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A systems biology approach to study the genetic variability of proteome responses to water deficit in sunflower

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Context

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.

Strategies & Objectives

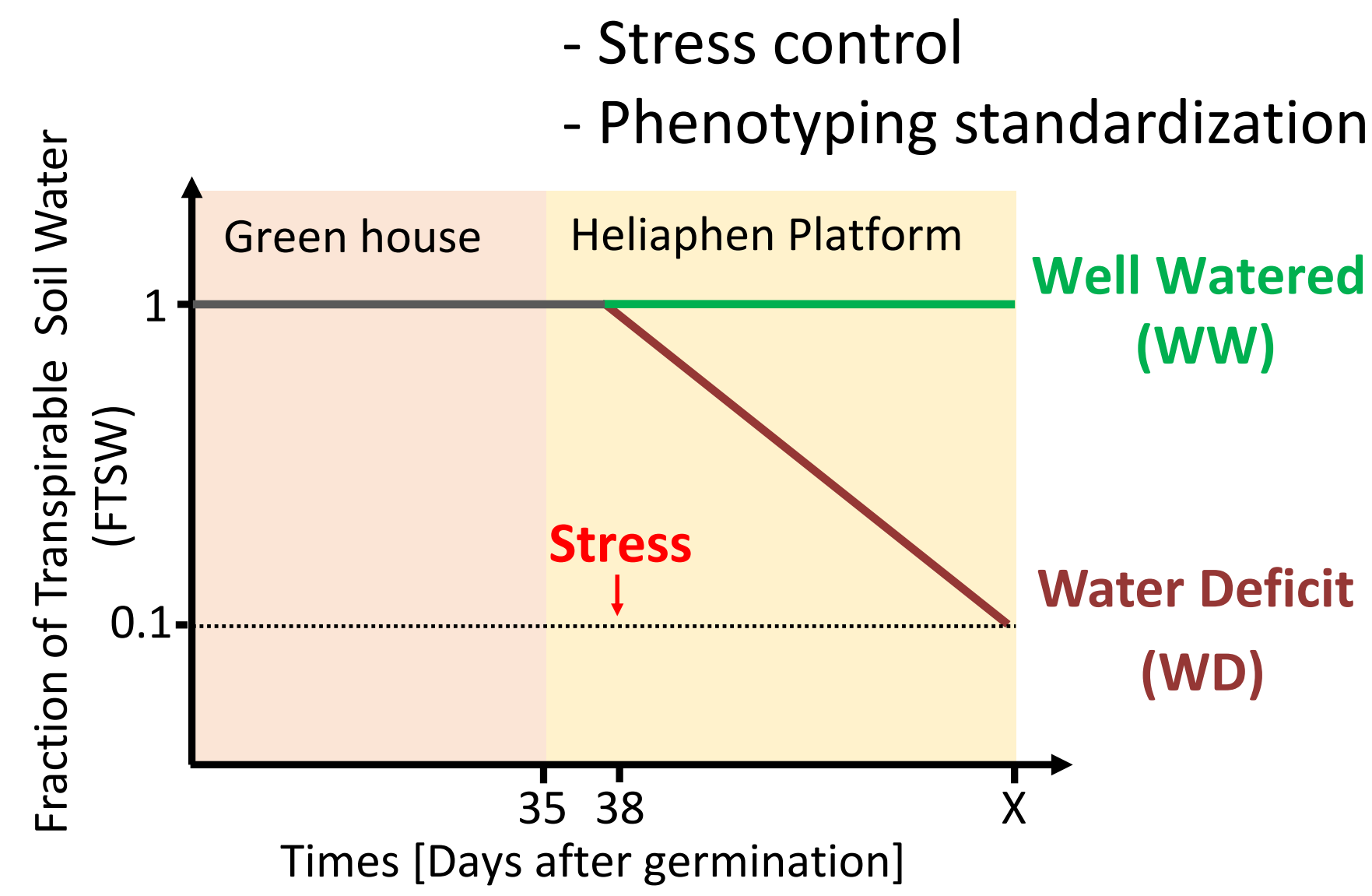
Characterization of the response of leaf proteome to drought and its genetic variation between parental lines and hybrids

24 genotypes (8 parental lines and 16 hybrids)

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

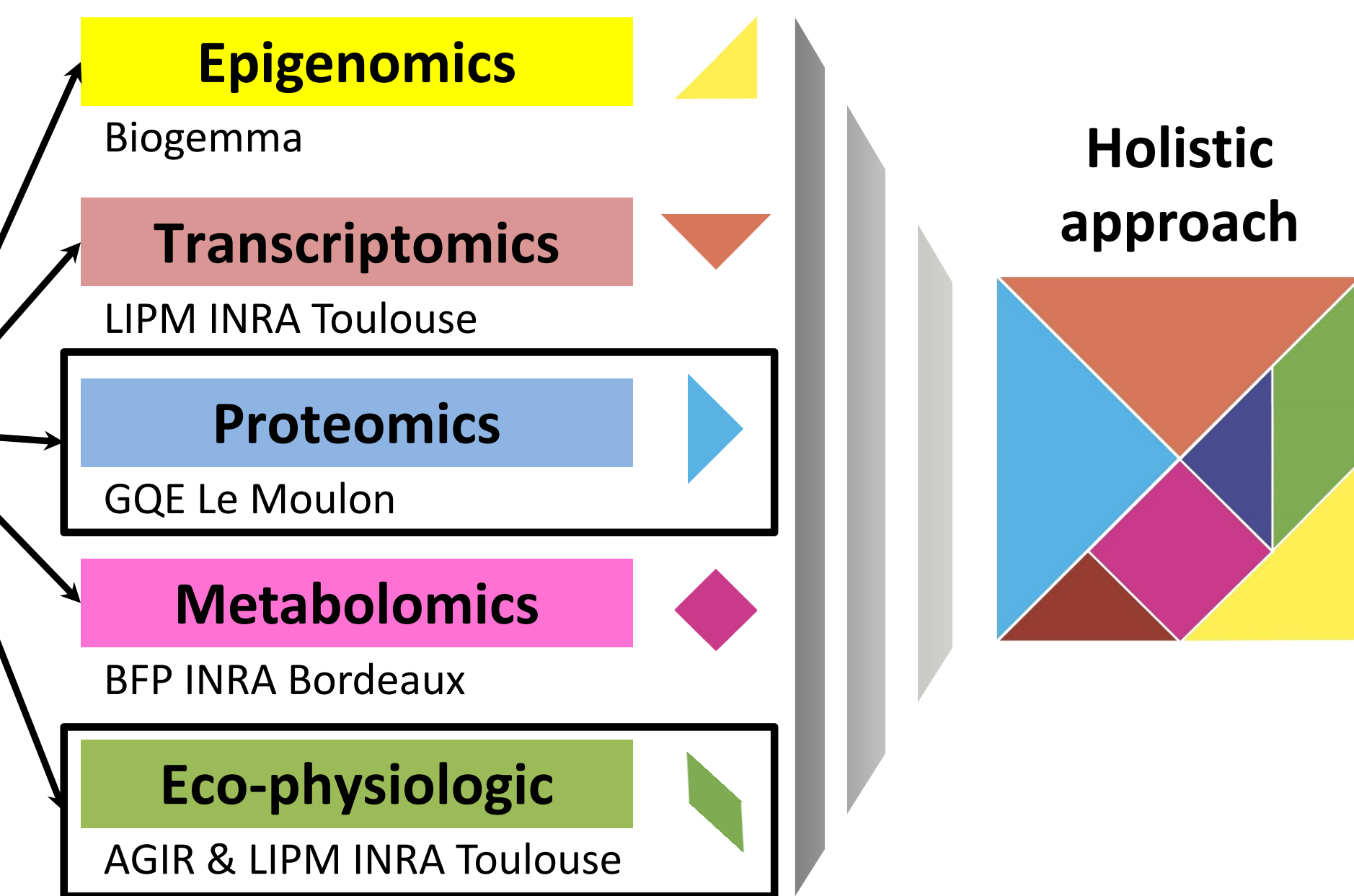
x3 biological replicates

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

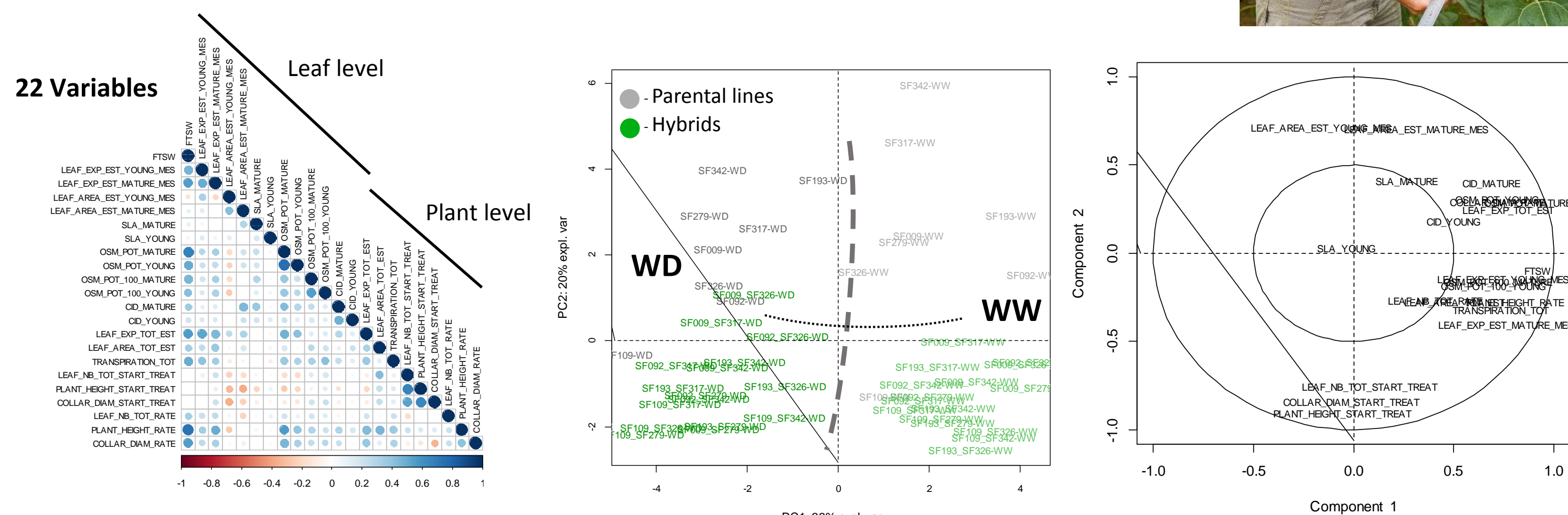


- Stress control
- Phenotyping standardization

A transdisciplinary and multi-partner project

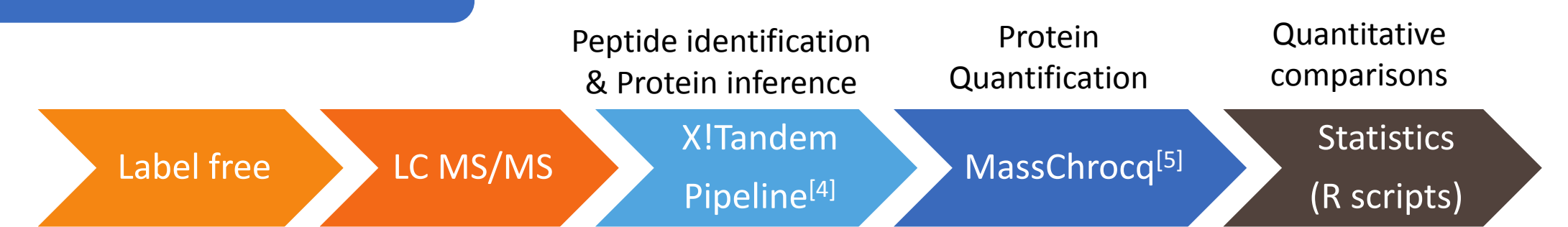


Eco-physiological data



- Strong impact of the water status:
 - Physiological variables
- Types of genotype (parental lines or hybrids) show different behaviors:
 - Architecture variables independent to the stress

Proteomics data

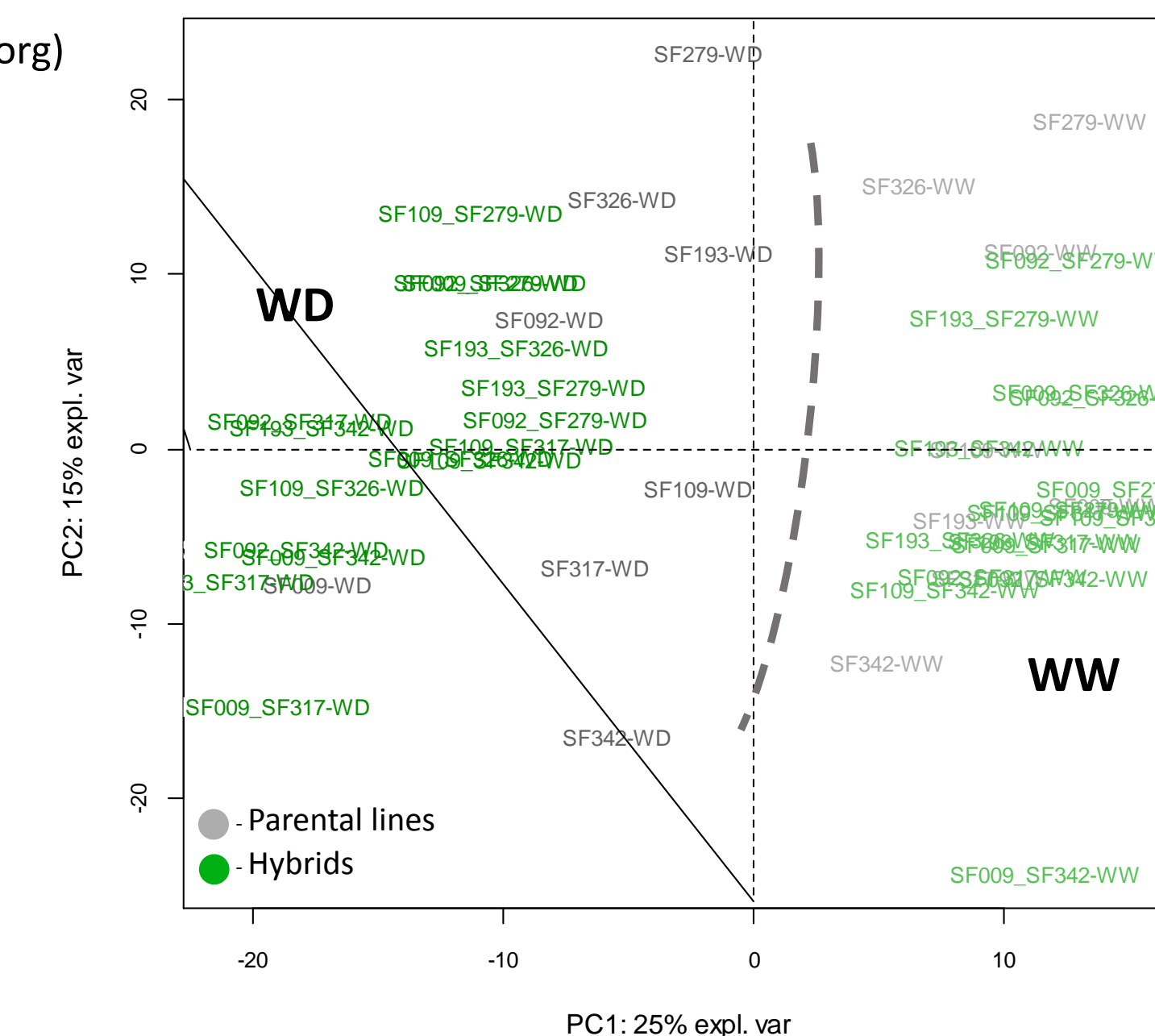


Identification
- Database : *Helianthus annuus* Non redundant Peptides XHQ (Heliagene.org)
- 2506 proteins identified

Quantification
- Quantitative analysis on 1211 proteins (after filtering) : ANOVA
- 575 DAPs (Differential Abundant Proteins) identified

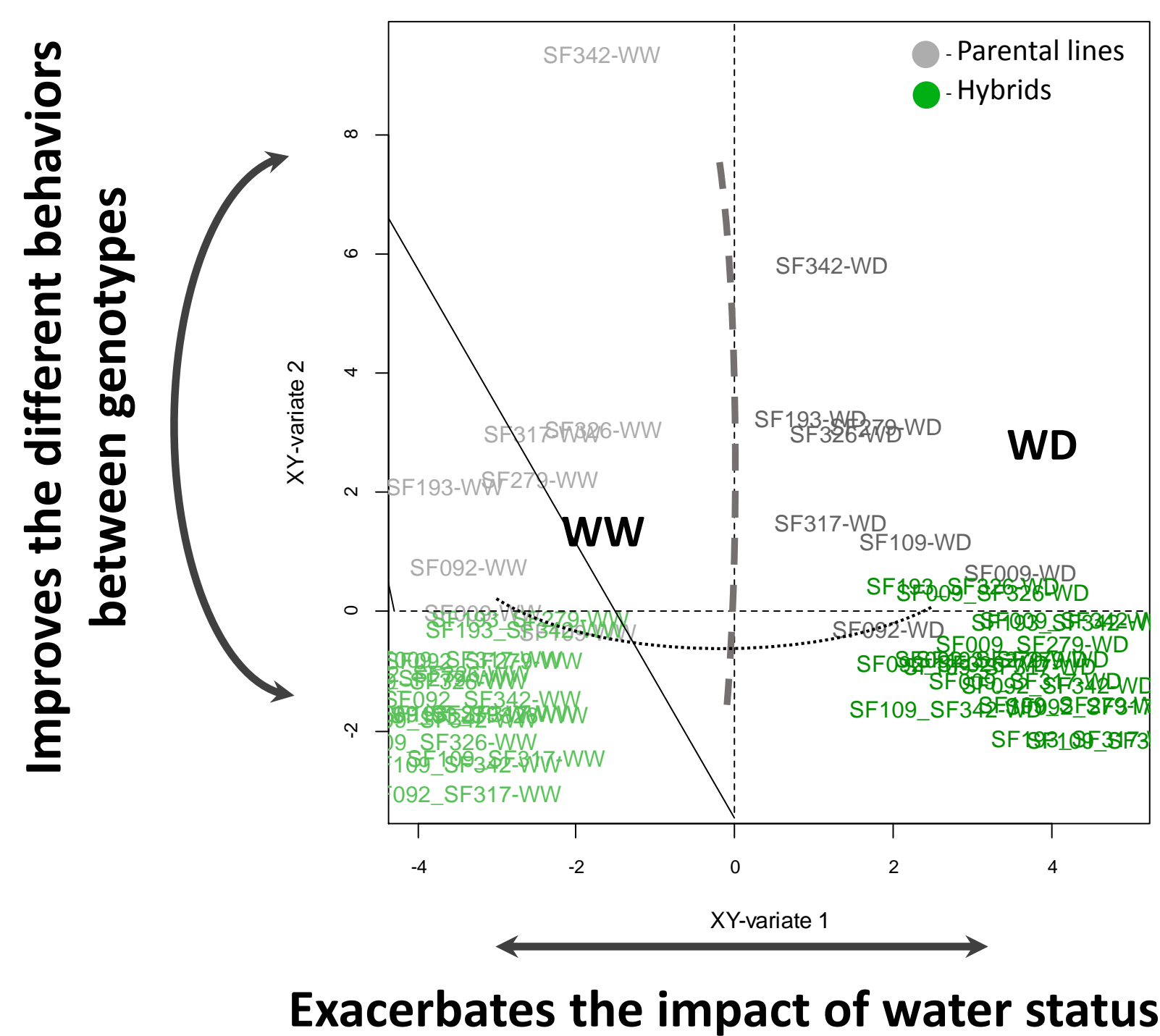
	Genotype	Treatment	Heterosis	Interaction
Nb of DAPs	446	210	84	6

- Strong influence of drought of the proteome
- Parental lines less impacted by the water stress



Integrative analysis

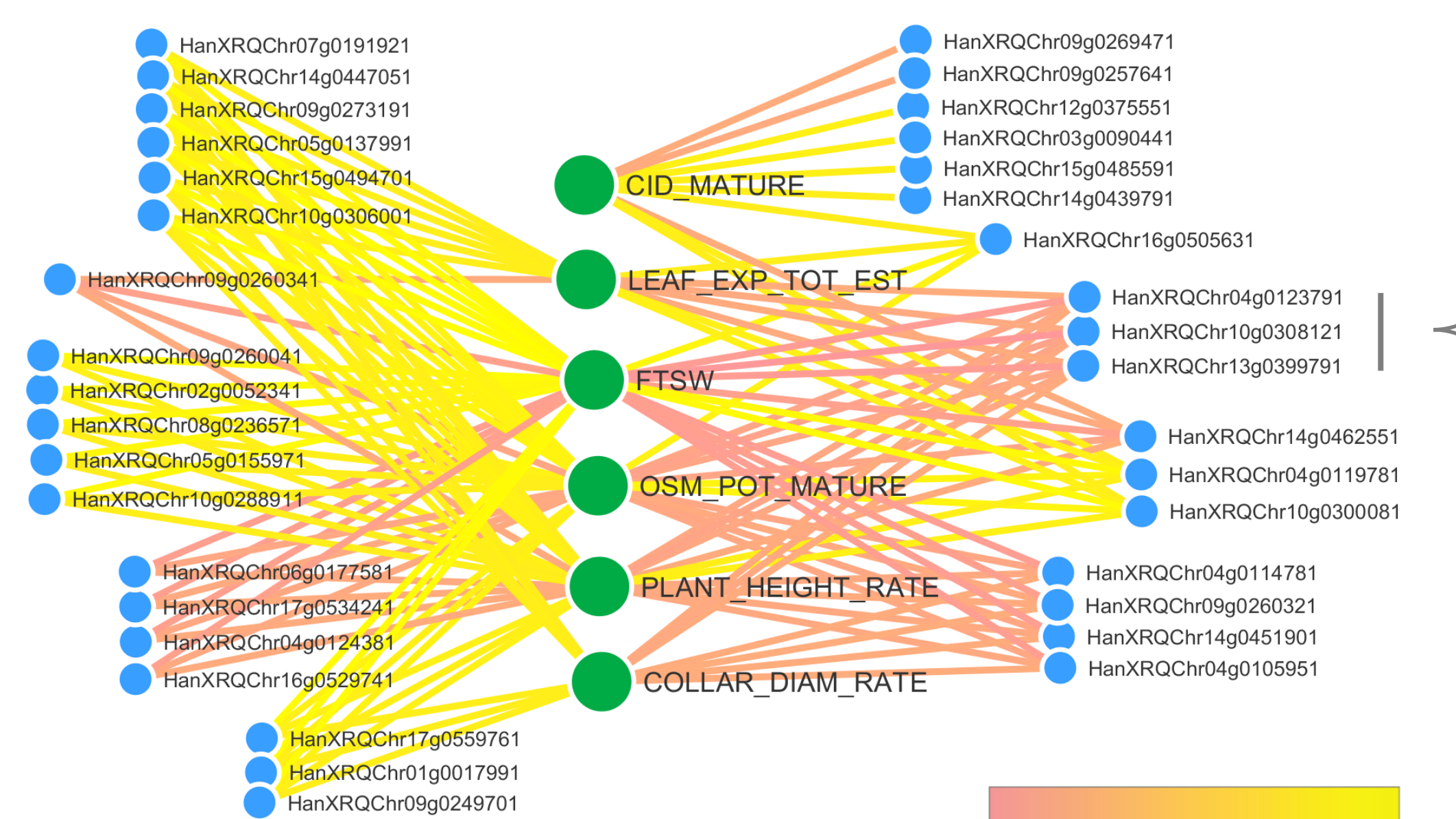
Eco-physiological data SPLS-DA Proteomics data



Improves the different behaviors between genotypes

Exacerbates the impact of water status

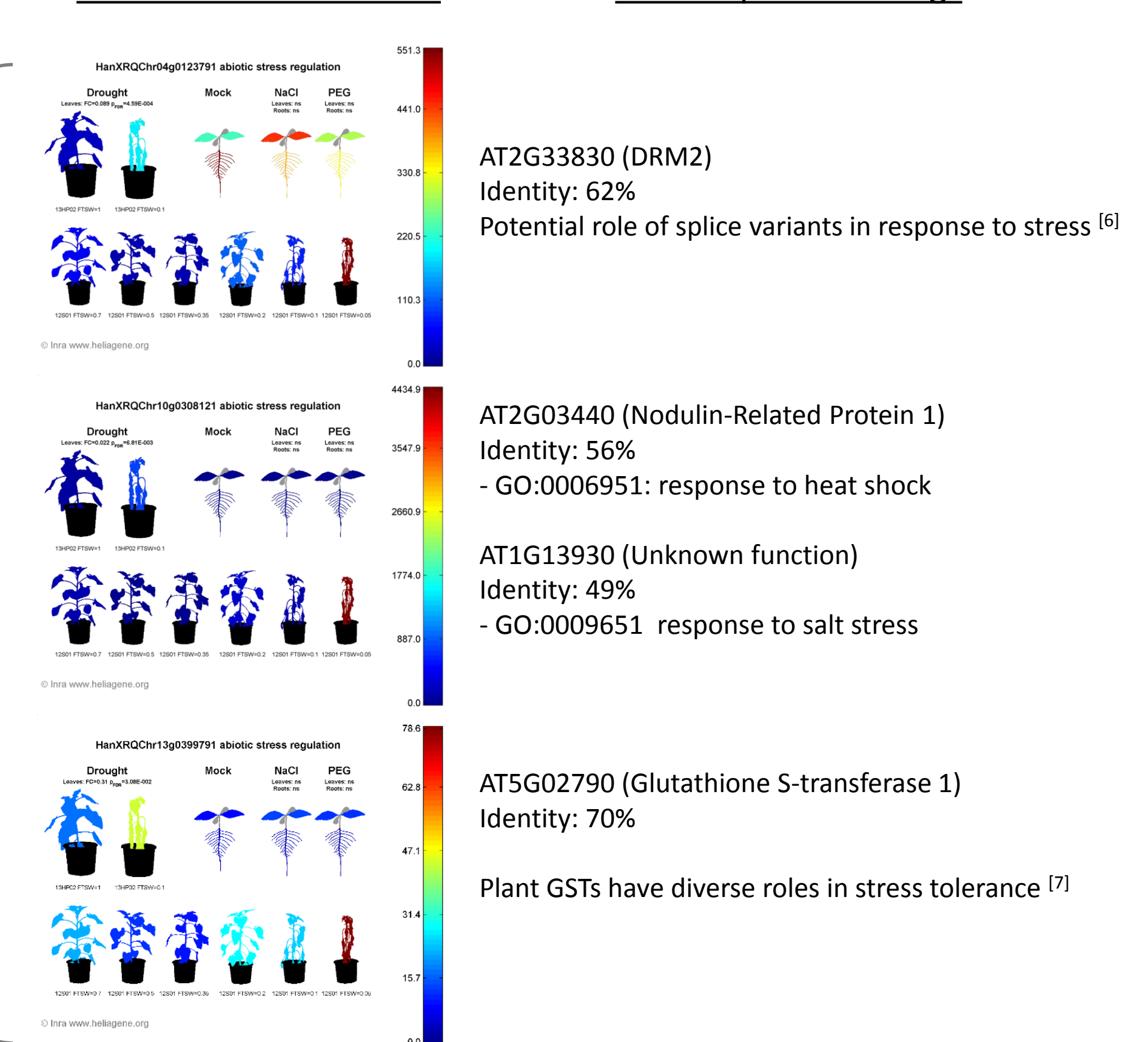
Systems biology approach without *a priori* highlights sunflower behaviors impacted by water deficit



Network displaying the correlation between the top proteins (60, blue) and eco-physiological variables (green) selected by a PLS model to discriminate the water status (cutoff: 0.55).
CID_MATURE: Carbon isotope discrimination (13C/12C) measured on the mature leaf; LEAF_EXP_TOT: leaf expansion of the entire plant estimates for the stress period; FTSW: fraction of transpirable soil water; OSM_POT_MATURE: osmotic potential of the mature leaf; PLANT_HEIGHT_RATE and COLLAR_DIAM_RATE: Differential measurement of collar diameter and plant height calculated between the beginning and the end of the stress normalised using the degree-day of this period.

Examples of candidate genes

Sunflower eFP Browser Arabidopsis homologs



Conclusion & Perspectives

To conclude, we demonstrated that sunflower has a strong response to water deficit and we observed different behaviors between hybrids and parental lines. The integrative analysis helped to provide interesting candidates^[8], to explain these differences and to understand relationships between eco-physiological and proteomics responses.

In perspective, we will characterize the most relevant candidates and study their roles using functional validation and genetic diversity evolution and breeding. Moreover, the heterosis effect (non additivity of abundance in the hybrids) and its role during drought stress will be characterised. This study is part of a larger project and other biological levels will be implemented soon to achieved a more holistic view.

References: [1] USDA, FAS. 2018; [2] Badouin *et al.*, Nature. 2017; [3] Gosseau *et al.*, bioRxiv. 2018; [4] Langella *et al.*, J Proteome Res. 2017; [5] Valot *et al.*, Proteomics. 2011; [6] Rae *et al.*, Mol. Genet. Genomics. 2014; [7] Nianiu-Obeidat *et al.*, Plant Cell Rep. 2017; [8] Duruflé *et al.*, bioRxiv. 2018