Multi-omics systems biology approach to reveal heterosis and drought response genomic processes in sunflower

Harold Duruflé

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SUNRISE

Multi-omics systems biology approach to reveal heterosis and drought response genomic processes in sunflower

Harold Duruflé

BioForA




General context

Why are we studying sunflower?

Long-time model in ecology and evolution

Hybrid speciation accompanied by genomic reorganization in wild sunflowers

Loren H. Rieseberg, Chrystal Van Fossen & Andrée M. Desrochers

Nature, 1995

Origin of extant domesticated sunflowers in eastern North America

Abigail V. Harter, Keith A. Gardner, Daniel Falush, David L. Lentz, Robert A. Bye & Loren H. Rieseberg

Nature, 2004

ndhF sequence evolution and the major clades in the sunflower family

K J Kim and R K Jansen

PNAS, 1995

Major Ecological Transitions in Wild Sunflowers Facilitated by Hybridization

Loren H. Rieseberg[1,*], Olivier Raymond[2], David M. Rosenthal[3], Zhao Lai[1], Kevin Livingstone[1], Takuya Nakazato[1], Jennifer L....

Science, 2003

Genomic islands of divergence are not affected by geography of speciation in sunflowers

S. Renaut, C. J. Grassa, S. Yeaman, B. T. Moyers, Z. Lai, N. C. Kane, J. E. Bowers, J. M. Burke & L. H. Rieseberg

Nature Communication, 2013

Genetics of alternative splicing evolution during sunflower domestication

Chris C. R. Smith, Silas Tittes, J. Paul Mendieta, Erin Collier-zans, Heather C. Rowe, Loren H. Rieseberg, and Nolan C. Kane

PNAS, 2018

The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution

Hélène Badouin, Jérôme Gouzy [...] Nicolas B. Langlade

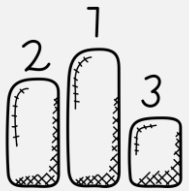
Nature, 2017

The genomics of linkage drag in inbred lines of sunflower

Kaichi Huang, Mojtaba Jahani, Jérôme Gouzy, +26, and Loren H. Rieseberg Authors Info & Affiliations

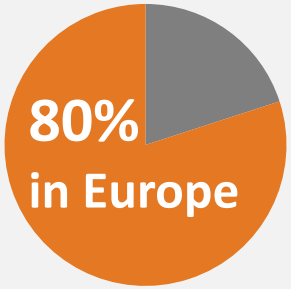
PNAS, 2023

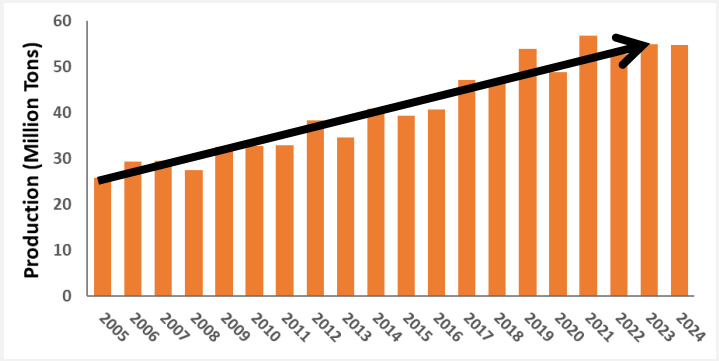
And … the third largest oilseed crop in the world



Sunflower, an important crop for Europe

45 Million tons of seed produced worldwide



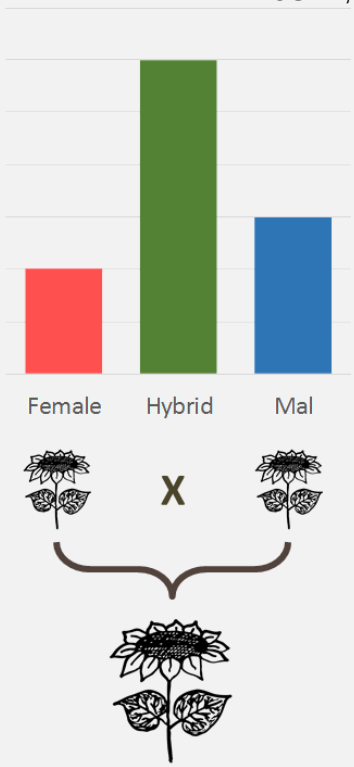


USDA, 2024

Hybrid production : > 90 % of sunflower production

Heterosis / Hybrid vigour: phenomenon who given progeny more vigorous than either of the two parents

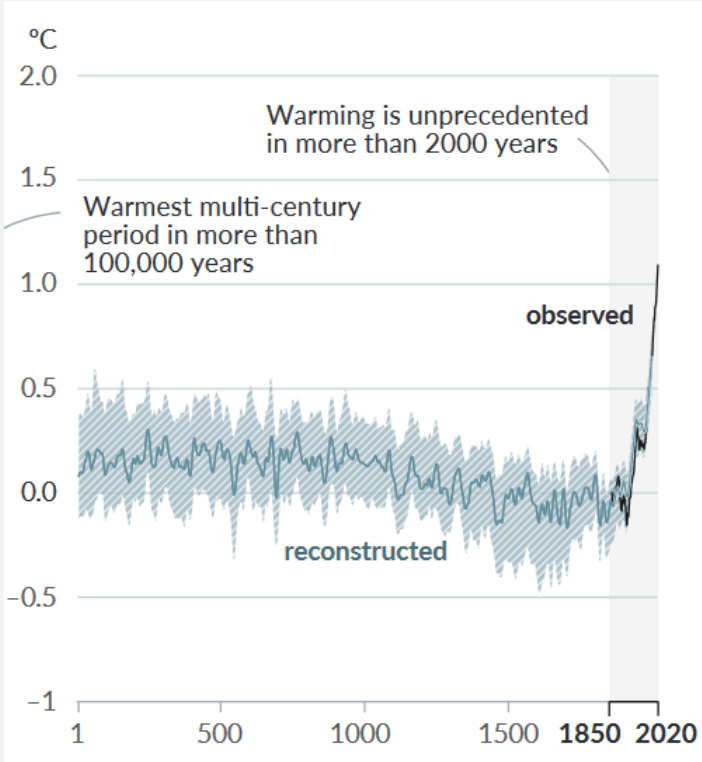
Washburn et., al. 2017



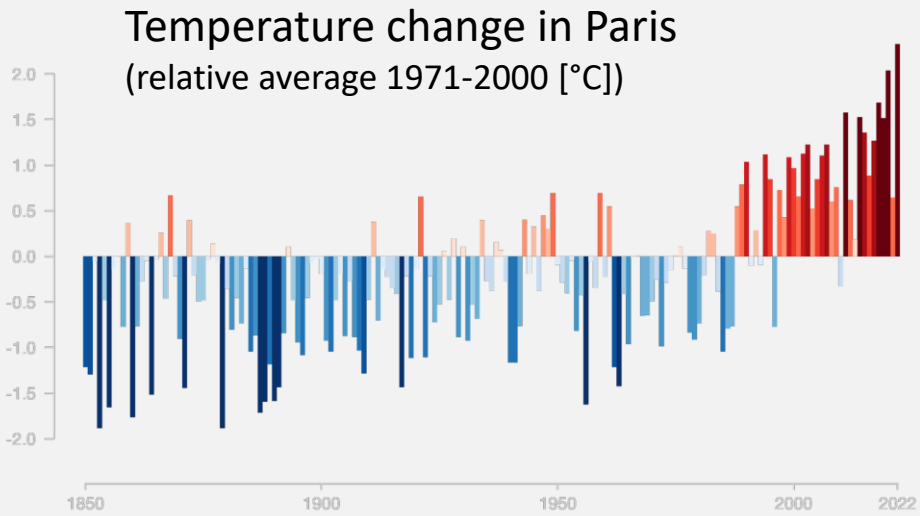
e.g. Higher yields and oil content, Disease resistance, Drought tolerance

Environmental context

Strong impact expected by the climate change



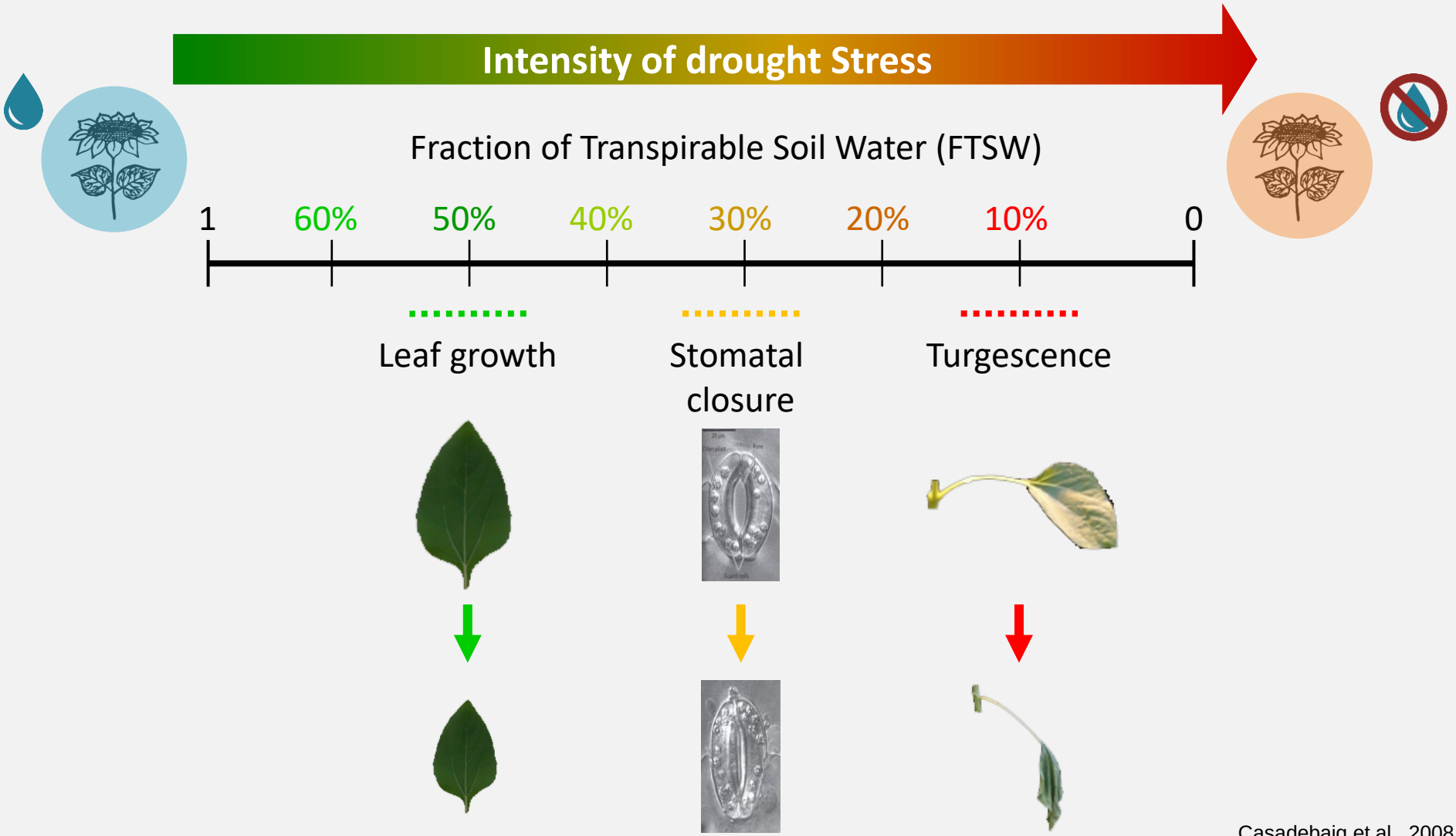
IPCC, 2021



Berkeley Earth, 2022

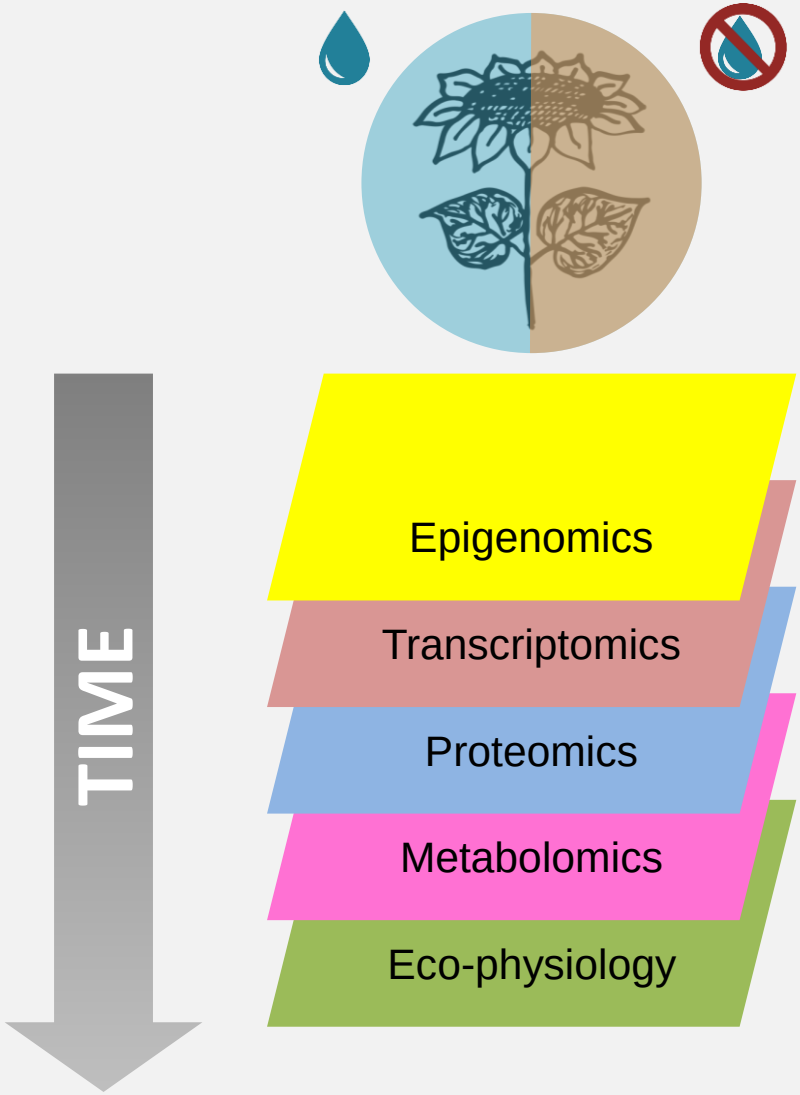
The drought stress response: complex responses

At the Agronomic, physiology, Molecular levels…



Casadebaig et al., 2008

The drought stress response: a complex response at multiple scales



Objectives & Strategies

How to characterize the response to sunflower drought and its genetic variation between parental lines and hybrids?

Experimental design

24 genotypes (8 parental lines and 16 hybrids)

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

2 environmental conditions

Water Deficit (WD)

Well Watered (WW)

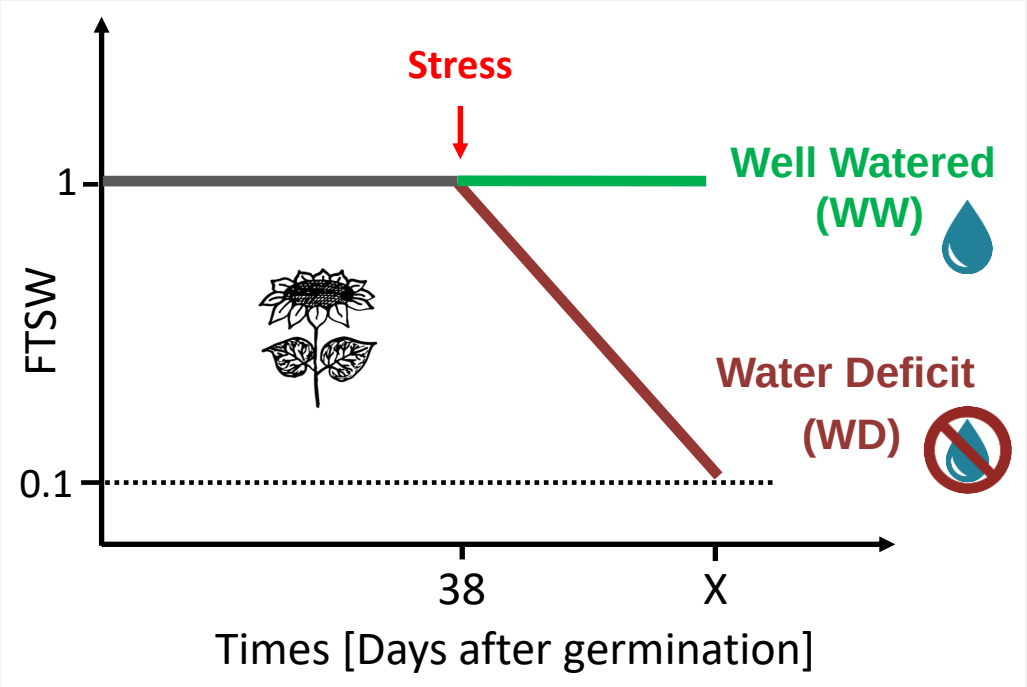
3 biological replicates

Objectives and experimental design

Realized with *Heliaphen* robot:

- **Controlled stress**
- **Phenotyping standardization**

Heliaphen platform (LIPM, INRA Toulouse)
(Gosseau et., al. 2019)



A transdisciplinary and multi-partner project

Epigenomics

innolea (ex Biogemma)

Transcriptomics

lipme

Proteomics

Génétique Quantitative et Évolution Le Moulon

PAPPSO

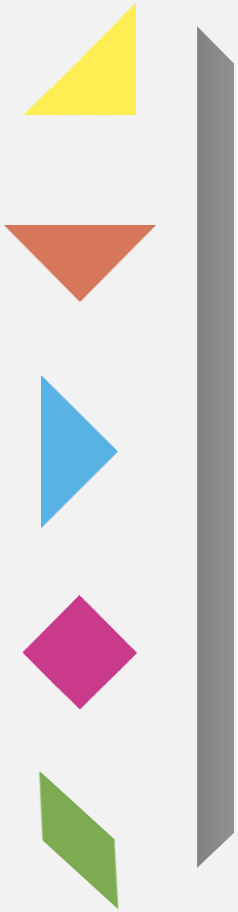
Metabolomics

bfp

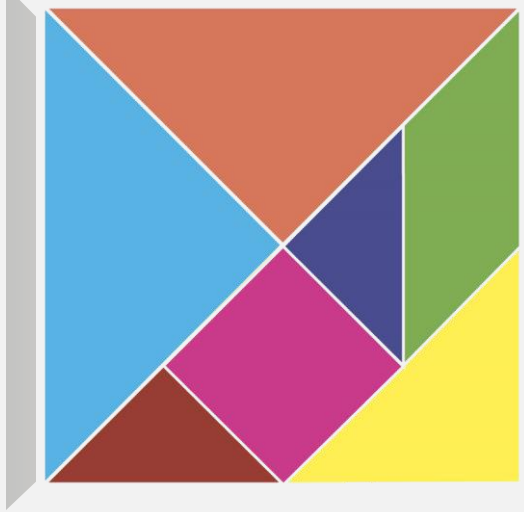
Eco-physiology

AGIR

lipme



Holistic approach



A transdisciplinary and multi-partner project

Epigenomics

Transcriptomics

Data Paper : Gody et., al. 2020

Proteomics

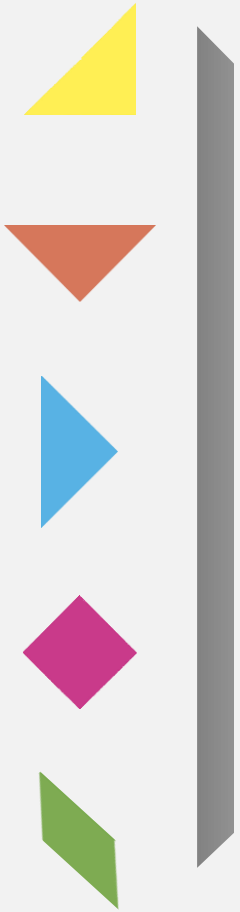
Data Paper : Baillau et., al. 2021

Metabolomics

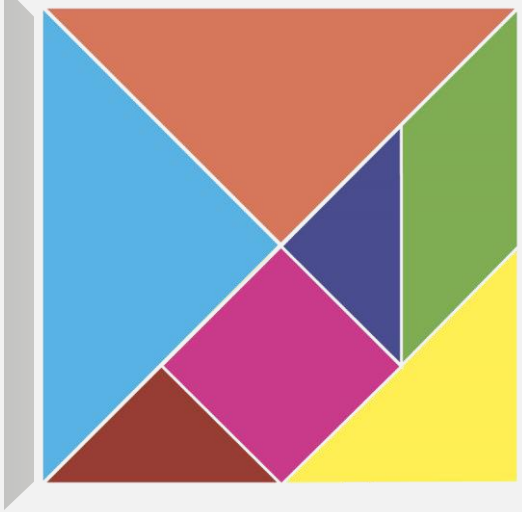
Data Paper : Berton et., al. 2021

Eco-physiology

Data Paper : Blanchet et., al. 2018



Holistic approach



Results

Eco-physiology

Nicolas Blanchet, Pierre Maury

Eco-physiological data

Eco-physiology

22 Variables

Physiological

e.g. Specific Leaf Area,
Osmotical potential,
Carbon Isotope Discrimination

Morphological

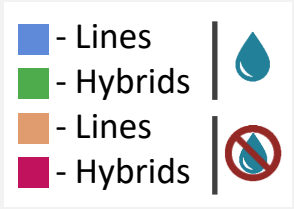
e.g. Plant height,
Number of leaves,
Leaf expansion

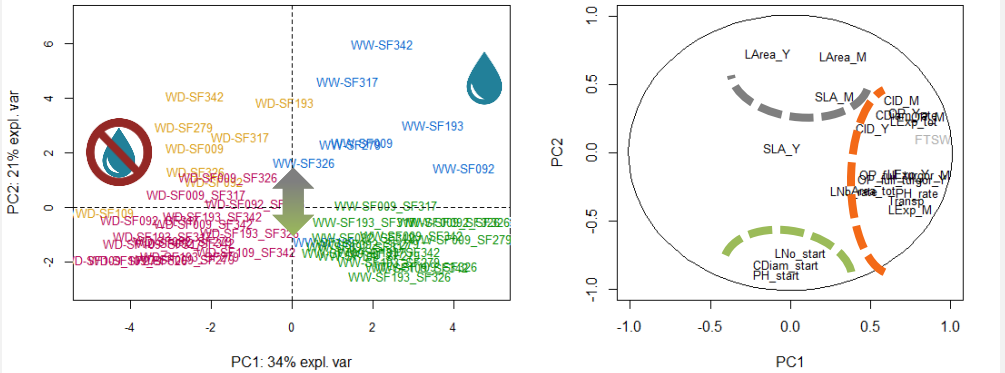
- At the beginning of the stress
- During the stress period
- At the end of the stress

Blanchet et. al., 2018

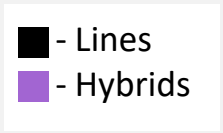
Eco-physiological data: multivariate analysis

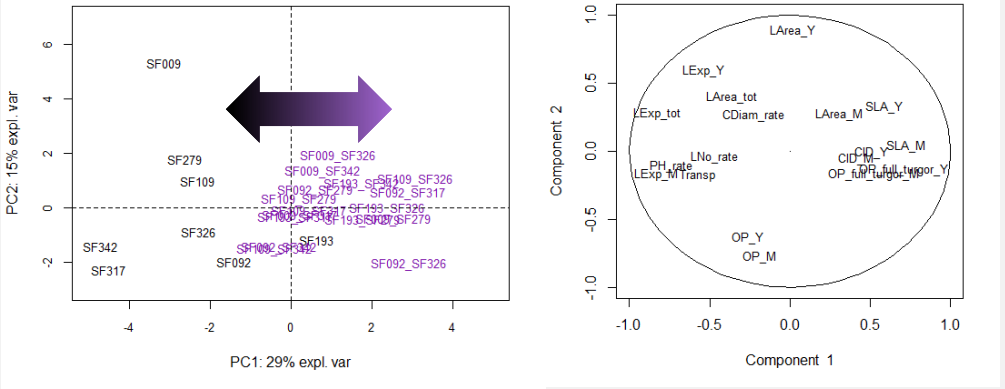
PCA of the traits





PCA of the trait responses to WD (WD-WW)





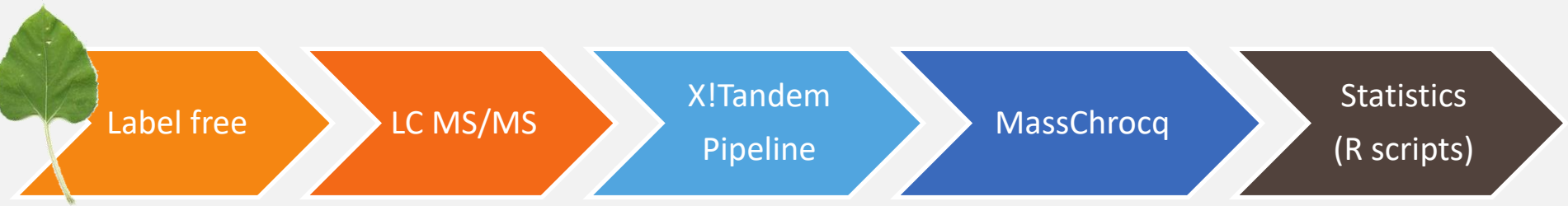
Duruflé et. al., 2023

- Strong impact of the water status: Physiological variables
- Types of genotype show different behaviors: Morphological variables
- Hybrids doesn't have the same behaviour than the parental lines during the stress.

Proteomics

Thierry Balliau, Mélisande Blein-Nicolas, Michel Zivy

Proteomics workflow



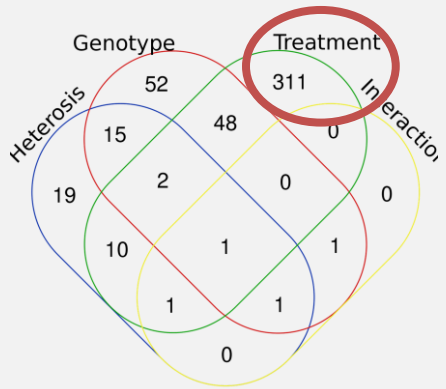
144 samples | Q-Exactive | Peptide identification & Protein inference (Langella et. al., 2017) | Protein Quantification (Valot et. al., 2011) | Quantitative comparisons

Identification

- Database : *Helianthus annuus* Non redundant Peptides XRQ (Heliagene.org)
- **3062 proteins identified**

Quantification

- Quantitative analysis on **1211 proteins** (after filtering) : Anova



471 DAPs identified with statistical tests

- Treatment, Genotypes, Heterosis, Interaction
- Pvalue < 0.05 (adjusted for multiple comparisons)
- Mixed model using kinship matrix

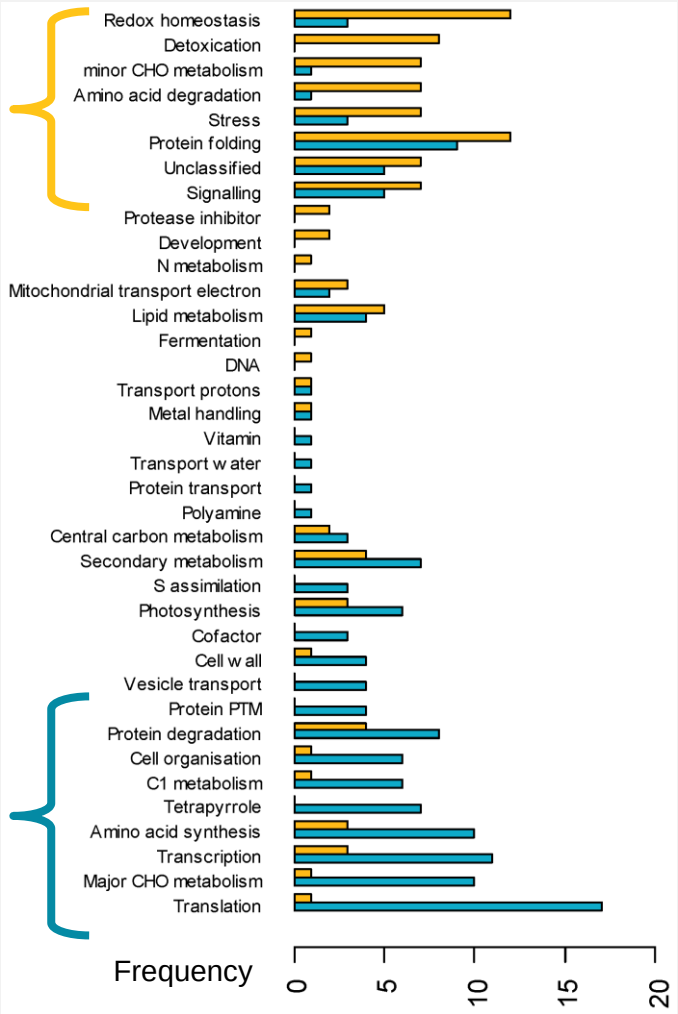
Duruflé et. al., 2023

Main protein categories involved in the response

Functional category of proteins in response to Water Deficit

Upregulated

Downregulated



- Classical global response to the stress

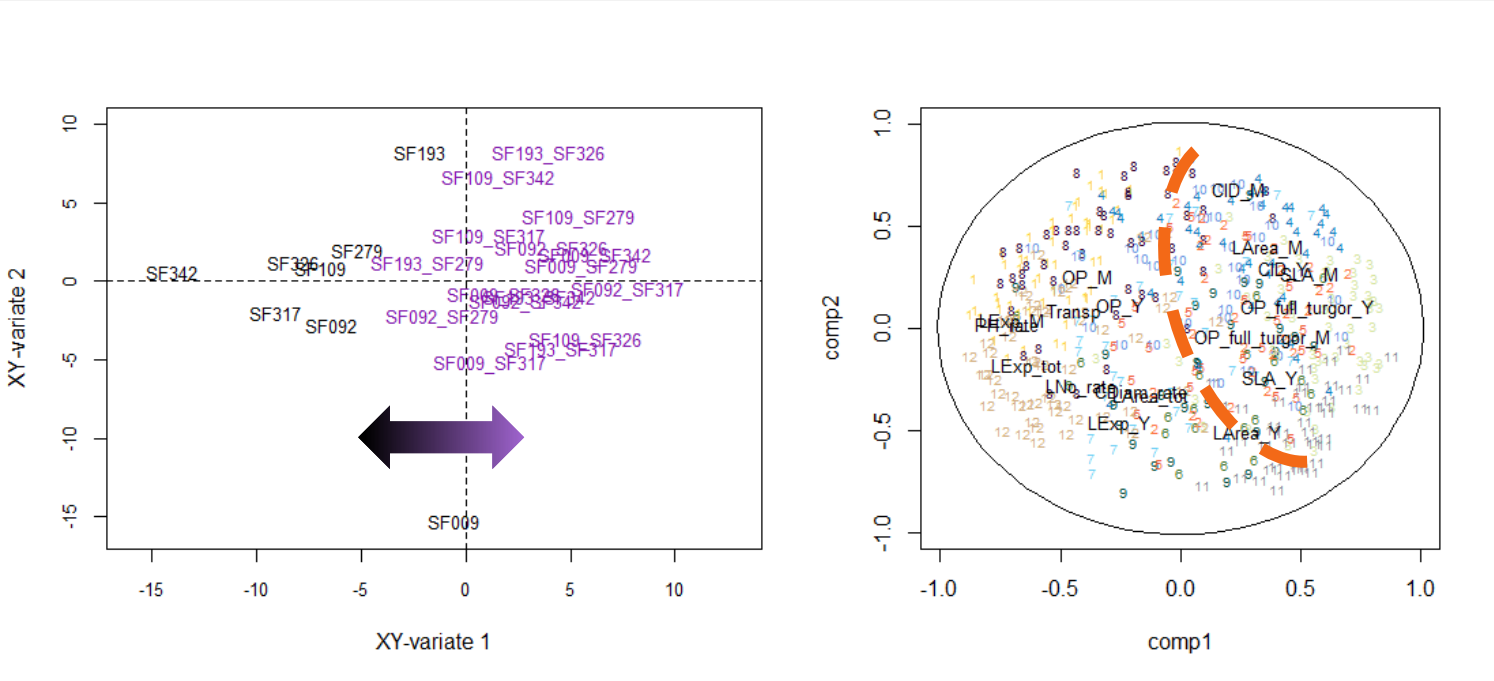
Duruflé et. al., 2023

Proteomics: Integrative analysis

PLS of trait responses to WD

DAPs (12 clusters by the K-means method & **Eco-Physiological** (EP)

- Lines
- Hybrids



Duruflé et. al., 2023

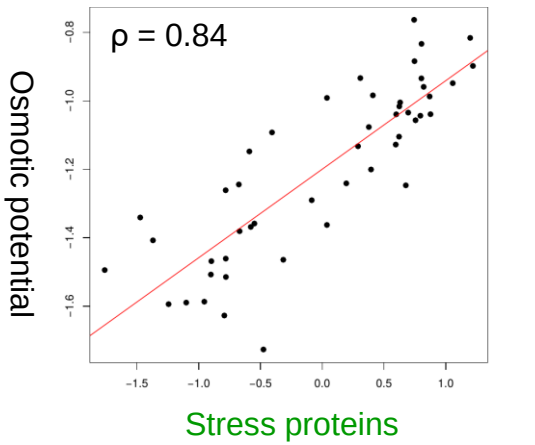
- Co-variation between eco-physiological responses and protein abundances
- Identification of clusters of DAPs upregulated in hybrids than in lines.

Basic correlation

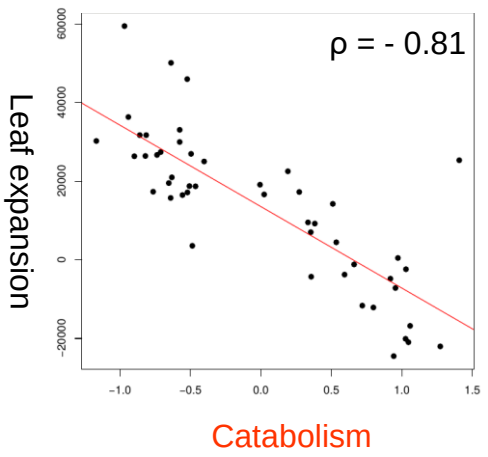
Examples of correlation based on the water status (and)

(48 genotype/treatment means)

Proteins decreasing upon



Proteins increasing upon

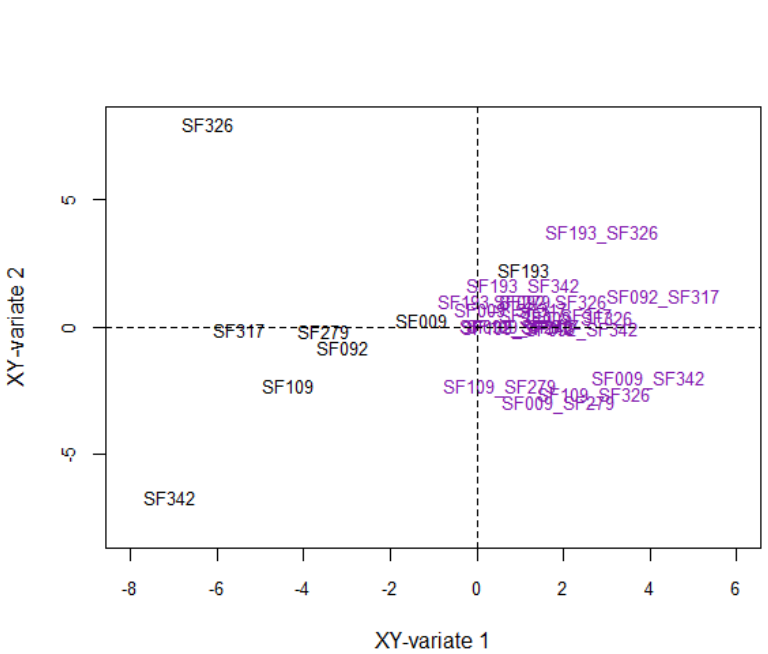


- Highlighted some correlations between proteins and ecophysiological variables
- **Is it possible to predict WD response with protein levels under WW conditions?**

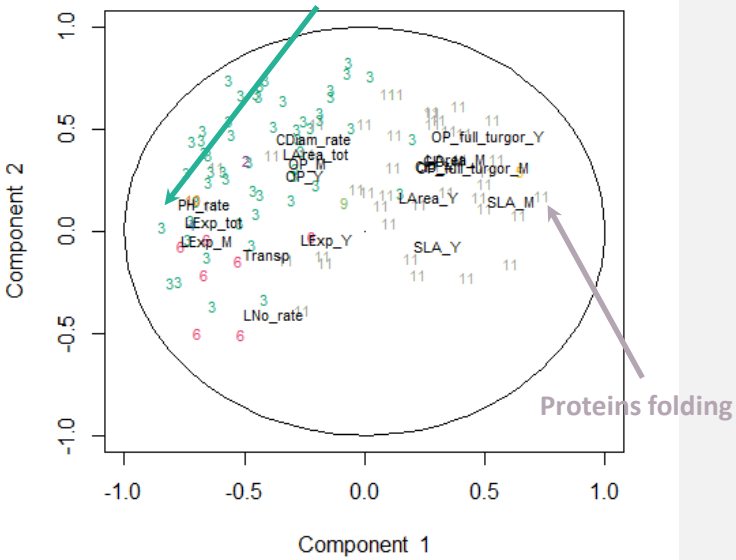
Proteomics and Predictions

PLS of 3 clusters of **DAPs upregulated under WW** conditions &
the response of the **EP traits**

- Lines
- Hybrids



Proteins involved in cell wall growth & synthesis of the osmoprotectant glycine-betaine



Duruflé et. al., 2023

- Positive correlation between the abundance of upregulated proteins under the WW condition and the maintenance of growth under WD (e.g. Cluster 3)

Metabolomics

Olivier Fernandez, Thierry Berton, Stéphane Bernillon, Yves Gibon, Annick Moing

Metabolomics (2019) 15:56
https://doi.org/10.1007/s11306-019-1515-4

ORIGINAL ARTICLE

Check for updates

Metabolomic characterization of sunflower leaf allows discriminating genotype groups or stress levels with a minimal set of metabolic markers

Olivier Fernandez[1,5] · Maria Urrutia[1,2,6] · Thierry Berton[1,7] · Stéphane Bernillon[1,3] · Catherine Deborde[1,3] · Daniel Jacob[1,3] · Mickaël Maucourt[1,3,6] · Pierre Maury[4] · Harold Duruflé[4] · Yves Gibon[1,3] · Nicolas B. Langlade[4] · Annick Moing[1,3]

Network

Simon De-Givry, Lise Pomiès, Céline Brouard

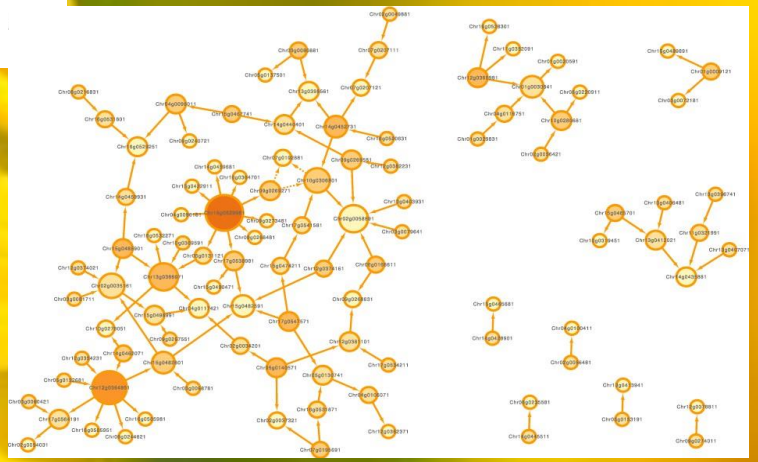
Bioinformatics, 38(17), 2022, 4127–4134
https://doi.org/10.1093/bioinformatics/btac445
Advance Access Publication Date: 6 July 2022
Original Paper

OXFORD

Gene expression

Gene regulatory network inference methodology for genomic and transcriptomic data acquired in genetically related heterozygote individuals

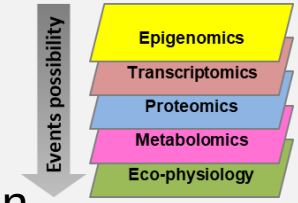
Lise Pomiès [1], Céline Brouard[1], Harold Duruflé[2], Élise Maigné[1], Clément Carré[1], Louise Gody[2], Fulya Trösser[1], George Katsirelos[3], Brigitte Mangin[2], Nicolas B. Langlade[2] and Simon de Givry [1,*]



Conclusions & Perspectives

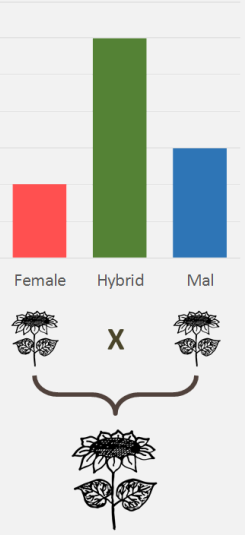
Conclusions and perspectives

- Large and complex effect of water deficit at multi biological scales
- Hybrids seem to be more reactive to water deficit than parental lines
- Multi-level analysis allows to see impact of the accumulation of regulation
- But, 3 biological replicates is not enough for complex statistical models



Perspectives:

- Give biological and evolutionary meaning of the integrative studies
  - Functional validation of the most relevant candidates
  - Genetic diversity evolution and breeding
- Improve our knowledge of the regulatory networks underlying heterosis



Challenges:

- Quantitative genetics approaches to study plasticity
- Increase the amount of protein per variety / genotype

lipme **ASTR team**

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Nicolas Blanchet
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Florie Gosseau
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Ludovic Legrand

Génétique Quantitative et Évolution Le Moulon — PAPPSO

Thierry Balliau
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Michel Zivy

bfp BORDEAUX METABOLOME

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Yves Gibon
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SUNRISE
UNE CULTURE POUR LE FUTUR

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Simon De-Givry
Lise Pomiès
Céline Brouard
Élise Maigné

Thanks to all people involved…

…and thank you for your attention

innolea
Magalie Leveugle

ANR — Investissements d'avenir — GIS bV — INRAE — syngenta — innolea — Terres Inovia — SOLTIS — RAGT 2n — LEREPS — mas seeds — SORBONNE UNIVERSITÉ — caussadesemences group