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# An integrative systems biology approach to study the genetic variability and the molecular involved in sunflower heterosis responses to drought stress

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Climate change is a current issue of major concern because of its potential effects on biodiversity and the agricultural sector. To better understand the adaptation of plants to this recent phenomenon is therefore a major interest for crop science and society. The domesticated sunflower, *Helianthus annuus* L., is the fourth most important oilseed crop in the world<sup>[1]</sup> and is promising for agriculture adaptation because it can maintain stable yields across a wide variety of environmental conditions, especially during drought stress<sup>[2]</sup>. As drought stress response involves a large number of molecular pathways and subsequent physiological processes, it constitutes an archetypical systems biology model.

## Two major studies

### 1- Characterization of leaf response to drought stress and its genetic variation between parental lines and hybrids

#### Strategies

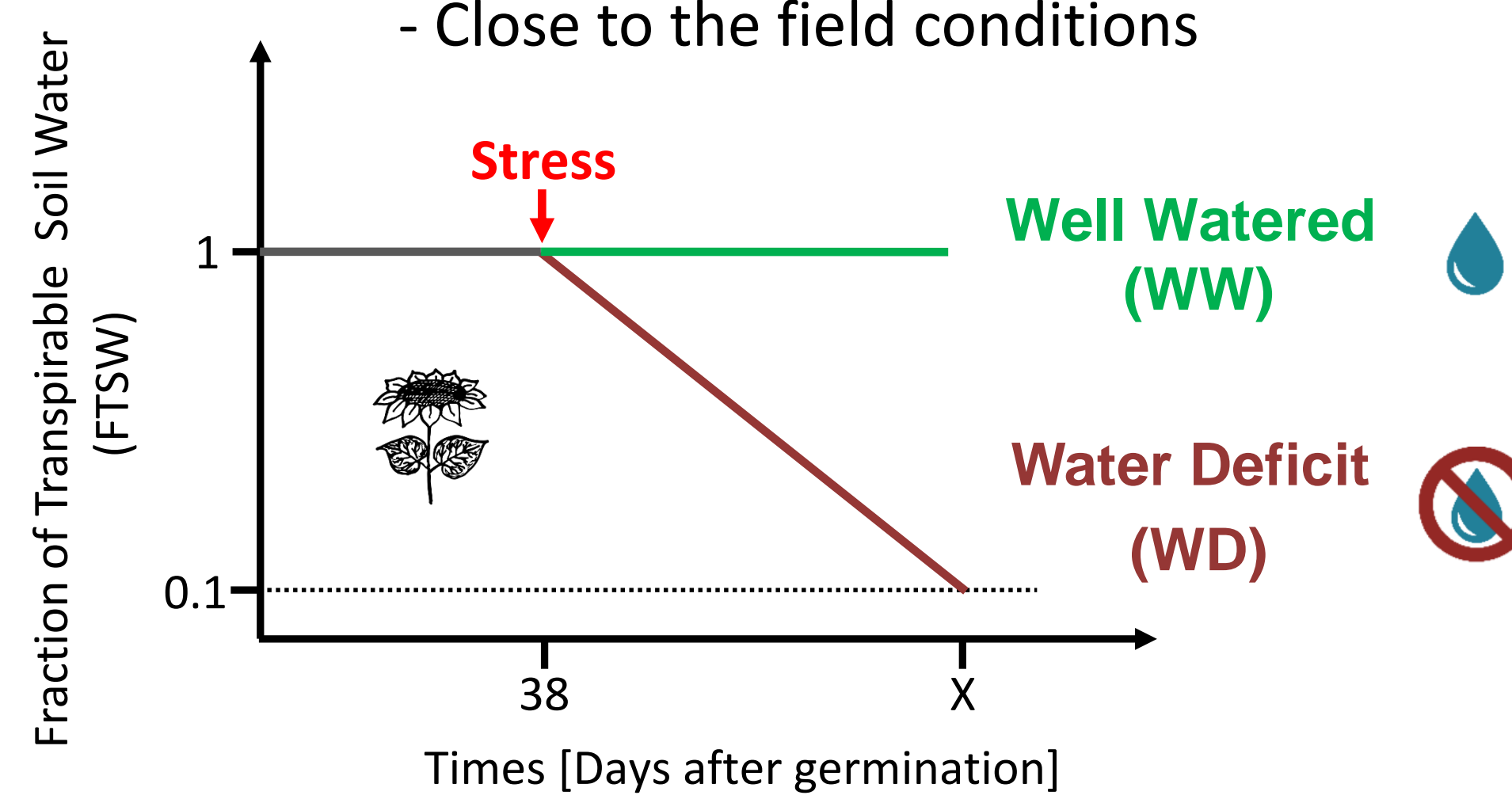
24 genotypes (8 parental lines and 16 hybrids)

| ♀ \ ♂ | SF279 | SF317 | SF326 | SF342 |
|-------|-------|-------|-------|-------|
| SF009 | ✓     | ✓     | ✓     | ✓     |
| SF092 | ✓     | ✓     | ✓     | ✓     |
| SF109 | ✓     | ✓     | ✓     | ✓     |
| SF193 | ✓     | ✓     | ✓     | ✓     |

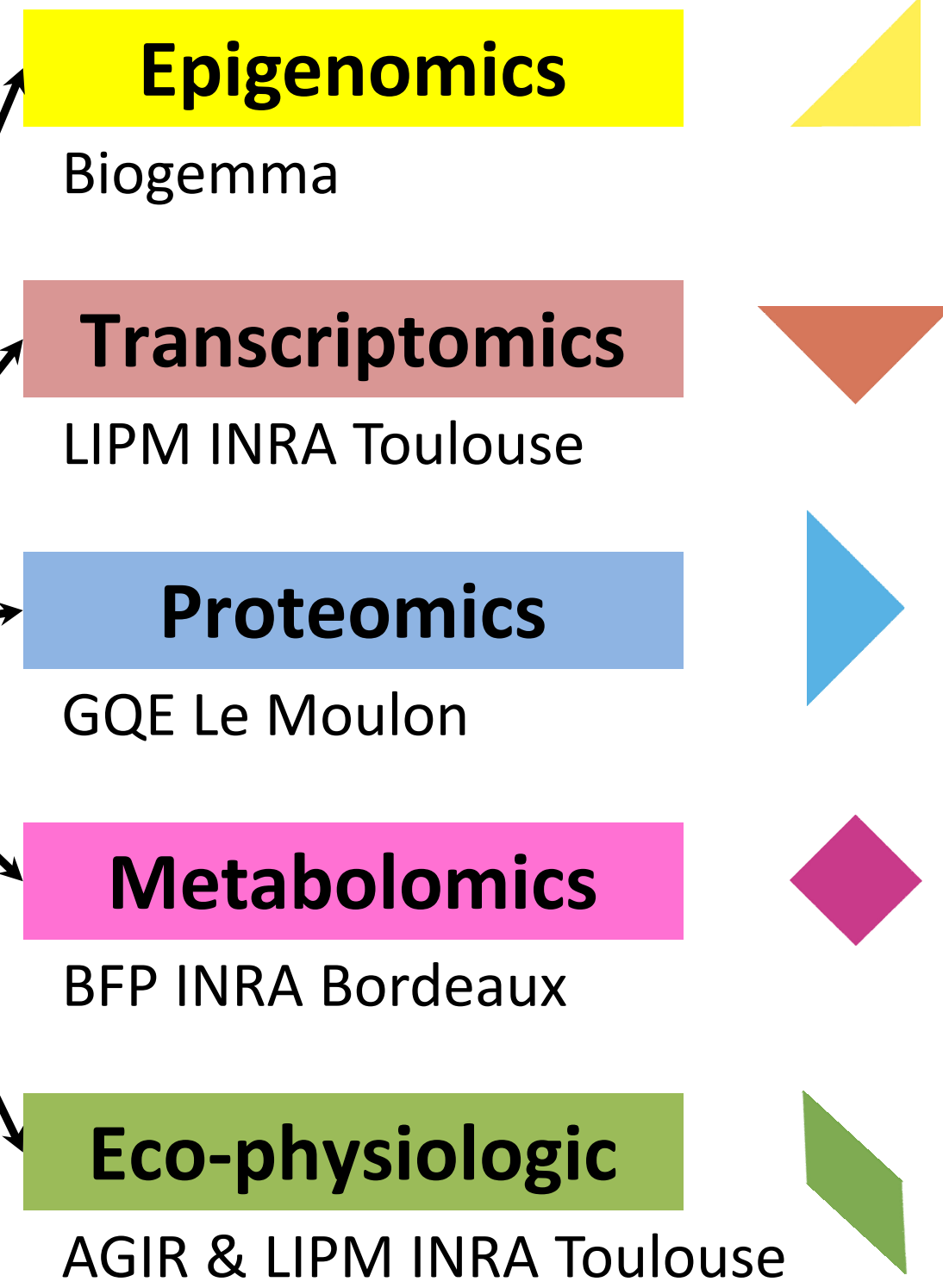
x3 biological replicates

x2 environmental conditions managed by the *Heliaphen* robot<sup>[3]</sup>:

- Stress control
- Phenotyping standardization
- Close to the field conditions



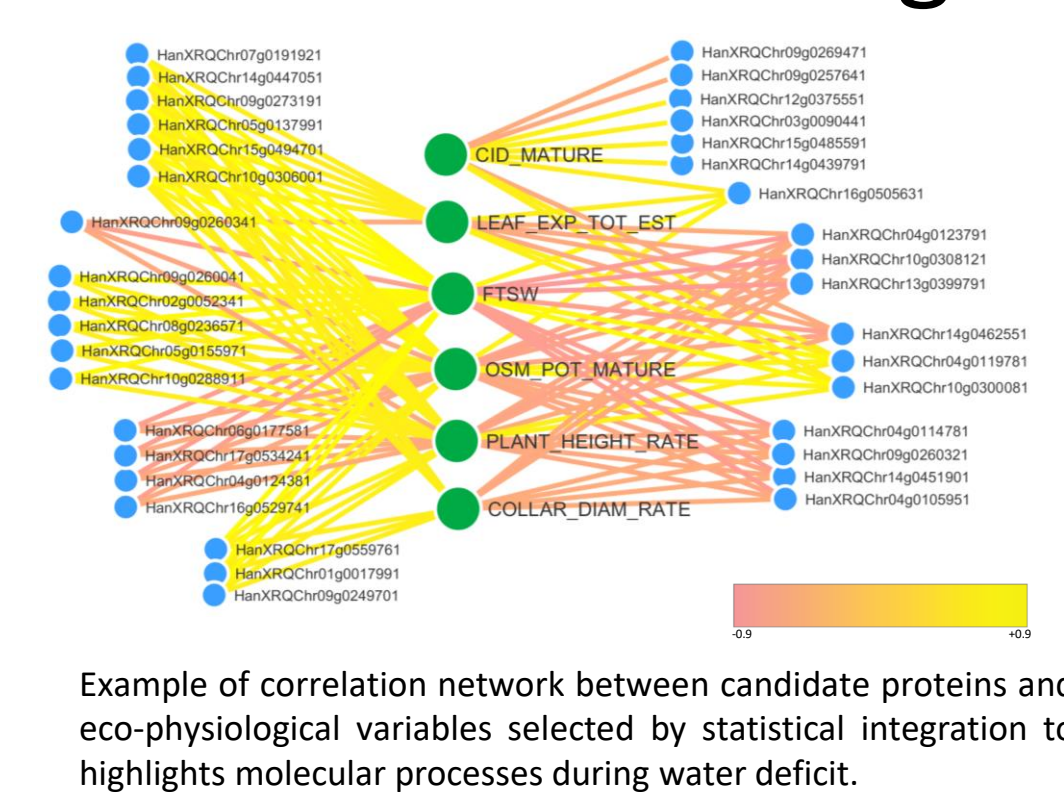
#### A transdisciplinary and multi-partner project



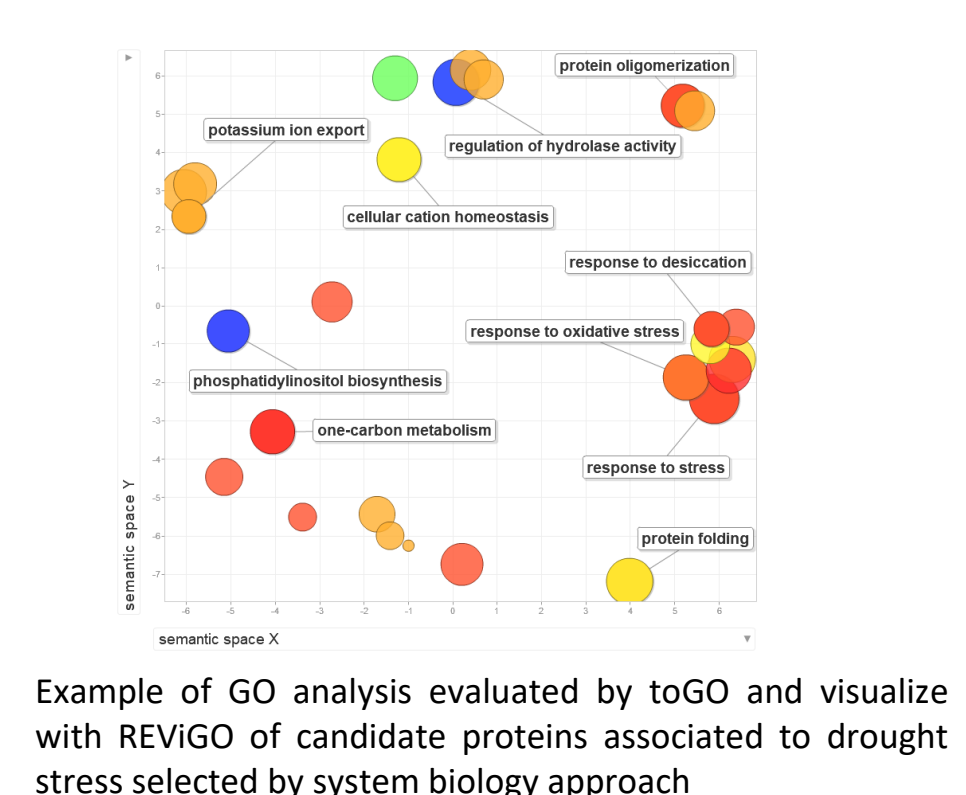
#### Holistic approach

#### Conclusion & Perspectives

The integrative analysis helped to provide interesting candidates<sup>[4]</sup>, to explain the differences of behaviors observed between genotypes and to understand relationships between heterogeneous omics datasets.



Example of correlation network between candidate proteins and eco-physiological variables selected by statistical integration to highlights molecular processes during water deficit.



Example of GO analysis evaluated by toGO and visualize with REVIGO of candidate proteins associated to drought stress selected by system biology approach

### 2 - Using mathematical models to better understanding sunflower response to drought and heterosis

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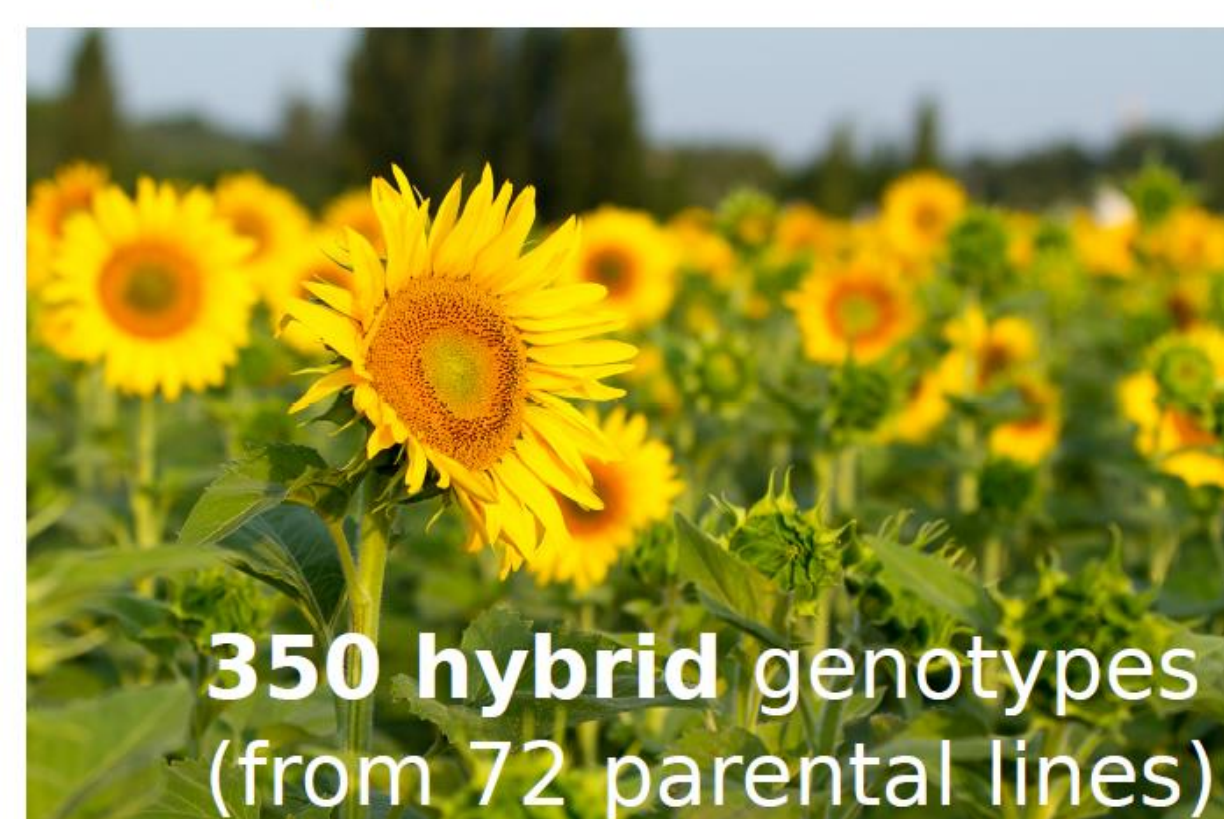
180 genes  
 to study plant response  
 to drought and heterosis

edge number of observation  
 (RNA expression, SNP, etc.)

MATHEMATICAL MODELS

hypothesis of regulation

Field experiment

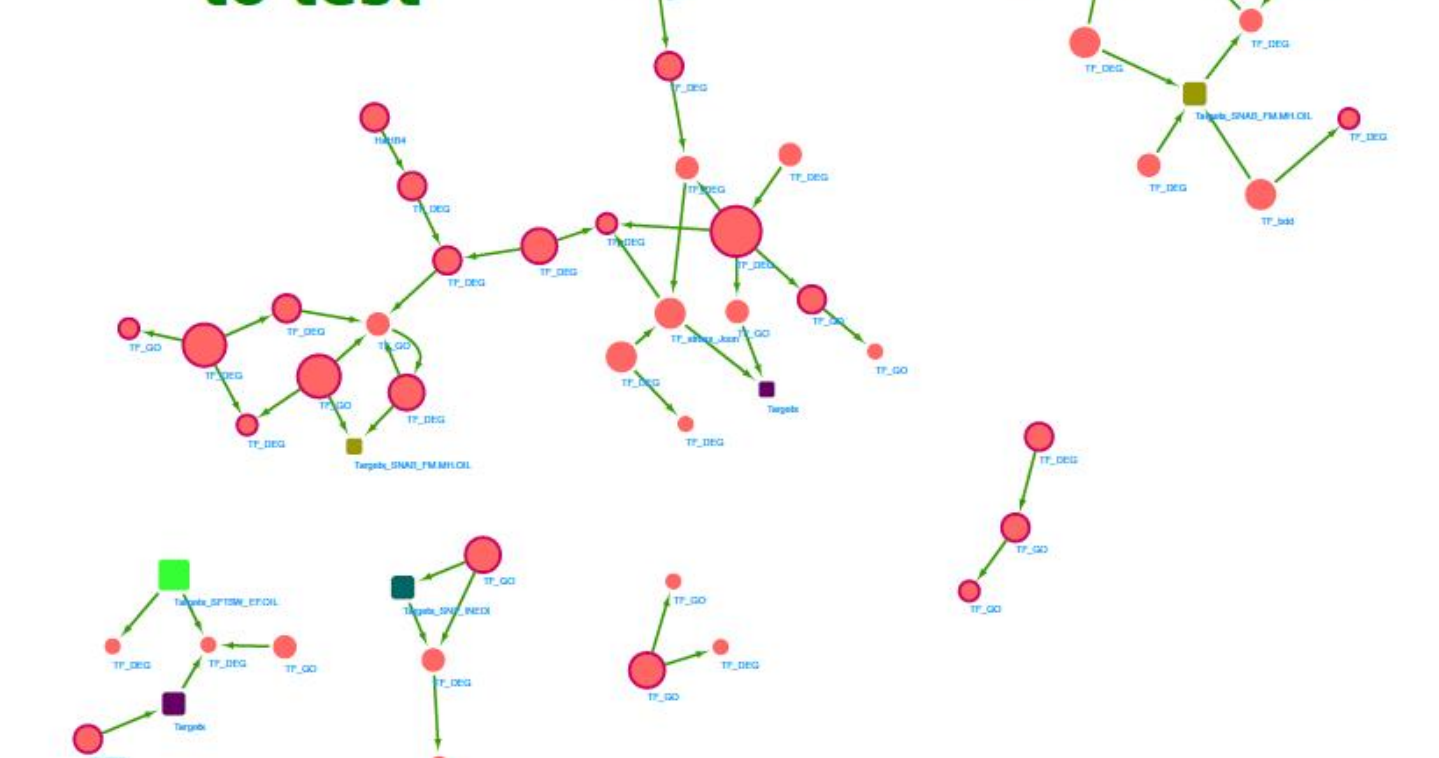


350 hybrid genotypes  
 (from 72 parental lines)

for the 180 genes :  
 - expression measured (fluidigm)  
 - SNP measured

lasso  
 random forest  
 bayesian network  
 OLS  
 PE-MRF  
 meta-analyse

75 régulations  
 to test



test on in silico data show that 80%  
 of found regulations are true