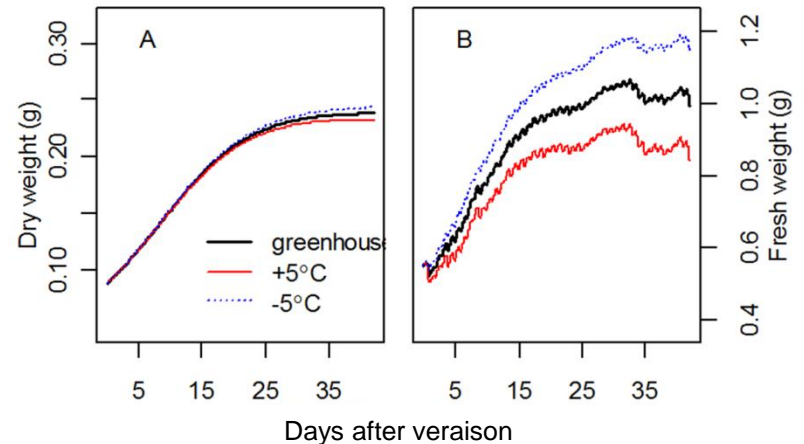
High



Low



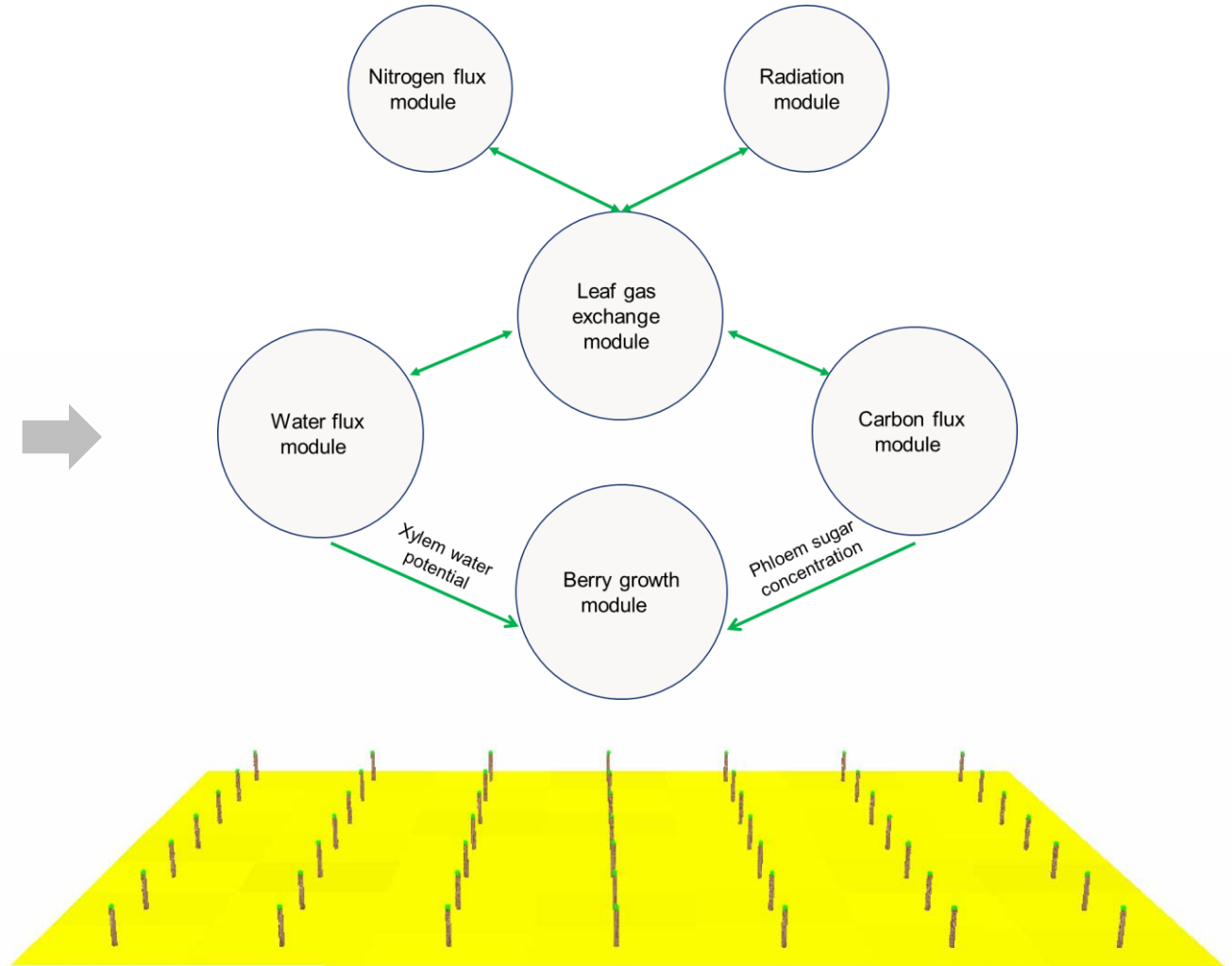
## Effect of temperature (E)



## Where are we ? Example 3/3



Integrating water and sugar fluxes into a 3D functional-structural plant model (FSPM).



# Grapevine PBM: where to go ?

- ✿ PBM predicts quantitative traits of a given G in any E
- ✿ **PBM** combined to **genetic** approaches for analysing genetic diversity of traits and enhancing plant breeding.

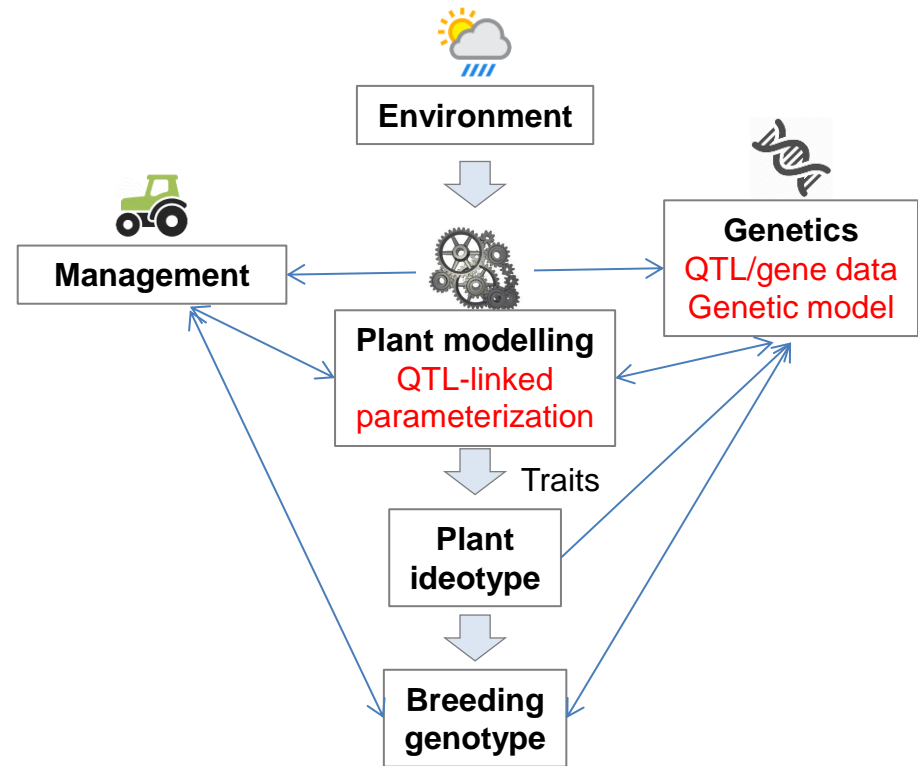


## STEP 1

Dissecting the genotypic variations of a given trait into model parameters.

## STEP 2

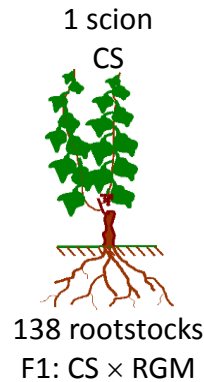
Analysing co-localizations (or not) between QTLs for that trait and QTLs for model parameters.



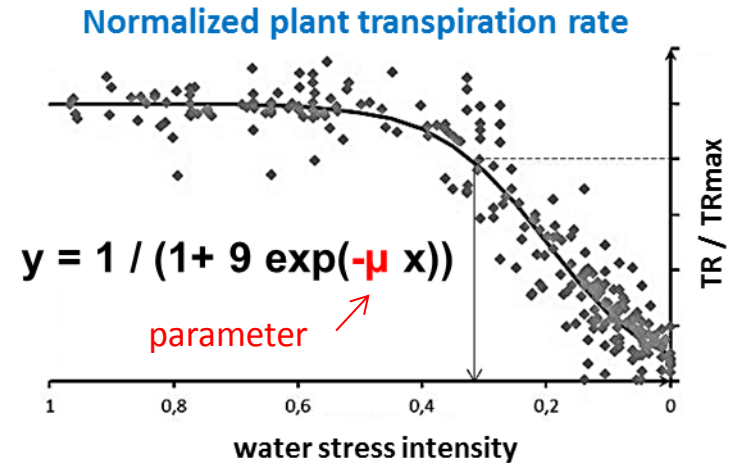
➡ First step to design and test *in silico* plants for future E



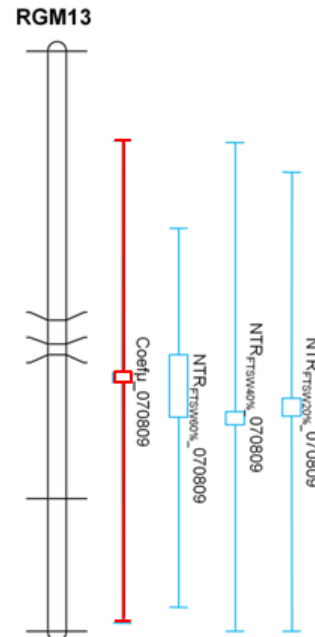
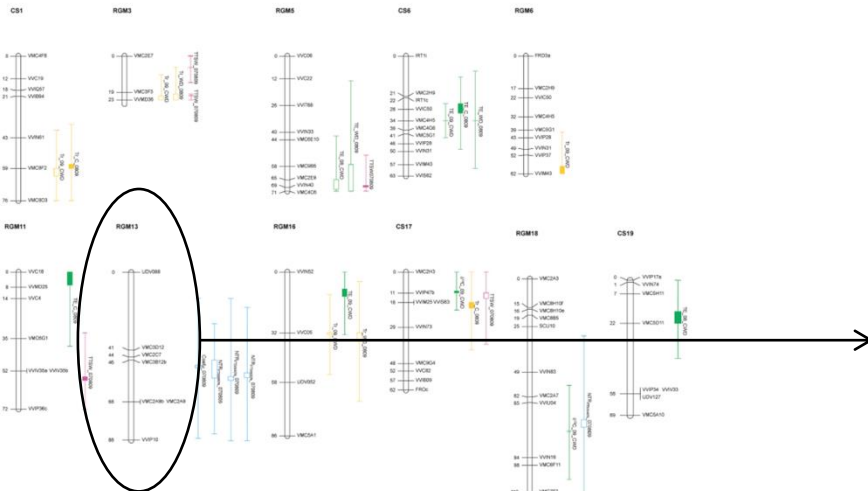
## 1 Phenotyping a progeny (138 genotypes)



## 2 Fitting plasticity response curves



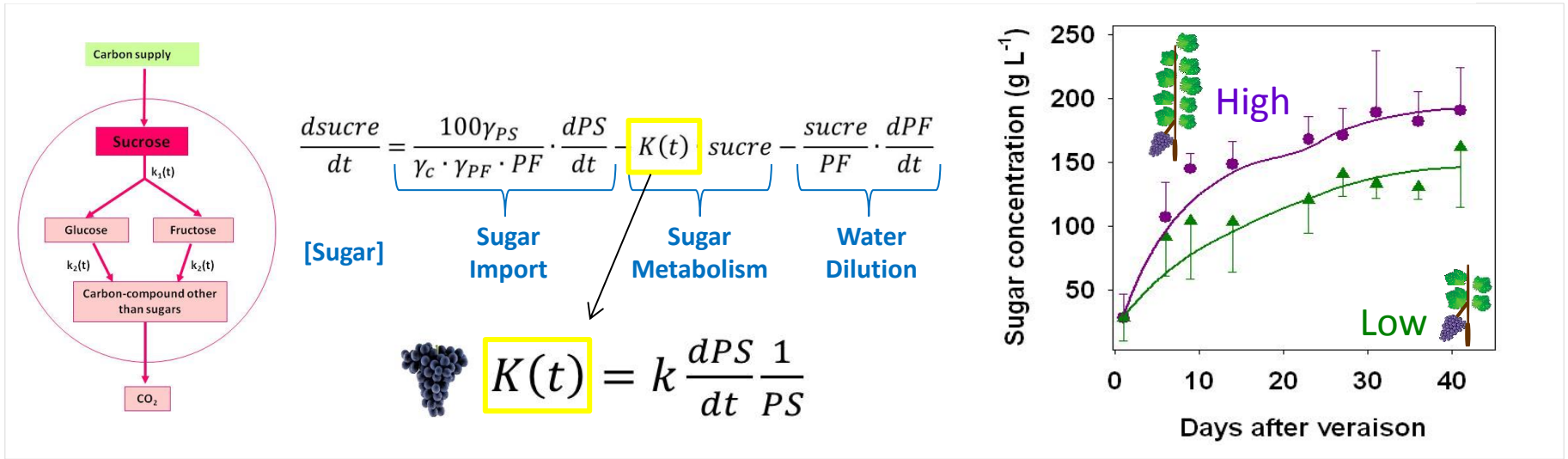
## 3 Genetic mapping



## 4 QTLs analysis

- > Measured traits
- > Model parameter

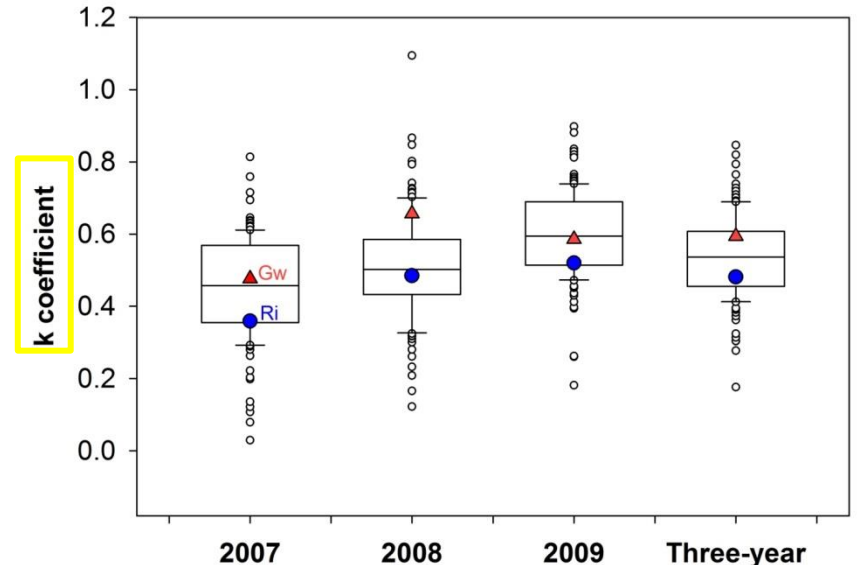
1 Developing a PBM of sugar accumulation.



Dai et al. 2009, 2011

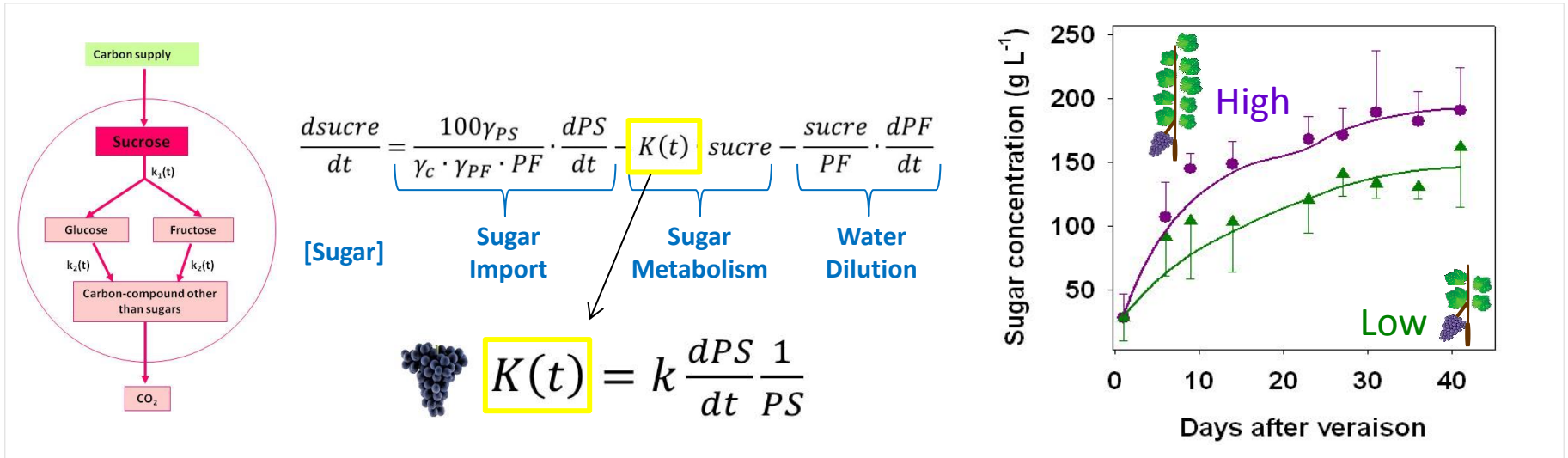
2 Deciphering the genetic variability of berry sugar content with the model.

- 120 genotypes, progeny from a **Riesling** x **Gewurztraminer** cross.
- K is dependent on G but independent of E.
- K values segregate in the population and explain the genetic variability in berry [sugar].

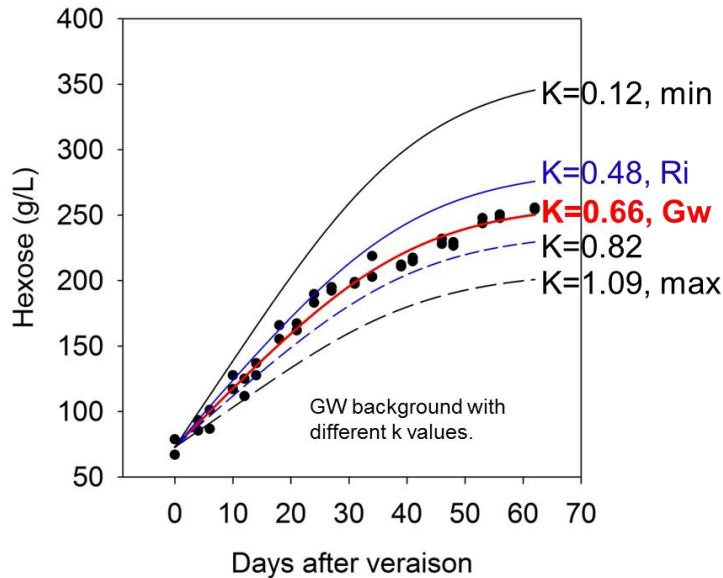


Duchêne et al., unpublished

1 Developing a PBM of sugar accumulation.



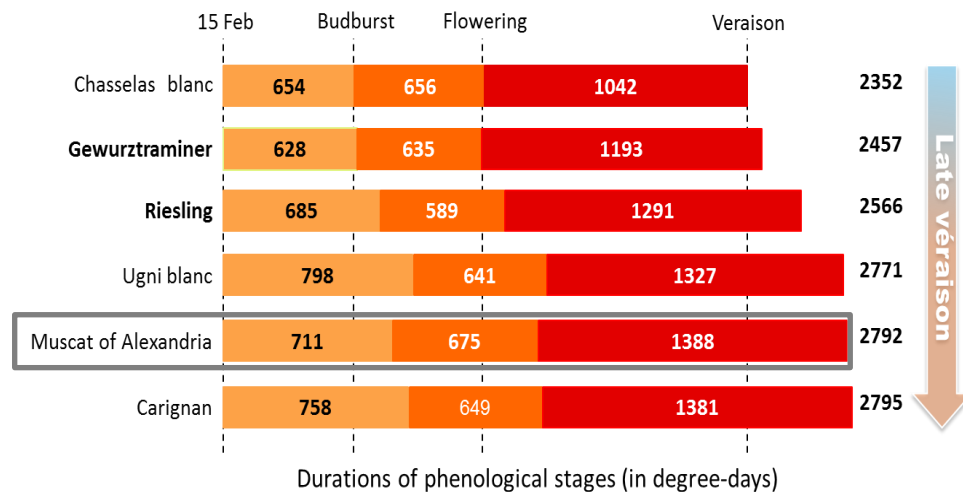
Dai et al. 2009, 2011



3 Identifying target genotypes with distinct sugar concentrations.

1 Modelling phenological stages.

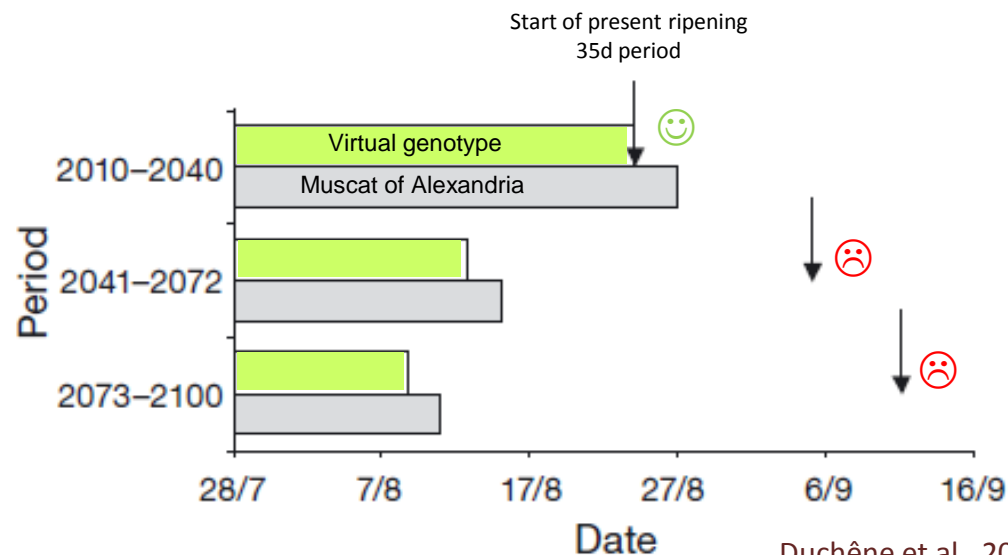
$$HS = \sum_{i=1}^n \text{Max}(T_i - T_b ; 0)$$



2 Analyzing the genetic variability of the parameters in a **Ri** x **Gw** progeny.

3 Creating a **virtual** late ripening genotype ( $\approx$  ideotype).

4 Assessing its performance to projected climatic scenarios.



Predicting G-to-P relationships under contrasted E is still a challenge ...  
**but we are in progress !**



**'All models are wrong but  
some are useful'**

(Georges E.P. Box)

Thank you for your attention