SUNRISE
SUNflower Resources to Improve yield Stability in a changing Environment

Nicolas Langlade
INRAE LIPME Toulouse

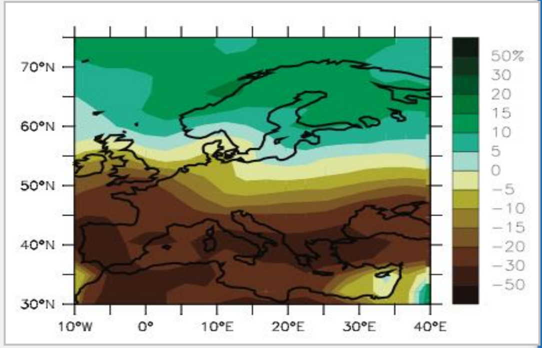
Climate change impact

Moriondo *et al.*, Climatic Change, 2010

Sunflower grain yield:

-20% in France in 2100

-50% in South-Eastern Europe



Precipitation deficit

SUNRISE data

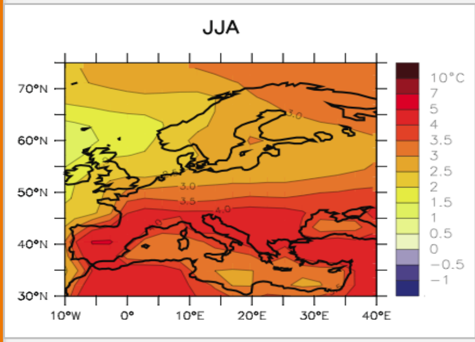
0.4q /ha /day stress

France: 750k ha ➔ 30 M€ / day

35d (2010s) → >50d (2030)/ year

World: 25 M ha

Temperature increase (°C)



Intergovernmental Panel on Climate Change (IPCC) Fourth Assessment Report
Moriondo et al., Climatic Change, 2010

A partnership centered around Toulouse

Seed industry research centres

- Innolea (Biogemma)
- Caussade (Lidea)
- MAS Seeds
- RAGT
- Soltis
- Syngenta

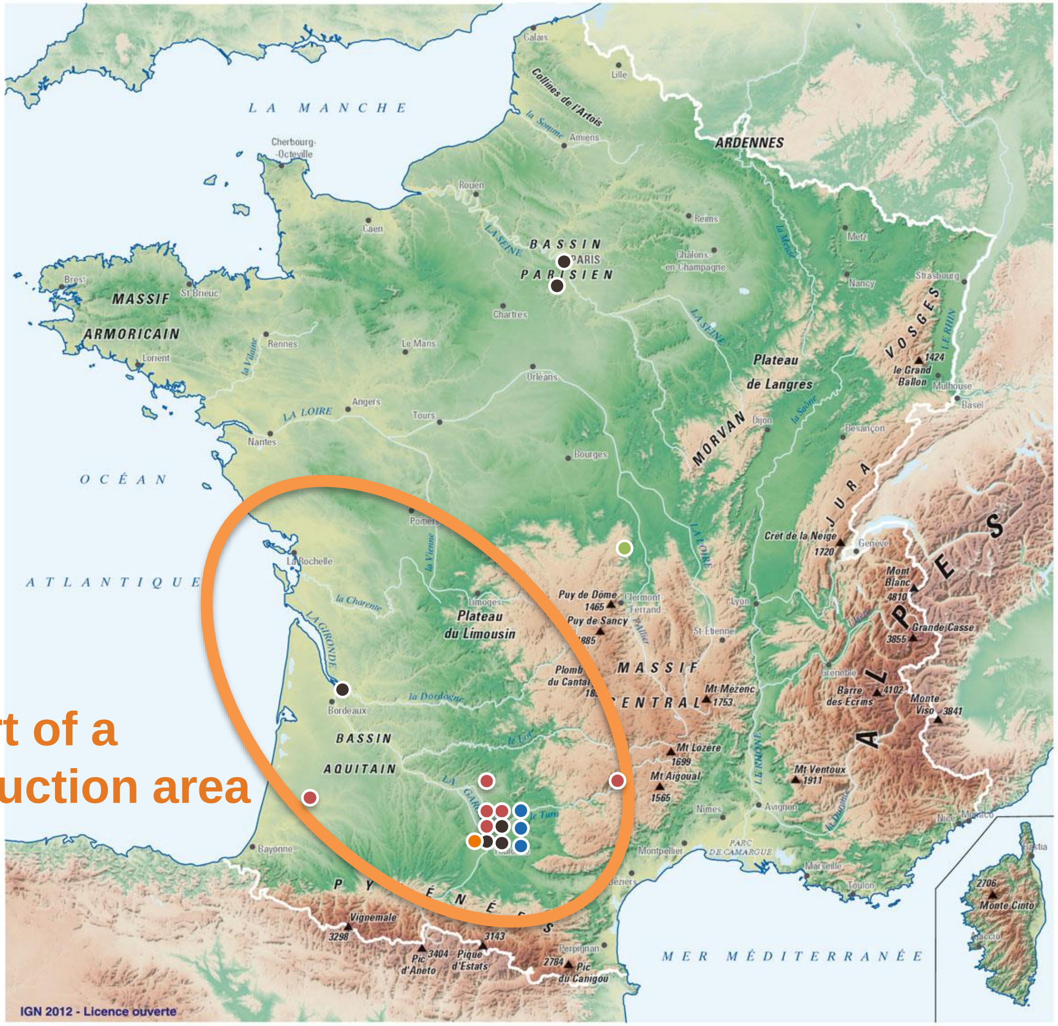
A technical institute:

- Terres Inovia

A multi-disciplinary public research centre for sunflower

- Agronomists
- Geneticists
- Bioinformaticians
- Mathematicians
- Genomics platform
- 2 phenotyping platforms

In the heart of a large production area



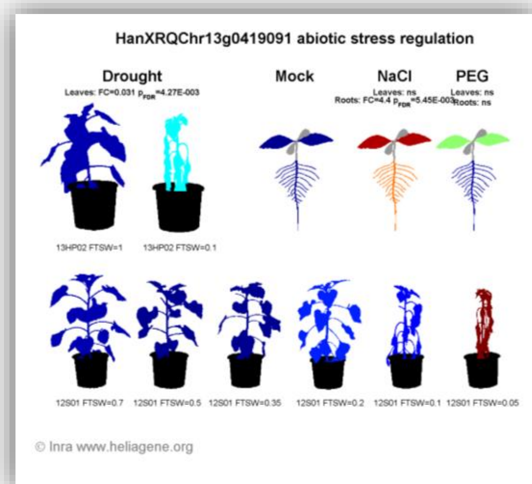
2 main scientific goals

Drought tolerance

At the genetic and molecular levels

In controled and field conditions

In a multistress context



Drought stress response

Heterosis

At the genetic and molecular levels

In controled and field conditions

Hybrid vigour

3 main scientific axis


Genomics and systems biology approach

Combined genetics and crop modeling approach

Socio-economic approach

Socio-economics analysis

Eco-service Pollination

Farm incomes

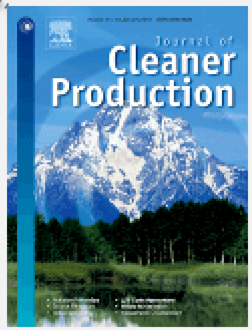
IMPACT OF POLICY

2012 · 2013 · 2014 · 2015 · 2016 · 2017 · 2018 · 2019 · 2020→

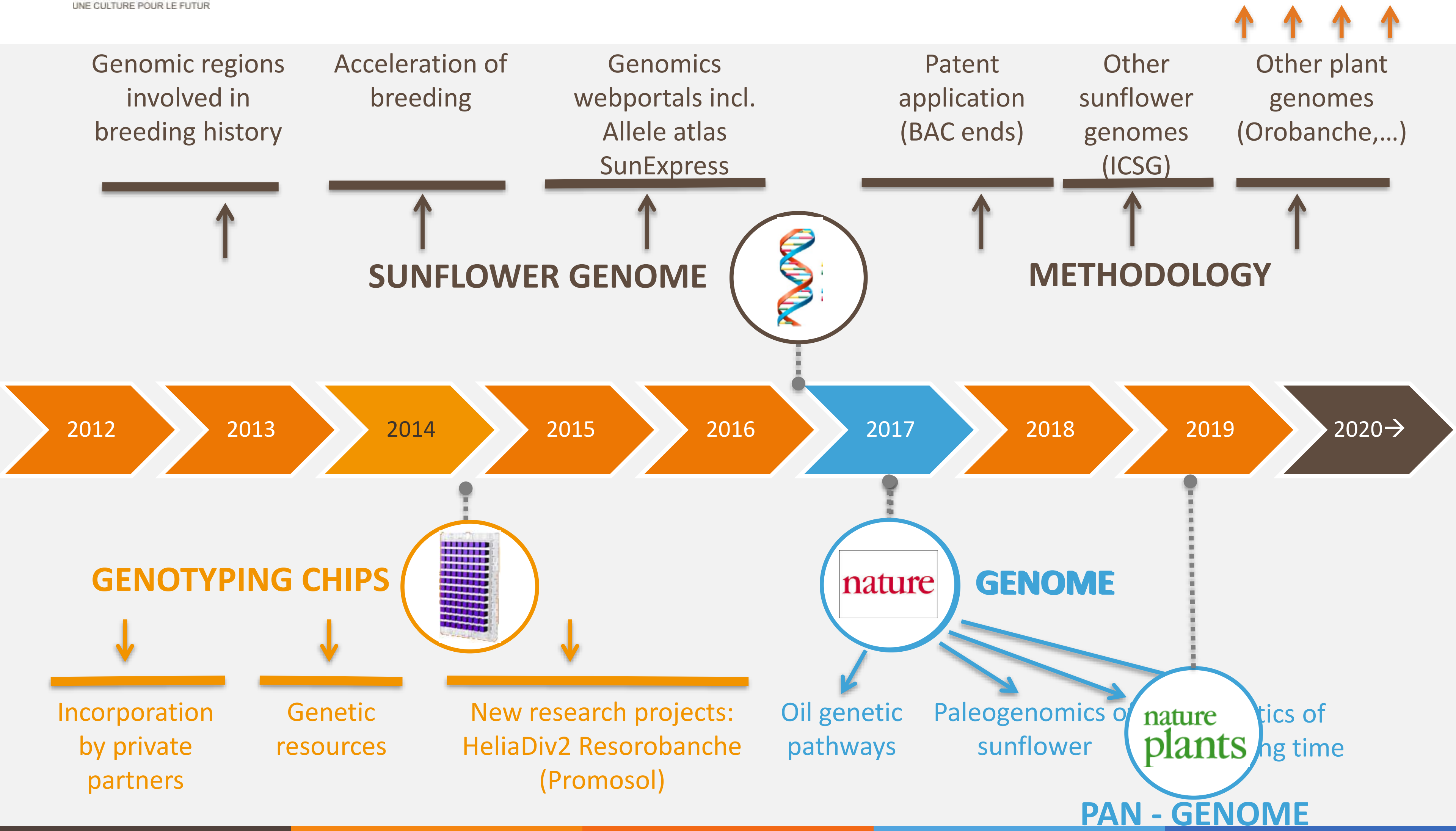
SUNFLOWER INDUSTRIAL CHAIN

Valorization of oilcake in sustainable development

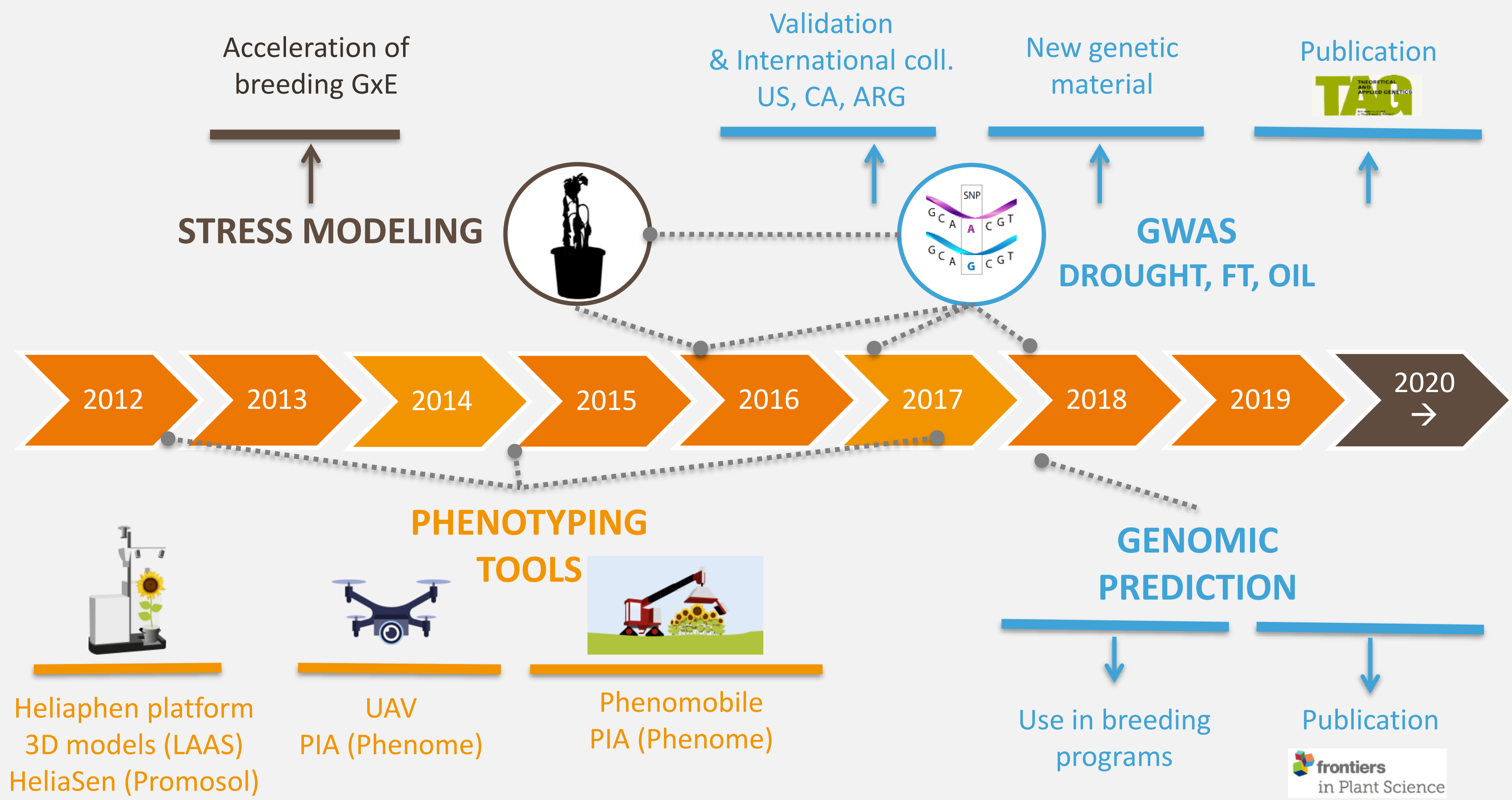
Plant Breeding and Eco-innovation



Impact of SUNRISE results
Genomics and Systems Biology



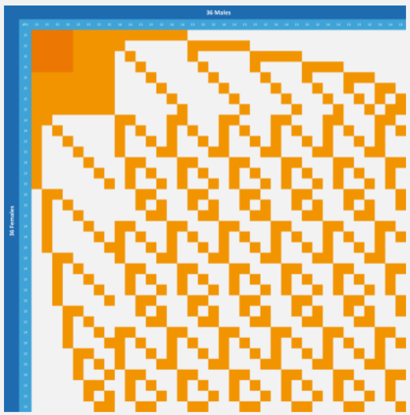
Impact of SUNRISE results
Genetics and Crop Modeling



Genetic designs to discover drought tolerance controling regions

Incomplete factorial hybrid panel

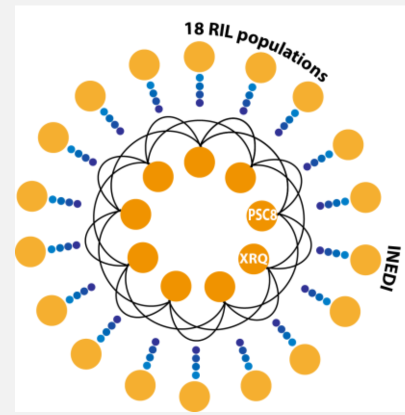
~450 hyb. ← 36 A * 36 R



- 2 original discovery networks
- Hybrid populations
- GWAS and genomic prediction

NAM population

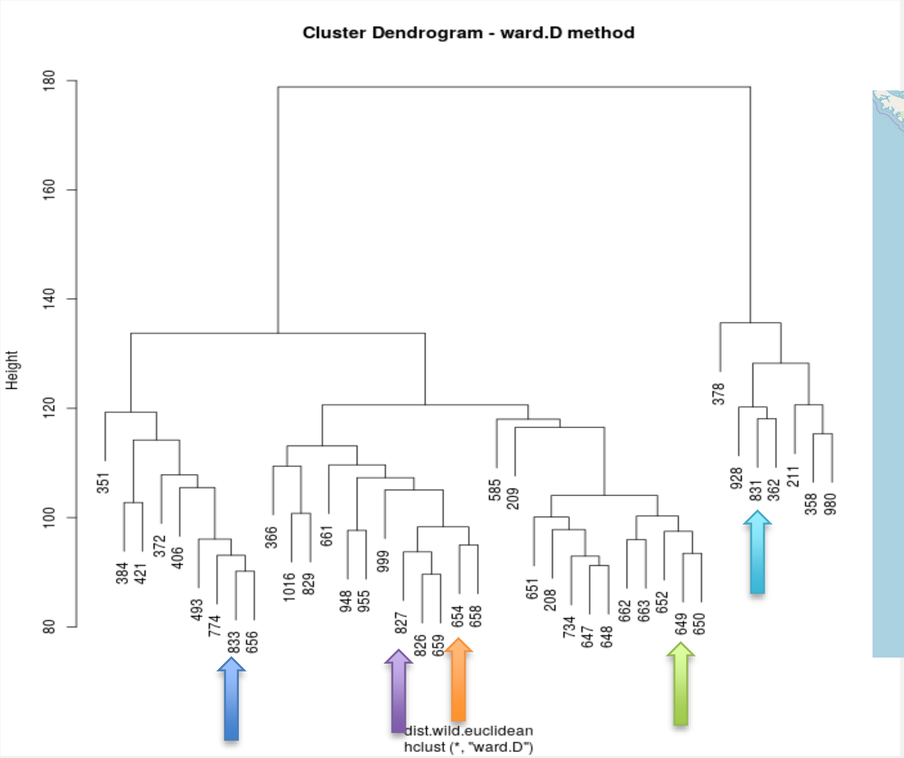
1513 hyb ← 576 RILs* 3 test.

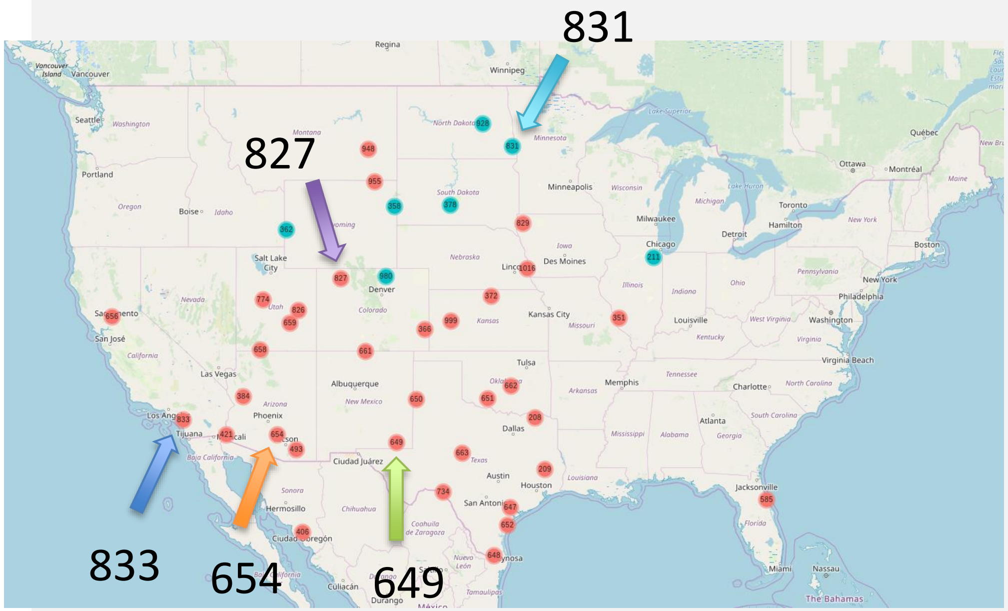


- 10 A and 5 R private lines
- Resequenced 10X
- ~14M SNPs → ~5M SNPs in R and B lines and MAF> 10%
  ➔ 461k non redundant SNPs

- 9 R and B public lines
- F5 or F6
- Genotyped AXIOM 600k SNPs
- ➔ 115k SNPs

Allelic Diversity platform

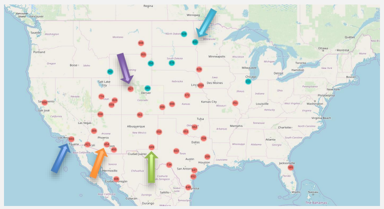


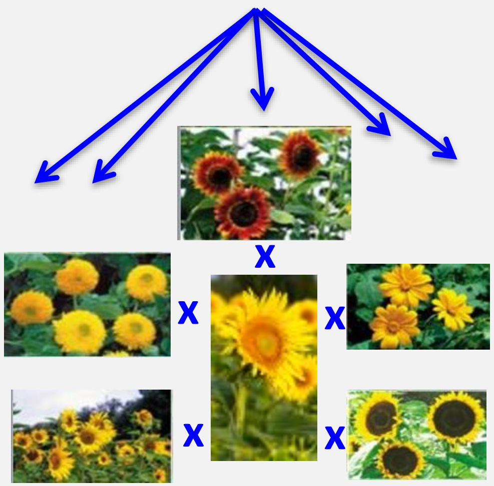


39 *H. annuus*
Resequenced 10X
Genotyped AXIOM 50k
→ **5 selected**

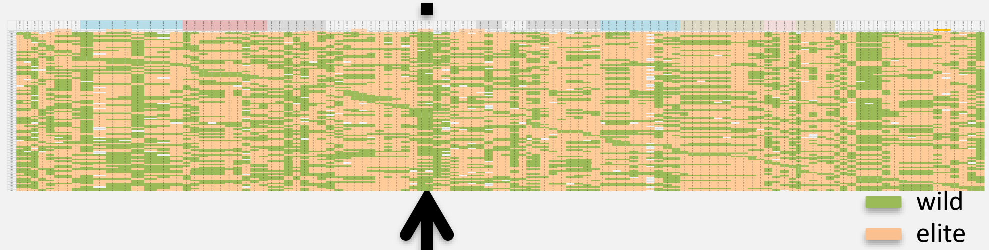
Coll. Promosol HeliaDiv2 Alexandra Duhnen

Allelic Diversity platform

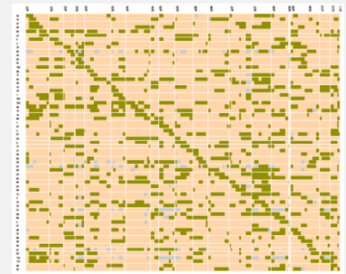




- **5 *H. annus* x 1 elite**



MAS

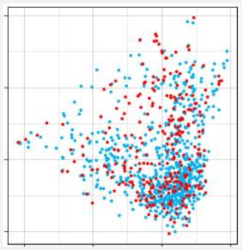


97+157+121+88+88
→ 551 ILs BC_2S_3
Genotyped AXIOM 50k

S. Muños, MC Boniface, N. Pouilly

Genetics of drought stress plasticity

Strategy to study genetics of abiotic stress plasticity



Core-collection

AXIOM
200k

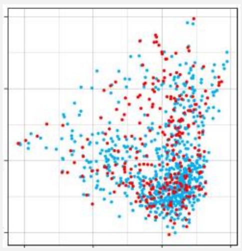
17 env. in FR
SUNFLO stress modeling
Yield plasticity to drought, cold, & nutritive stresses

Plasticity QTLs

9 6 21

Mangin *et al*. 2017 PCE

Strategy to study genetics of abiotic stress plasticity



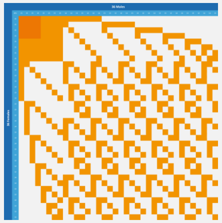
Core-collection

AXIOM 200k

17 env. in FR

Yield plasticity QTLs

9 6 21



IFD

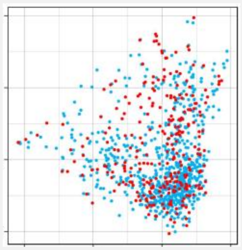
Reseq 461k

13 env. in FR, RO

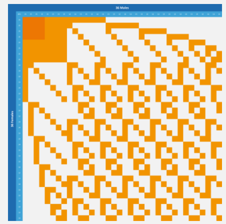
Yield plasticity QTLs

3 7 9

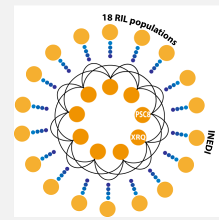
Strategy to study genetics of abiotic stress plasticity



Core-collection



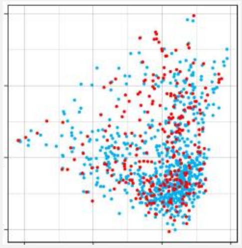
IFD



NAM DRR

Core-collection	IFD	NAM DRR
AXIOM 200k	Reseq 461k	AXIOM 600k
17 env. in FR	13 env. in FR, RO	13 env. in FR, RO, CL
Yield plasticity QTLs	Yield plasticity QTLs	Yield plasticity QTLs
9 / 6 / 21	3 / 7 / 9	33 / 17 / 18

Strategy to study genetics of abiotic stress plasticity



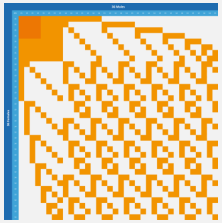
Core-collection

AXIOM 200k

17 env. in FR

Yield plasticity QTLs

9 6 21



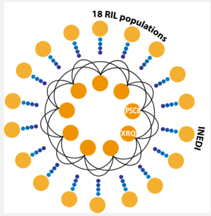
IFD

Reseq 461k

13 env. in FR, RO

Yield plasticity QTLs

3 7 9



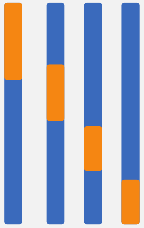
NAM DRR

AXIOM 600k

11 env. in FR, RO, CL

Yield plasticity QTLs

33 17 18



Biparental RIL

AXIOM 600k

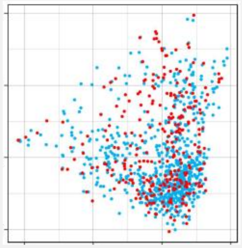
2 env. on Heliaphen

Yield plasticity QTLs

4

Gosseau *et al.* 2019 FiPS

Strategy to study genetics of abiotic stress plasticity



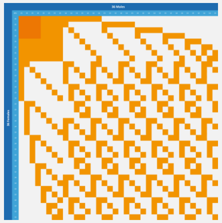
Core-collection

AXIOM 200k

17 env. in FR

Yield plasticity QTLs

9 6 21



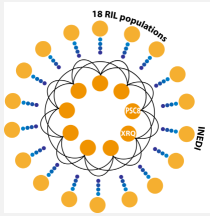
IFD

Reseq 351k

13 env. in FR, RO

Yield plasticity QTLs

3 7 9



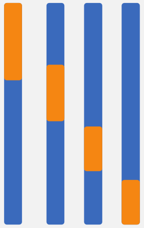
NAM DRR

AXIOM 600k

11 env. in FR, RO, CL

Yield plasticity QTLs

33 17 18



Biparental RIL

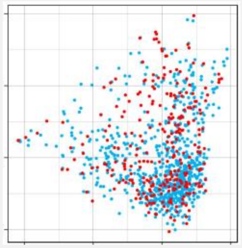
AXIOM 600k

2 env. on Heliaphen

Yield plasticity QTLs

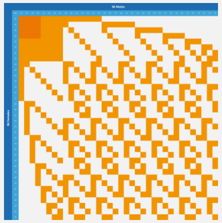
4

Strategy to study genetics of abiotic stress plasticity



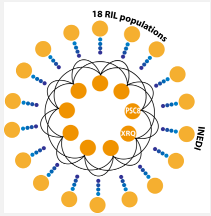
Core-collection

9 6 21



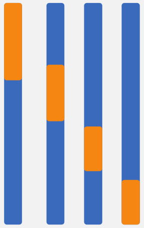
IFD

3 7 9



NAM DRR

33 17 18



Biparental RIL

4

34 QTL validated for yield plasticity

4 QTL in 3 pop (+7 in 2 pop)

2 QTL in 3 pop (+8 in 2 pop)

DYP03

DYP12

1 QTL in 3 pop (+12 in 2 pop)

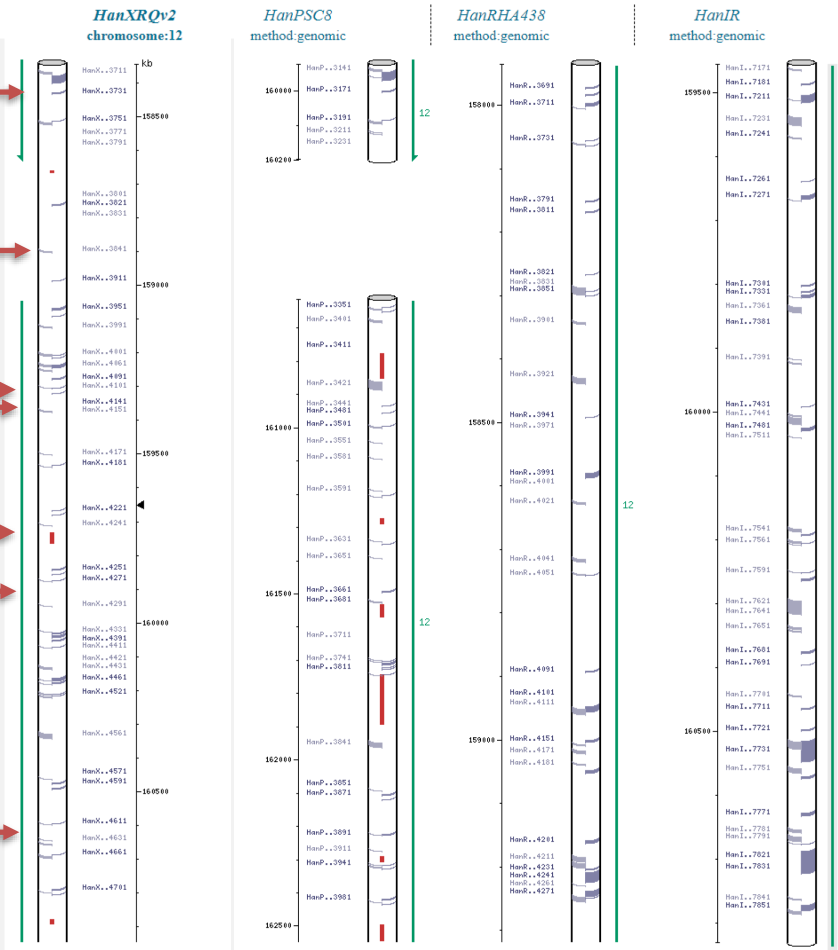
Colocalisation of SNPs associated to plasticity and yield related traits <100kb

Gosseau *et al.* 2019 FiPS

https://lipm-narcisse.toulouse.inrae.fr/multi/cgi-bin/narcisse.cgi

DYP12 genomic structure

XRQv2 PSC8 RHA438 IR



GWA Hybrid GY

GWA Hybrid GY

GWA hybrid GY drought plasticity

NAM-DRR SENESCENCE

INEDI TKW drought plasticity

Gosseau *et al.* 2019 FiPS

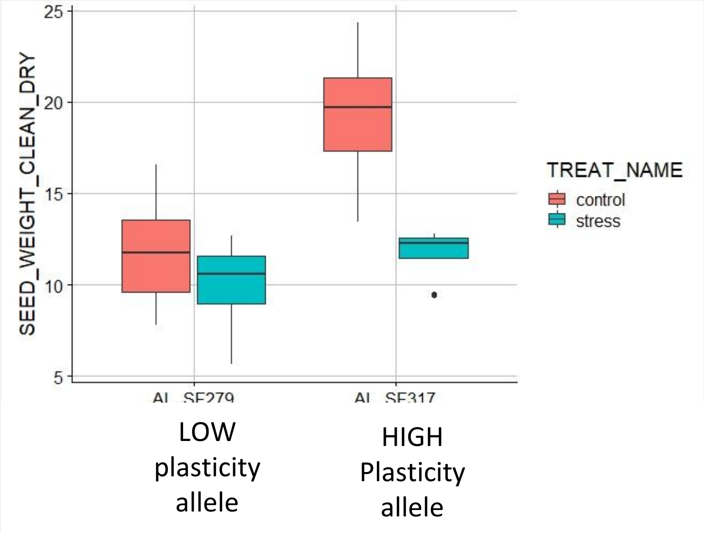
NAM-DRR OIL

NAM GY cold plasticity

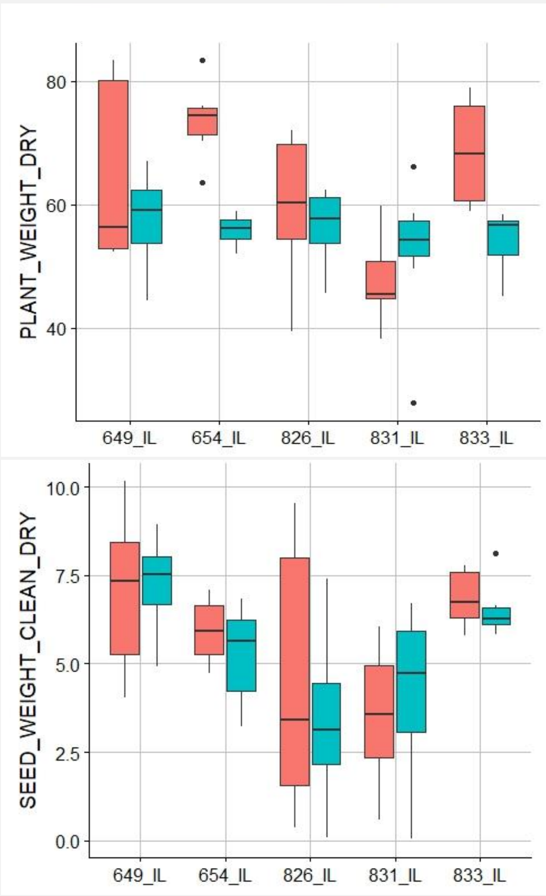
DYP12 high throughput phenotyping

N. Blanchet
Phenotoul Heliaphen platform

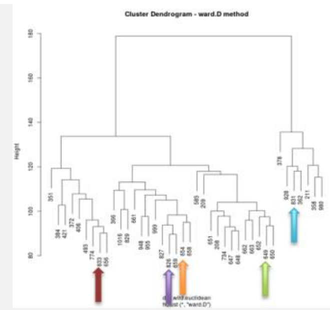
DYP 12 NILs



DYP12 new alleles from IL



CTL / DRY



New wild alleles from H. annuus

New replication experiment under way

Confirms DYP12 acts on biomass reallocation to seeds in drought conditions

DYP12 gene expression network

L. Pomiès
H. Duruflé
S. De Givry
E. Maigné
C. Brouard

GWA Hybrid GY

GWA Hybrid GY

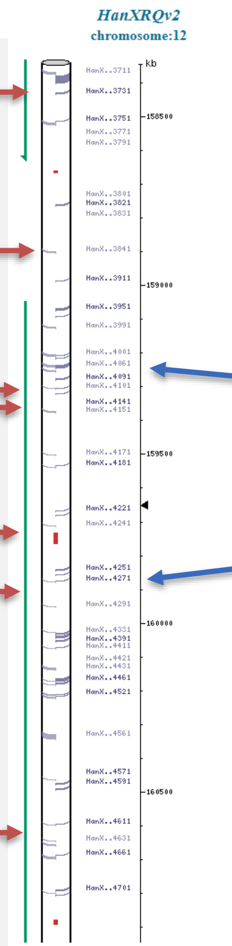
GWA hybrid GY drought plasticity

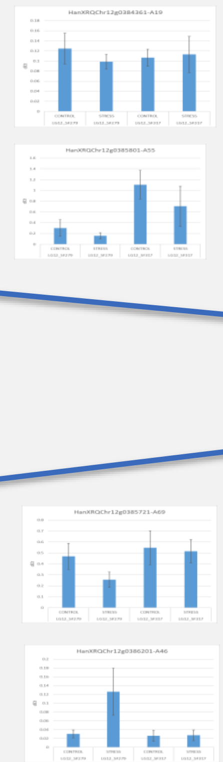
NAM-DRR SENESCENCE

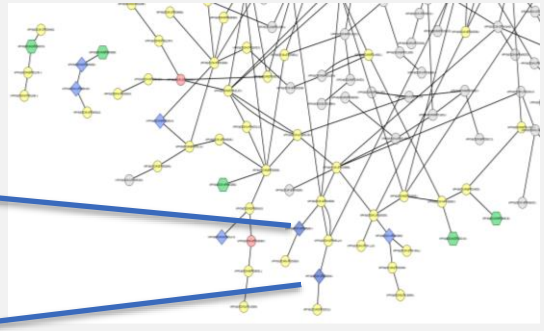
INEDI TKW drought plasticity

NAM-DRR OIL

NAM GY cold plasticity



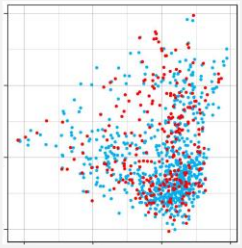




Gene Regulatory Network

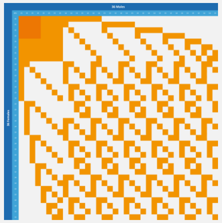
integrates DYP12 and other QTL and drought related candidate genes

Strategy to study genetics of abiotic stress plasticity



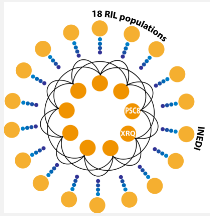
Core-collection

9 6 21



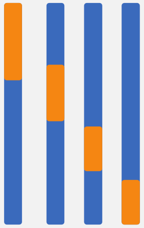
IFD

3 7 9



NAM DRR

33 17 18



Biparental RIL

4

34 QTL validated for yield plasticity

4 QTL in 3 pop (+7 in 2 pop)

2 QTL in 3 pop (+8 in 2 pop)

DYP03

DYP12

1 QTL in 3 pop (+12 in 2 pop)

Perspectives
for genetics of abiotic stress plasticity

Perspectives
for genetics of abiotic stress genetics

Objectives

→ identify the genomic polymorphism

→ identify the physiological processes

→ validate in new crop management that imply new stress scenarios

Needs

→ interdisciplinary approaches

Genomic structural variation

HT Phenotyping and eco-physiology

Agronomy

→ strong public-private partnership

Production stress scenarios

Accelerate breeding

Acknowledgements

Sunflower Genetics and Genomics
INRAE Toulouse LIPME

Florie Gosseau (Integration)
Brigitte Mangin (Genetical statistics)
Nicolas Blanchet (Heliaphen)
Stéphane Muños (genomics)
Marie-Claude Boniface
Fanny Bonnafous
Eléna Cadic
Olivier Catrice
Adeline Chaubet
Romain Dinis
Alexandra Duhnen
Harold Duruflé
Louise Gody
Marion Larroque
Jean Leconte
Lolita Lorenzon
Gwenola Marage
Marco Moroldo
Charlotte Penouilh
Prune Pégot-Espagnet
Nicolas Pouilly
Camille Tapy
Patrick Vincourt

Bioinformatics team
INRAE Toulouse LIPME

Jérôme Gouzy
Sébastien Carrère
Ludovic Legrand
Ludovic Cottret

VASCO team
INRAE Toulouse AGIR

Pierre Casadebaig (crop modeling)
Philippe Debaeke

INRAE Toulouse Experimental Unit

Gilles Tison
Philippe Burger
Paul Bataillon
Rémi Marandel
Mathieu Roy

Thank you for your attention

www.sunrise-project.fr

@SUNRISE_France

Financeurs

Partenaires