

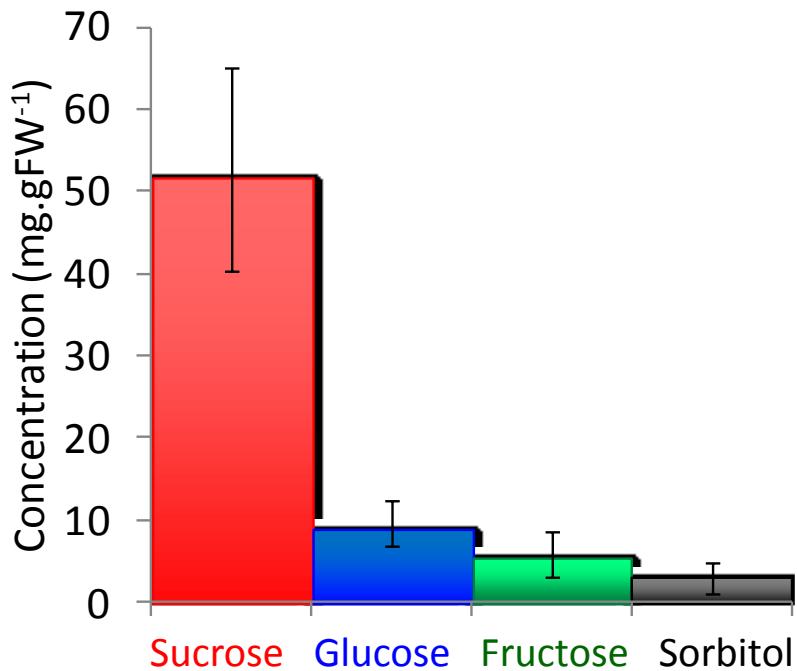
## *A kinetic model of sugar metabolism in peach fruit allows the exploration of genetic variability*



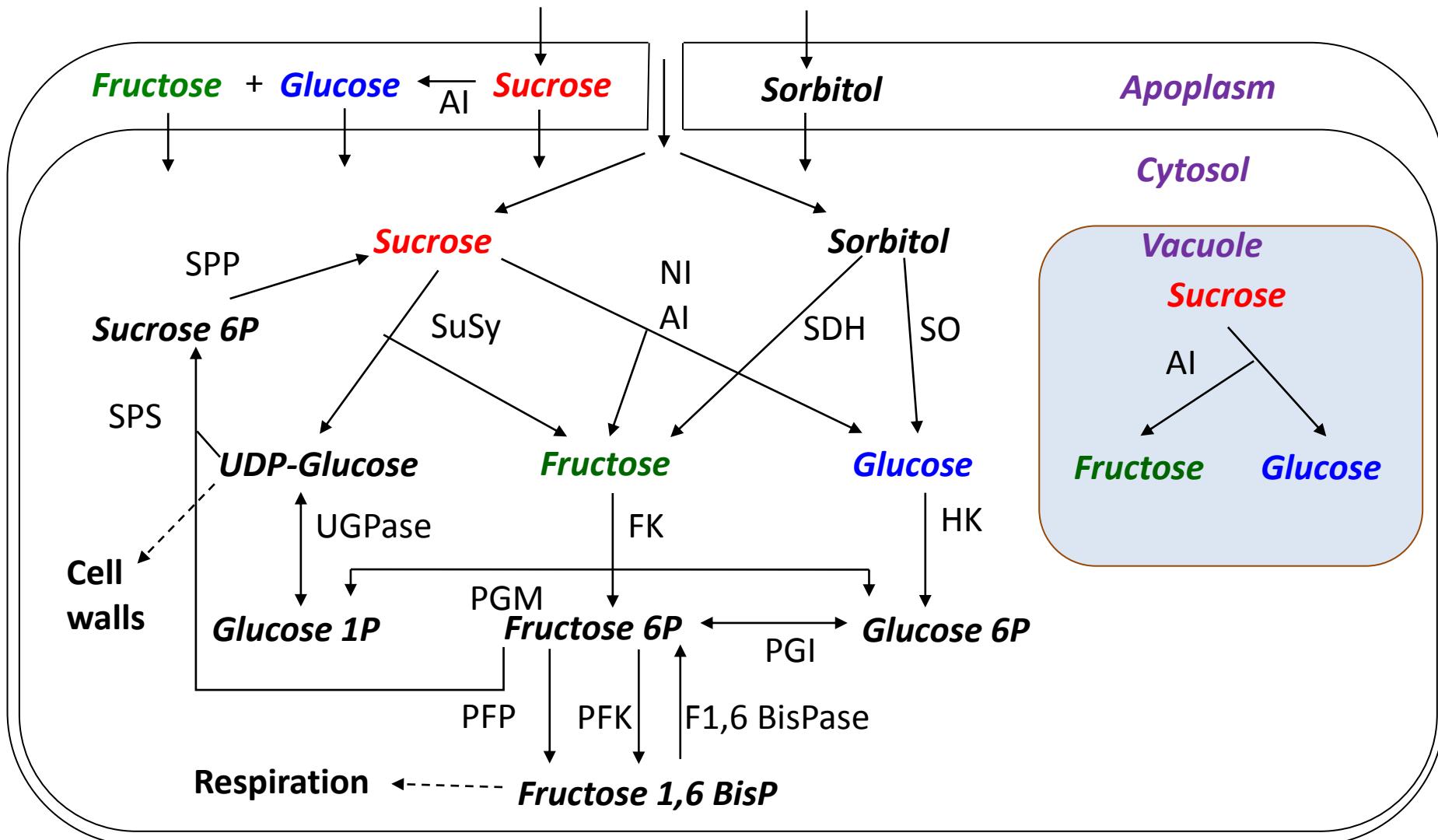
Elsa Desnoues, **Michel Génard**, Bénédicte Quilot-Turion, Valentina Baldazzi

Sugar concentration is an important factor of fruit quality

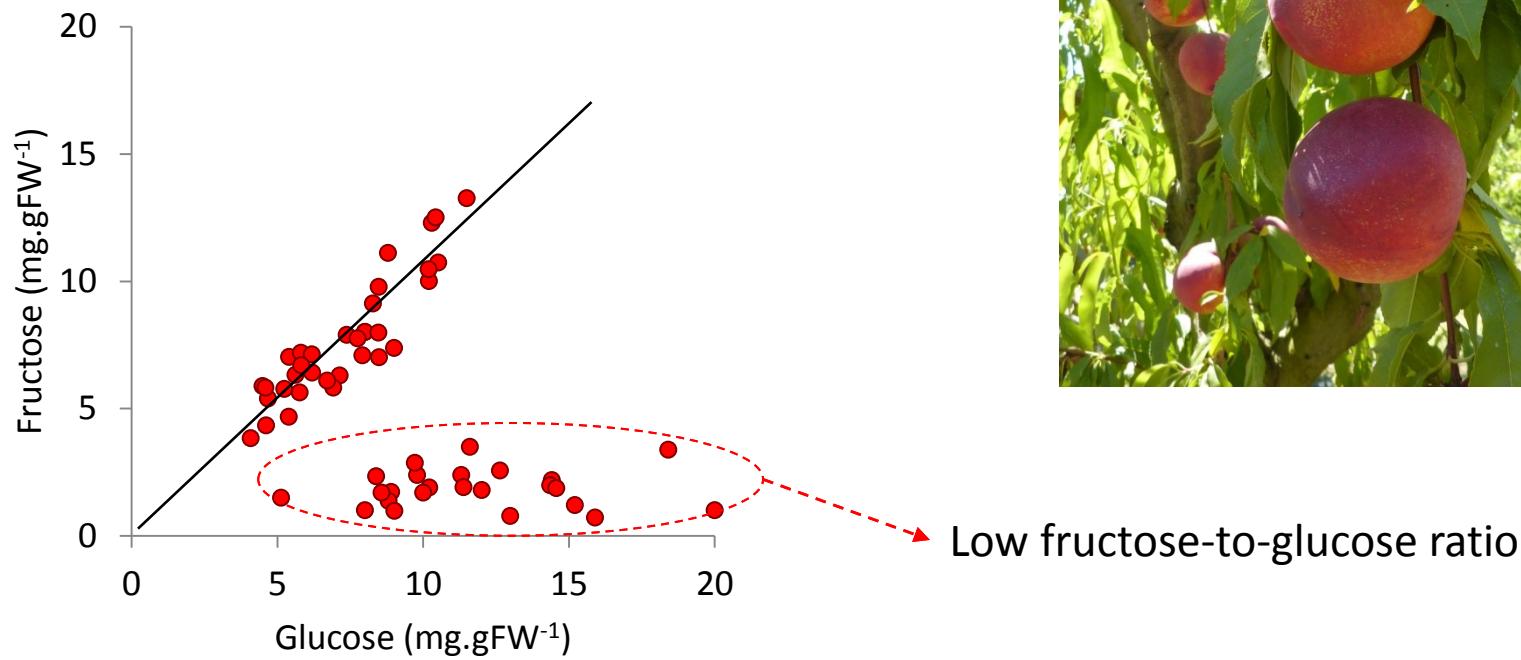
In peach fruit:



## Sugar metabolism in peach fruit



In peach fruit: high phenotypic variability  
of sugar concentration



**Objectives:** better understand the mechanisms of sugar accumulation during peach fruit development and **investigate hypotheses to explain the major change in fructose concentration between genotypes.**

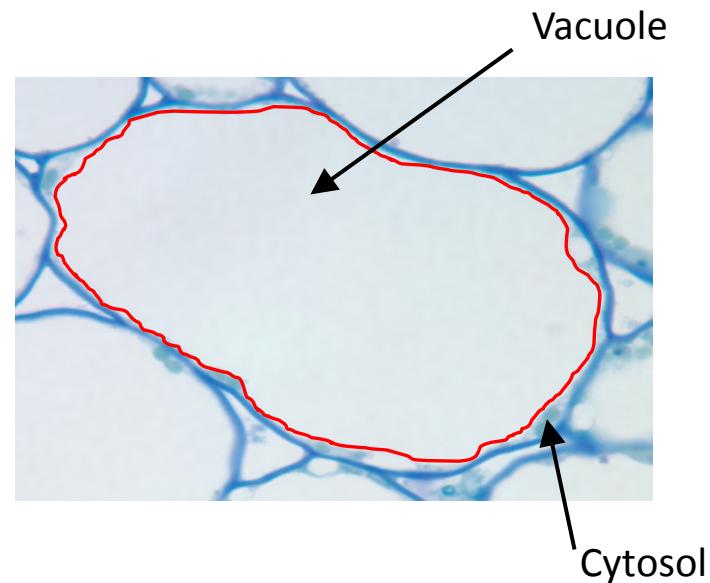
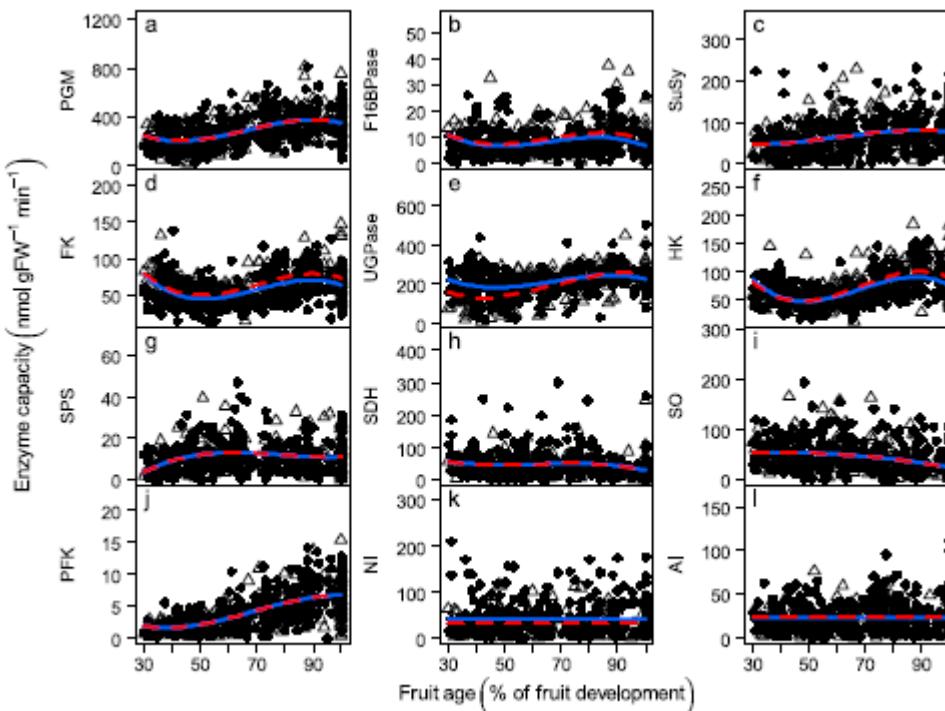
→ a kinetic model of sugar metabolism with :

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→ a kinetic model of sugar metabolism with :

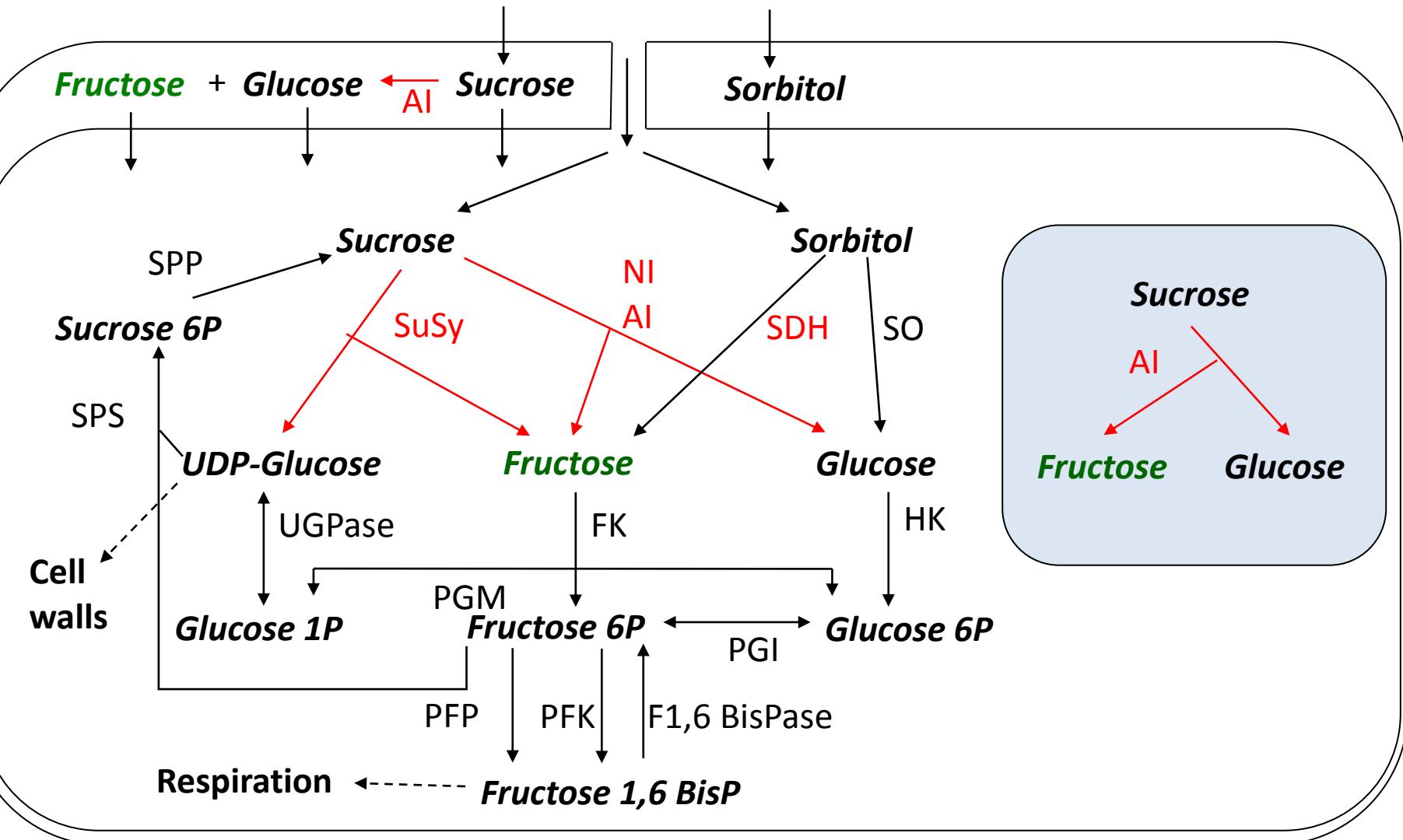
- data-driven enzymatic capacities

- an explicit representation of cellular compartmentation



Functional hypothesis to explain 'low fructose' phenotype:

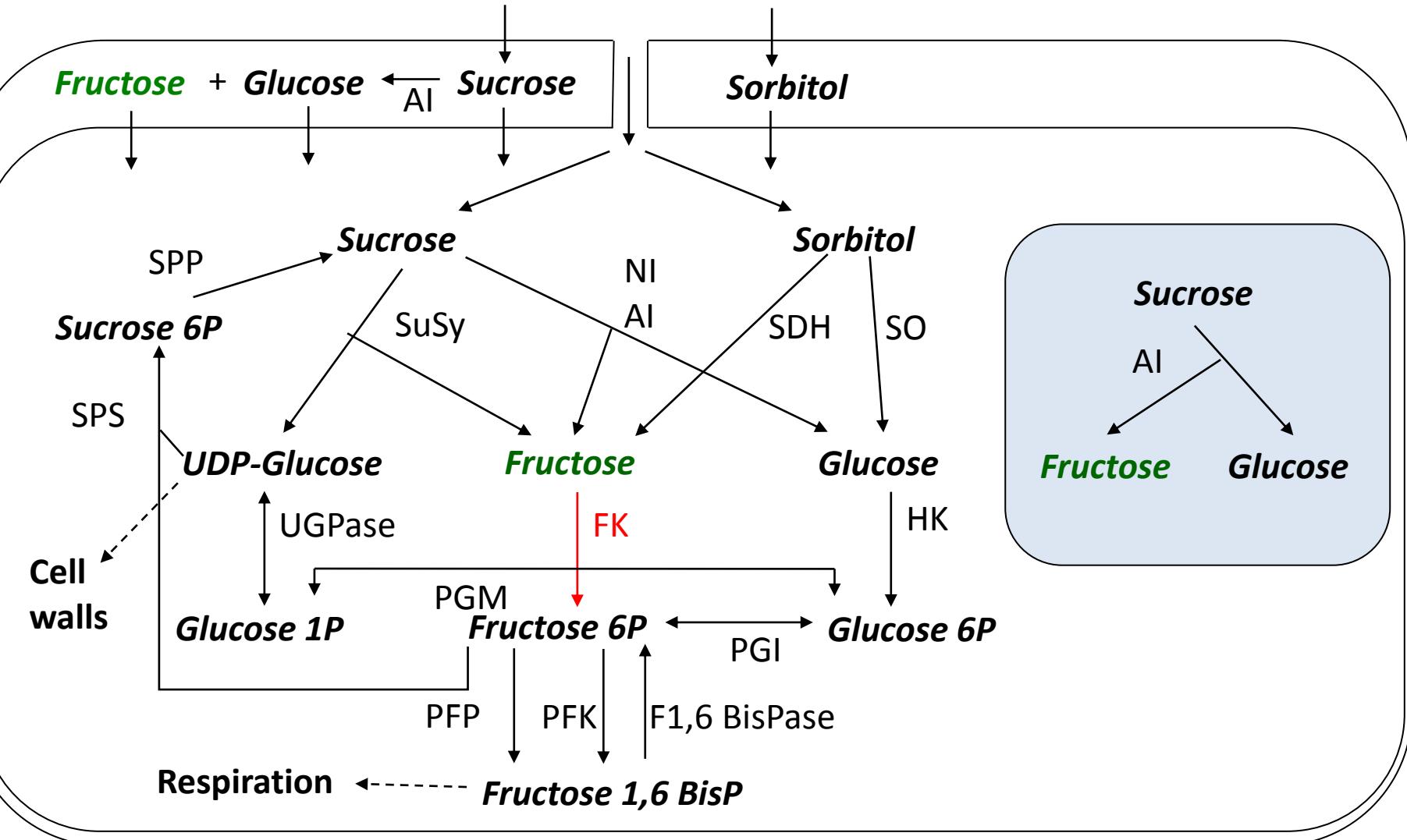
- Synthesis



Functional hypothesis to explain 'low fructose' phenotype:

- Synthesis

- Degradation

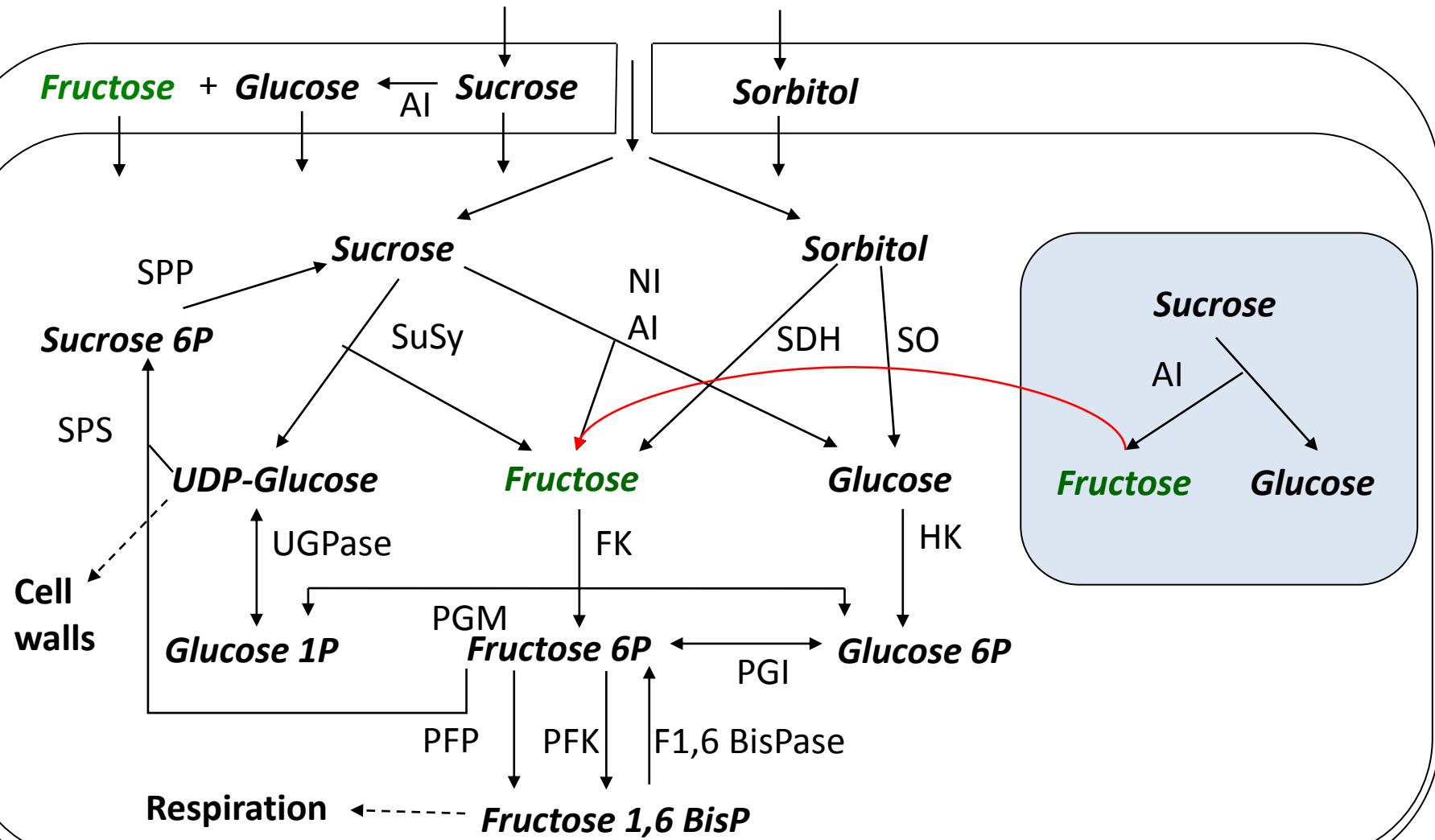


Functional hypothesis to explain 'low fructose' phenotype:

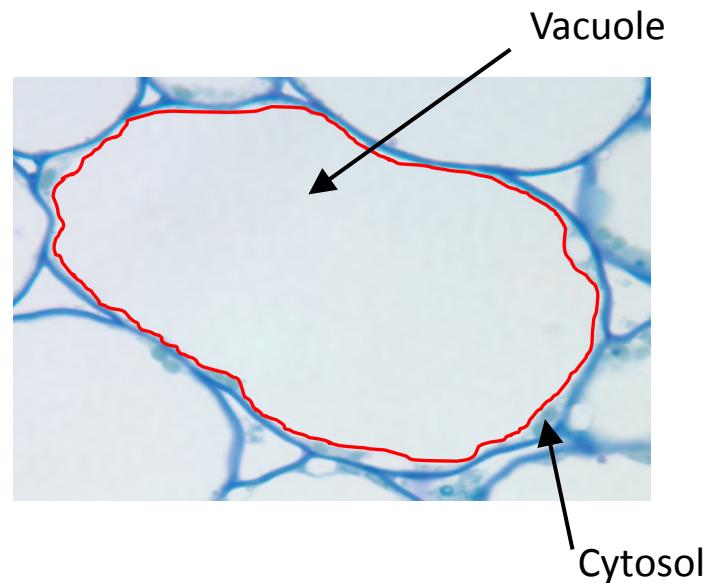
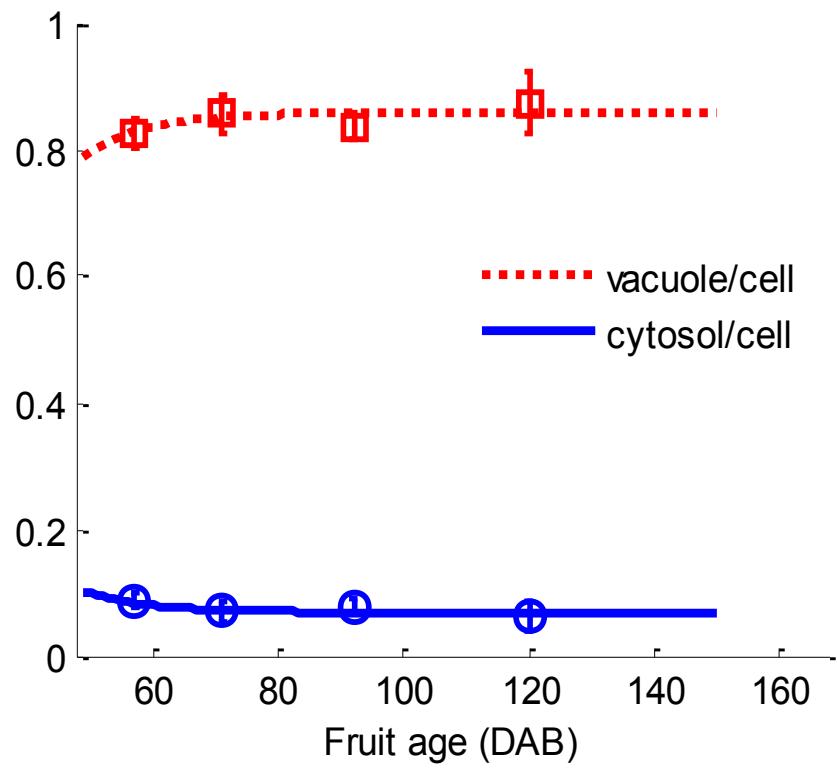
- Synthesis

- Degradation

**- Storage modification**



The vacuole volume is more than 80% of cell volume



- **set of 9 ordinary differential equations**

$$\frac{d[\text{Sucrose}]_{\text{Cytosol}}}{dt} = F1 + F16 - F4 - F9 - F10$$

$$\frac{d[\text{Sorbitol}]_{\text{Cytosol}}}{dt} = F2 - F11 - F12 - F19$$

$$\frac{d[\text{Fructose}]_{\text{Cytosol}}}{dt} = F3 + F8 + F9 + F10 + F11 - F7 - F14$$

$$\frac{d[\text{Glucose}]_{\text{Cytosol}}}{dt} = F3 + F6 + F10 + F12 - F5 - F15$$

$$\frac{d[\text{HexosesPhosphates}]_{\text{Cytosol}}}{dt} = F9 + F14 + F15 - F17 - F18 - F16$$

$$\frac{d[\text{Sucrose}]_{\text{Vacuole}}}{dt} = F4 - F13$$

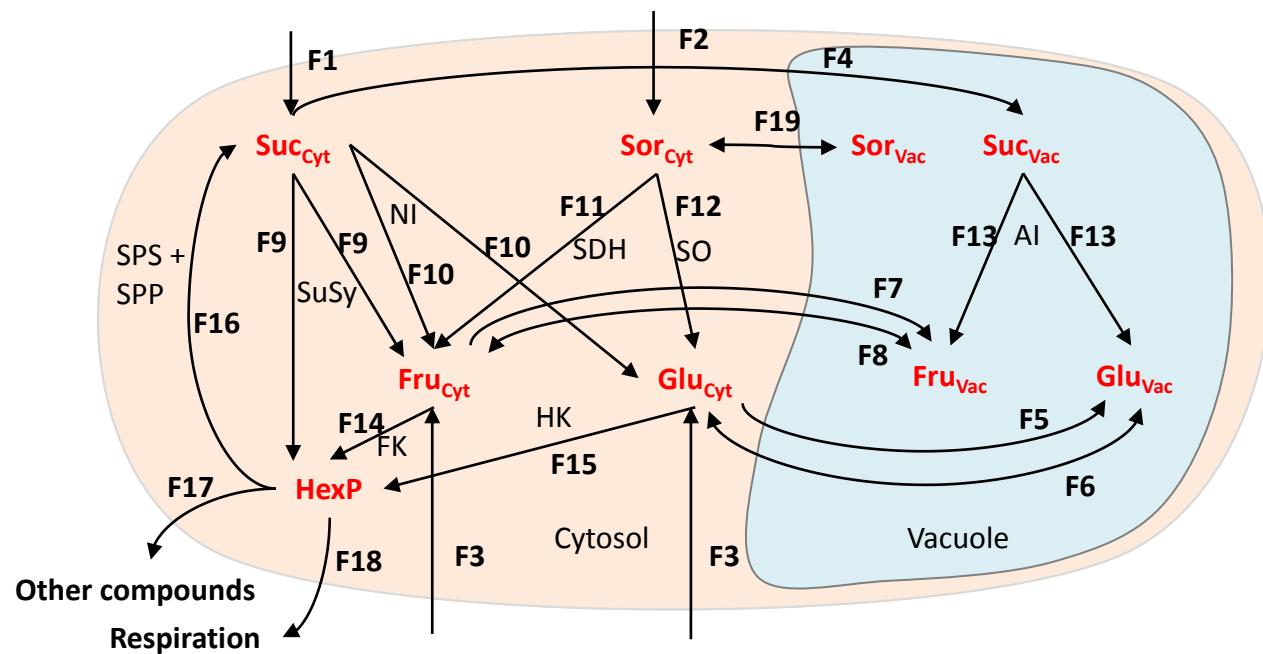
$$\frac{d[\text{Fructose}]_{\text{Vacuole}}}{dt} = F7 + F13 - F8$$

$$\frac{d[\text{Glucose}]_{\text{Vacuole}}}{dt} = F5 + F13 - F6$$

$$\frac{d[\text{Sorbitol}]_{\text{Vacuole}}}{dt} = F19$$



- set of 9 ordinary differential equations
- 19 flows



- **set of 9 ordinary differential equations**
- **19 flows**
- **30 parameters :**
  - 8 from phenotyping data
  - 8 from literature data
  - 14 numerically estimated

Simulation of 8 genotypes from an interspecific population *Prunus davidiana* x *Prunus persica*.



X

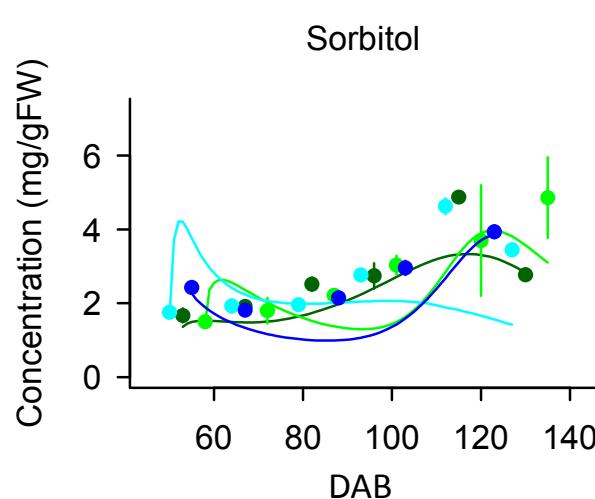
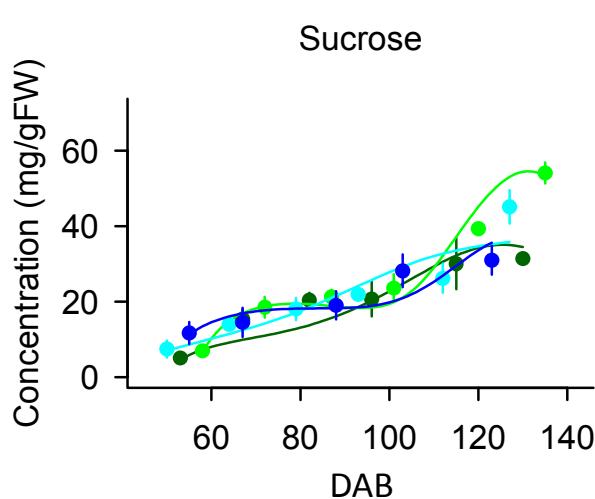
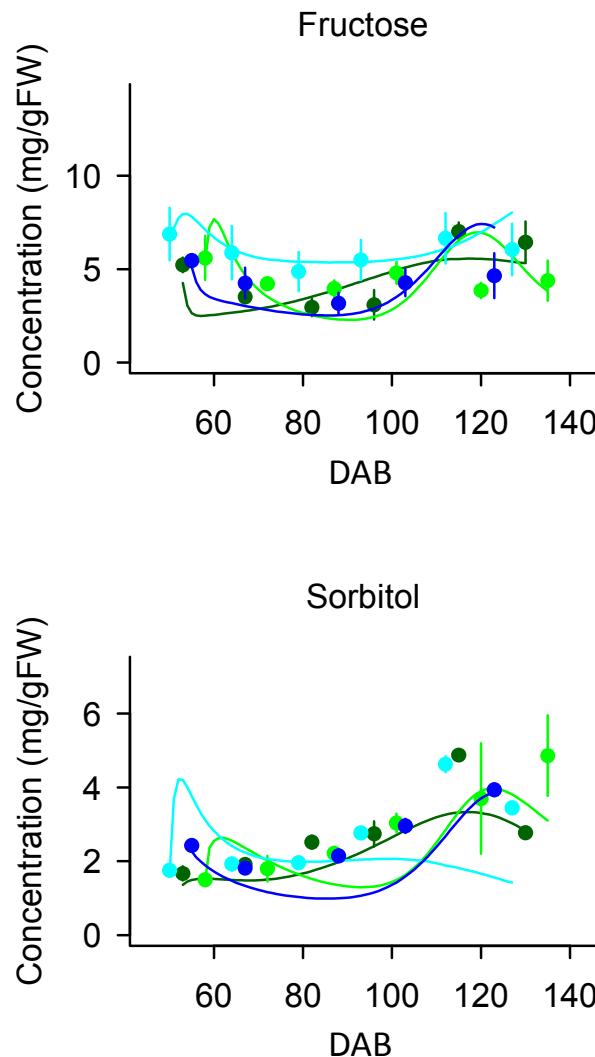
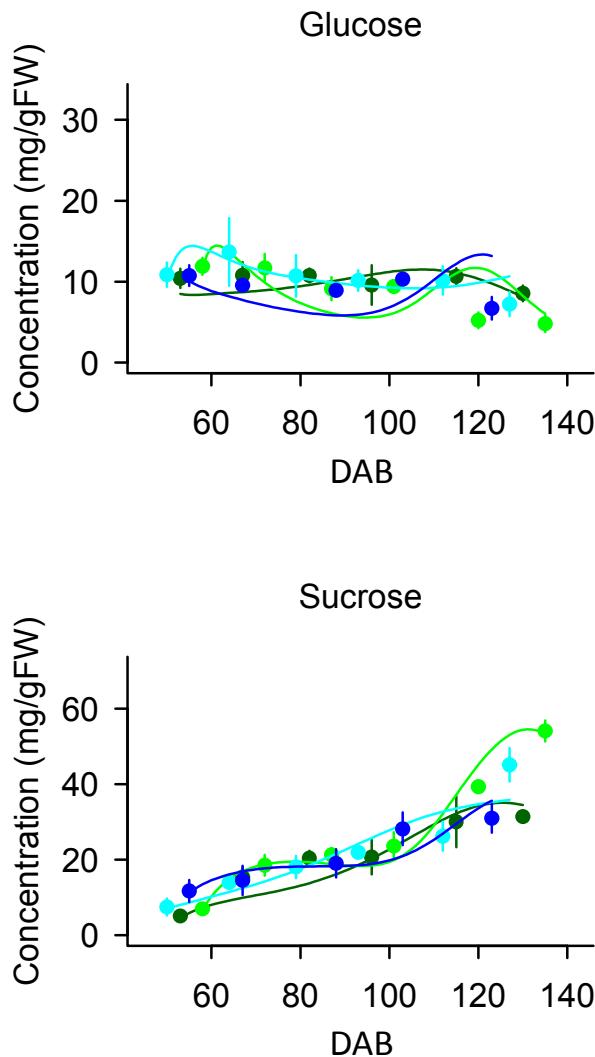
- Input:

- temperature → **identical**
- dry mass variation → **different for each genotype**

- 30 parameters :

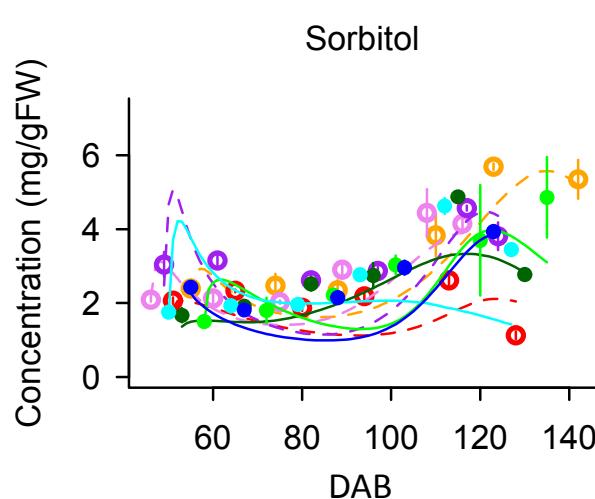
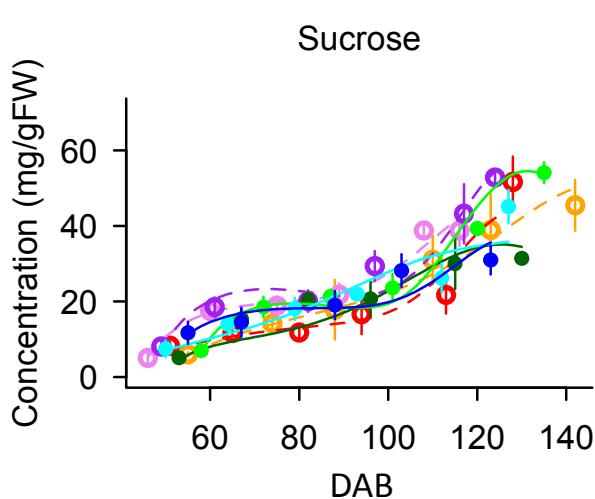
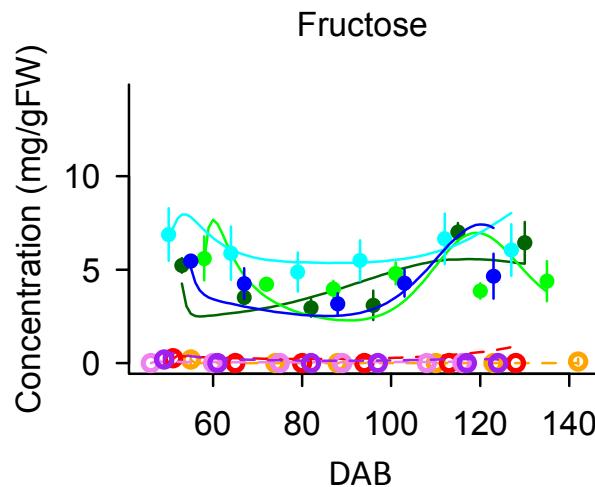
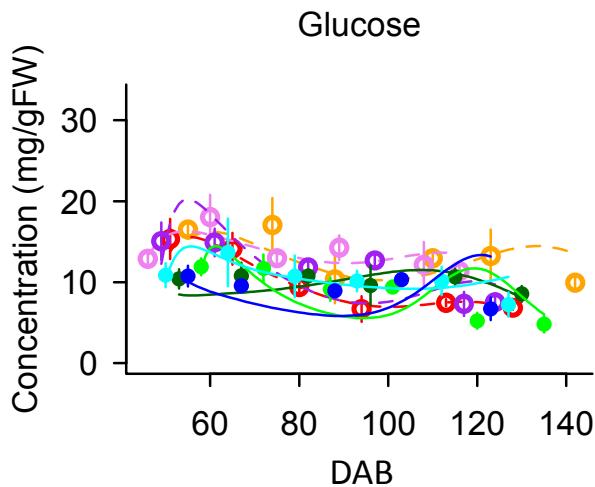
- 8 from phenotyping data → **identical**
- 8 from literature data → **identical**
- 14 numerically estimated → **different for each genotype**

Predictions of sugar concentration during fruit growth for : 4 'standard' genotypes



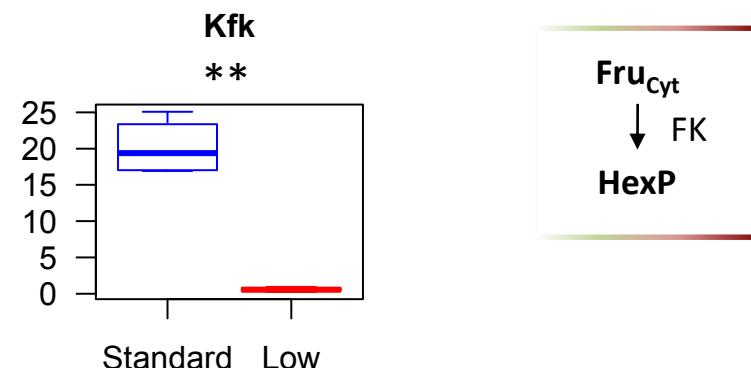
- Experimentales data
- Simulations

Predictions of sugar concentration during fruit growth for : 4 'standard' genotypes  
4 'low fructose' genotypes

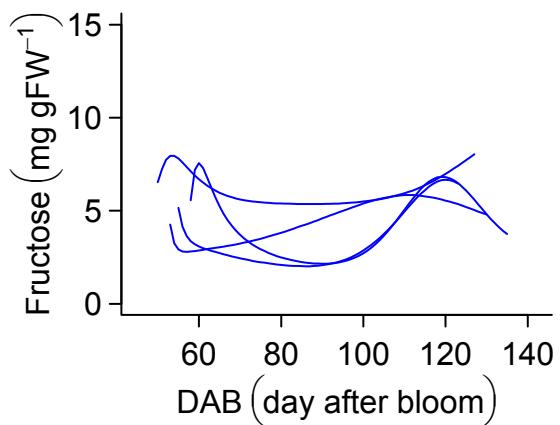


- Experimentales data
- Simulations

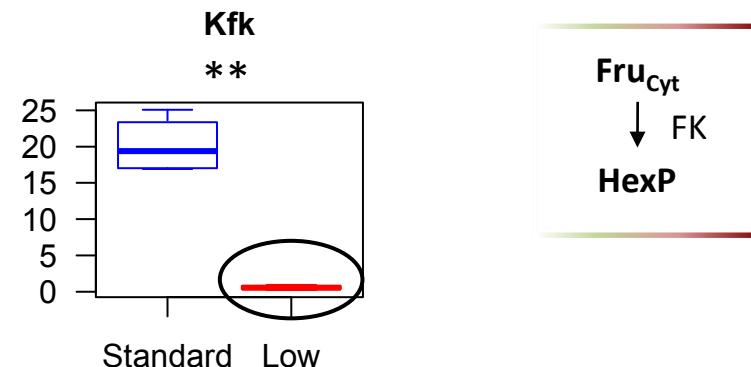
14 parameters numerically estimated :  
Kfk (FK affinity for fructose) significantly **lower** for 'low fructose' genotypes



Simulation of fructose concentration for:  
- 'standard' genotypes

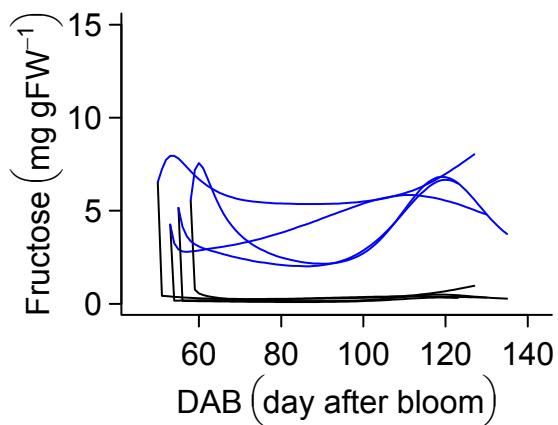


14 parameters numerically estimated :  
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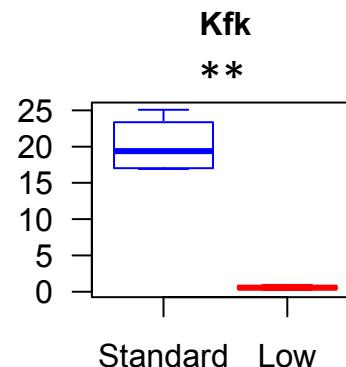
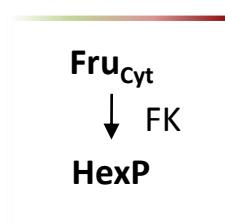


Simulation of fructose concentration for:

- 'standard' genotypes
- 'standard' genotypes with average value of Kfk estimated on 'low fructose' genotypes

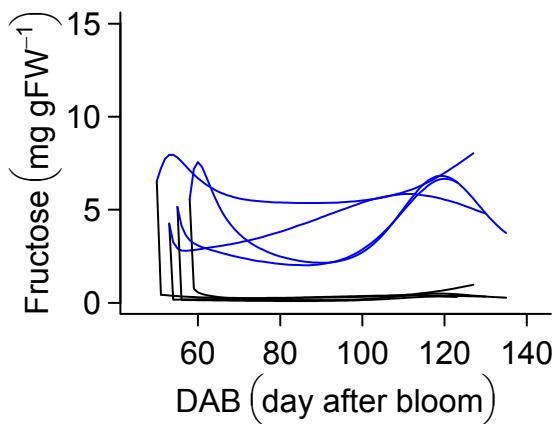


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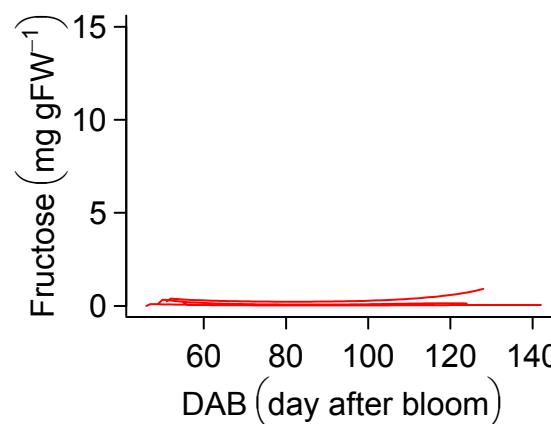
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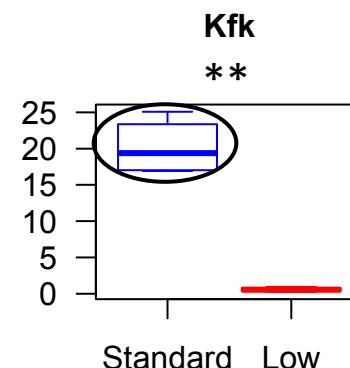
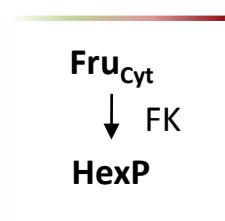


Simulation of fructose concentration for:

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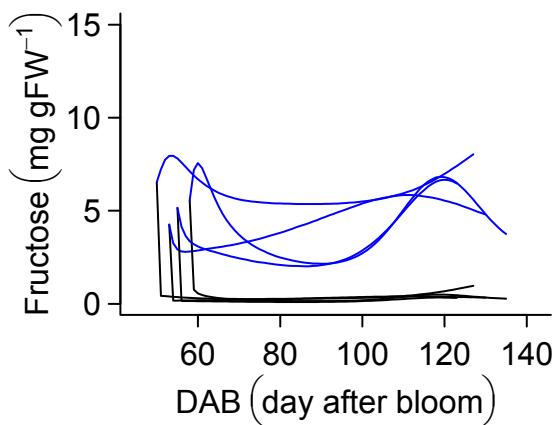


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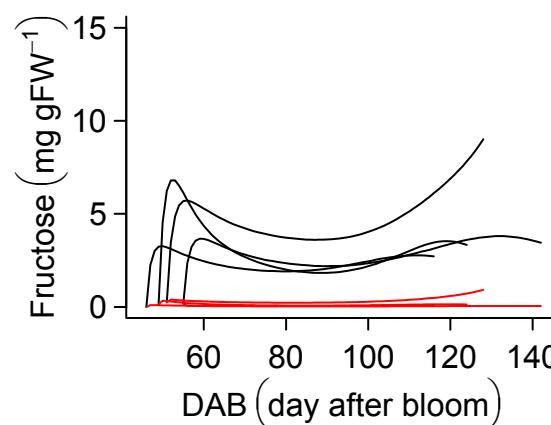
Simulation of fructose concentration for:

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- 'standard' genotypes with average value of Kfk estimated on 'low fructose' genotypes



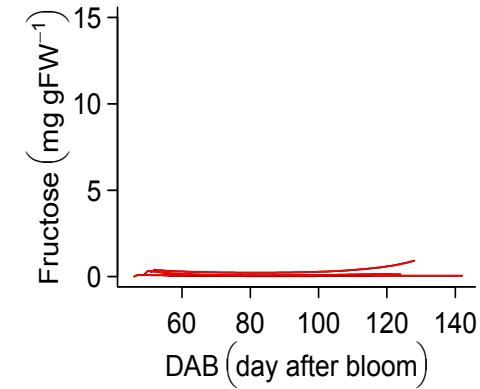
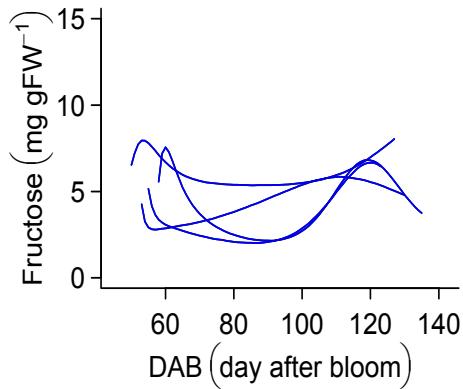
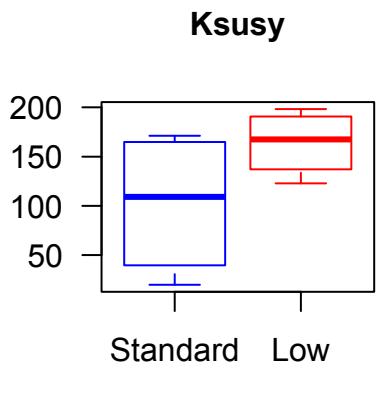
Simulation of fructose concentration for:

- 'low fructose' genotypes
- 'low fructose' genotypes with average value of Kfk estimated on 'standard' genotypes

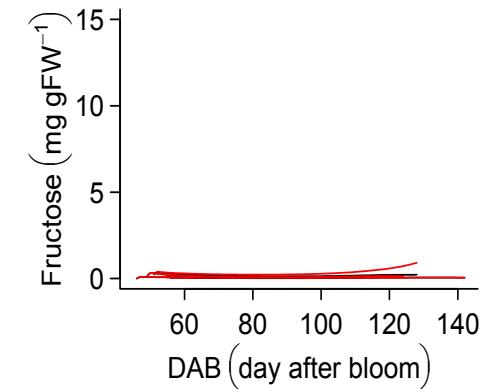
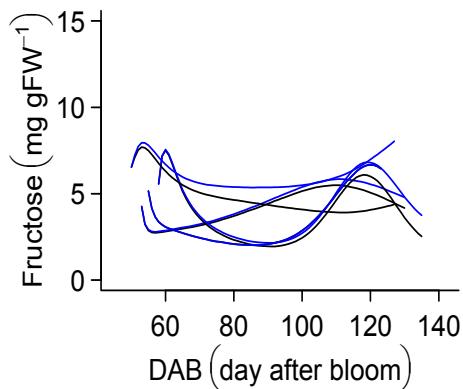
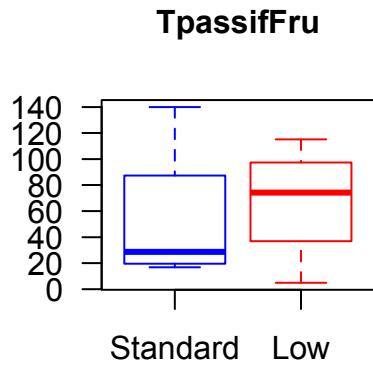


Modification of other parameters does not allow to change the fructose concentration

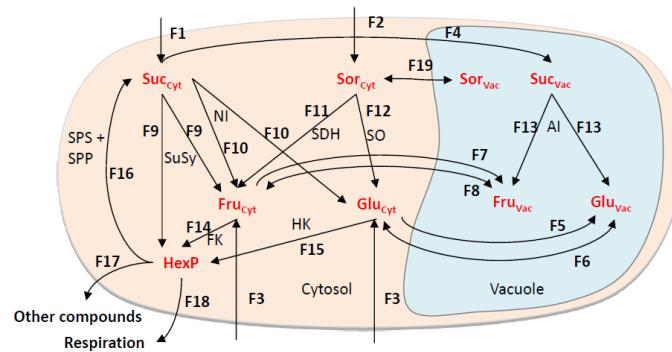
## Synthesis



## Transport



## Development of a kinetic model to simulate sugar concentration during fruit growth



→ a difference in **fructokinase affinity** can be responsible for the 'low-fructose' phenotype

Helpful tool for the investigation of sugar metabolism in fruit and the identification of the mechanisms underlying phenotypic variability

# Thank you



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