



Global Science Conference

March 16-18, 2015
Le Corum, Montpellier France

Towards genotypes adapted to climate change

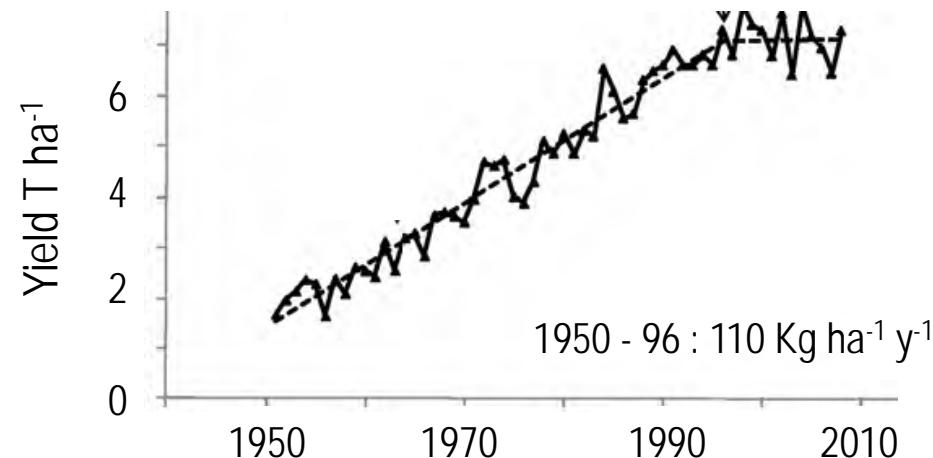
via combination of phenotyping and modelling: The projects DROPS and Phenome

Francois Tardieu
INRA Montpellier

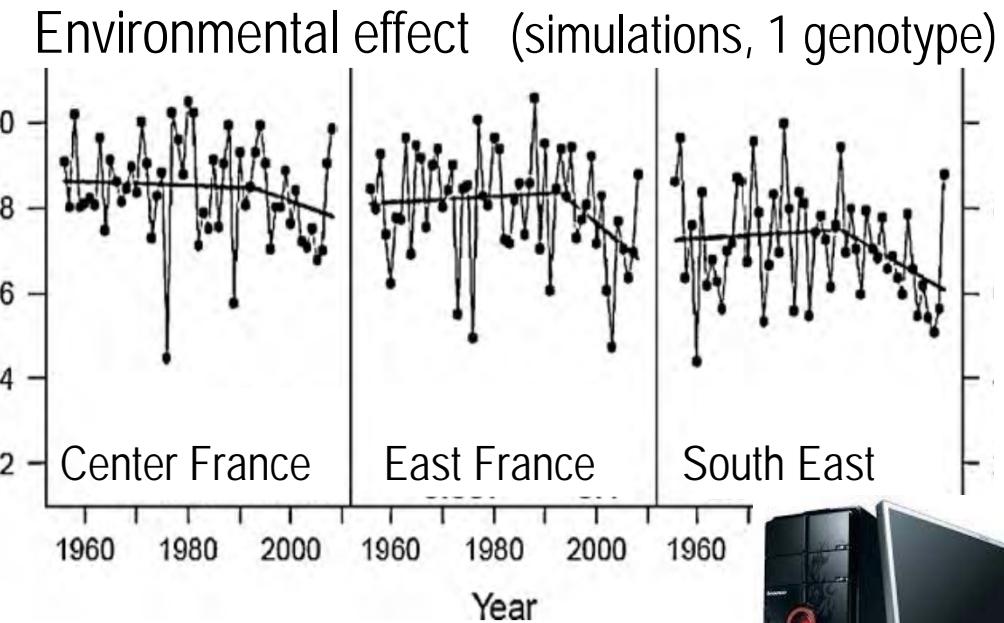
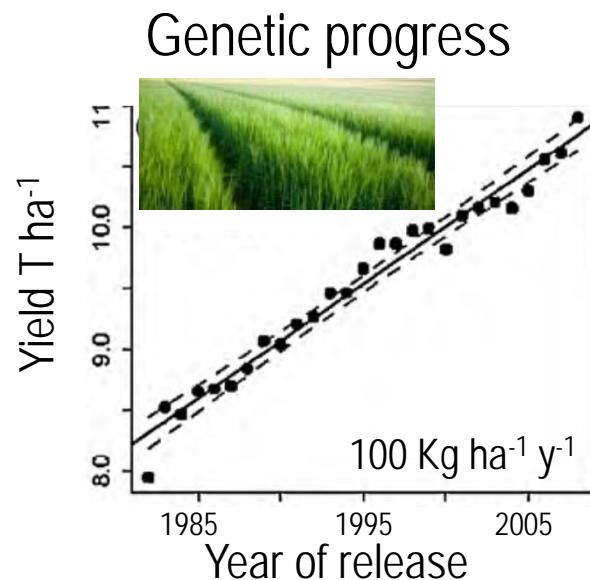


A continuous genetic progress challenged by climate change

	NW	NE	SW	SE
1950	2.1	2.4	2.7	2.7
1955	2.3	1.9	1.5	1.5
1960	3	3.1	3.3	3.3
1965	3.5	3.3	3.8	3.6
1970	4.1	4.1	4.3	4.2
1975	4.5	4.1	3.7	3.9
1980	5.1	5.0	5.4	5.2
1985	5.5	5.6	5.8	5.5
1990	6.3	5.8	6.1	5.9
1995	7.1	7.3	7.1	7.3
2000	7.2	7.1	7.5	7.4
2005	7.1	6.8	6.8	7.2
2010	7	7.3	7.8	8.0
2015	7.1	6.7	6.6	6.2



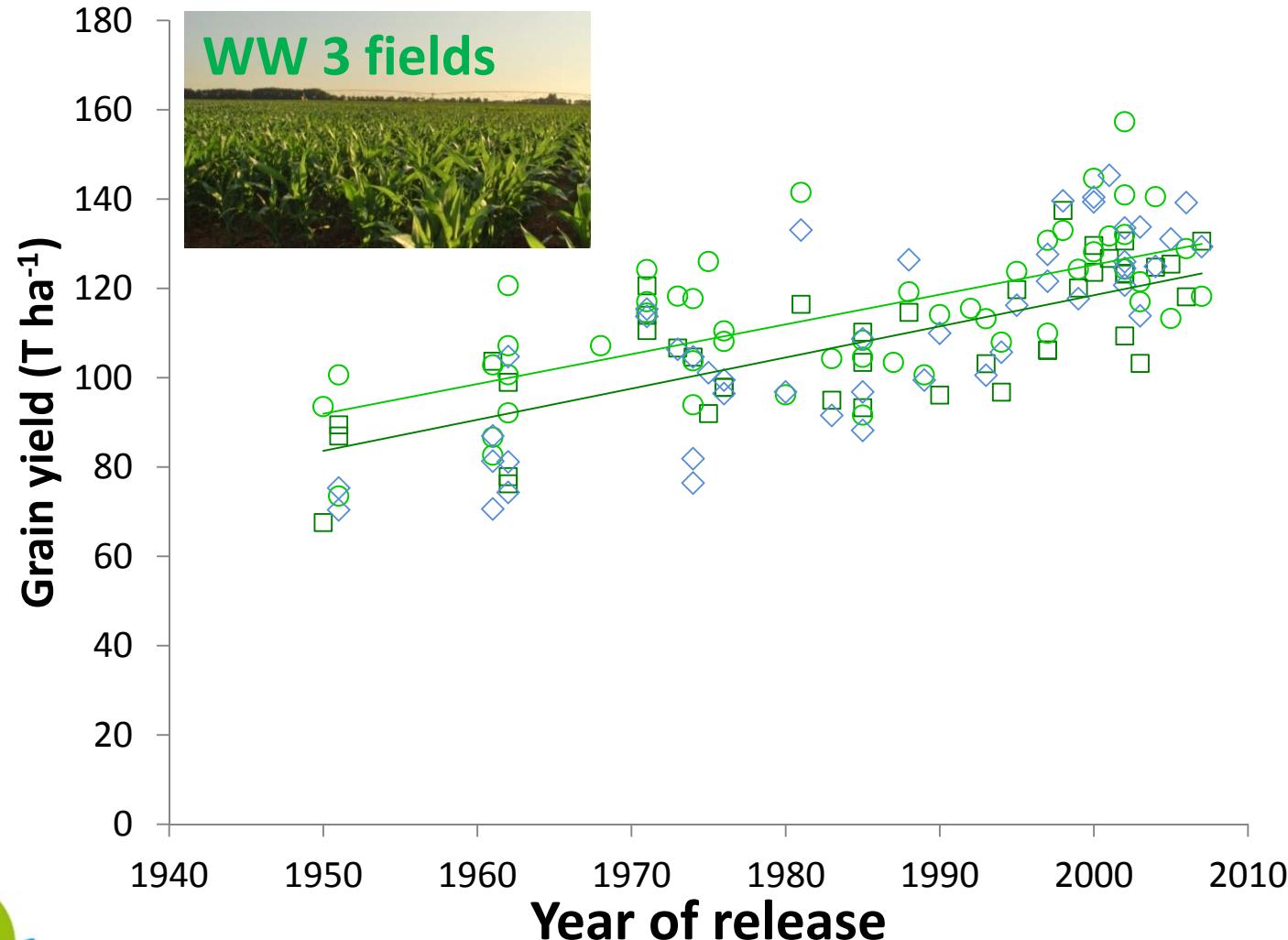
similar in all EU,
barley, canola, sunflower...



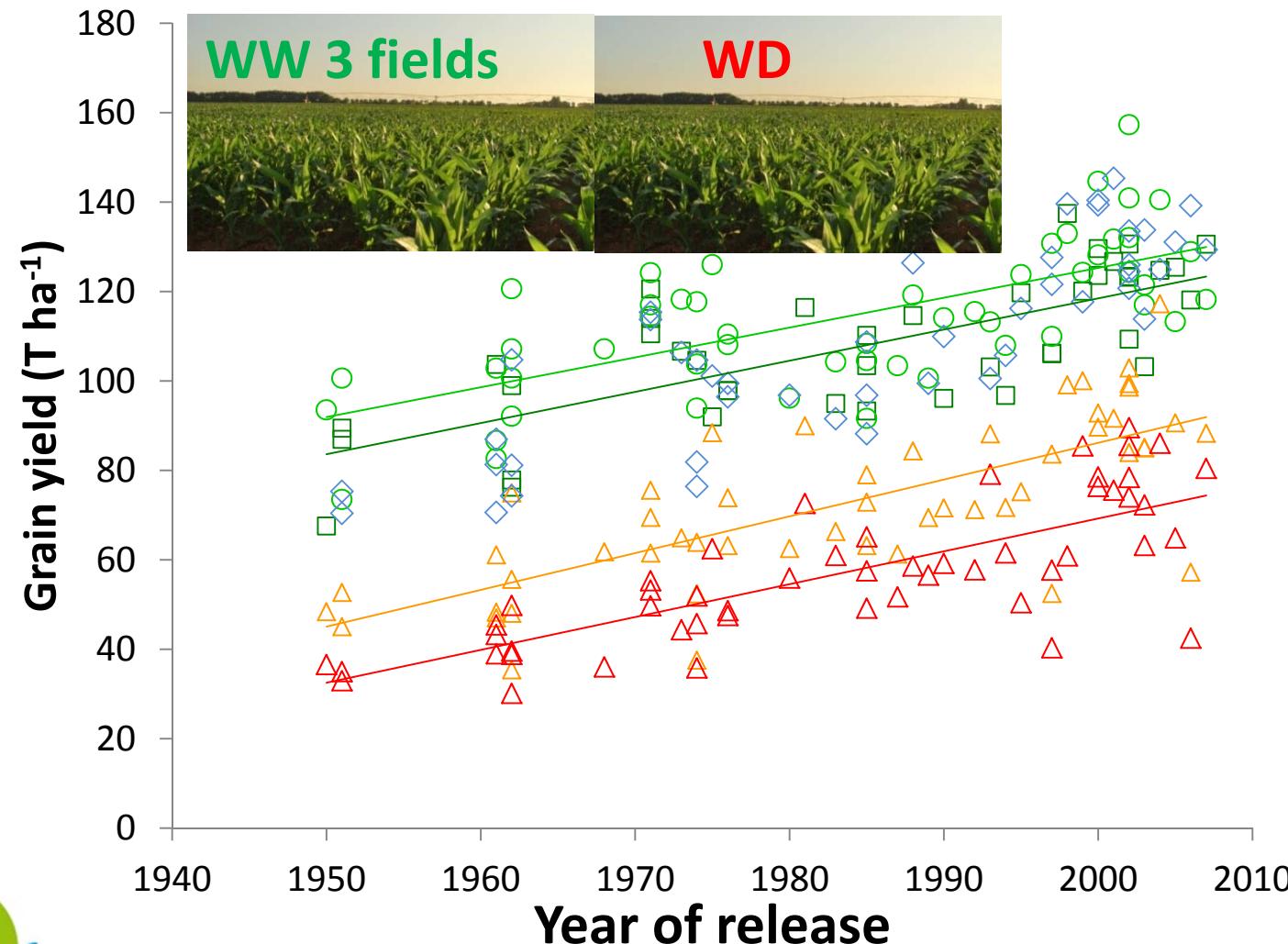
We need a new generation of genotypes better adapted

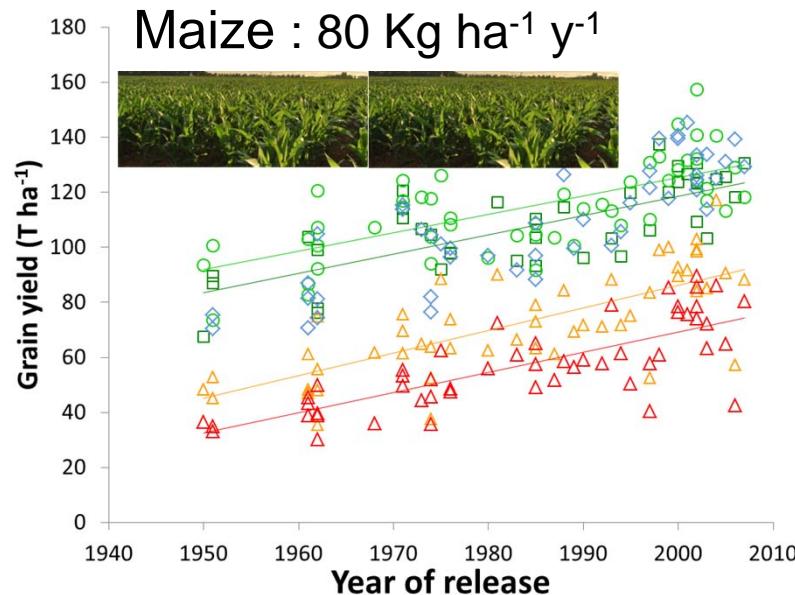


Maize : 80 Kg ha⁻¹ year⁻¹ in a European series,

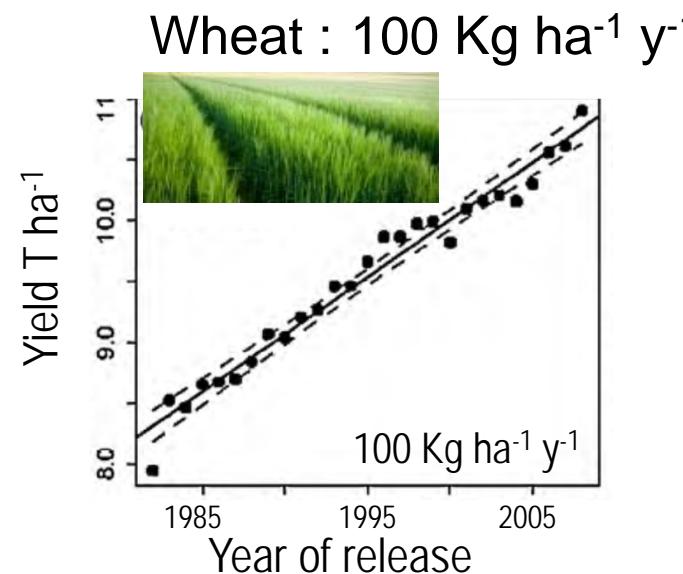


Maize : 80 Kg ha⁻¹ year⁻¹ in a European series,
same progress in water deficit

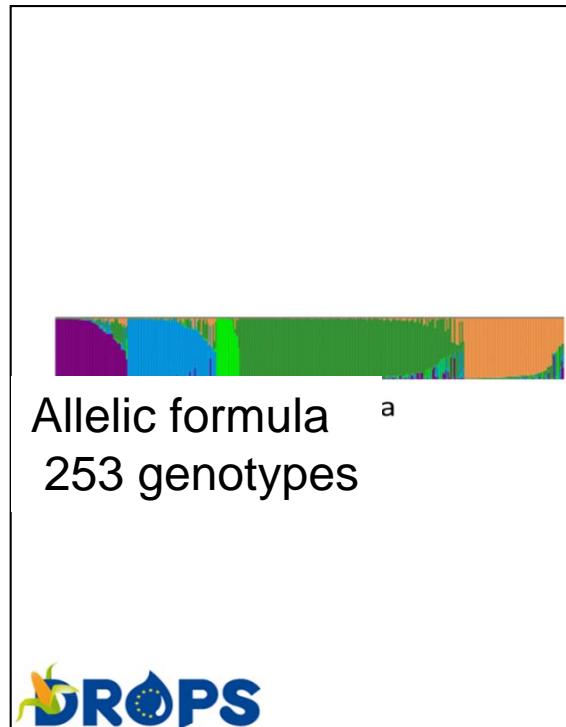




- Breeders have done their job...
- Crop models deal with 'maize' or 'wheat' not genotypes
Not the same plants in 2050 !
- We want progress to continue

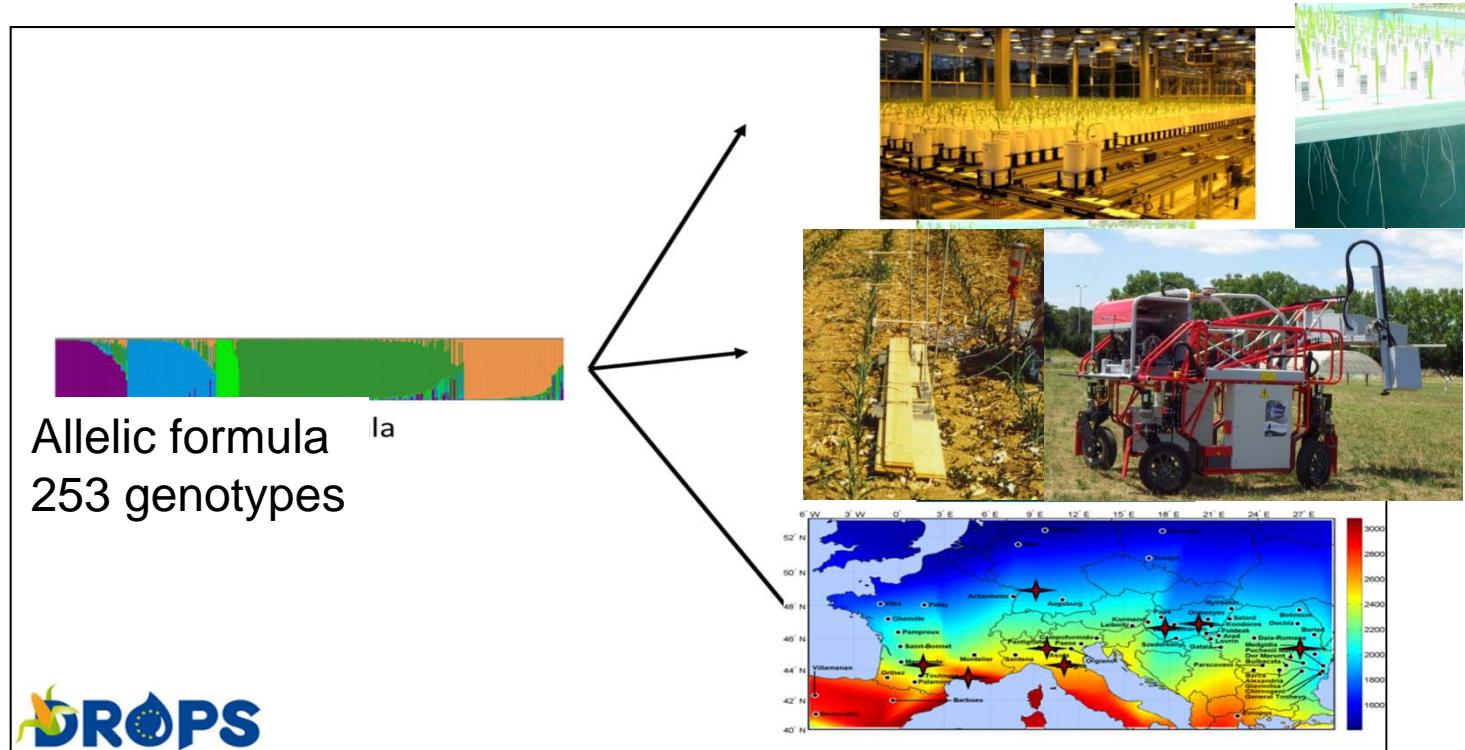


Approach



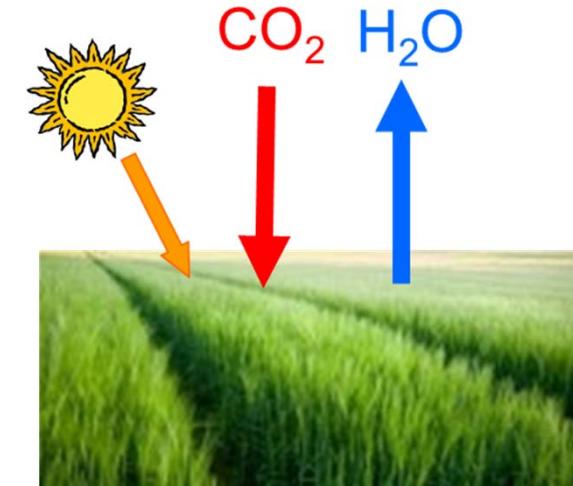
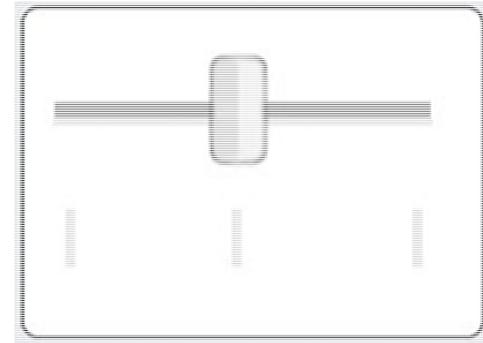
- Explore genetic resources

Approach



- Explore genetic resources
- Identify genomic regions that control traits and performances in a variability of climates *100s genotypes (throughput)*

Breeding for optimisation, not for resistance to stress



Optimisation between traits (alleles) of tolerance
traits (alleles) for productivity

- Explore genetic resources
- Identify genomic regions that control traits and performances in a variability of climates *100s genotypes (throughput)*
- **Where and when alleles are favorable ?**

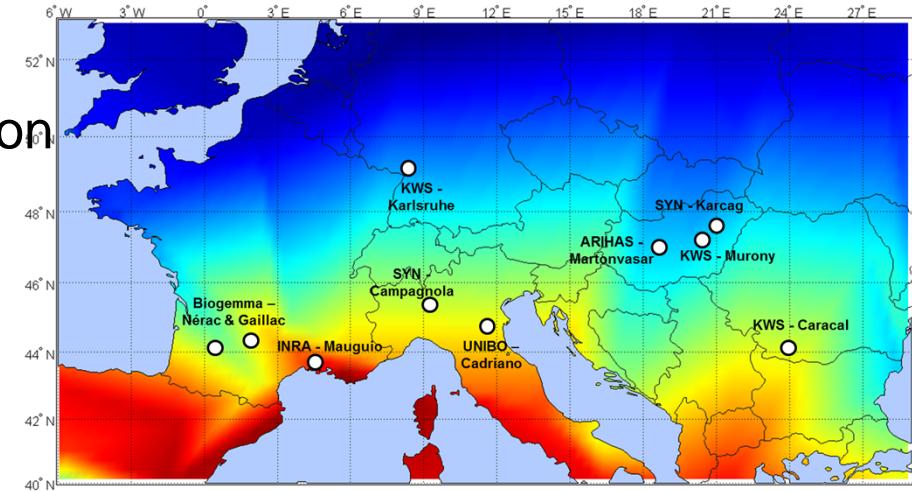
***measure environmental conditions (sensors),
many sites x years (throughput)***

A large genetic variability of yield, difficult to interpret



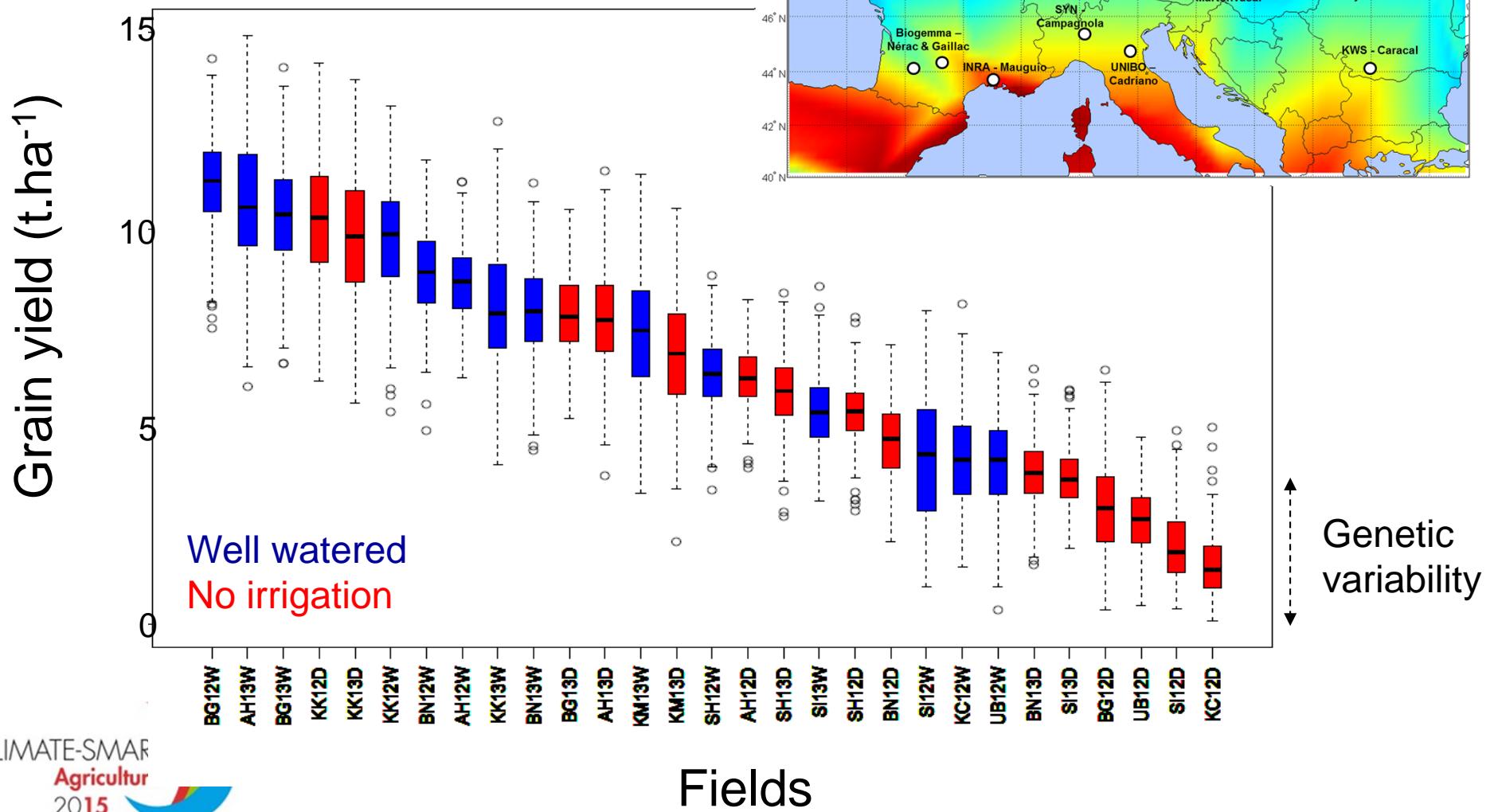
253 genotypes in 16 fields x 2 years

GxE = more than 50% of the total variation



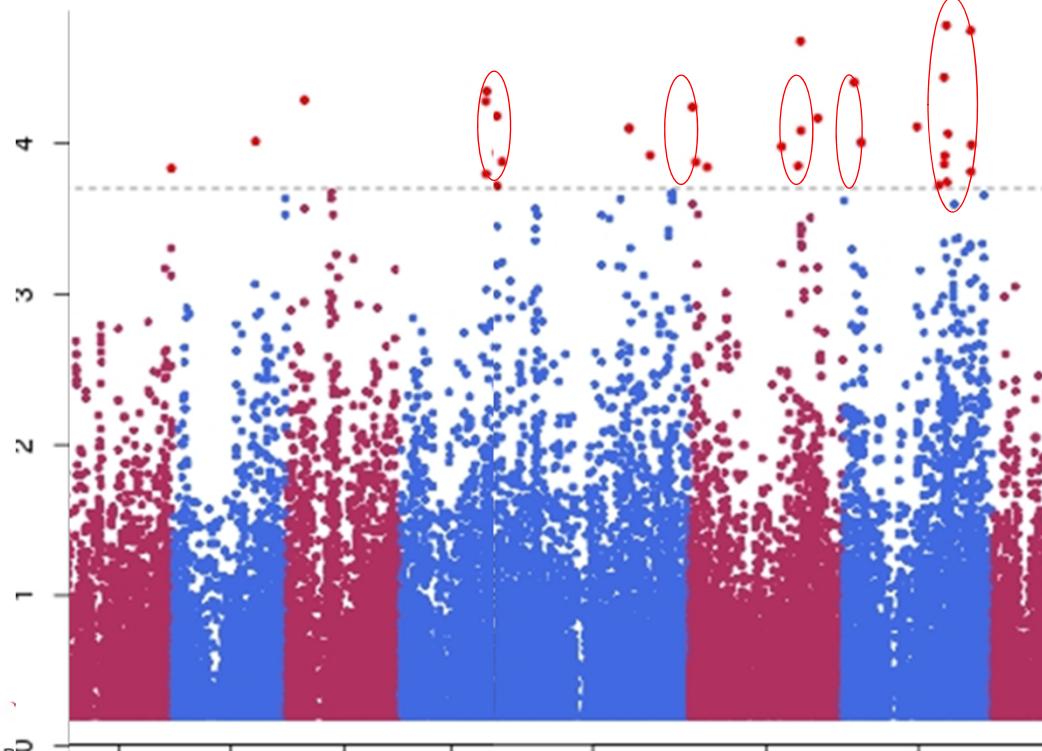
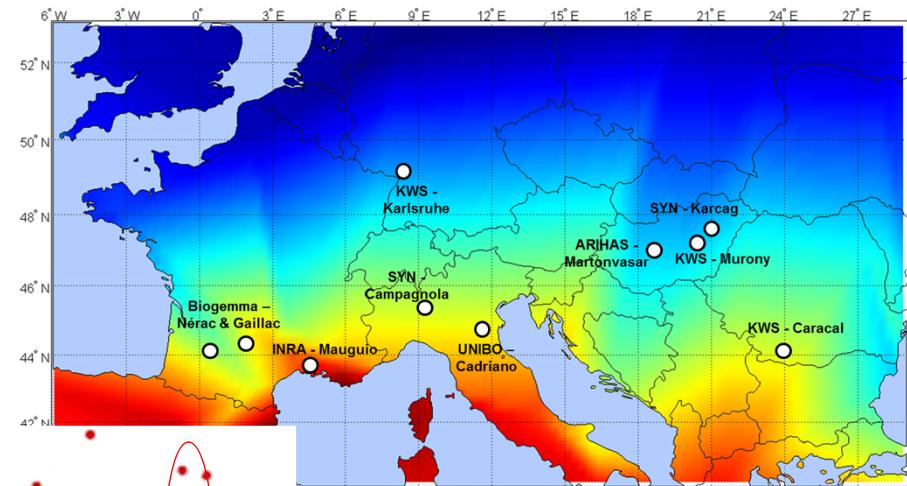
A large genetic variability of yield, difficult to interpret

252 genotypes in 16 fields x 2 years
GxE = more than 50% of the total variation



A large genetic variability of yield, difficult to interpret

Some genomic regions control yield
BUT highly unstable between fields



W. Kruijer & S. Negro
WUR INRA
Biometris Moulon



Disentangling the genetic variability



Disentangling the genetic variability

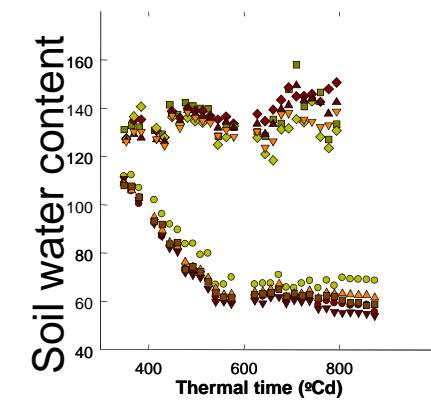
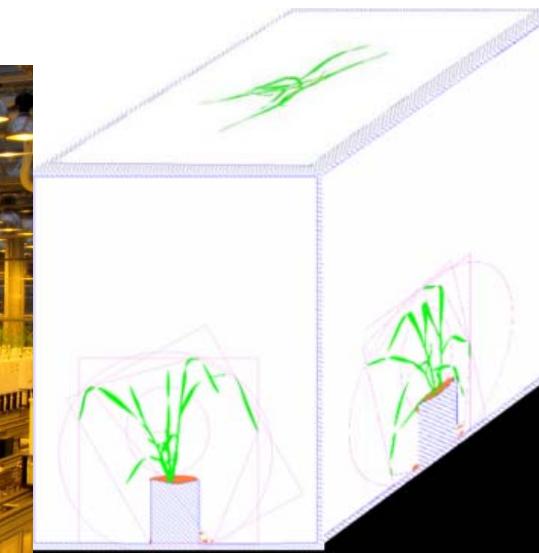


PhenoArch

<http://bioweb.supagro.inra.fr/PhenoArch/>



1650 plants



Disentangling the genetic variability

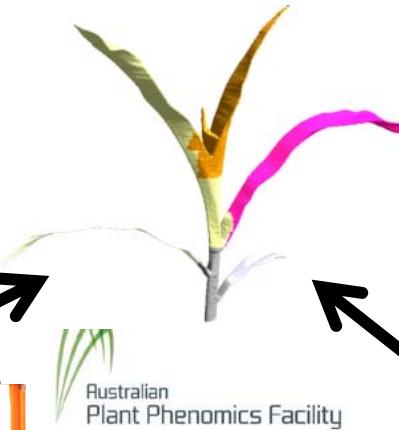


PhenoArch

<http://bioweb.supagro.inra.fr/PhenoArch/>



3D imaging



Model

Australian
Plant Phenomics Facility

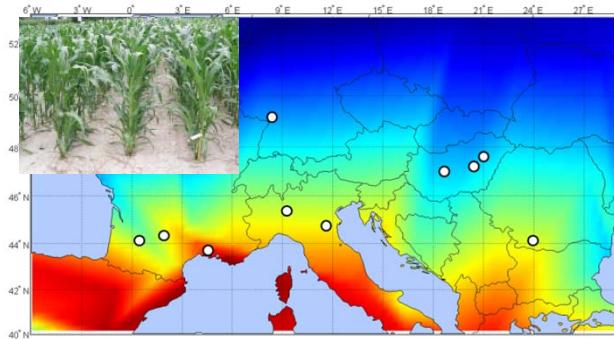
PHENOME
Réseau Français
Phénomique végétale
FPPN

CLIMATE-SMART
PHENOME
Réseau Français
Phénomique végétale



Li Cabrera C. Fournier

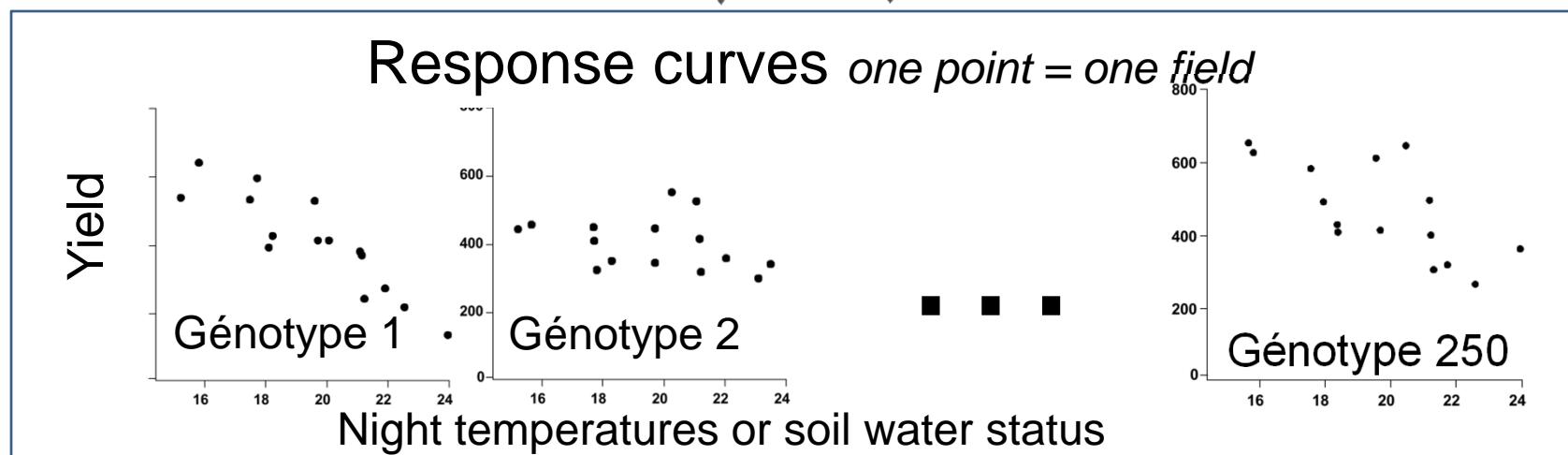
Disentangling the genetic variability



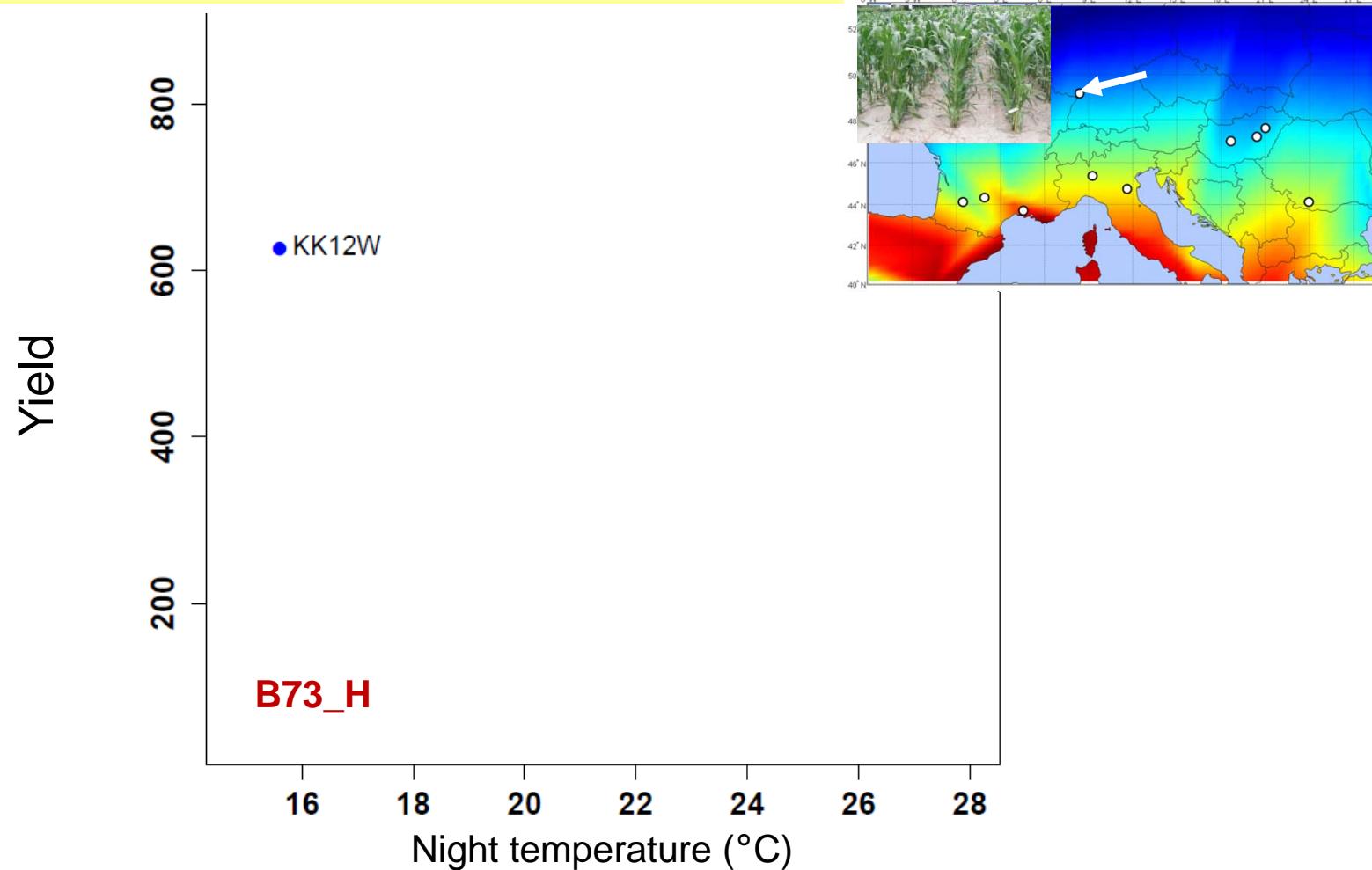
Climate and grain number



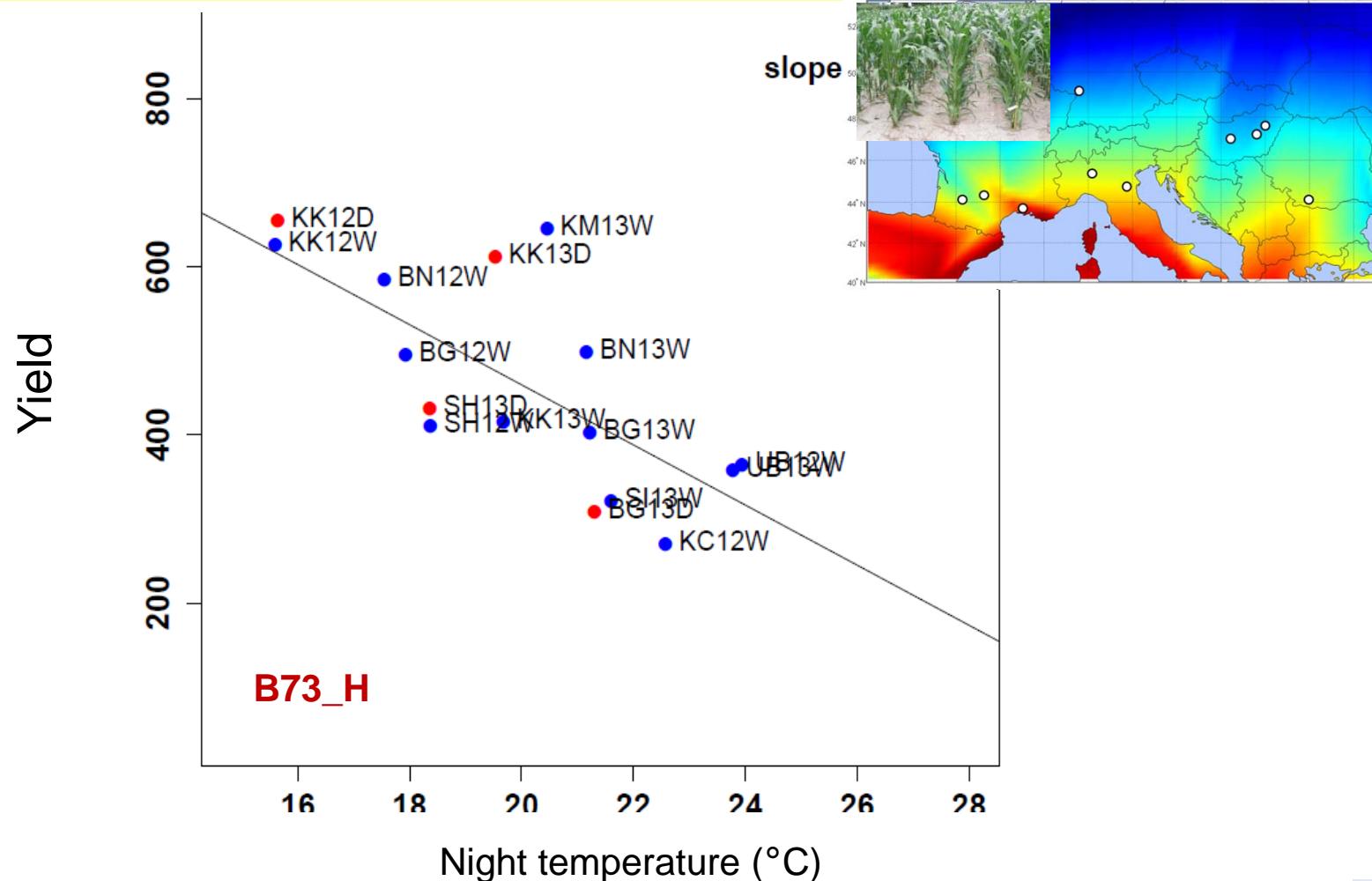
Precise development
250 genotypes



Disentangling the genetic variability



Disentangling the genetic variability

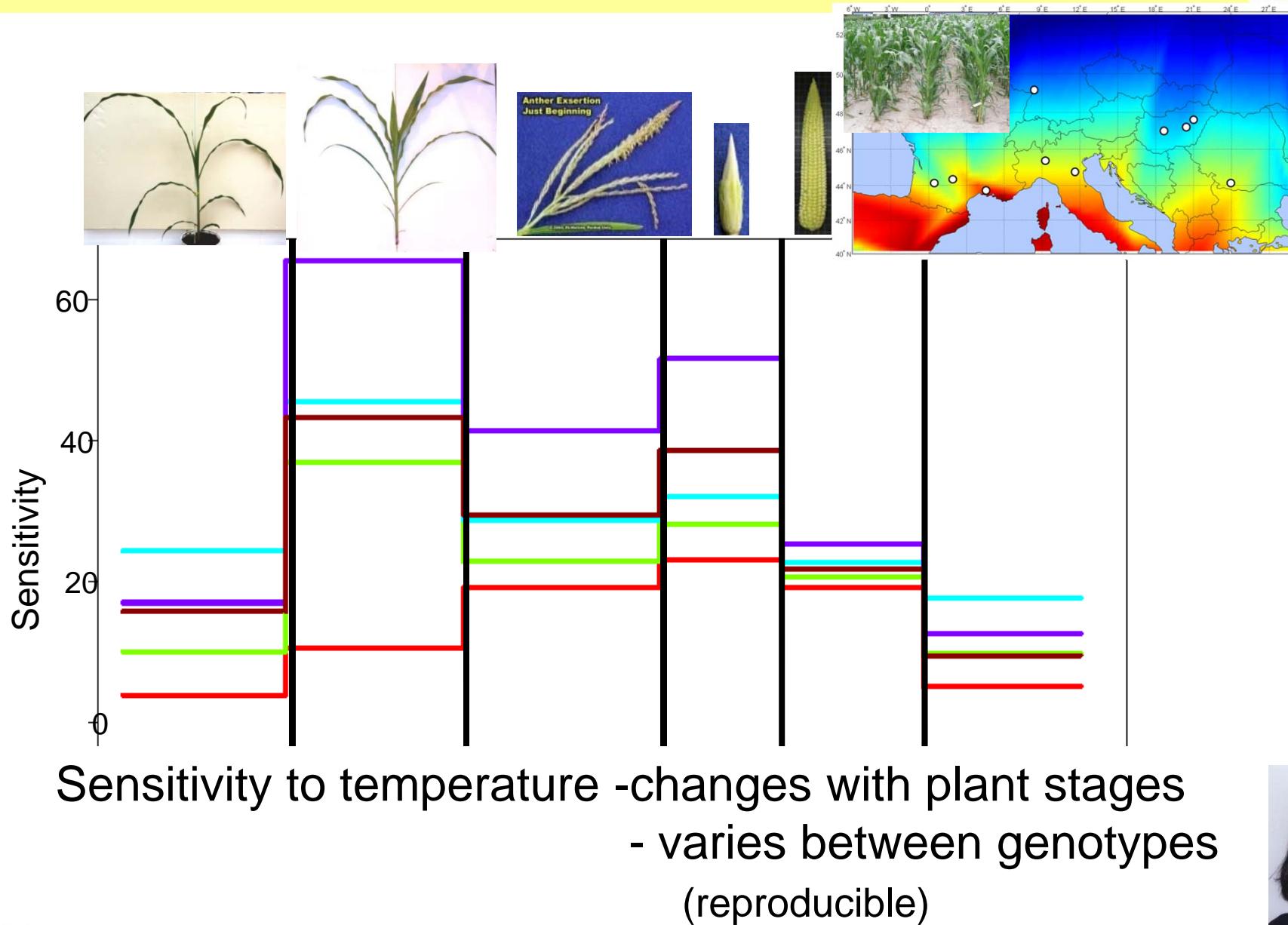


→ 50% of yield varies with night temperature around flowering



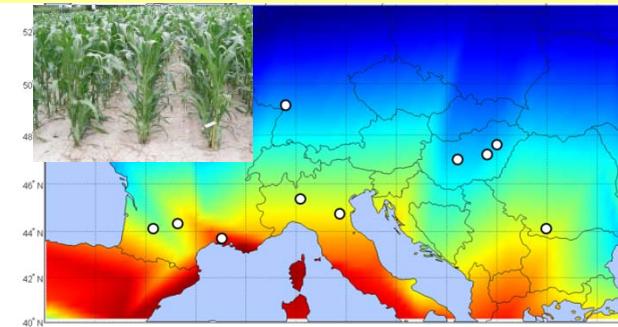
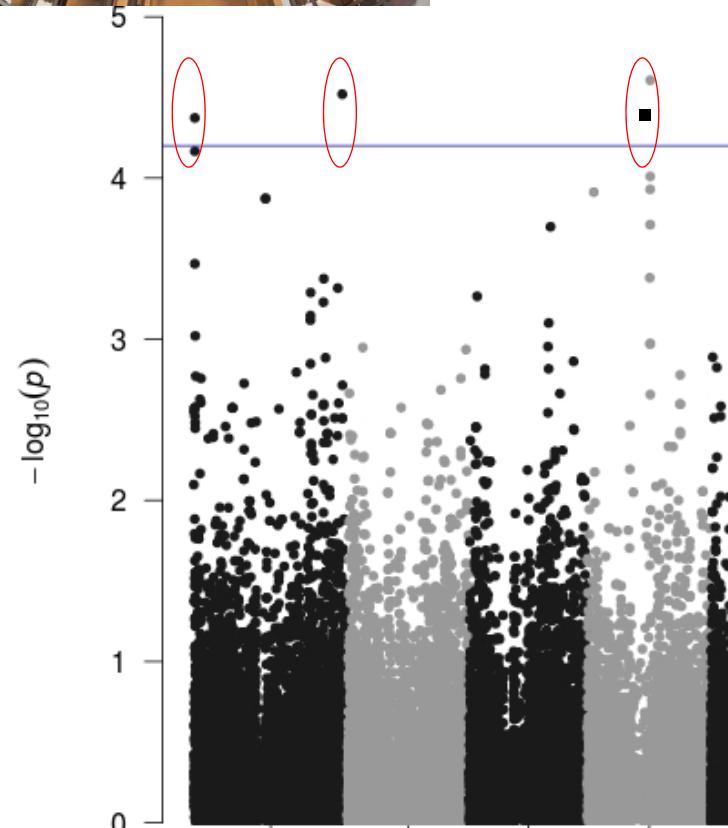
E. Millet

Disentangling the genetic variability



E. Millet

Disentangling the genetic variability



A large genetic variability of sensitivity, usable for breeding :

Genomic regions associated with sensitivity to temperature

in the field

But using a phenotyping platform



Disentangling the genetic variability : water deficit

PHENODYN

<http://bioweb.supagro.inra.fr/phenodyn/>



transpiration



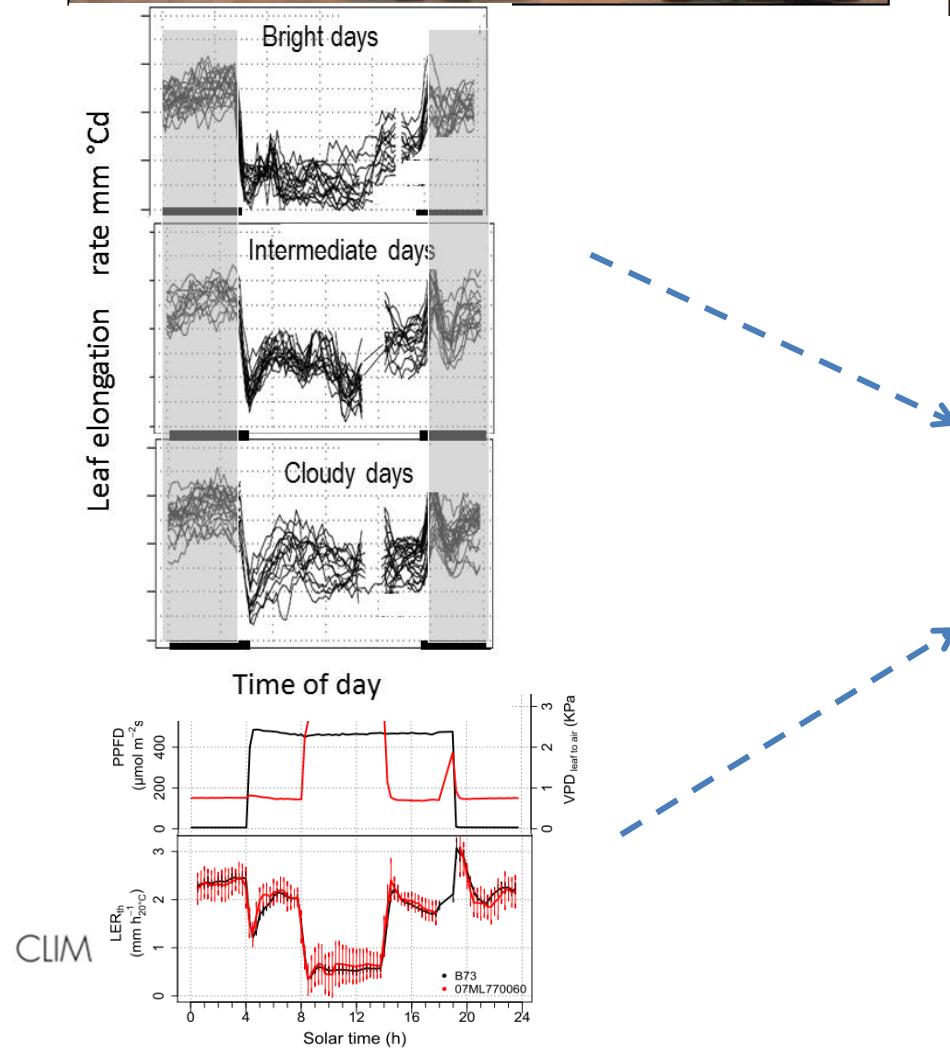
Environment



growth

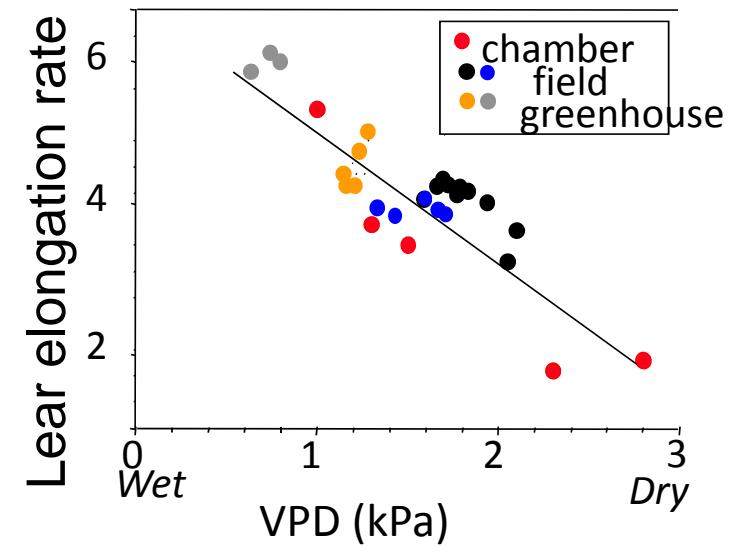


Disentangling the genetic variability : water deficit

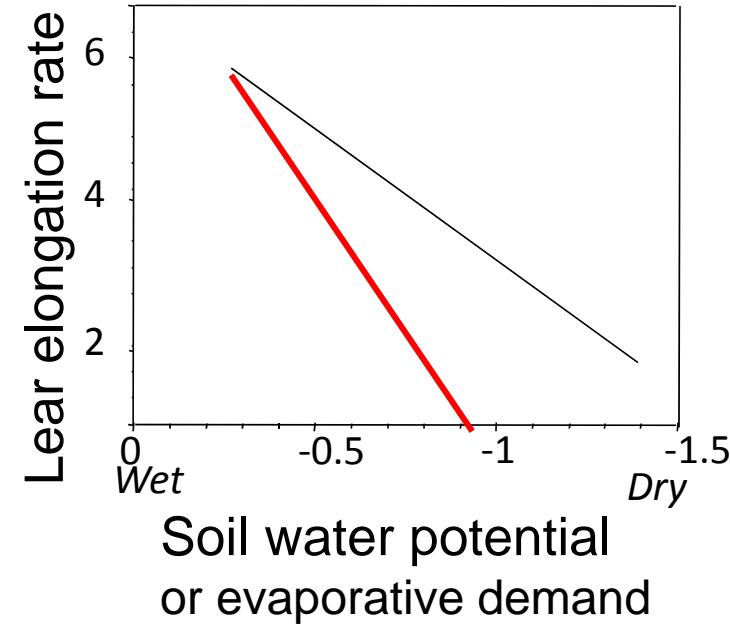
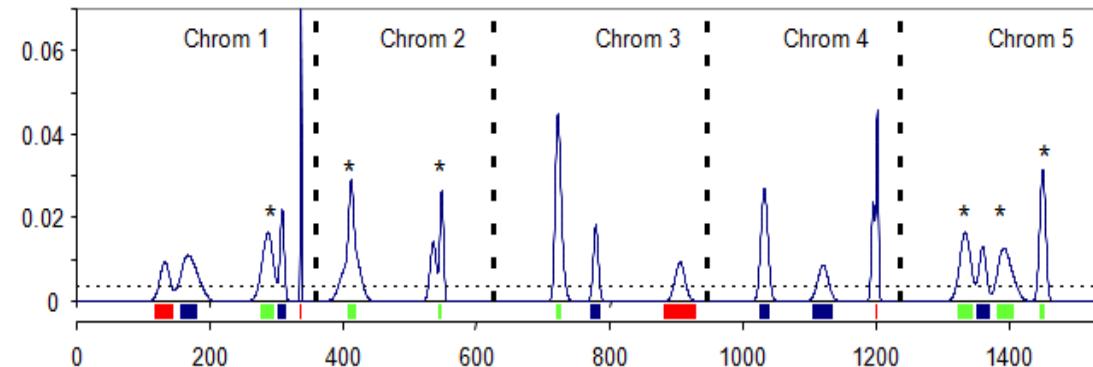
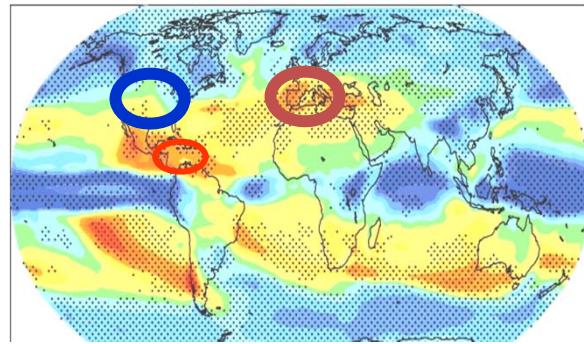


Response to water deficit

Stable between experiments



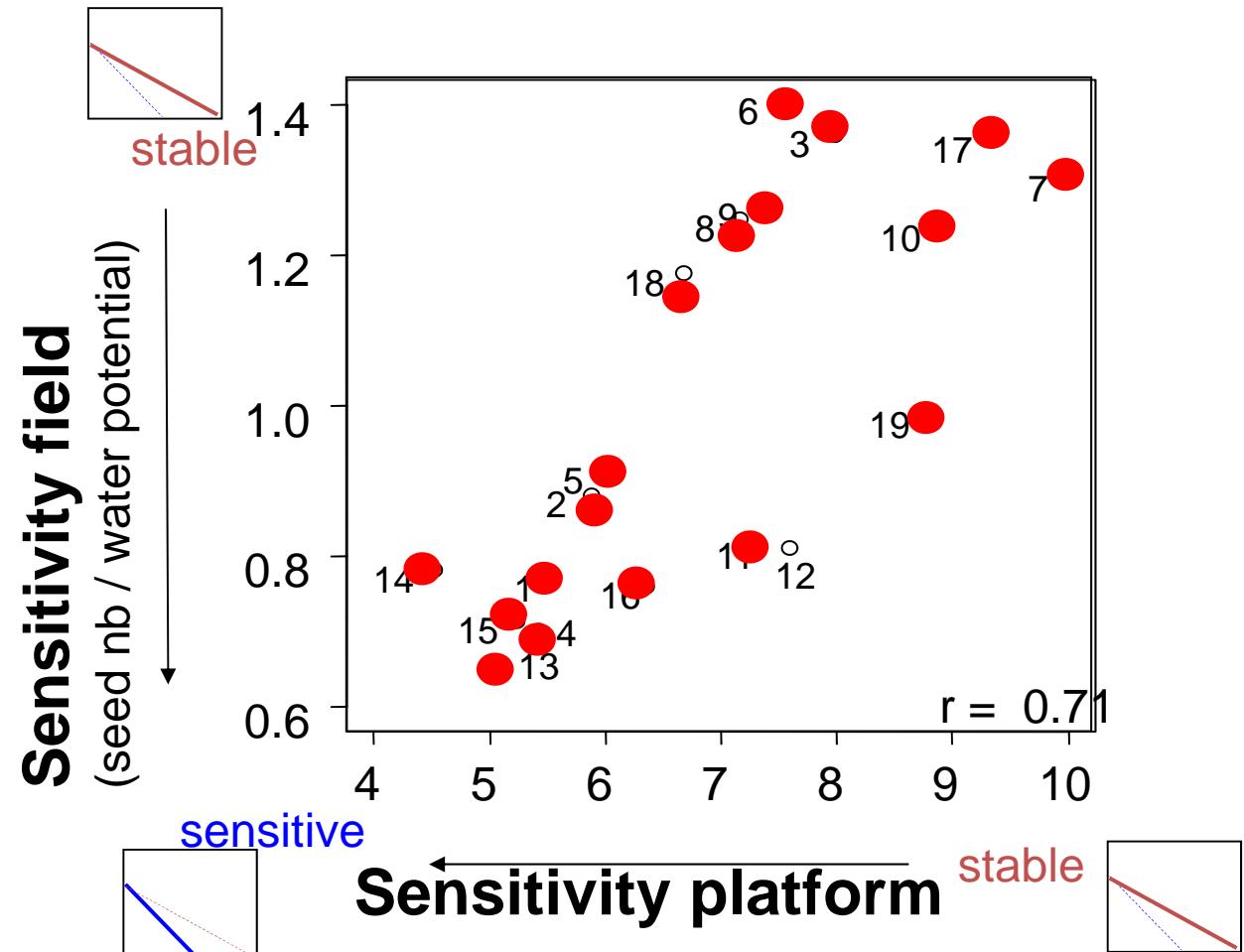
Mapping sensitivity on the maize genome (3 mapping populations)



C. Welcker

Welcker et al. 2011 *Plant Physiol.*

Sensitivity to water deficit in field and platforms

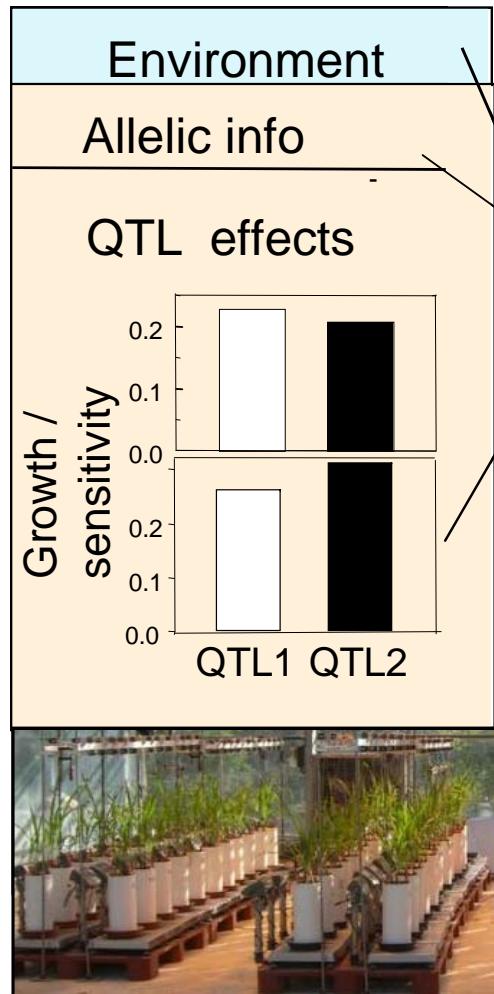


C. Welcker

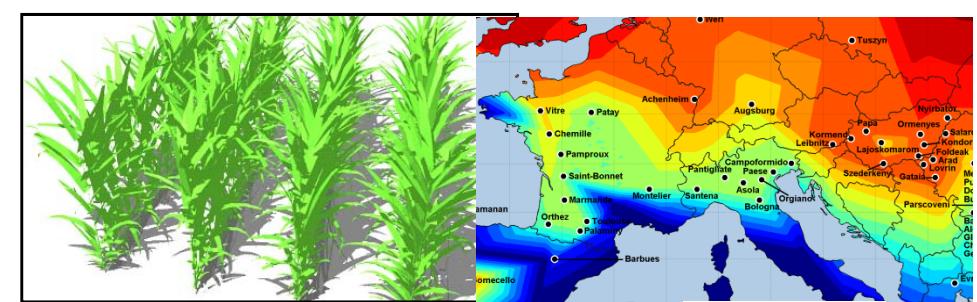
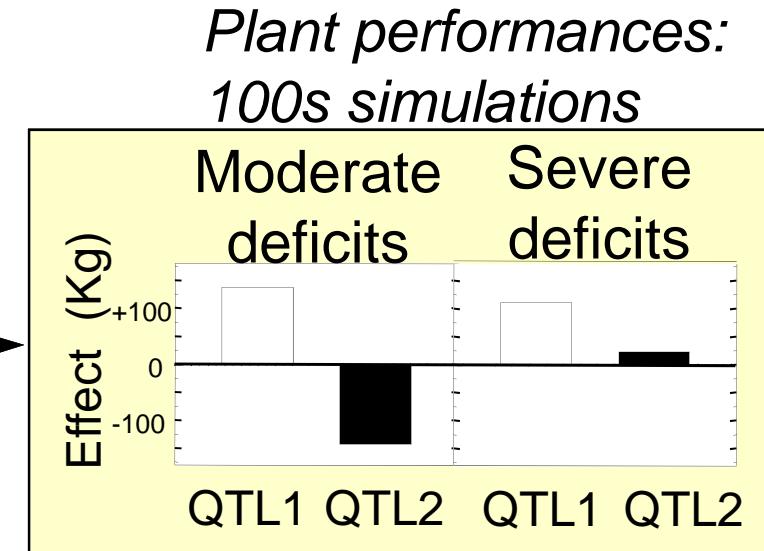
Welcker et al. 2011 *Plant Physiol.*
Chapuis et al 2012 EJA



Yield simulation from QTLs identified in platforms :

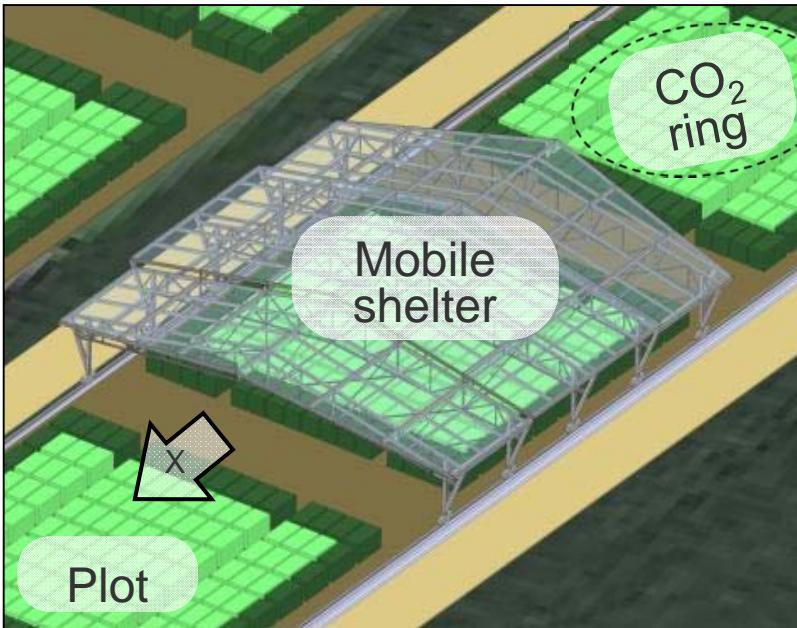


Model :
Leaf area
Biomass
Transpiration
Yield



DROPS

Going further with phenotyping



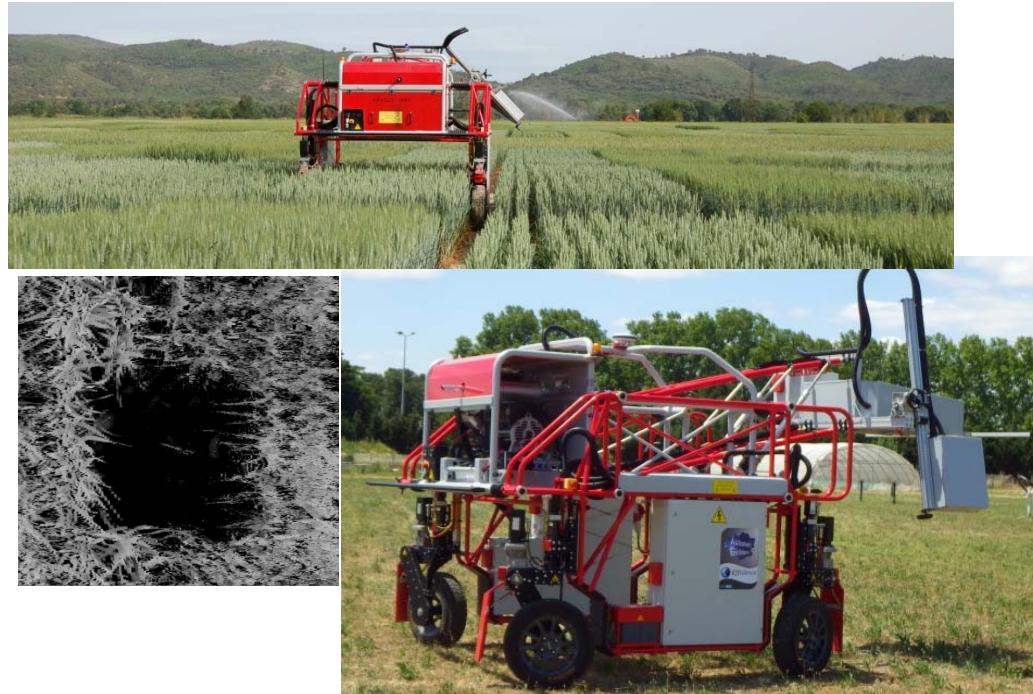
CO₂ enrichment (FACE)
INRA Clermont Ferrand

...



Rainout shelters
Ouzouer
PhenoField

Going further with phenotyping

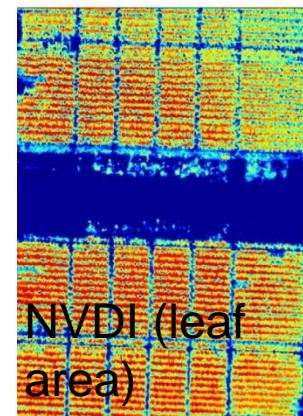
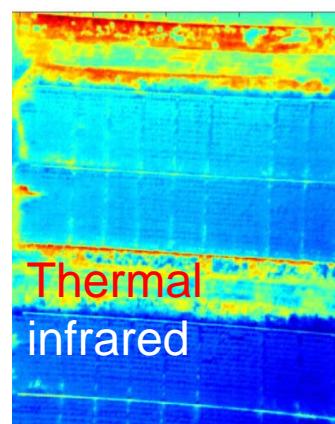
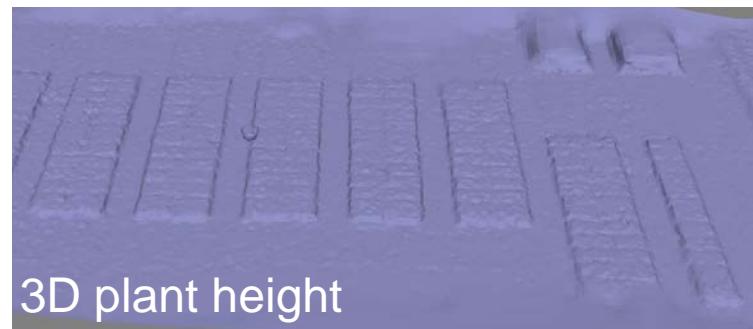
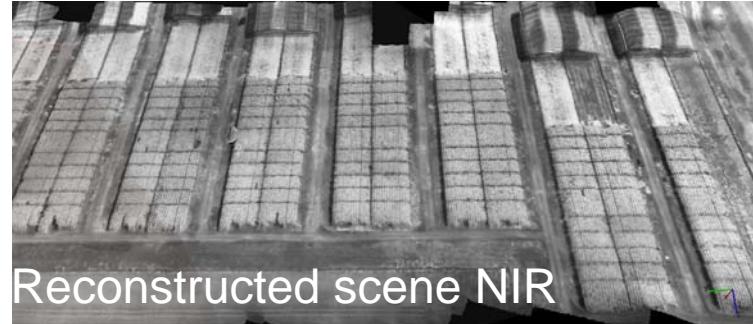


PHENOME
Réseau Français
Phénomique végétale
F P P N

100s genotypes :
biomass, leaf area, nb spikes, [N],
leaf angles, transpiration...

LiDAR, imaging in RGB, NIR, Nbands etc

Going further with phenotyping



Essential to take into account the genetic progress
in models of climate change impacts

A large genetic variability of sensitivities to high temperatures
water deficit

... Progress continues

Combining equipped field experiments and phenotyping
platforms is a key for breeding for mitigating the effects of CC