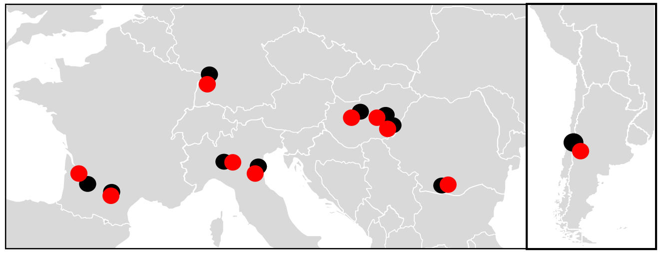
Multi scale phenotyping for crop performance in precise environmental scenarios: combining phenomics in controlled conditions with multi-site field experiments

F. Tardieu



Multi scale phenotyping for crop performance in precise environmental scenarios: combining phenomics in controlled conditions with multi-site field experiments

What to measure ?

We are interested by physiological mechanisms but

- Genetics needs 100s genotypes: physiology at high throughput
- To what extent are they related to yield or yield-related traits

Phenotypic distance: the temporal, spatial, and organization scales to be crossed between two phenotypic traits; can be measured via the number of equations, parameters, and input variables necessary to derive one trait from the other

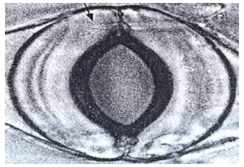
Traits have increasingly conditional effects with phenotypic distance

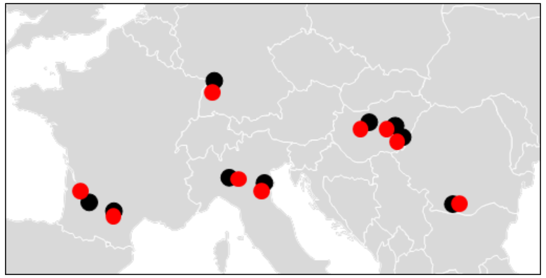
Tardieu et al 2018 Ann rev Plant Biol

ABA – yield : large phenotypic distance, context dependent effect
Photosynthesis – yield : large
grain number – yield : small

What to measure ?

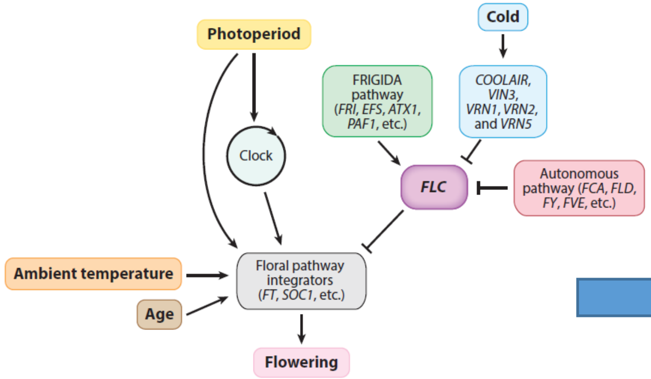
Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Multi-environment field network Weeks to months
	'Physiology community'	*'FSPM community'*		*'Crop models community'*



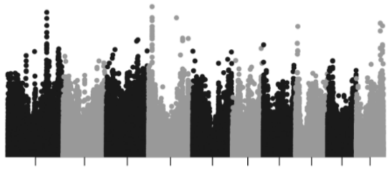


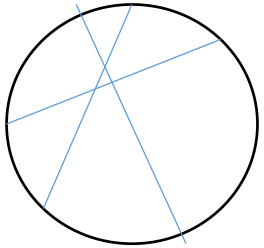
What to measure ?

Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Multi-environment field network Weeks to months
Genetic complexity	*10s of genes, combinations*			*Millions of polymorphisms* *100s of QTLs*



Gene networks with explicit gene actions



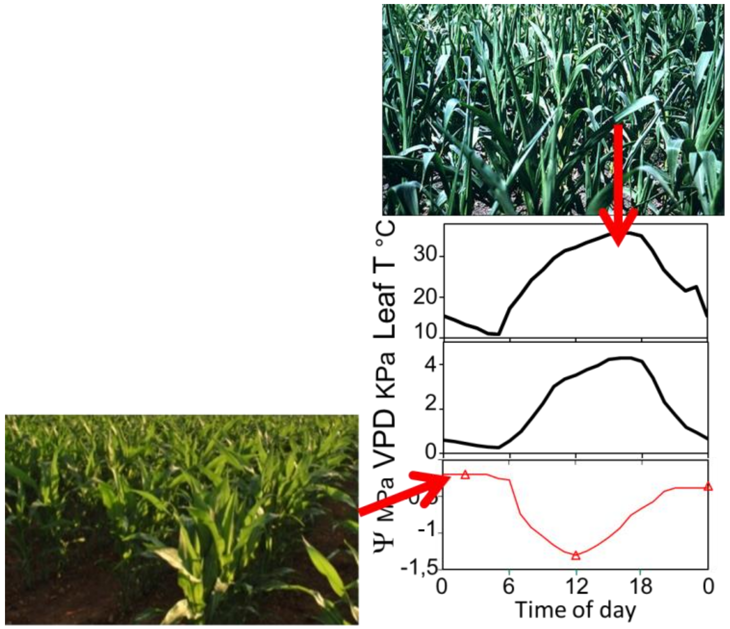


Gene networks with a statistical base

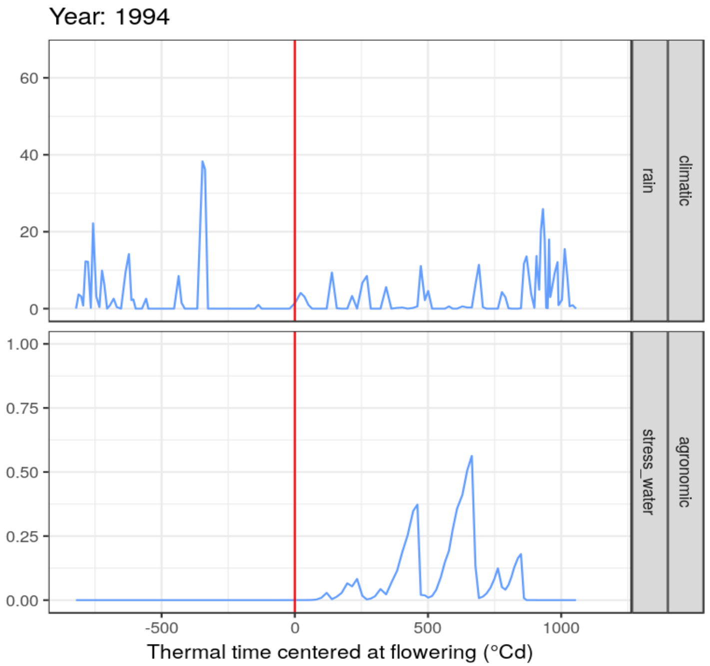
What to measure ?

Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Multi-environment field network Weeks to months

Physiological mechanisms and gene networks over minutes, yield over months

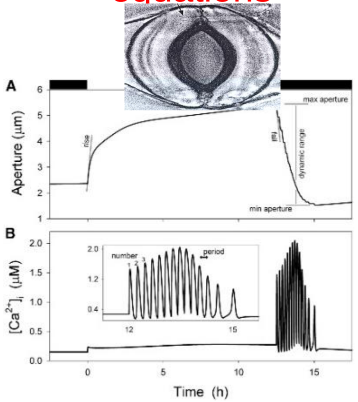


Tardieu et al 2017 Current Biology.



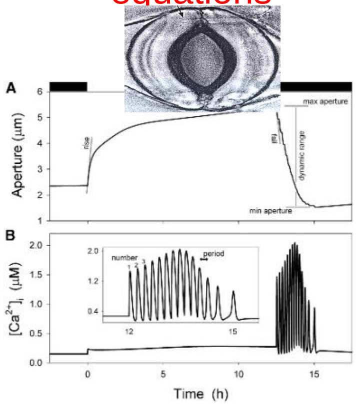
Casadebaig P 2016 EJA

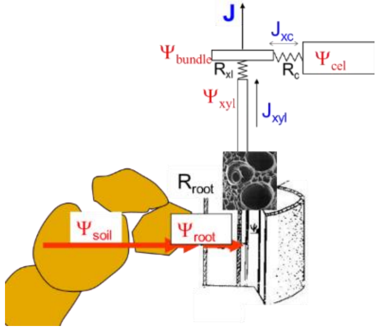
What to measure ?

Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Canopies in a range of environments Weeks to months
Genetic complexity	Single genes, combined	→	→	Genome wide allelic composition
Mechanisms	Transcripts Ion channels Biophysics			
Models Abstraction (most often)	Networks Boolean and differ. equations  *Explicit genes/metabolites, no explicit organs,*			

Vialet Chabrand et al 2017
Plant Phy

Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Canopies in a range of environments Weeks to months
Genetic complexity	Single genes, combined	→	→	Genome wide allelic composition
Mechanisms	Transcripts Ion channels Biophysics	Hydraulics Metabolism hormones		
Models Abstraction (most often)	Networks Boolean and differ. equations *Explicit genes/metabolites, no explicit organs,*	Differential Equ. ; gradients Conserved fluxes *No explicit genes, no explicit organs, Explicit fluxes ($m^{-2}s^{-1}$),*		





Vialet Chabrand et al 2017 Plant Phy

Caldeira et al 2014 Nat Com

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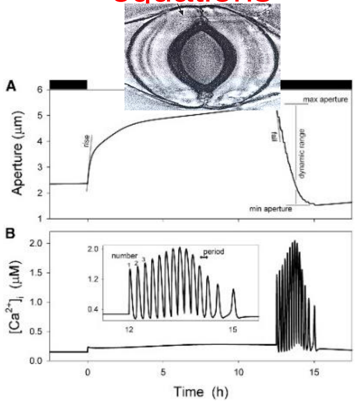
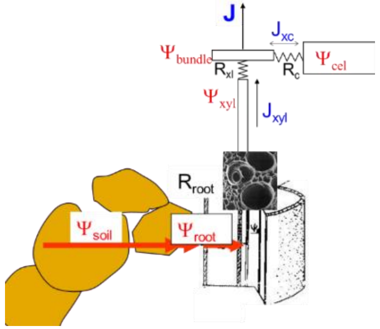
Scale	Cell- cm^2 Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Canopies in a range of environments Weeks to months
Genetic complexity	Single genes, combined	→	→	Genome wide allelic composition
Mechanisms	Transcripts Ion channels Biophysics	Hydraulics Metabolism hormones	Coordination Hormones, nutrients	
Models	Networks Boolean and differ. equations	Differential Equ. ; gradients Conserved fluxes	Fonctional/ Structural (FSPM)	
Abstraction (most often)	*Explicit genes/metabolites, no explicit organs,*	*No explicit genes, no explicit organs, Explicit fluxes ($m^{-2}s^{-1}$),*	*No explicit genes, Explicit organs (x,y,z), No explicit fluxes*	



Vialet Chabrand et al 2017
Plant Phy

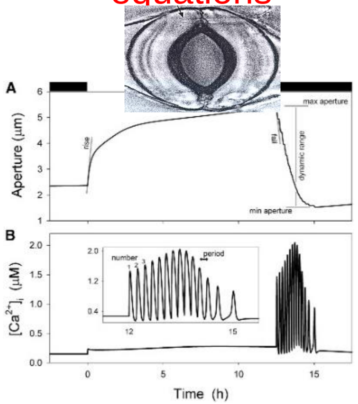


Caldeira et al 2014
Nat Com

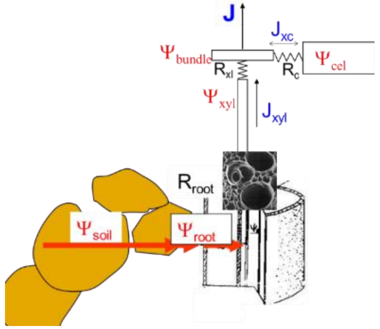
Mairhofer et al 2012
Plant Phy
Pradal et al 2015

What to measure ?

Scale	Cell- cm² Minutes / days	Organ(s) Minute/days	Plant or Canopy Minute to weeks	Canopies in a range of environments Weeks to months
Genetic complexity	Single genes, combined	→	→	Genome wide allelic composition
Mechanisms	Transcripts Ion channels Biophysics	Hydraulics Metabolism hormones	Coordination Hormones, nutrients	Feedbacks, Water/C/N balances coordination
Models	Networks Boolean and differ. equations	Differential Equ. ; gradients Conserved fluxes	Fonctional/ Structural (FSPM)	Regression models $$GY_{ij} = (\mu + e_j + g_i + \sum_{l=1}^{s} \beta_{l,i}\, cov_{l,i,j}) \times GW_i$$ Crop models (fin. differences)
Abstraction (most often)	*Explicit genes/metabolites, no explicit organs,*	*No explicit genes, no explicit organs, Explicit fluxes ($m^{-2}s^{-1}$),*	*No explicit genes, Explicit organs (x,y,z), No explicit fluxes*	*No explicit genes, No explicit organs, No explicit fluxes in plants*

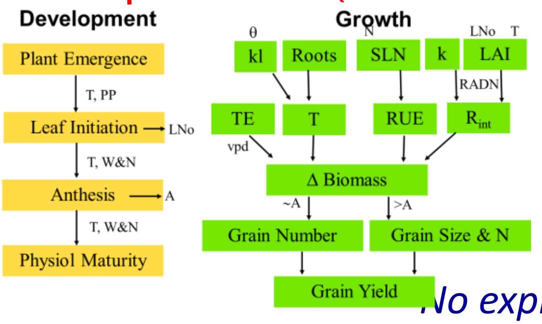


Vialet Chabrand et al 2017 Plant Phy



Caldeira et al 2014 Nat Com

Mairhofer et al 2012 Plant Phy
Pradal et al 2015



Millet et al 2019 Nat Gen
Wu et al 2019 Nat Plants

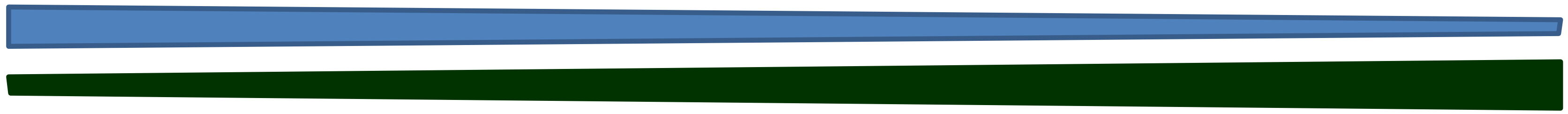
What to measure ? A ‘fractal’ complexity

Physiological mechanisms — Integrative ‘metamechanisms’

	Leaf cm^2 Minutes / days	Cell- Organ Minute/days	Plant or Canopy Minute to weeks	Canopies in a range of environments Weeks to months
Genetic complexity	*Single genes, combined*	→	→	*Genome wide allelic composition*
Mechanisms in models	Transcripts Ion channels Biophysics	Hydraulics Metabolism hormones	Coordination, Hormones, nutrients	Feedbacks, Water/C/N balances coordination

Biology

Evolution



Tardieu et al 2017 Current BIol. ; Taylor et al 2019, PNAS

I propose:

Mechanisms at higher level involve evolution (mechanisms constrained into strategies)

‘not all genotypes possible everywhere’

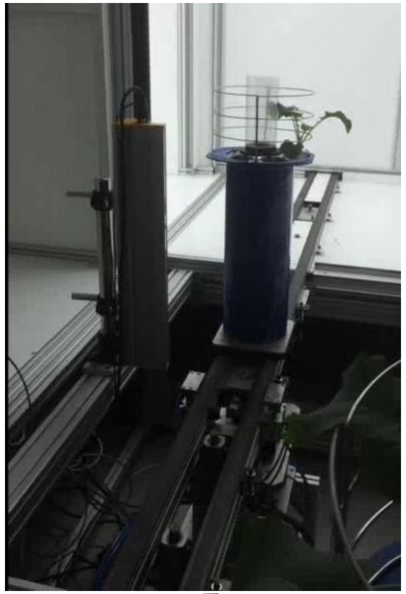
So the genetic variability can be modelled at all scales

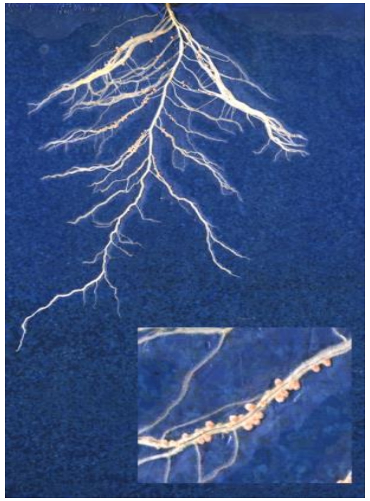
“High throughput physiology”: stomatal conductance and photosynthesis at plant level

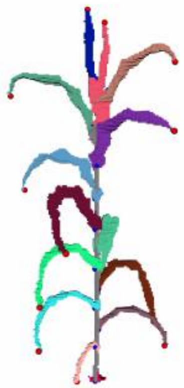
“High throughput physiology”: stomatal conductance and photosynthesis at plant level

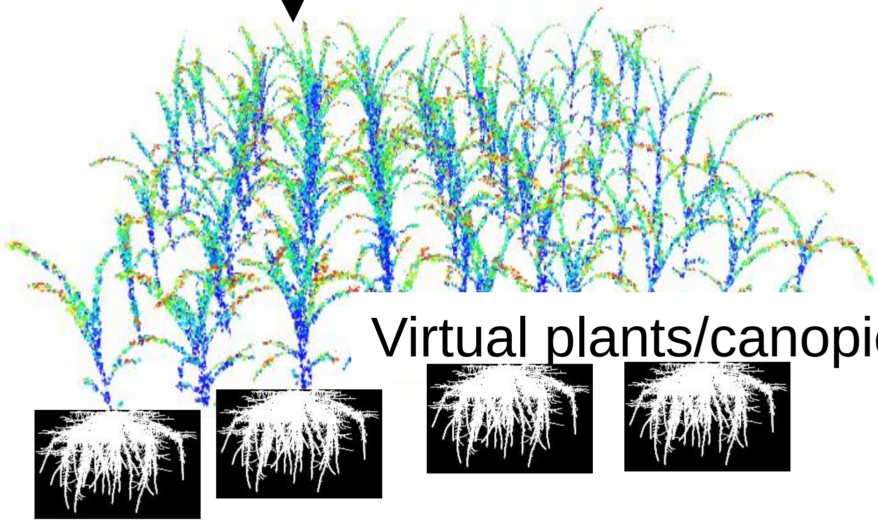
2400 plants (Montpellier

1800 rhizotrons (Dijon)







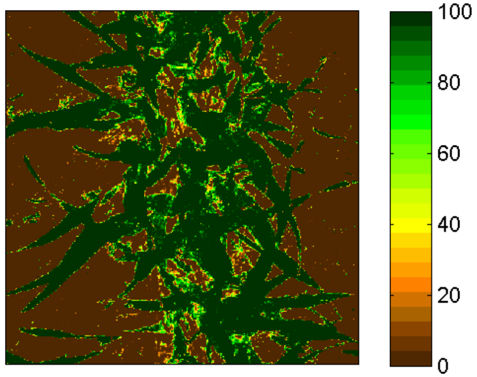


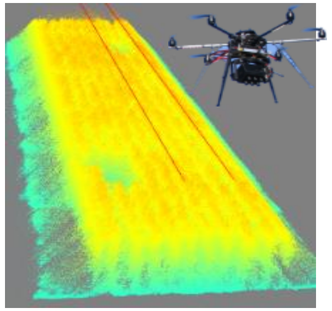
Virtual plants/canopies

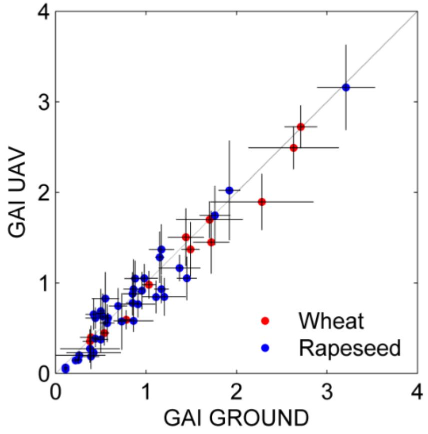
“High throughput physiology”: stomatal conductance and photosynthesis at plant level

Field phenotyping (Phenomobiles / gantries / drones)

Image analysis for traits : ***Green fraction, light interception, photosynthesis biotic status***







Liu et al 2017
Ag. Forest Met

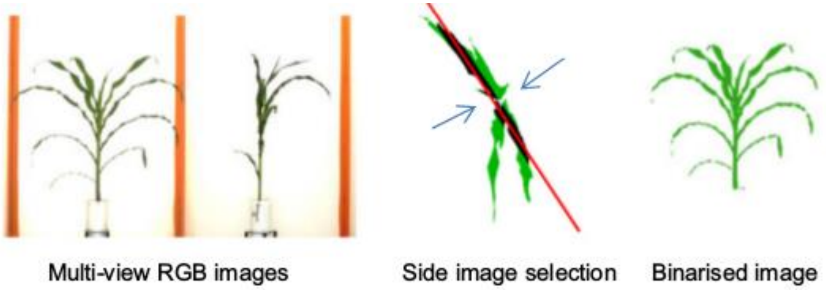
“High throughput physiology”: stomatal conductance and photosynthesis at plant level

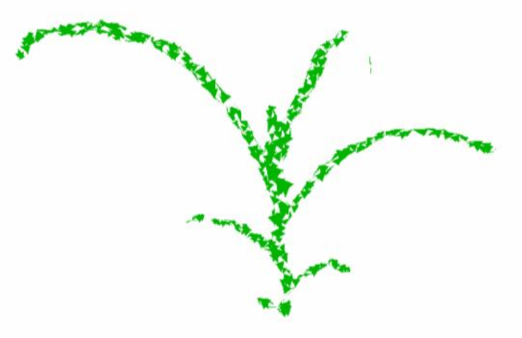
Light interception and RUE from Imaging and Modelling

Imaging

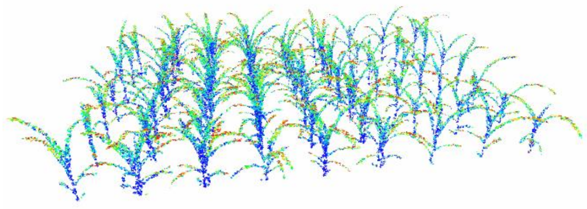
250 hybrids

Reconstruction



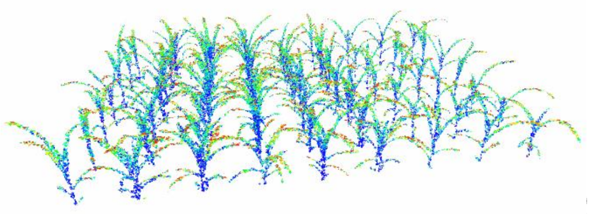


Field
(virtual or real)



Radiation interception efficiency

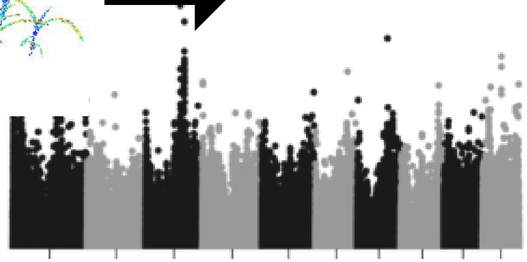
Platform



Radiation Use efficiency

$h^2 = 0.6$

Genetic dissection



Perez et al. 2019 PCE
Chen et al 2019 J .Exp Bot

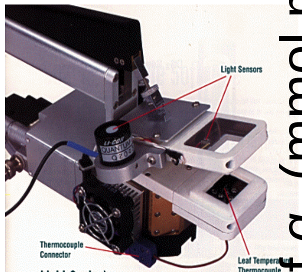
Tardieu et al 2017 Current Biol

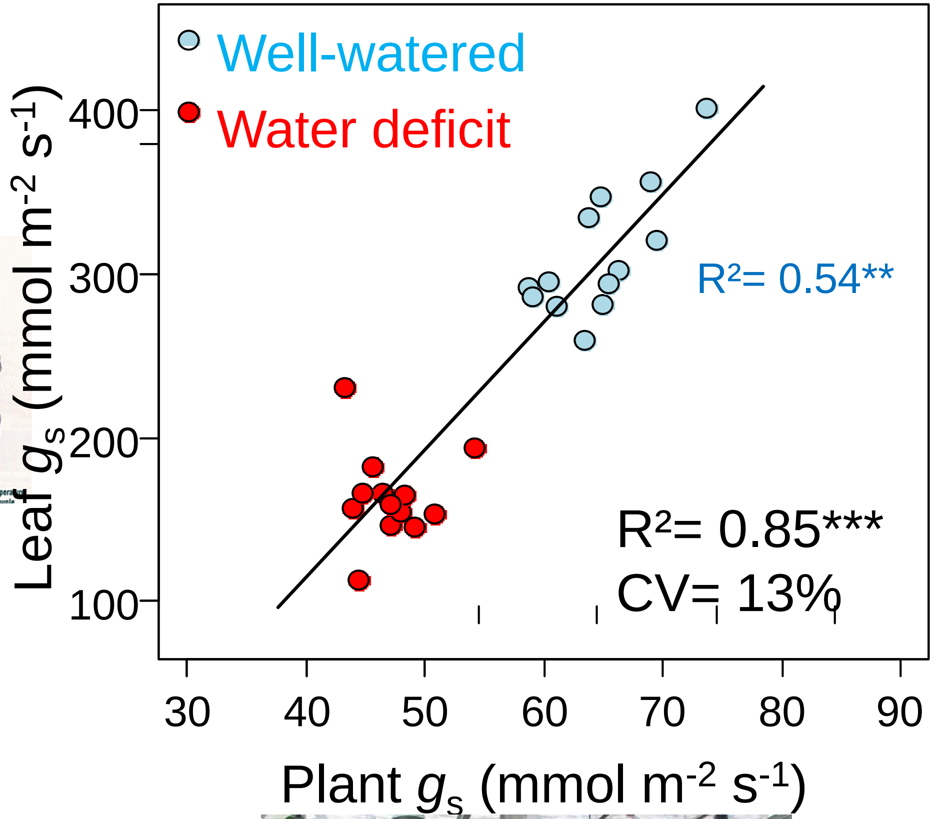
“High throughput physiology”: stomatal conductance and photosynthesis at plant level

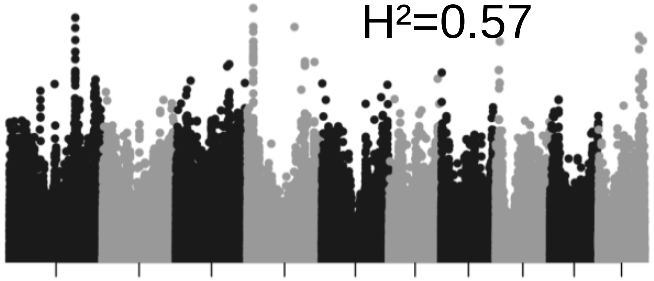
Maximum stomatal conductance from water flux

(inversing the Penman Monteith equation)

$$J_w = \frac{s\,(\Phi_n - G) + \rho_a c_p\, VPD_{air}\, g_a}{\lambda\,[\,s + \gamma(1 + g_a / g_s)]}$$







Genetic dissection

Alvarez Prado et al 2017
Plant Cell Environment

INRAE science for people, life & earth

We can predict traits and model parameters from the genotype

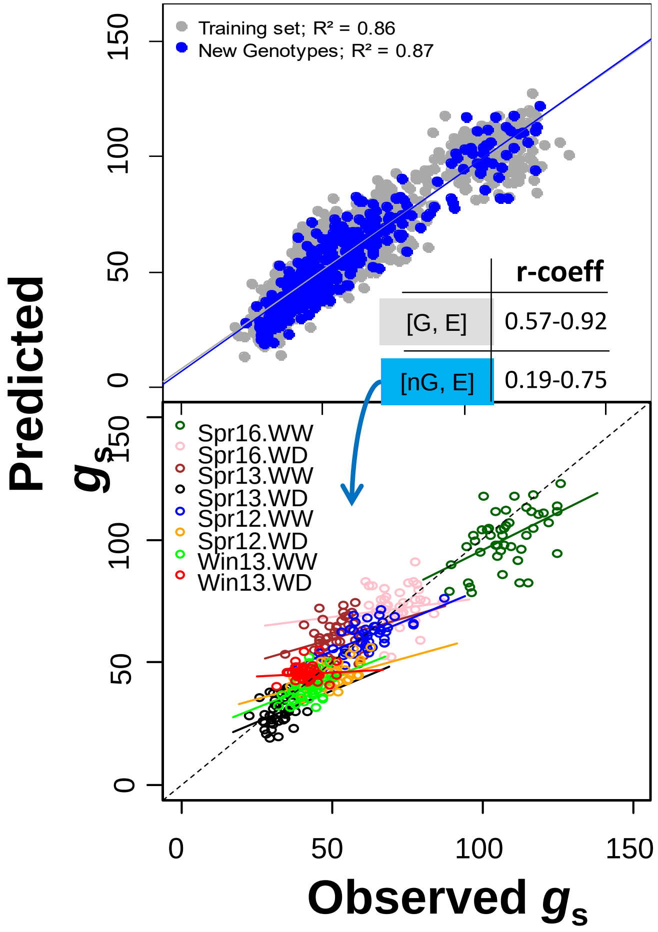
regression of phenotypic values with 750 000 marker values)

Maximum stomatal conductance)

[G, E] Training set (200 hyb)

[nG, E] Testing set (46 hyb)

X 20 permutations



Alvarez Prado et al 2017
Plant Cell Environment

To what extent are detailed phenotypes related to yield ?

For us, straightforward that phenotyping participates to breeding
BUT trait-based selection not in current breeding pipe lines

For us, straightforward that phenotyping participates to breeding
BUT trait-based selection not in current breeding pipe lines

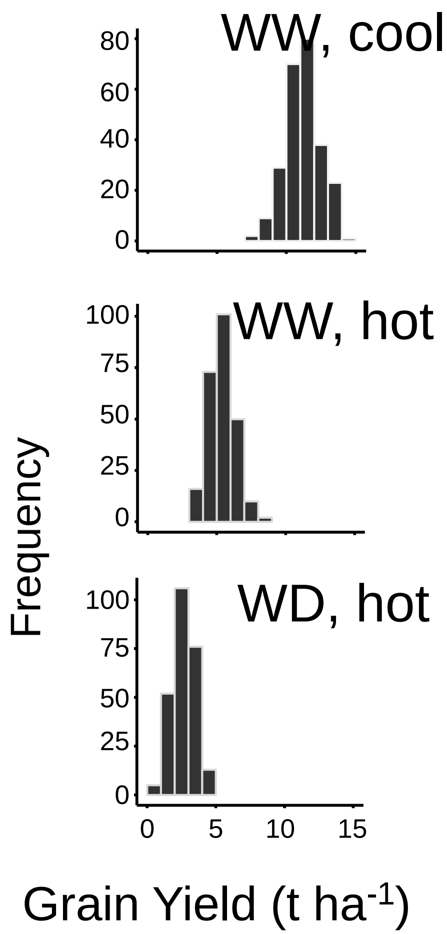
Richard and Sadras 2014 J Exp Bot (as a sample)

- *'The limited success of indirect selection to improve crop yield'*
- *'Indirect methods, based on secondary traits (…) a complement to direct selection for yield'*

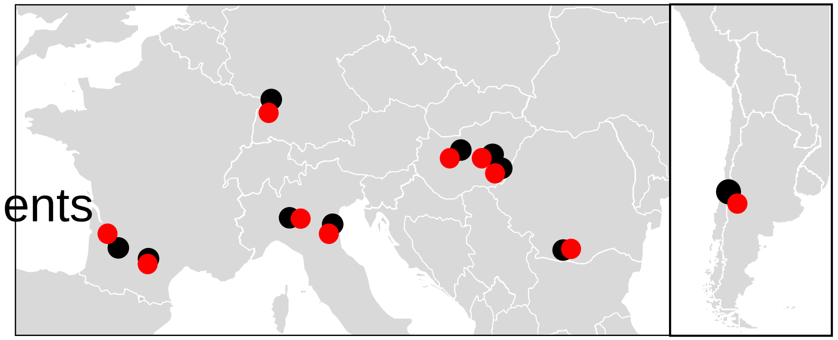
… Is Phenomics useful at all for improving crop performance ?

But what is THE yield and THE genetic control of yield ?

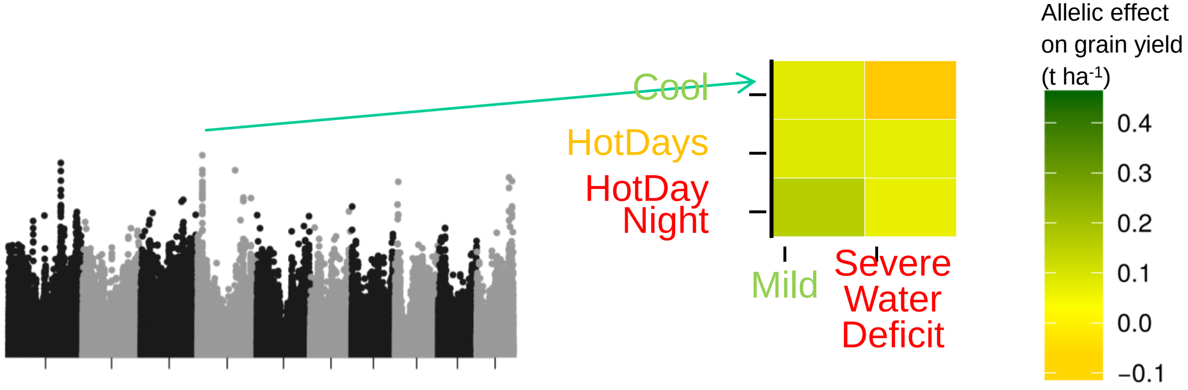
To what extent are detailed phenotypes related to yield ? Conditional effect of alleles



16 fields
x
2 years
x
2 W treatments



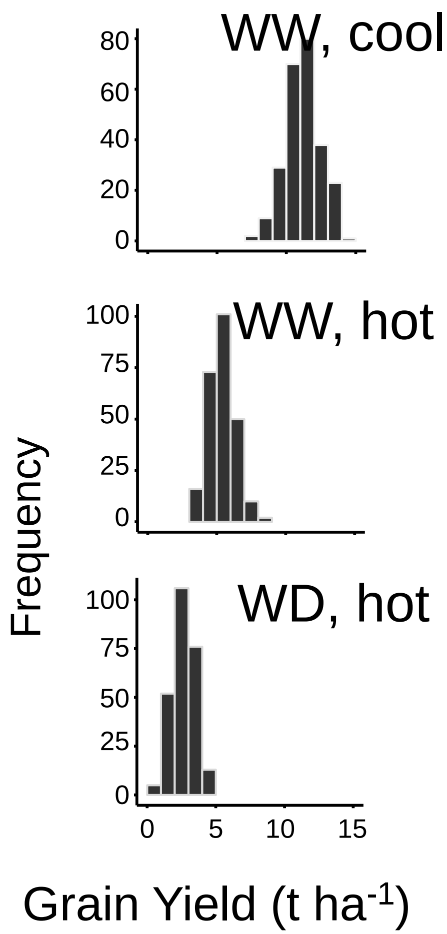
Allelic effects 1 QTL. each square, one scenario



Millet et al. 2016 Plant Phys

Yield and ranking of genotypes differ between fields
Most QTLs have positive, negative or no effects depending on scenarios

To what extent are detailed phenotypes related to yield ? Conditional effect of alleles



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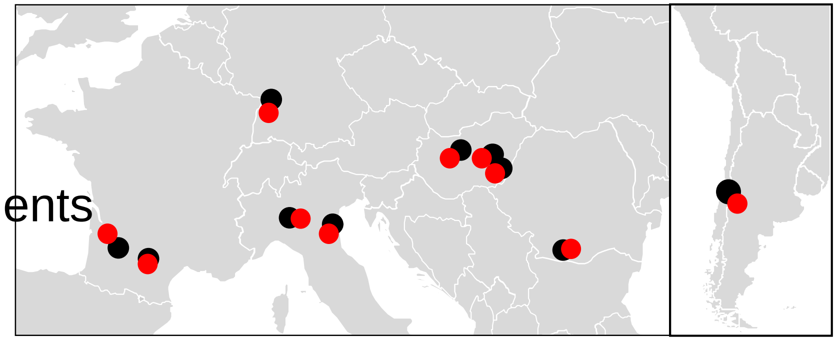

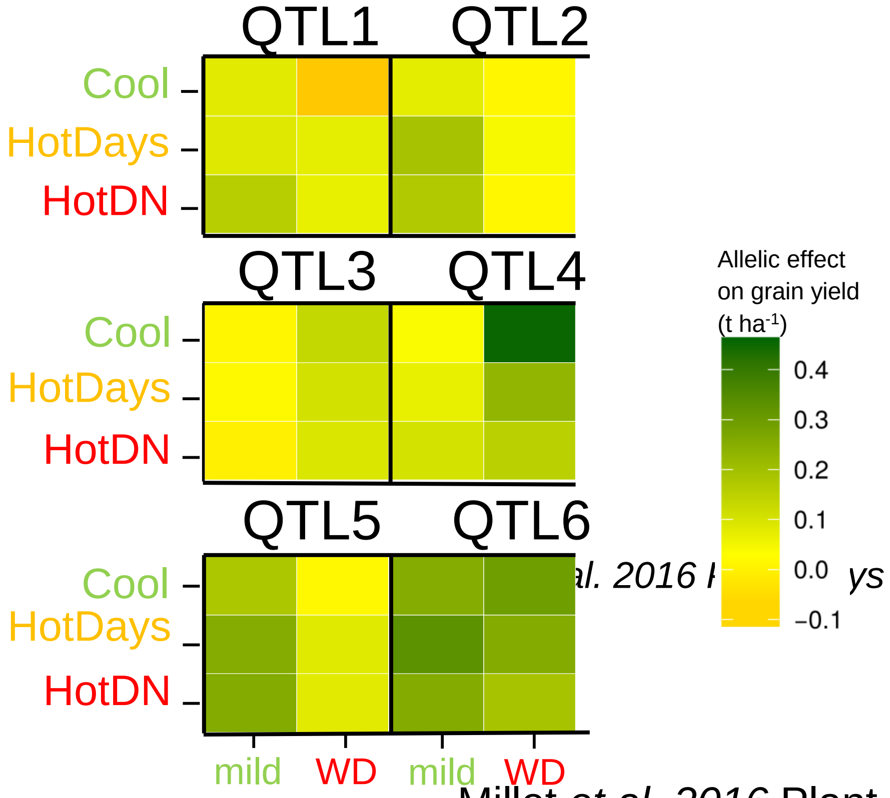

Millet *et al. 2016* Plant Phys

Yield and ranking of genotypes differ between fields

Most QTLs have positive, negative or no effects depending on scenarios

To what extent are detailed phenotypes related to yield ? Conditional effect of traits

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		Consequence on yield per soil and climate scenario				
		1	2	3	4	5
	targeted phenotypic traits	Early (around sowing) and mild WD mild ET, shallow soil	Terminal and mild to strong WD, high ET, shallow soil	Terminal and mild to strong WD, high ET, deep soil	Mild WD high ET, high T, deep soil	Mild WD high ET, high T, shallow soil
short-term traits	Stringent stomatal control					
	slow/sensitive leaf growth					
intrinsic / integrated traits	early flowering					
	sensitive grain abortion					
	High hydraulic conductance					
	Efficient root system upper layers					
	Deep rooting /efficient RS depth					
	high transpiration (intrinsic)					
	Long coleoptile (seedling establishment)					
	CAM					
	glaucousness					

Tardieu et al 2018 Ann Rev Plant Biology.

To what extent are detailed phenotypes related to yield ? Conditional effect of traits

		Consequence on yield per soil and climate scenario				
		1	2	3	4	5
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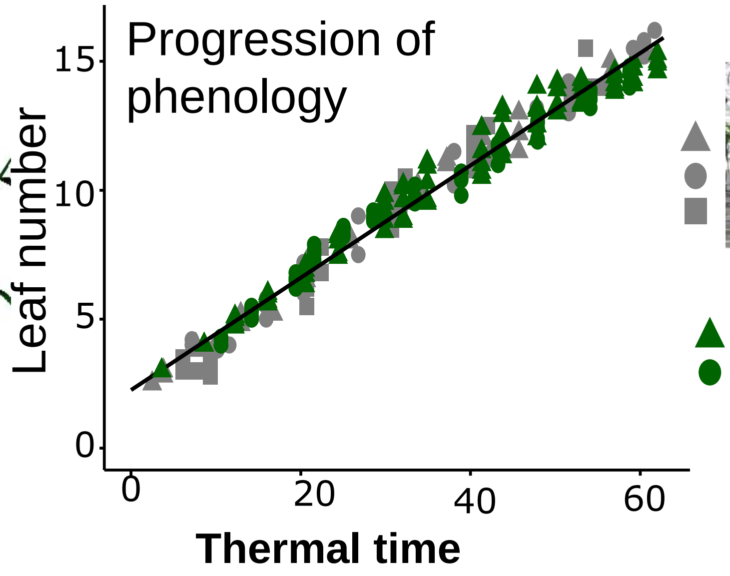
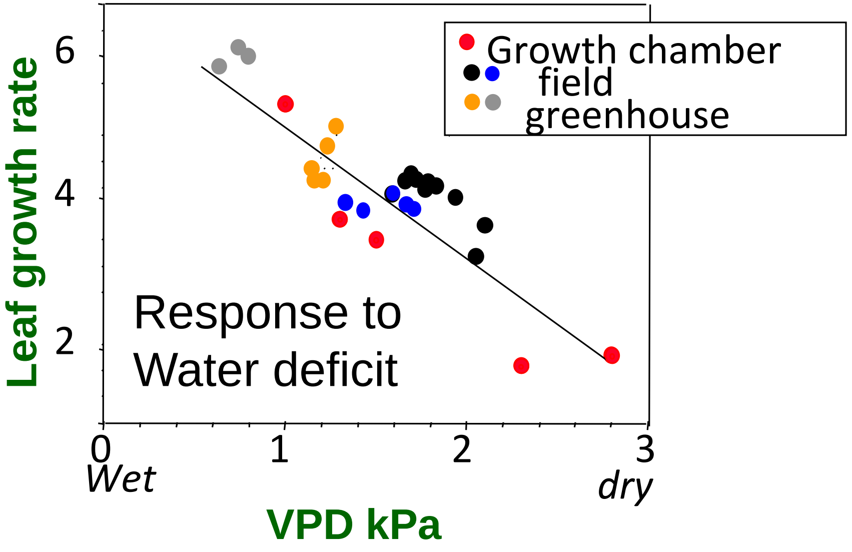
short-term traits	Stringent stomatal control	-	+	=/+	-	-
	slow/sensitive leaf growth	-	+	=/+	-	+
intrinsic / integrated traits	early flowering	+	++	+	-	+/=
	sensitive grain abortion	--	++	+	-	+/=
	High hydraulic conductance	+	-	+	++	-
	Efficient root system upper layers	+	-	-	+	+
	Deep rooting /efficient RS depth	-	-	+	+	-
	high transpiration (intrinsic)	=	--	-	++	-
	Long coleoptile (seedling establishment)	+	=	=	=	=
	CAM	-	=/+	-	-	-
	glaucousness	+	=	=	+	+

Tardieu et al 2018 Ann Rev Plant Biology.

Traits, *1 genotype*

One can measure genotype-specific traits in platforms
(platforms can represent field, after some effort)

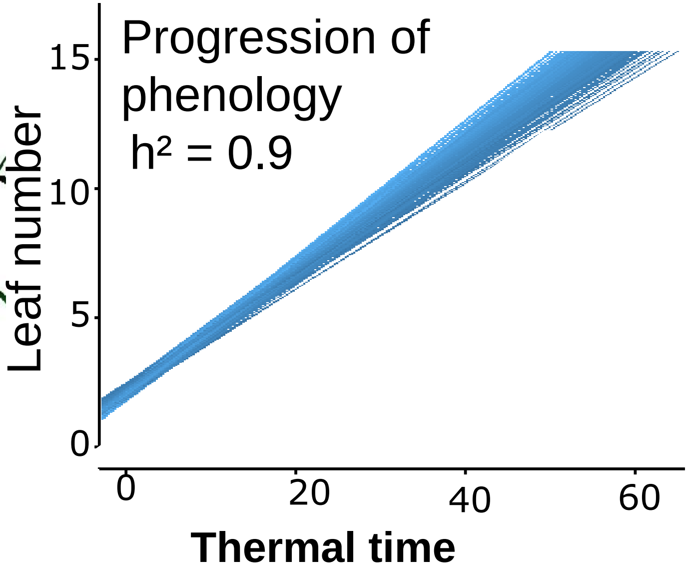


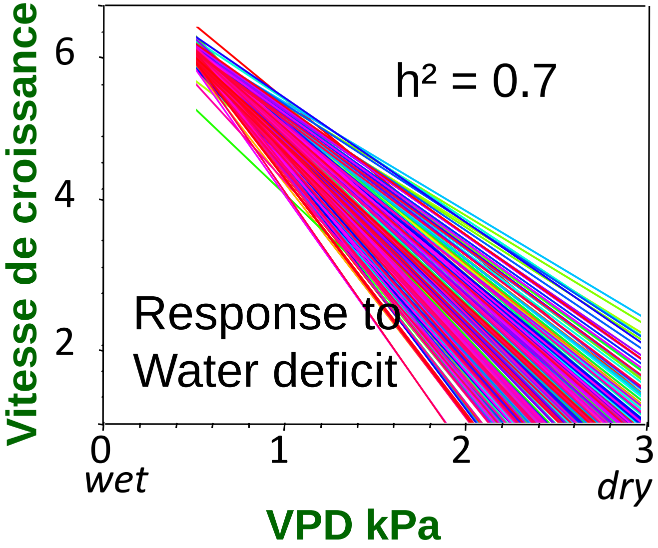


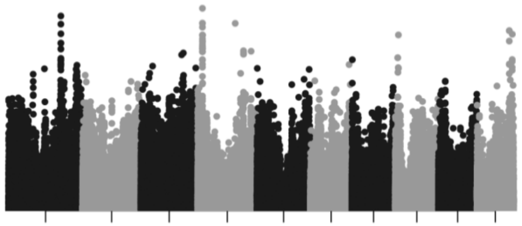
Traits, *250 genotype*

One can measure genotype-specific traits in platforms

Traits are heritable







Genetic dissection

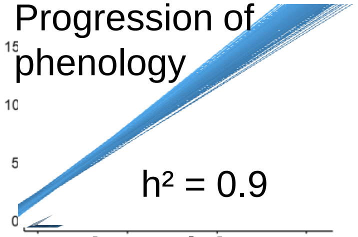
S. Alvarez Prado

Combining phenomics, modelling and genomic prediction

Genomic prediction of maize yield across European environmental scenarios

Millet et al 2019 Nature Genetics

1. Plateform, 250 geno



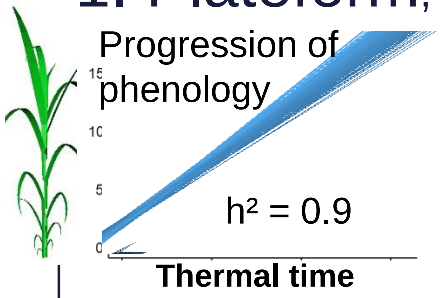
Floral transition — Silk initiation — End abortion — Grain maturity

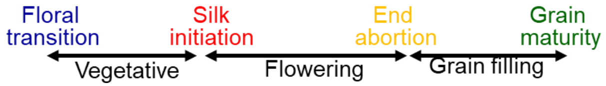
Vegetative ↔ Flowering ↔ Grain filling

Genomic prediction of maize yield across European environmental scenarios

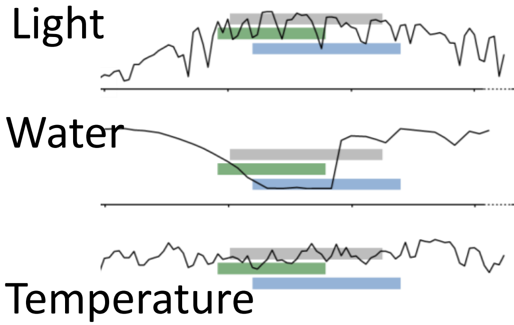
Millet et al 2019 Nature Genetics

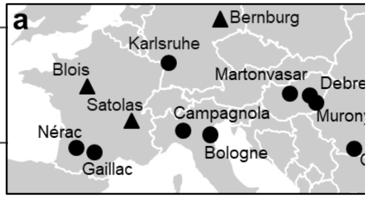
1. Plateform, 250 geno





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

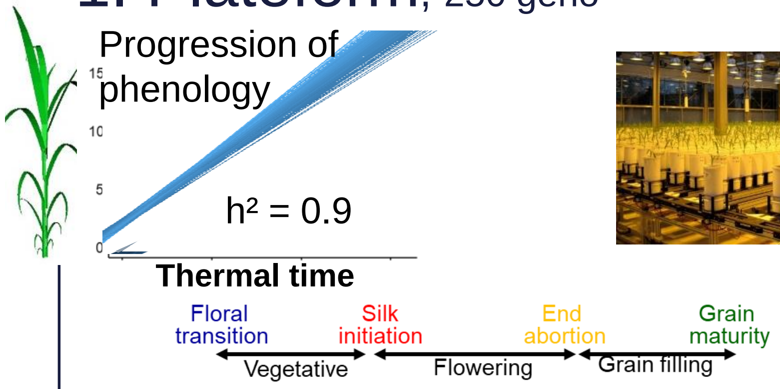




Genomic prediction of maize yield across European environmental scenarios

Millet et al 2019 Nature Genetics

1. Plateform, 250 geno



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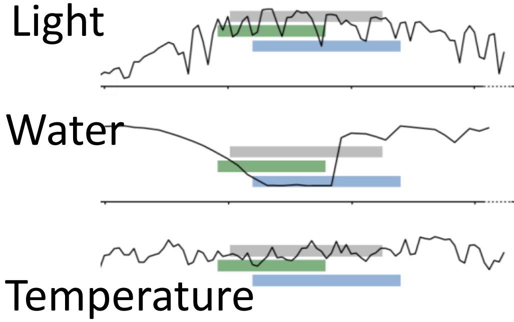
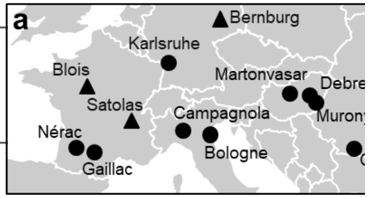
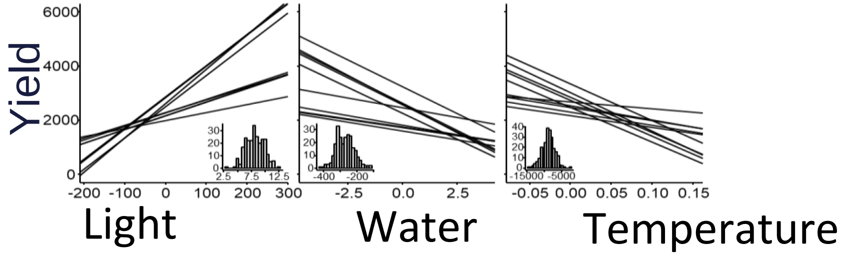




3. Response curves, 250 geno



4. Genomic prediction, 250 geno

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

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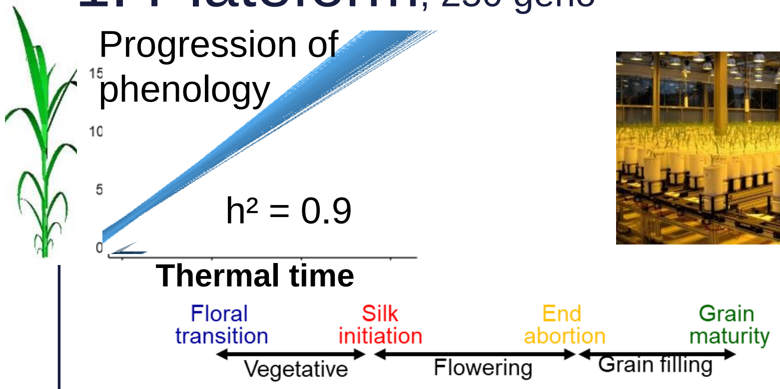

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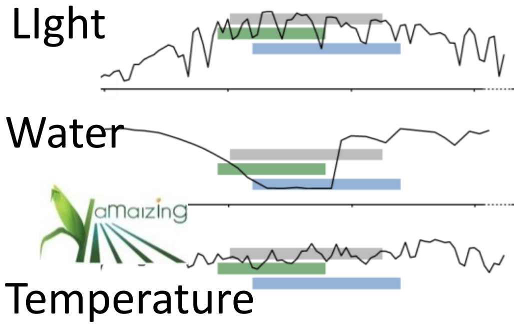

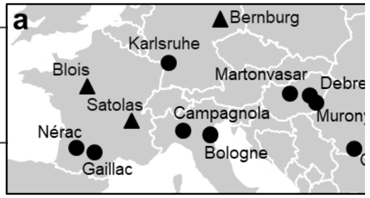

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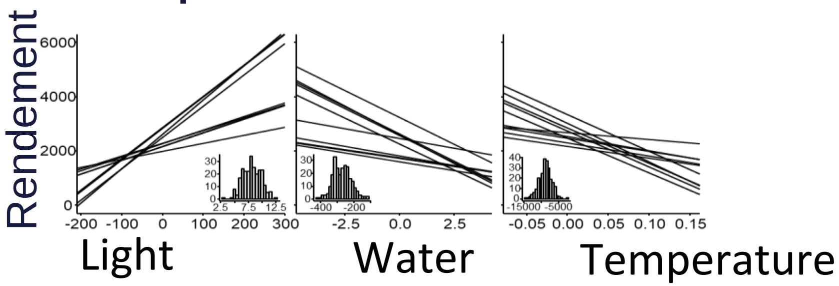

4. Genomic prediction, 250 geno

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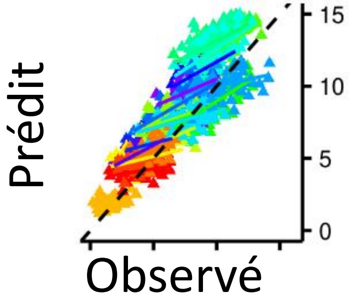
5. Test, New geno in new fields



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

A multi-scale problem, multi scale solutions

- Physiological mechanisms can be measured in high precision platforms
  Their effects, and that of underlying alleles, depends on environmental scenarios

- Platforms cannot represent fields
  … but a field does not represent another field!

- Multi site field experiments: where and when alleles are favourable
  for yield, and increasingly for traits

- Difficult to disentangle environmental effects and to measure some traits in the field
  High throughput still essential : relate the genetic variabilities of traits and yield.

Future of phenomics : development of methods to link phenotypic scales (modelling) and include them in genomic prediction

FAIR Data management

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Field experiments

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Platform experiments, modelling, GWAS

C Welcker

B. Parent

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O. Turc

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