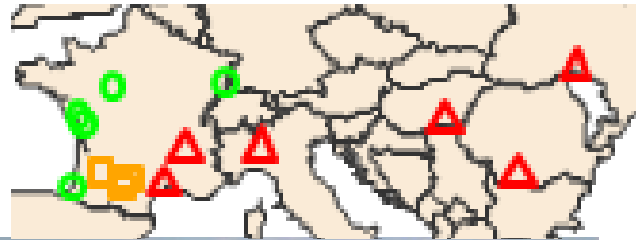


Most cost effective experiments are those in databases : Using and reusing indoor and multisite field experiments for assessing the genetic variability of plant responses to environment

F. Tardieu, C Welcker, LI Cabrera Bosquet, I. Alic, P Neveu, C Pommier



Using and reusing indoor and multisite field experiments for assessing the genetic variability of plant responses to environment

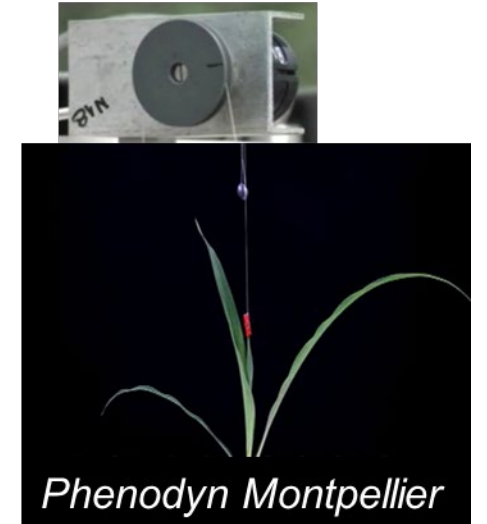
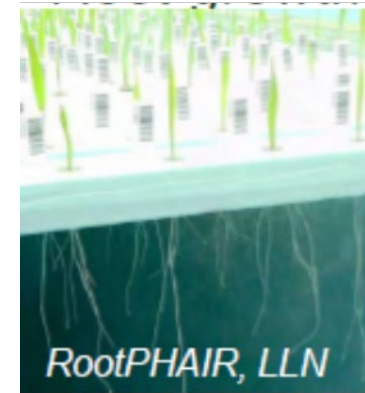
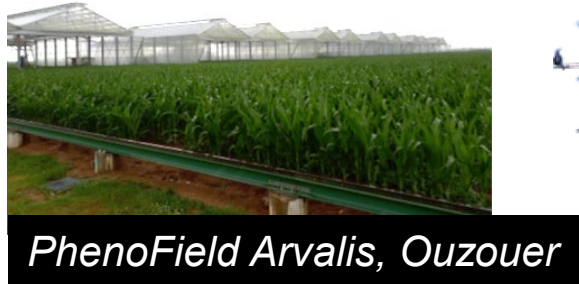
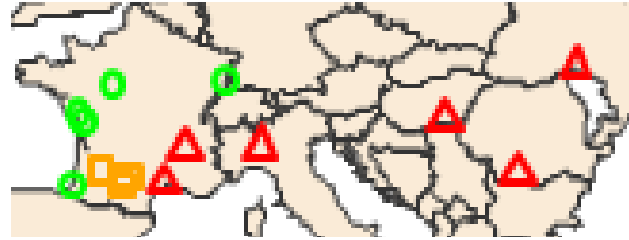
Assessing the responses to environmental conditions of panels of genotypes needs hundreds of genotypes (accessions) tested in:

- Tens of field experiments in contrasting environmental scenarios:
capture the responses of yield to environmental conditions for each genotype
- Experiments in field phenotyping platforms with different treatments:
capture integrated traits related to differences in yield responses
- Experiments in indoor platforms with treatments
disentangle environmental effects at phenotyping and omic scales

Impossible to collect such datasets in one single project : needs data reuse

For instance, 250 maize hybrids

- Yield in 24 field experiments
- Traits in 10 detailed experiments in phenotyping platforms
- Traits in 3 equipped fields



Impossible to collect such datasets in one single project : needs data reuse

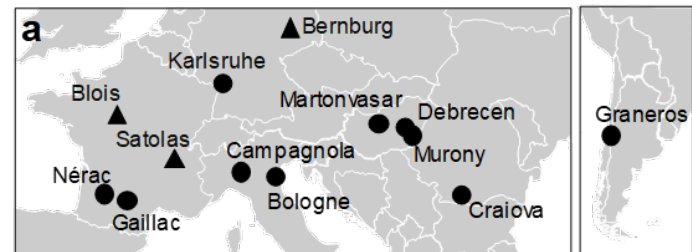
Phenotyping platform



Genetic variability of traits/
omics

Diversity panel: 250 unrelated hybrids

Field network



Genetic variability of yield

Plant, Cell & Environment 2019 PC E

Phenomics allows identification of genomic regions affecting maize stomatal conductance with conditional effects of water deficit and evaporative demand Santiago Alvarez Prado

Physiology Platform

Cabrera-Bosquet | Antonin Grau | let | Claude Welcker | François Tardieu

Stomatal conductance with Penman Monteith equation

LETTERS 2019 nature genetics

<https://doi.org/10.1038/s41588-019-0414-y>

Genomic prediction of maize yield across European environmental conditions

Emilie J. Millet^{1,2,4}, Willem Kruijer¹, Aude Coupel-Ledru^{2,5}, Santiago Alvarez Prado^{2,6}, Llorenç Cabrera-Bosquet², Sébastien Lacube², Alain Charcosset², Claude Welcker², Fred van Eeuwijk¹ and François Tardieu^{2*}

Genomics, modelling Field + (platform)

GP of response curves to environment

PNAS 2018

Maize yields over Europe may increase in spite of climate change, with an appropriate use of the genetic variability of flowering time

Boris Parent^a, Margot Leclere^{a,1}, Sébastien Lacube^a, Mikhail A. Semenov^b, Claude Welcker^a, Pierre Martre^a, and François Tardieu^{a,2}

Process based modelling, Field

Traits and yield prediction 2050 vs present

Plant Physiology[®], Maistrioux, Chaumont 2024

Genetic variability of aquaporin expression in maize From eQTLs to a MITE insertion regulating PIP2;5 expression

Functional genomics, Physiology, Platform

GWAS of PIP transcripts

Plant Physiology[®], Emilie J. Millet, 2016

Genome-Wide Analysis of Yield in Europe: Allelic Effects Vary with Drought and Heat Scenarios^{1|OPEN}

Genetics, Field

Environment-specific yield QTLs

Journal of Experimental Botany, 2020

Simulating the effect of flowering time on maize individual leaf area in contrasting environmental scenarios

Process based modelling, Field + platform

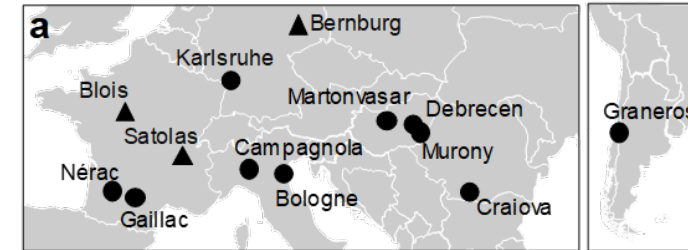
Modelling traits and yield of 100s genotypes

Phenotyping platform



Genetic variability of traits/
omics

Field network



Genetic variability of yield

Genetic progress panel: 64 hybrids commercialized from 1950 to 2010

Plant, Cell & Environment

2019

PCE

Changes in the vertical distribution of leaf area enhanced light interception efficiency in maize over generations of selection

Raphaël P.A. Perez^{1,2} | Christian Fournier¹ | Llorenç Cabrera-Bosquet¹ | Simon Artzet¹ | Christophe Pradal² | Nicolas Brichet¹ | Tsu-Wei Chen^{1,3} | Romain Chapuis⁴ | Claude Welcker¹ | François Tardieu¹

Ecophysiology, 3D modelling
Platform

Architectural traits + genetic progress

2022

Physiological adaptive traits are a potential allele reservoir for maize genetic progress under challenging conditions

Claude Welcker, Nadir Abusamra Spencer... François Tardieu

Genetics, Ecophysiology
Field + platform

Selection for yield improved architecture
but not physiological drought responses



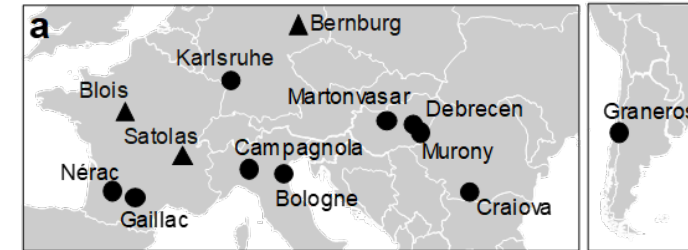
C Welcker

Phenotyping platform




Genetic variability of traits/
omics in phenotyping platform

Field network



Genetic variability of yield in a
network of fields

Two panels (for training) + one (for validation)


2023

Robotized indoor phenotyping allows genomic prediction of adaptive traits in the field

Jugurta Boudghaghen^{1,4}, Laurence Moreau², Katia Beauchêne³, Romain Chapuis⁵, Nathalie Mangel⁶, Llorenç Cabrera-Bosquet¹, Claude Welcker¹, Matthieu Bogard² & François Tardieu¹✉

Genetics Genomics, ecophysiology
Field + platform

Indoor vs field traits, genomic prediction



Jugurta
Boudghaghen

1 – The same datasets were used for addressing different questions

genomics, genetics, imaging, crop modelling, methodology

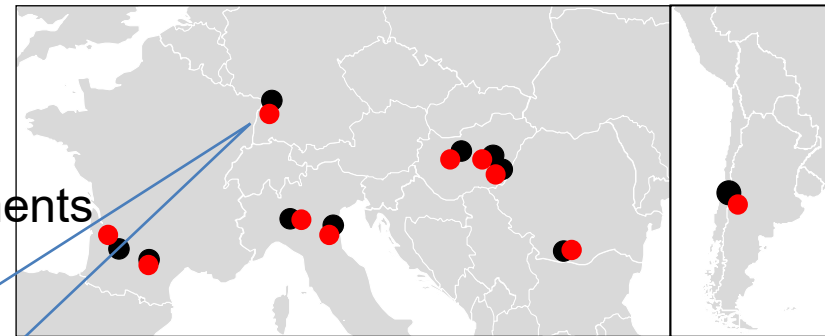
Success story per se:

*Datasets generated in 2014-2017 resulted in 12 papers till 2024,
+ at least 6 in prep, + many afterwards*

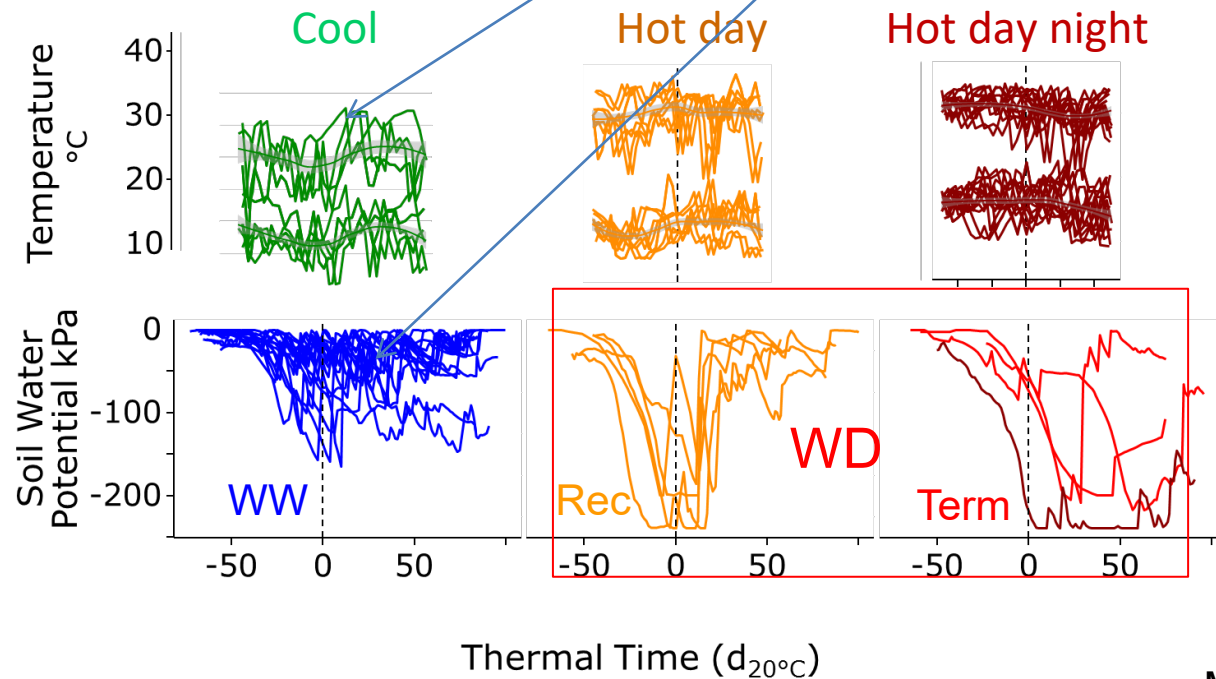
Typical joint analyses : Envirotyping



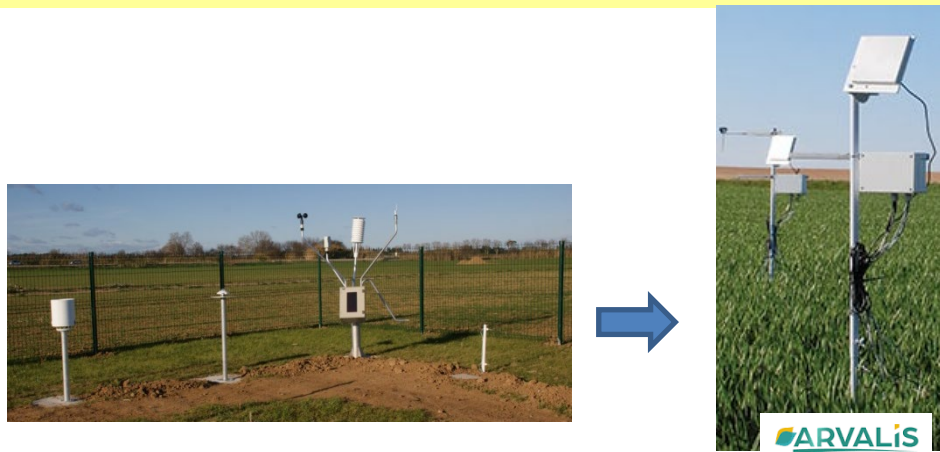
16 fields
X
2 years
X
2 W treatments



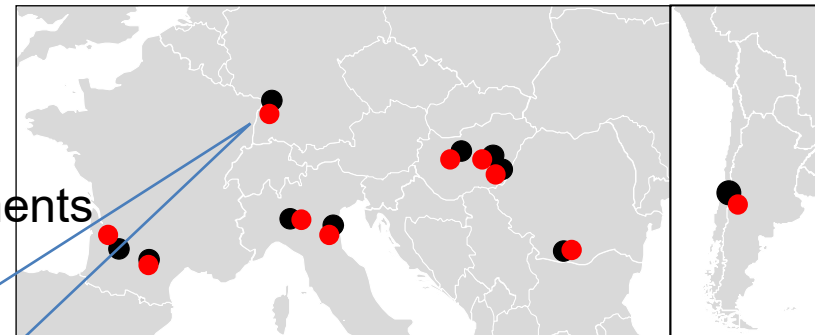
Environmental scenarios (clustering experiments)



Typical joint analyses 1 : Envirotyping + climate change

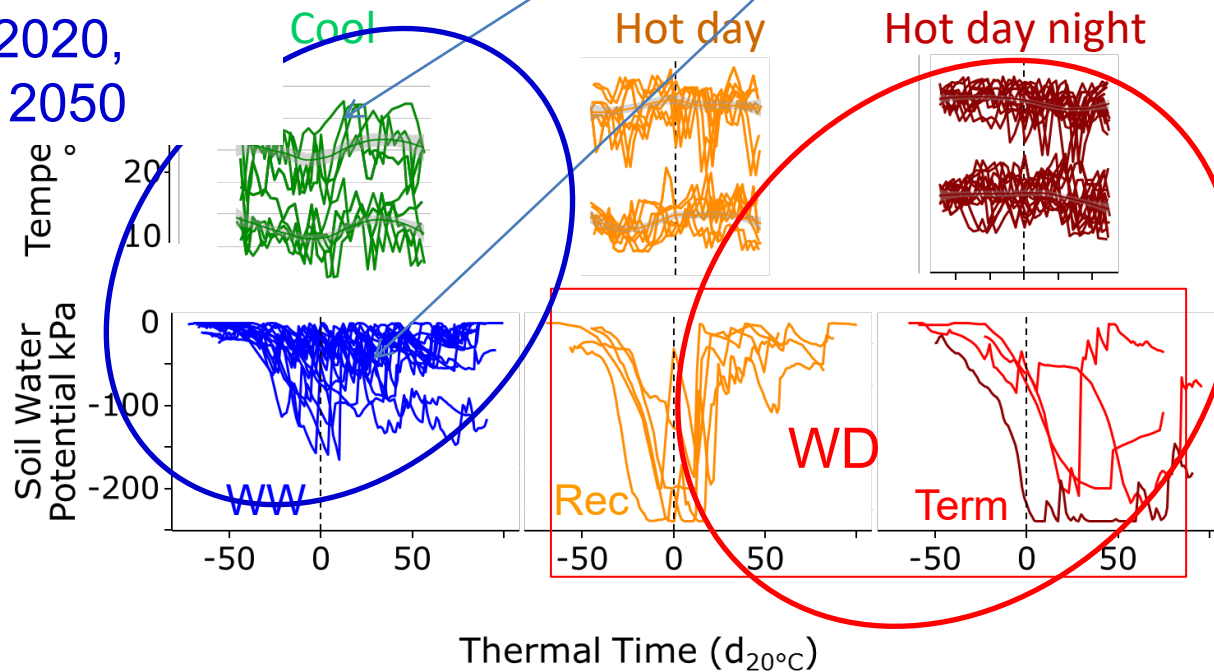


16 fields
X
2 years
X
2 W treatments



Environmental scenarios (clustering experiments)


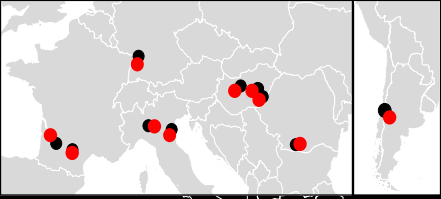
90% frequency 2020,
20% frequency 2050



5% frequency 2020,
25% frequency 2050


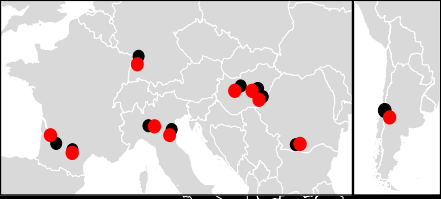


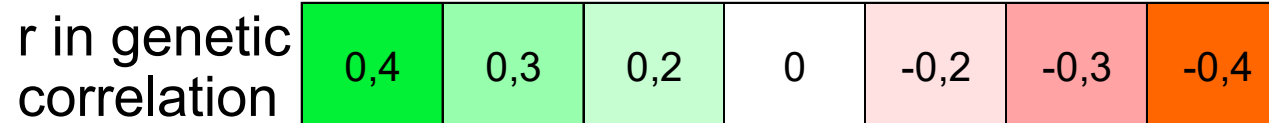
Parent et al 2018 PNAS

Yield per environmental scenario		Traits in platform						
		Anthesis	Architecture RH _{PAD}	Stomatal conductance	Light interception	Leaf area	WUE	Sensitivity growh
 	WW Cool							
	WW high VPD							
	WW Hot night							
	WD Cool							
	WD Hot							



Some traits well correlated with yield: architecture, stomatal conductance
BUT correlations depend on climatic scenarios for stomatal conductance

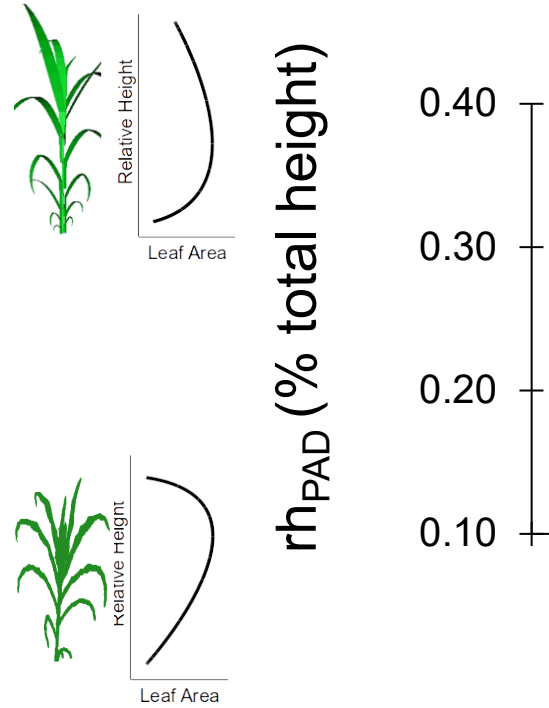
Yield per environmental scenario		Traits in platform						
		Anthesis	Architecture RH _{PAD}	Stomatal conductance	Light interception	Leaf area	WUE	Sensitivity growth
 	WW Cool	Green	Light Green	Green	White	White	White	White
	WW high VPD	Green	Light Green	Green	White	White	White	White
	WW Hot night	Green	Green	White	White	White	Light Green	Light Green
	WD Cool	Green	Green	White	Light Pink	White	Light Pink	White
	WD Hot	Green	Green	Red	Light Pink	Light Pink	White	White



Typical joint analyses 2: Do indoor phenotyping platforms represent field ? (a thesis with 90% data in databases)



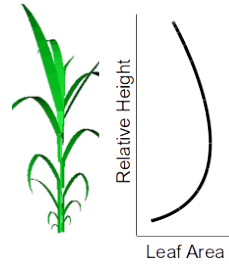
3D image analysis



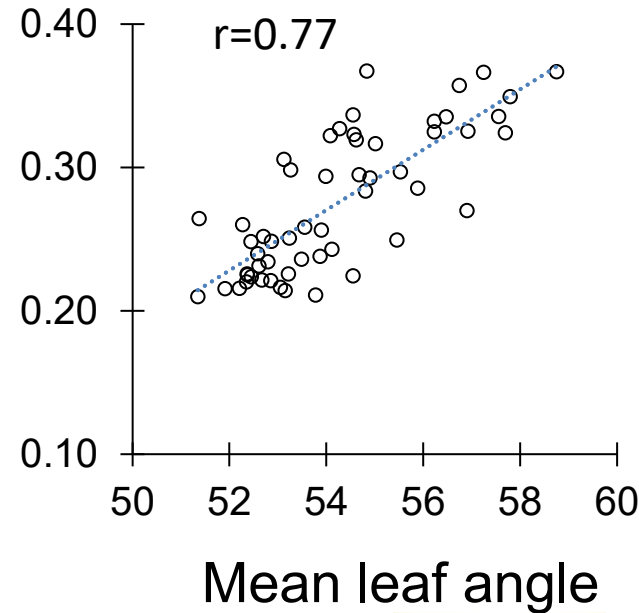
Typical joint analyses 2: Do indoor phenotyping platforms represent field ? (a thesis with 90% data in databases)



3D image analysis



rh_{PAD} (% total height)



Images, inversion of the Prosail model



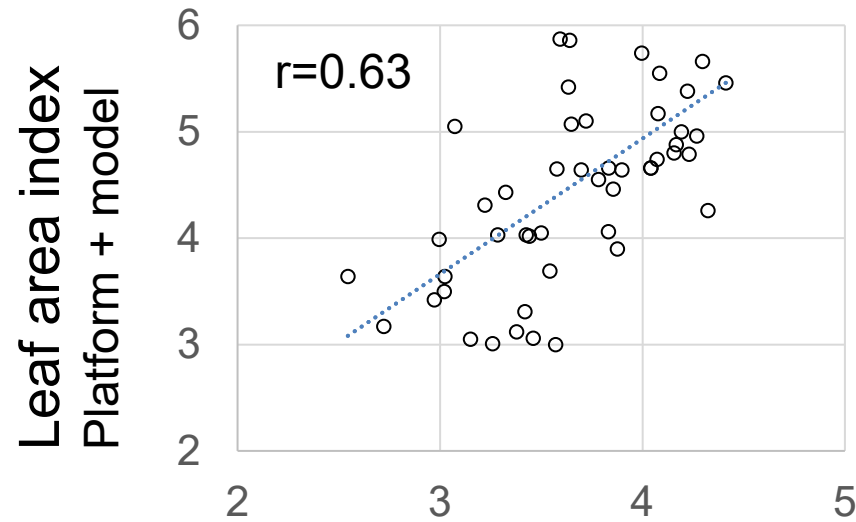
Traits translate from indoor platform to field, with modelling

Typical joint analyses 2: Do indoor phenotyping platforms represent field ? (a thesis with 90% data in databases)

No correlation between leaf area indoor and in fields BUT



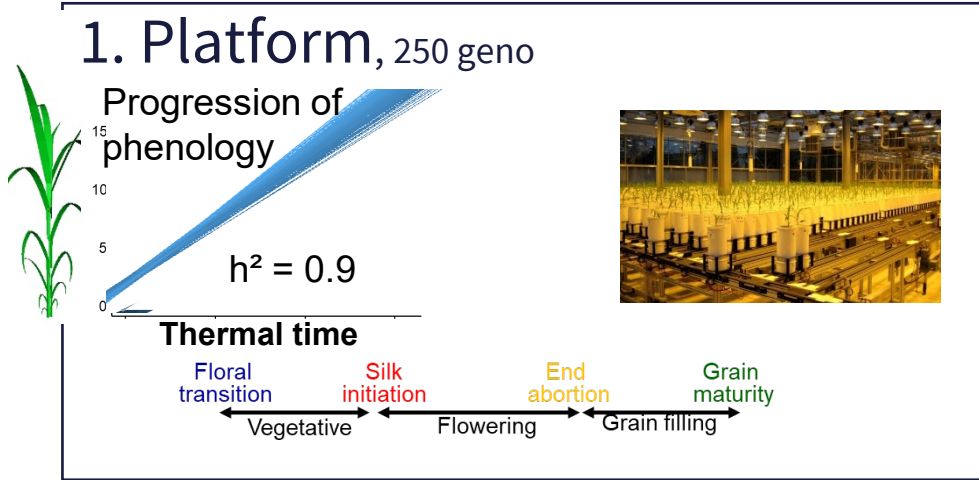
- Simulations based on*
 - *Genotypic values (platform)*
 - Phenology + leaf number*
 - Leaf growth rate*
 - *Environmental conditions in the field*



Traits translate from indoor platform to field, with modelling

images, inversion of the ROSAT model

Bouidghaghen et al 2023 Nature Com

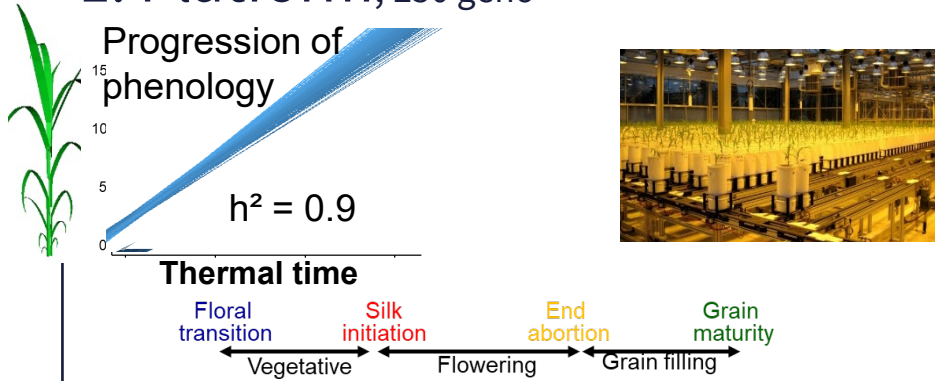


C. Welcker

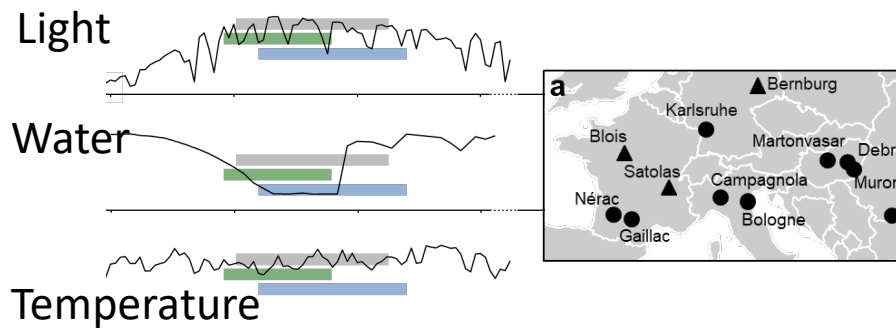


E. Millet

1. Platform, 250 geno



2. Field, Conditions felt by 250 genotypes in 25 fields

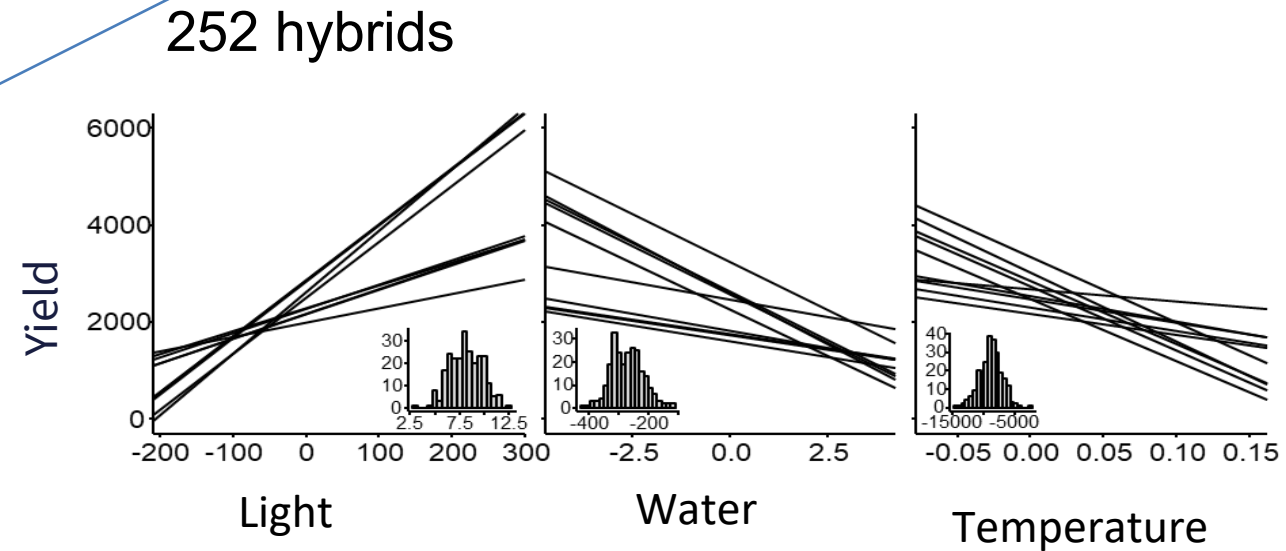
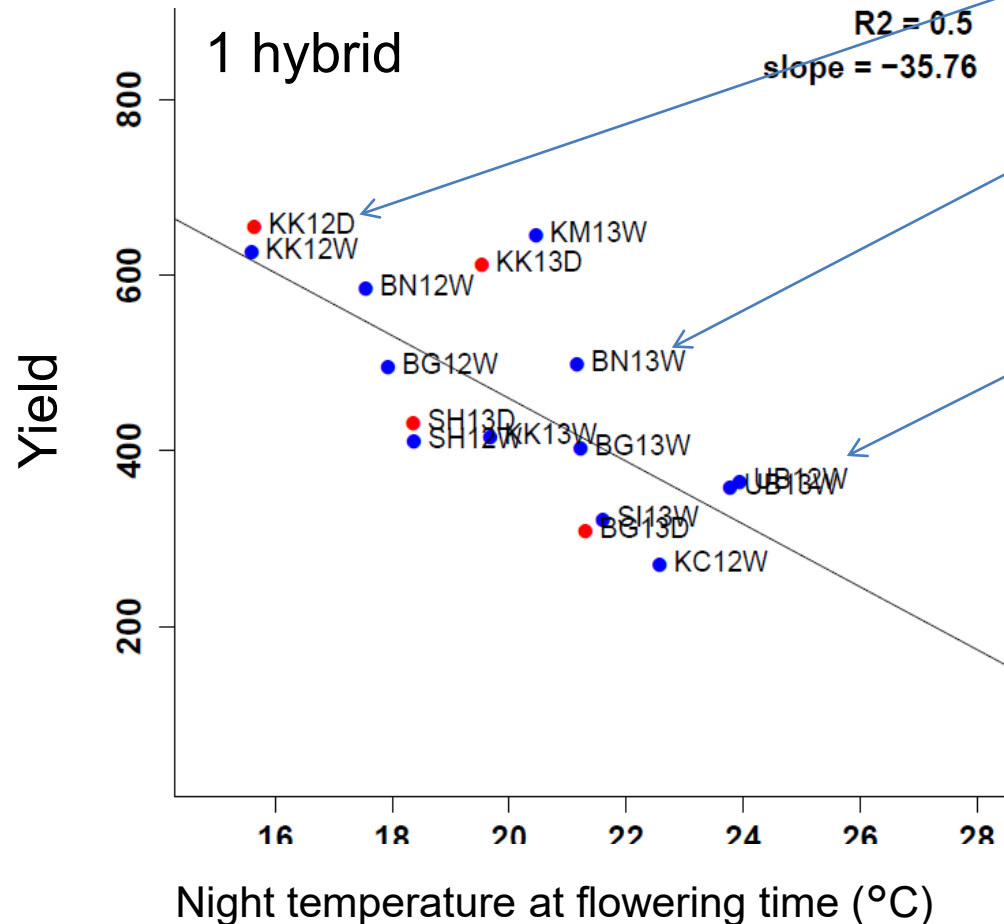
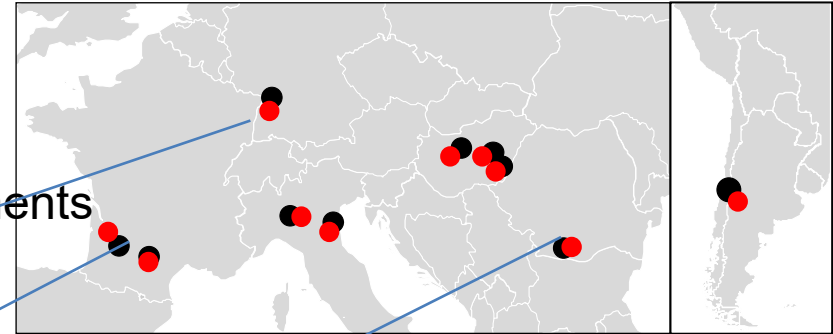


C. Welcker

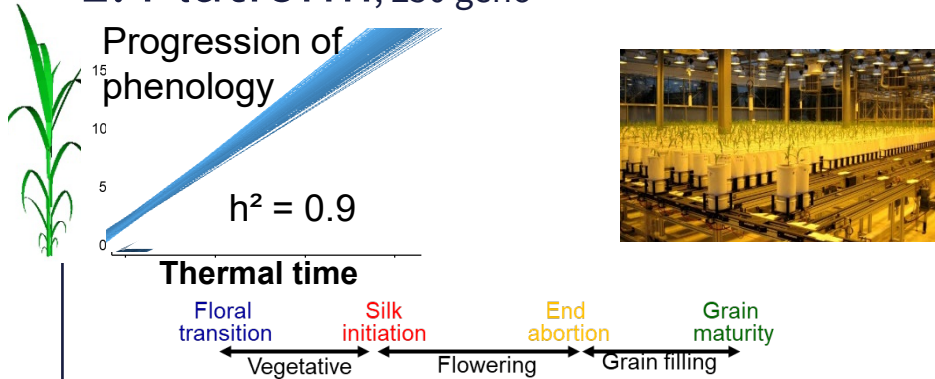


E. Millet

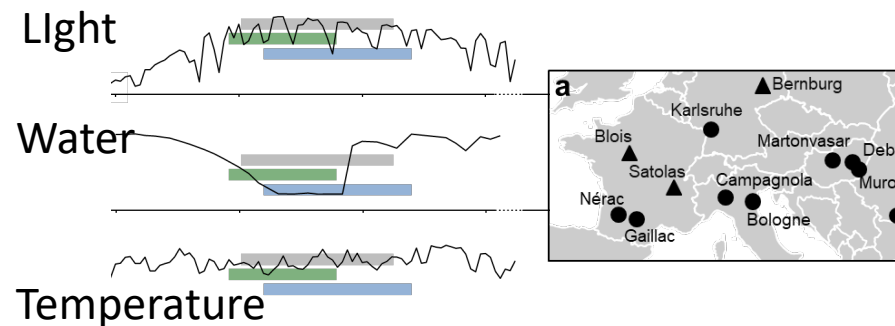
16 fields
X
2 years
X
2 W treatments



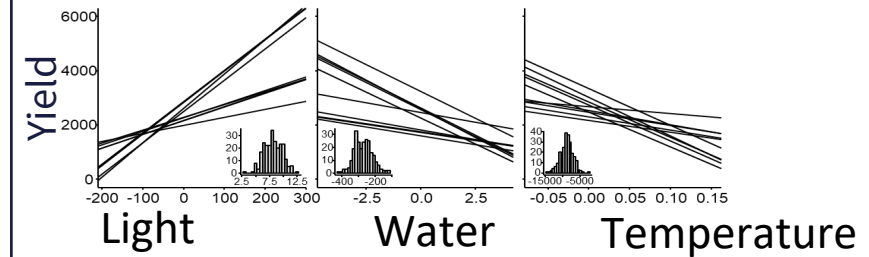
1. Platform, 250 geno



2. Field, Conditions felt by 250 genotypes in 25 fields



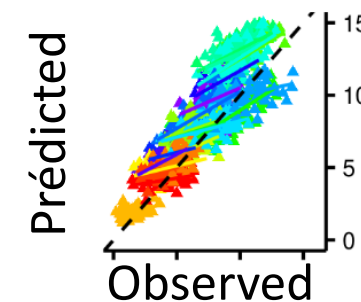
3. Response curves, 250 geno



4. Genomic prediction, 250 geno

$$GY_{ij} = (\mu + e_j + g_i + \sum_{l=1}^s \beta_{l,i} cov_{l,i,j}) \times GW_i$$

5. Test, New geno in new fields



Which geno (1000s) in which fields (1000s)



C. Welcker



E. Millet

1 – The same datasets were used for addressing different questions

genomics, genetics, imaging, crop modelling

Success story per se: 12 papers 2024, at least 6 in prep, + many afterwards

2 – Each question generated novel methods for statistical / modelling analysis

‘conceptual revolution’:

- classical representation : first the question then experiments

- Here, data availability BEFORE scientific hypotheses: a posteriori protocols

Success story per se: generated novel knowledge

3 – Overall (synthesis):

- Data reuse is possible, necessary and fruitful

A dataset collected in 2012-2016 is used for publications in 2024,

analysed jointly with other datasets: **Increasing added value with time**

- This allowed holistic analyse of the genetic variability of plant responses to environmental conditions / climate change

- BUT these panels are neither maintained nor really available. HELP ?

- BUT this needs a very careful (and demanding) data management
(Cyril Pommier’s presentation later today)





Field experiments



T. Presterl



A Murigneux
S. Praud



K Beauchène
J. Lorgeou



C. Guillaume



S. Melkior



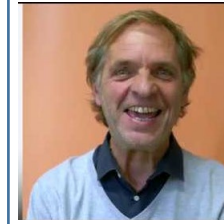
Genetic analyses

Moulon,
A Charcosset
L Moreau



Wageningen
F van Eeuwijk
Willem Kruijer

Data management



P. Neveu, C Pommier, I Alic, A Tireau



Platform experiments, modelling, GWAS, genomic prediction



C Welcker



LI Cabrera



B Parent



E. Millet



N Abou
Samra
Spencer



Italo
Granato



Romain
Chapuis



Jugurta
Boudghagen



S. Alvarez
Prado



R. Perez



C Fournier