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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^[1] and is promising for agriculture adaptation because it can maintain stable yields across a wide variety of environmental conditions, especially during drought stress^[2]. 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

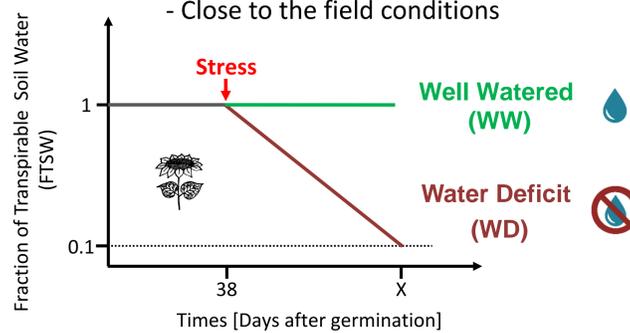
24 genotypes (8 parental lines and 16 hybrids)

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

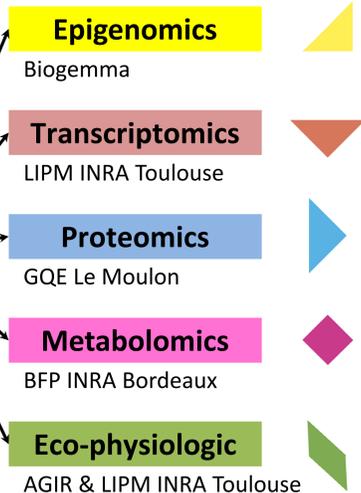
x3 biological replicates

x2 environmental conditions managed by the *Heliaphen* robot^[3]:

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

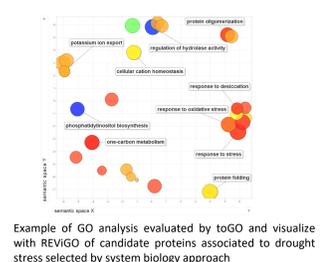
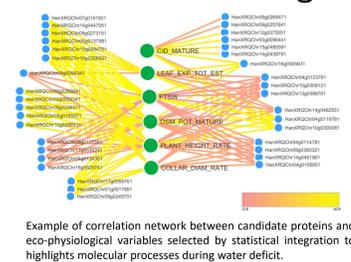


A transdisciplinary and multi-partner project



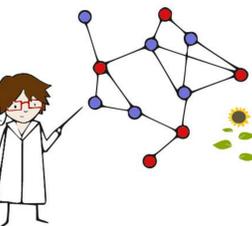
Conclusion & Perspectives

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



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

Lise Pomiès (Post doctoral position)
 Mathématiques et Informatique Appliquées de Toulouse (UR875)



180 genes
 to study plant response
 to drought and heterosis

32,320 possible regulations
 ~ 8 000 days of work in the
 lab to study all those possible
 regulations

Solution
 Reduce the number of
 regulation to test in the lab
 by using **inference network**

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

MATHEMATICAL
 MODELS

hypothesis of regulation

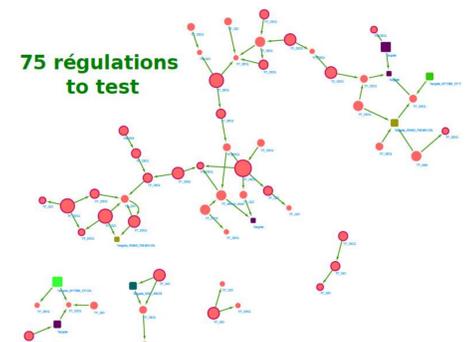
Field experiment



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



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