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Dissecting GxE and QTLxE of maize yield in contrasting scenarios of light, heat and water deficit

Emilie J. Millet, Willem Kruijer, Santiago Alvarez Prado, Llorenç Cabrera-Bosquet, Aude Coupel-Ledru, Sébastien Lacube, Yves Gibon, Sylvain Prigent, Claude Welcker, Alain Charcosset, et al.

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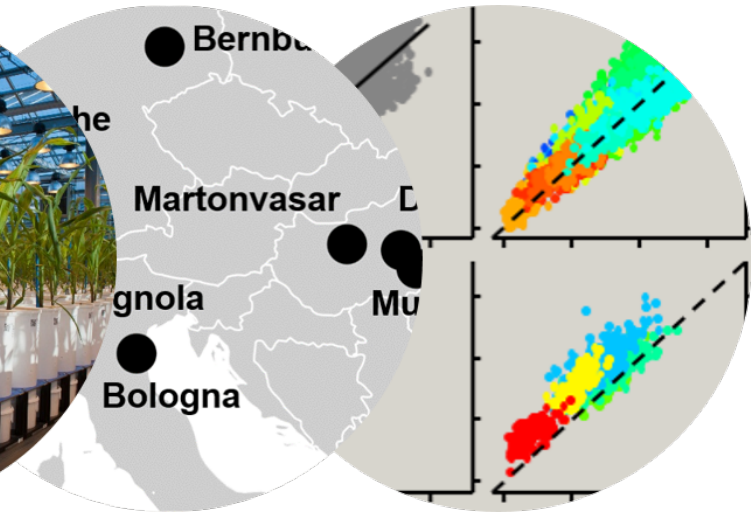
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Dissecting G×E and QTL×E of maize yield in contrasting scenarios of light, heat and water deficit.

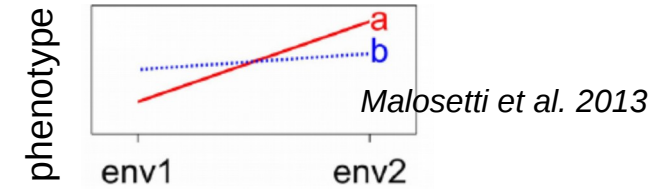
Millet E, Kruijer W, Alvarez Prado S, Cabrera-Bosquet L, Coupel-Ledru A, Lacube S, Gibon Y, Prigent S, Welcker C, Charcosset A, van Eeuwijk F, Tardieu F

XXIVth EUCARPIA Maize and Sorghum Conference, 8th October 2019, Munich

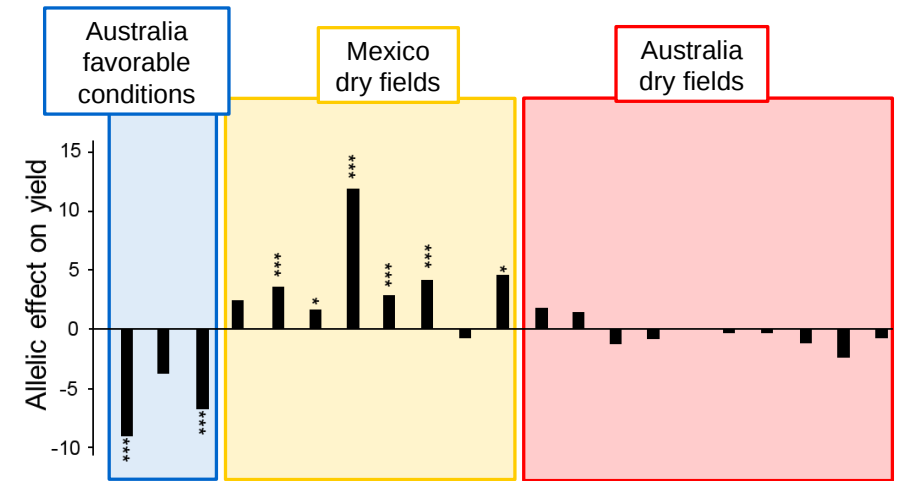


Background

Phenotypic response can differ for different varieties = $G \times E$

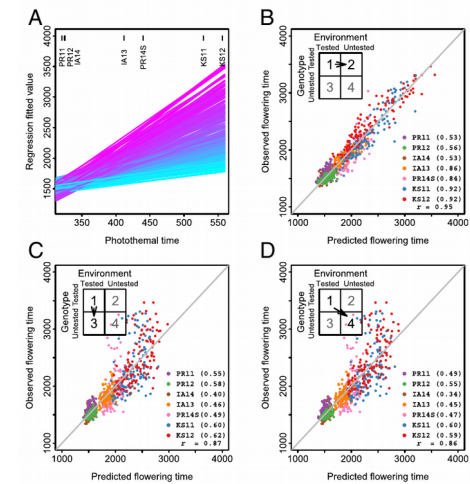
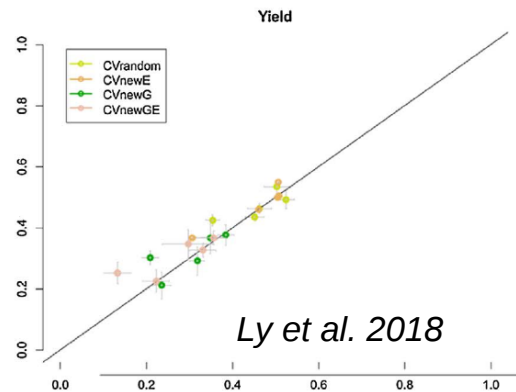
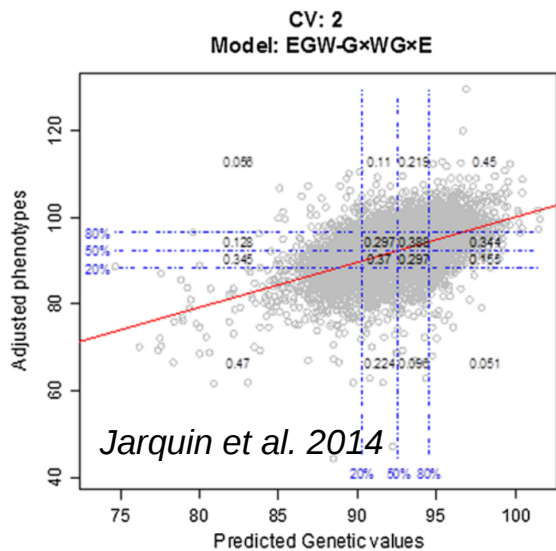


Detection of QTL will depend on the environment
 ⇒ environment dependent effects



Genomic prediction can assess the performances of thousands of genotypes but faces the difficulty $G \times E$
 ⇒ Few studies dissect the $G \times E$ for predicting grain yield

*redrawn from
 Bonneau et al 2013
 ACPFG Australia*



New tools and methods for dissecting the G×E: the «ics»

- Phenomic (new phenotyping)
→ field network, high throughput platform
- Genomic (High density genotyping)
- Environmental characterization (envirotyping, enviromic (Resende et al. 2019 bioRxiv))
→ sensor network, Geographic Information Systems
- Statistics (new class of models)

➔ New modelling strategies to incorporate new phenotyping information in different classes of genotype-to-phenotype (G2P) models

➔ From large numbers of basic and raw secondary phenotype data → relatively few genotype specific parameters with high predictive power

Size input data	Modelling step	Input	Model / strategy	Output	Model dependence output
Large	Feature extraction	Multiple pixels/wavelengths for each plot, genotype, time point and environment (low level traits)	Segmentation Organ Tracking Indices (e.g. NDVI) Machine learning	Trait value for each plot, genotype, time point and environment	Small
	Correcting for design factors and spatial trends	Trait value for each plot, genotype, time point and environment	Mixed models: - AR@ AR - SpATS	Adjusted trait value for each genotype, time point and environment	
	Dynamical modelling	Trait value for each genotype, time point and environment	Standard mathematical functions (Logistic, Gompertz) Repeated measures Splines Crop growth models	Genotype specific parameters for each environment (intermediate level traits)	
	Modelling dependence on environmental gradients	Genotype specific parameters for each environment	Standard mathematical functions Splines Crop growth models	Genotypic sensitivities to environmental covariables (higher level traits)	
	Target trait prediction	Higher order traits and environmental characterizations	Mixed models (multi-trait, factorial regression) Crop growth models	Genotype specific yield predictions per environment	

Novel approaches for dissection of genetic architecture of yield under drought and heat that combines:

- environmental characterization (sensor networks)
- statistical modelling
- genome-wide association
- phenomic tools
- genomic prediction

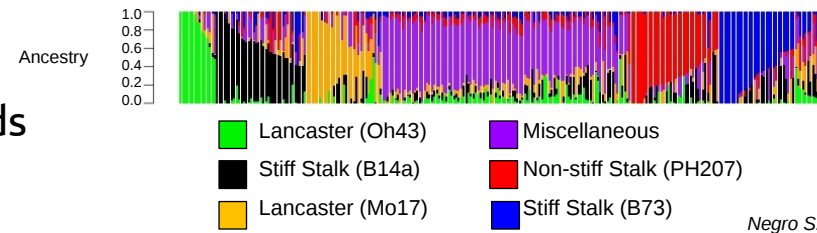


Weclker C. Tardieu F.

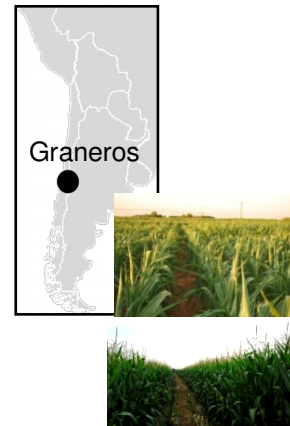
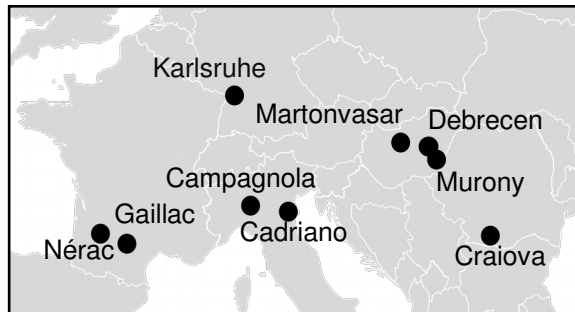


van Eeuwijk F. Charcosset A.

The DROPS panel ~ 250 maize hybrids
(Dent diversity group × flint tester)



Climatic transect over Europe + Chile :
10 Sites, 2 Years (2012, 2013)
diverse drought scenarios : 2 water regimes
→ 25 experiments (Site x Year x Regime)

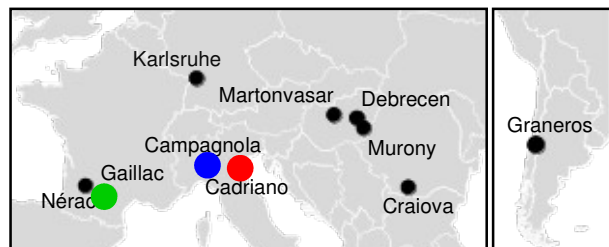


High throughput phenotyping platform
(Phenoarch):
3 experimental series
2 water regimes
→ 8 experiments

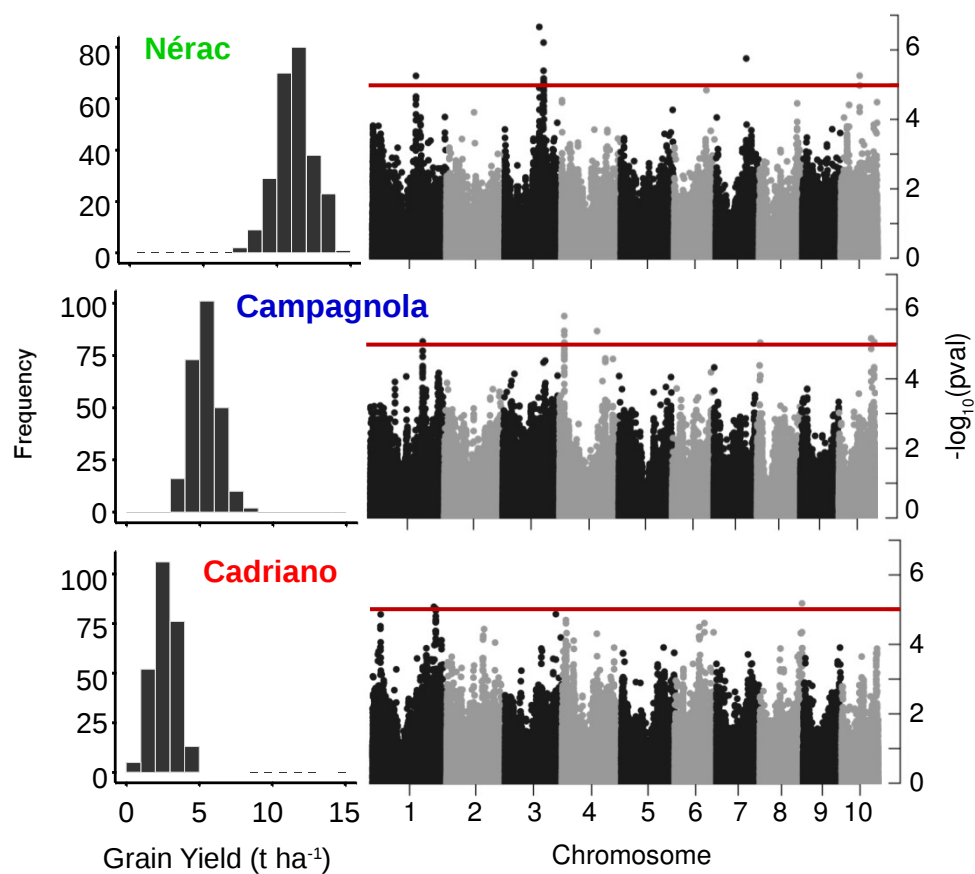


Large variation of grain yield linked to environment variability ?

Large distribution of grain yield within and between experiments with a large G×E



467 significant SNPs for grain yield => 48 QTLs
 QTL are significant in 7 experiments (from 2 to 23)
 => Can we use the environmental classification to explain the QTL×E ?



WW - Hot(day)

WW - Cool

WD - Hot



Weclker C.



Kruijer W.



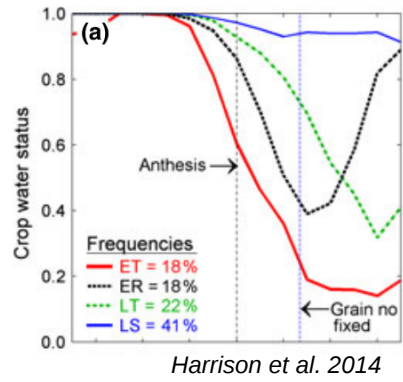
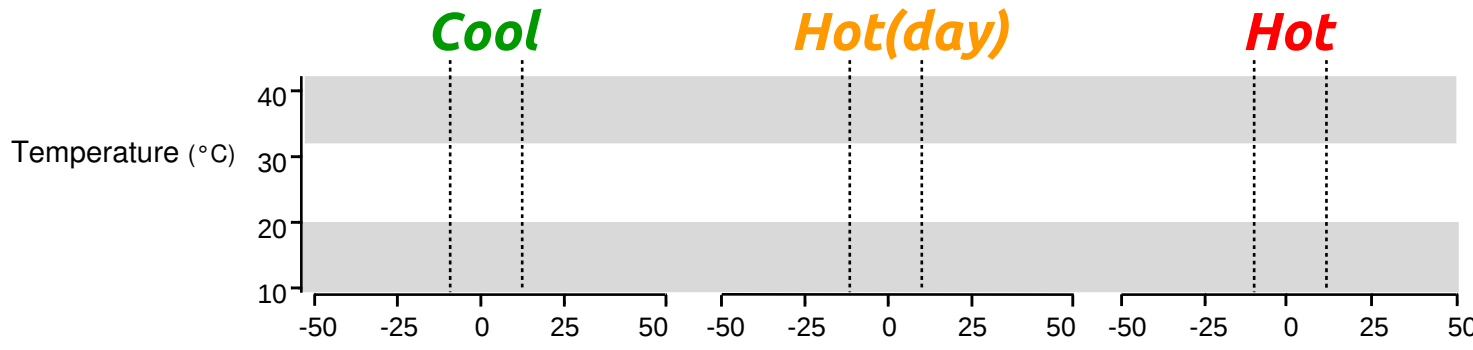
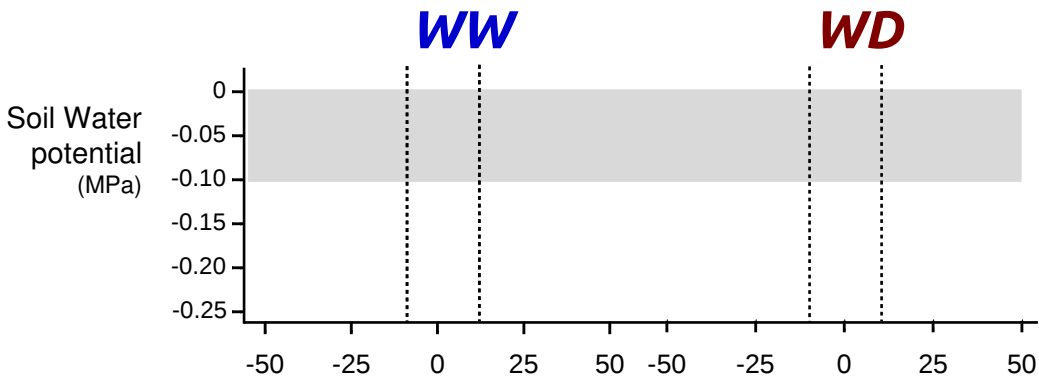
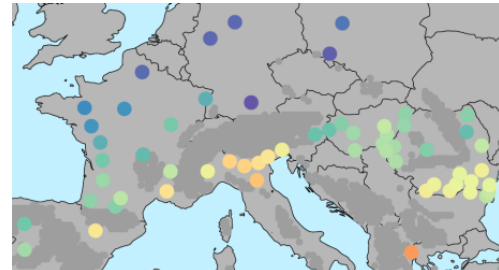
Coupel-Ledru A.



Nicolas S.

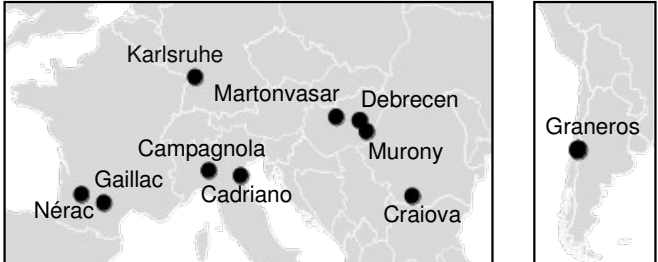
Environmental classification over Europe

Which scenarios in Europe ?
 Simulation of drought scenarios (APSIM) : 55 sites x 35 years
 ⇒ Typical scenarios of drought in Europe

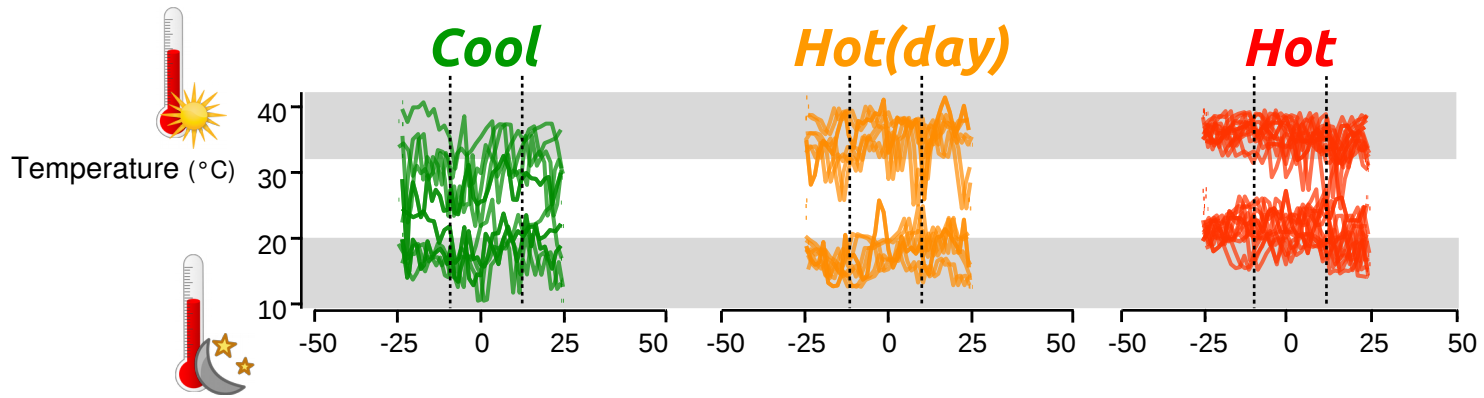
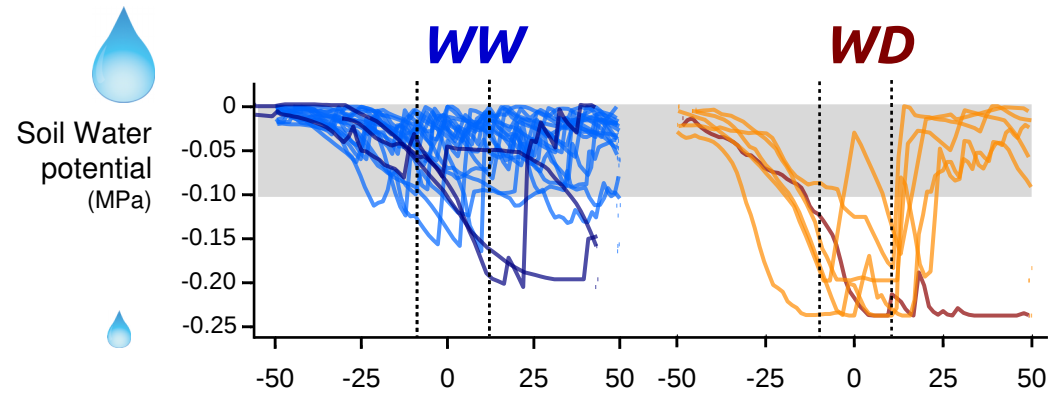


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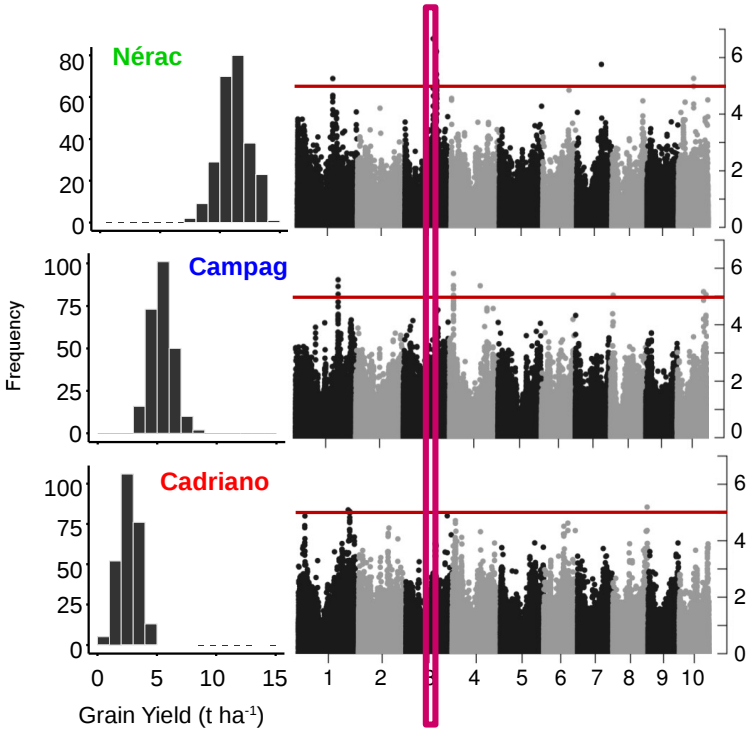


Clustering the experiments in these scenarios

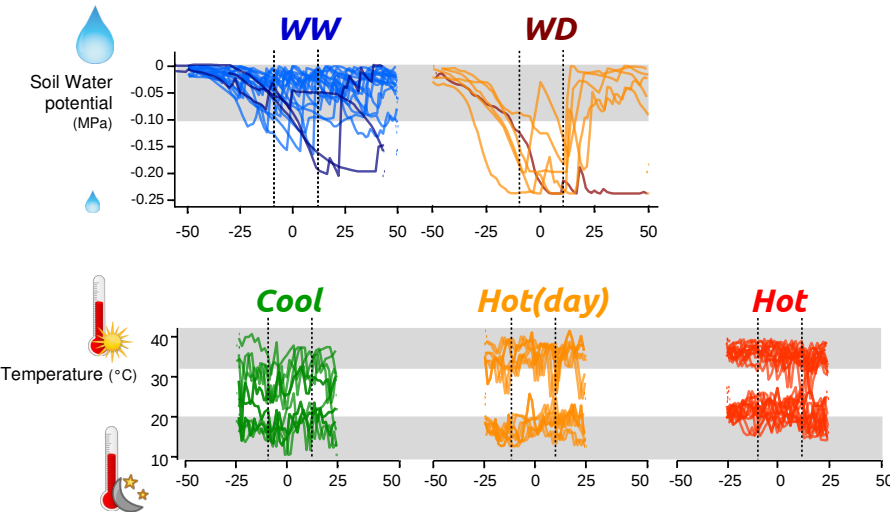


Environmental classification over Europe to explain the allelic effects

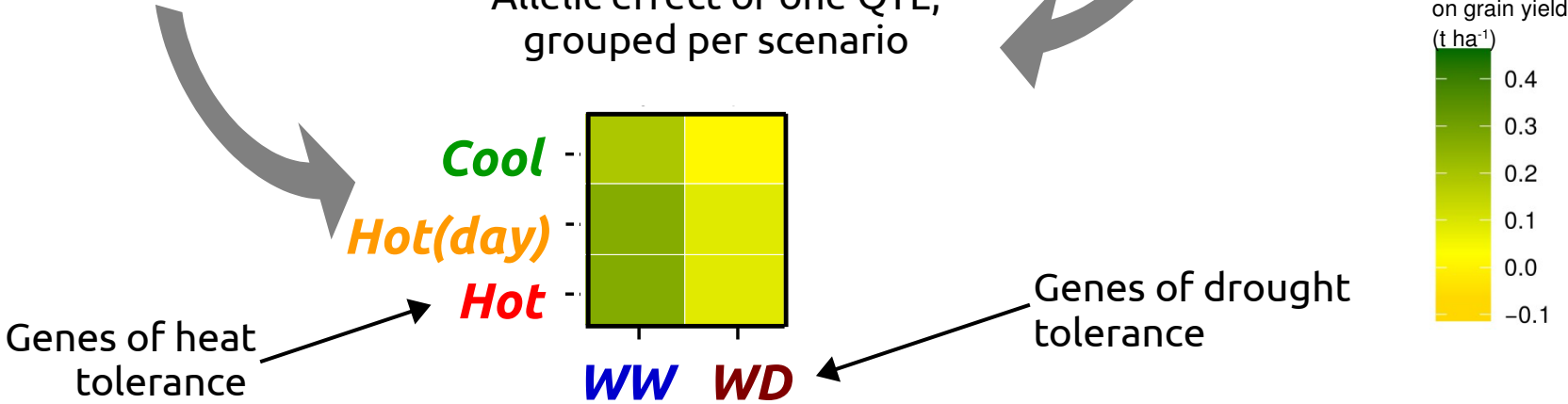
Allelic effect of one QTL



Clusters of experiments

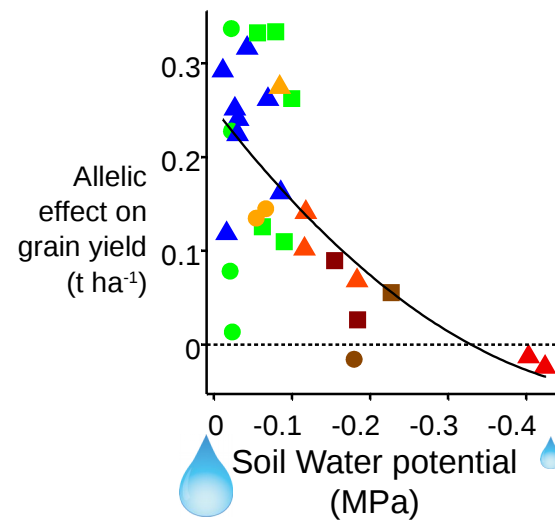
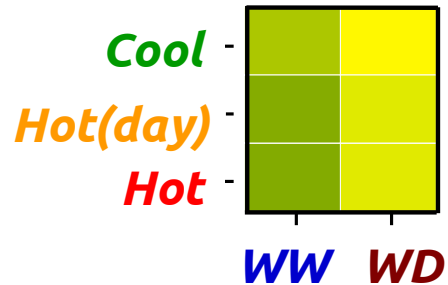


Allelic effect of one QTL, grouped per scenario

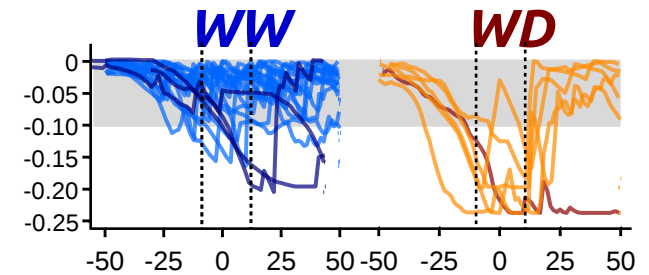


Genomic region displayed scenario-dependent effect

Classification of the QTLs using the QTL×Scenario and QTL×Co-variable



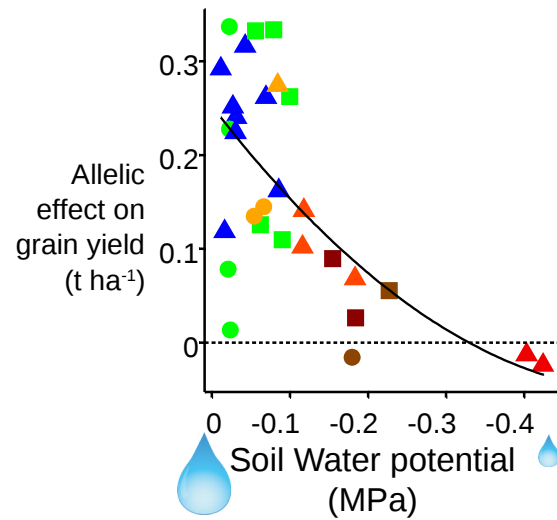
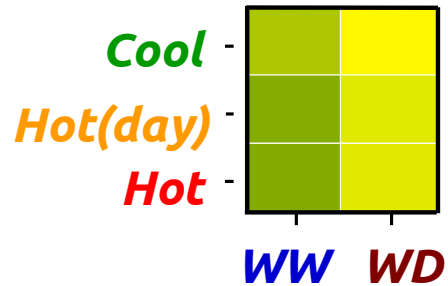
(environmental variable average around flowering time)



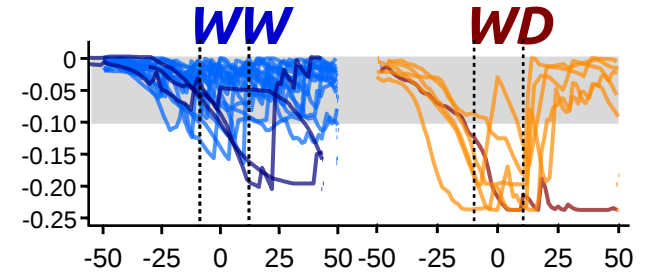
- 25 QTLs with larger allelic effect in favourable conditions
- 8 QTLs with high effects in *Hot* and null effect in *Cool*
- 12 QTLs with high effects in *WD* and no or lesser effect in *WW*
- 3 QTLs with no clear pattern of allelic effect

Genomic region displayed scenario-dependent effect

Classification of the QTLs using the QTL×Scenario and QTL×Co-variable



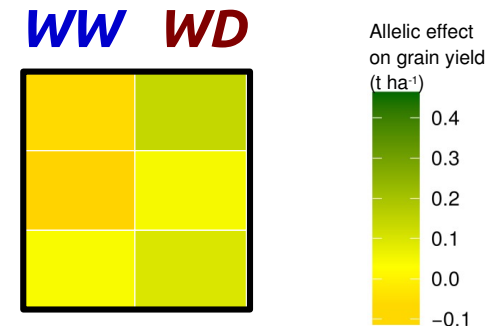
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- 25 QTLs with larger allelic effect in favourable conditions
- 8 QTLs with high effects in *Hot* and null effect in *Cool*
- 12 QTLs with high effects in *WD* and no or lesser effect in *WW*
- 3 QTLs with no clear pattern of allelic effect

Targeting the genes in the interval based on the response to environment:

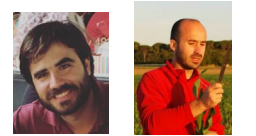
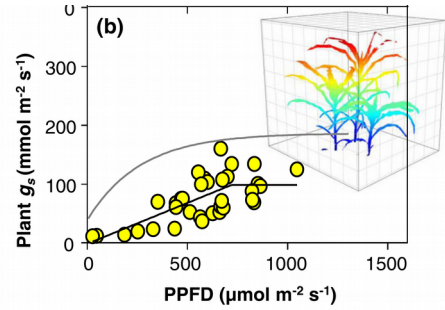
- Positive in *WD*, negative in *WW*
- QTL increases ABA in leaves (Giuliani et al., 2005)
- Gene involved in ABA biosynthesis
- high ABA can cause reduction in growth in *WW* while maintaining growth in *WD*



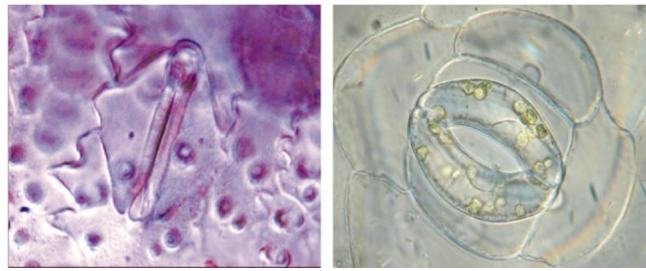
Genomic region displayed scenario-dependent effect: in platform too

Stomatal conductance from water flux in the DROPS panel (inversing the Penman Monteith equation)

$$ET_{ref} = \frac{s \times R_n + \rho \times C_p \times g_a \times VPD}{\lambda \times \left(s + \gamma \times \left(1 + \frac{g_a}{g_s} \right) \right)}$$



Alvarez Prado S.
Cabrera-Bosquet L.

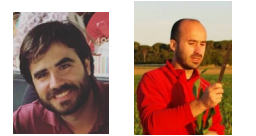
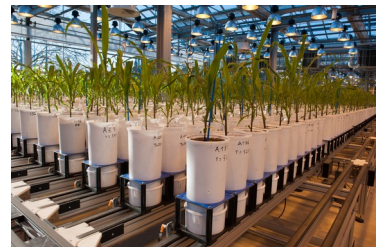
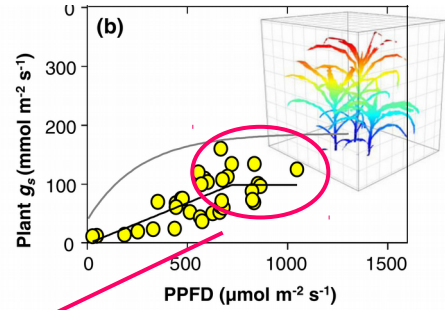


Hetherington & Woodward, 2003

Genomic region displayed scenario-dependent effect: in platform too

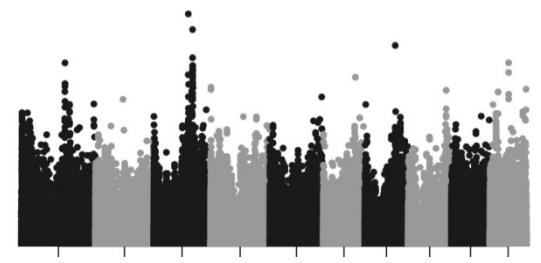
Stomatal conductance from water flux in 250 genotypes (inversing the Penman Monteith equation)

$$ET_{ref} = \frac{s \times R_h + \rho \times C_p \times g_a \times VPD}{\lambda \times \left(s + \gamma \times \left(1 + \frac{g_a}{g_s} \right) \right)}$$



Alvarez Prado S.
Cabrera-Bosquet L.

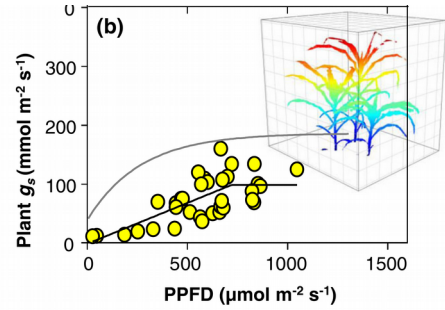
GWAS in each experiments on g_{smax} = 16 QTLs with large QTL×E



Genomic region displayed scenario-dependent effect: in platform too

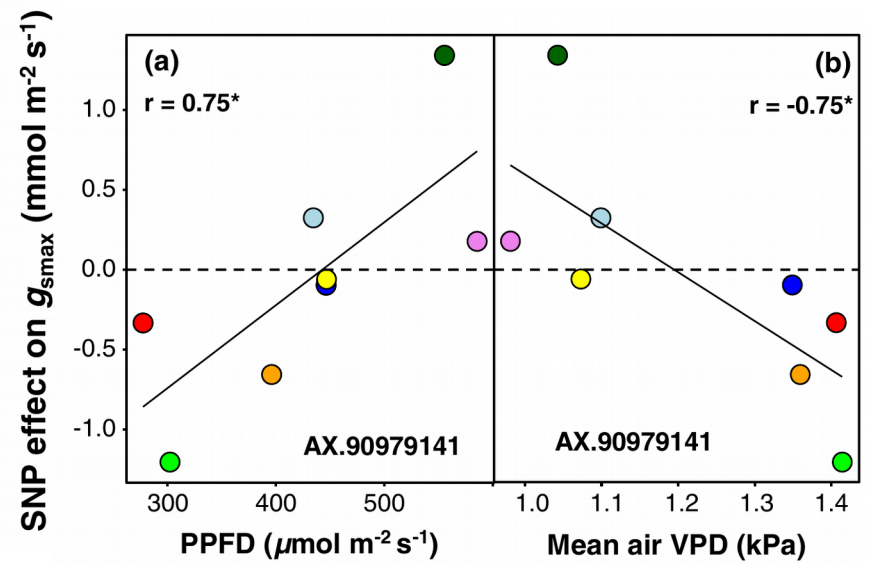
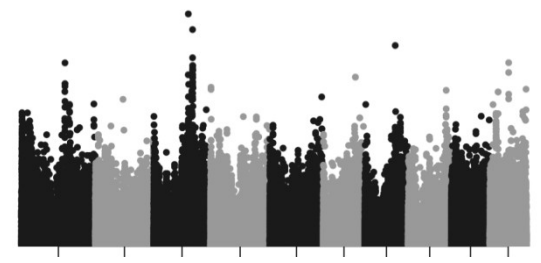
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Alvarez Prado S.
Cabrera-Bosquet L.

GWAS in each experiment on g_{smax} = 16 QTLs with large QTL×E
Using environmental variables to explain the QTL×E:



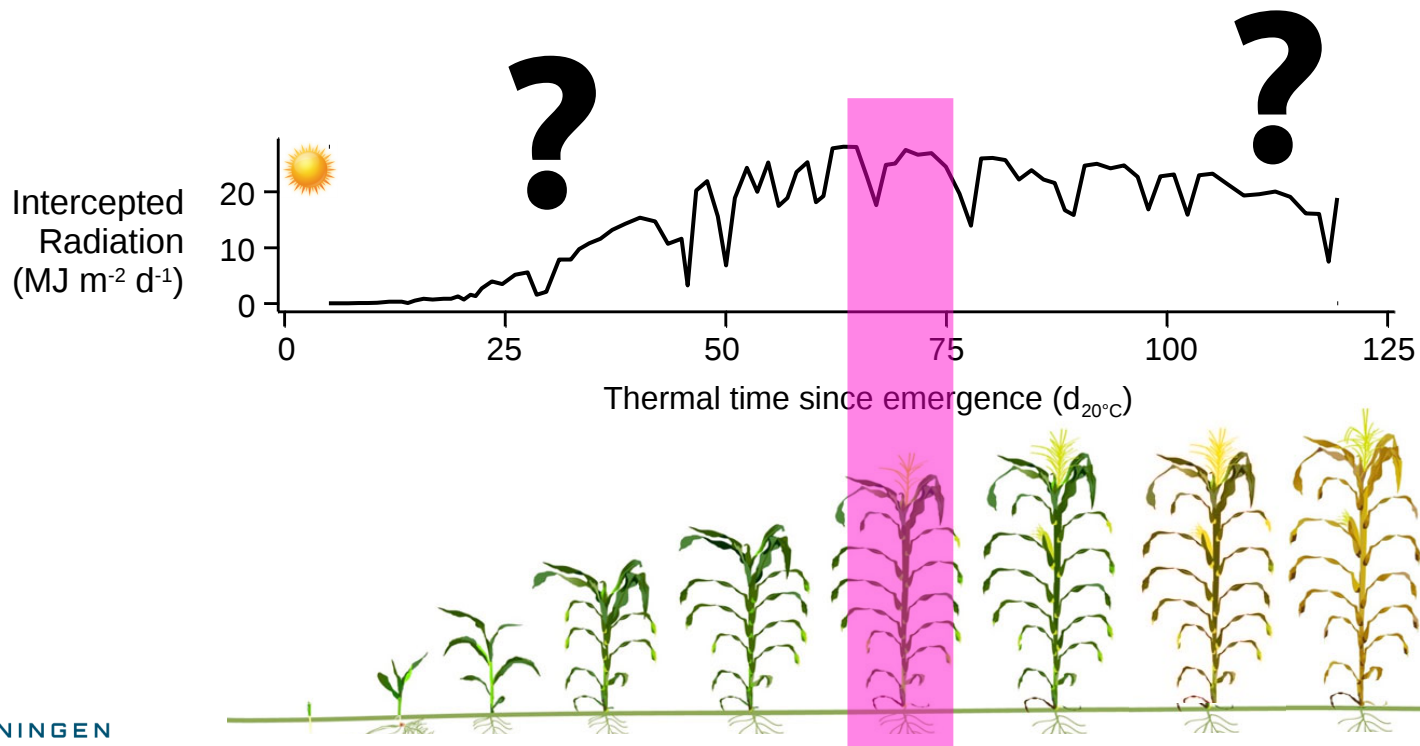
Vapour pressure deficit and light with opposite directions:
Genes of ABA transcription factors + two ethylene related proteins
→ involved in the drought-induced processes of stomatal closure

Dissecting QTL×E: a summary

Using sensor network only (no phenomic) we could classify QTLs and identify candidate genes linked with response of GY to change in environment

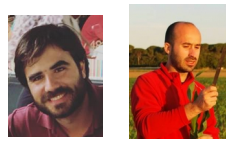
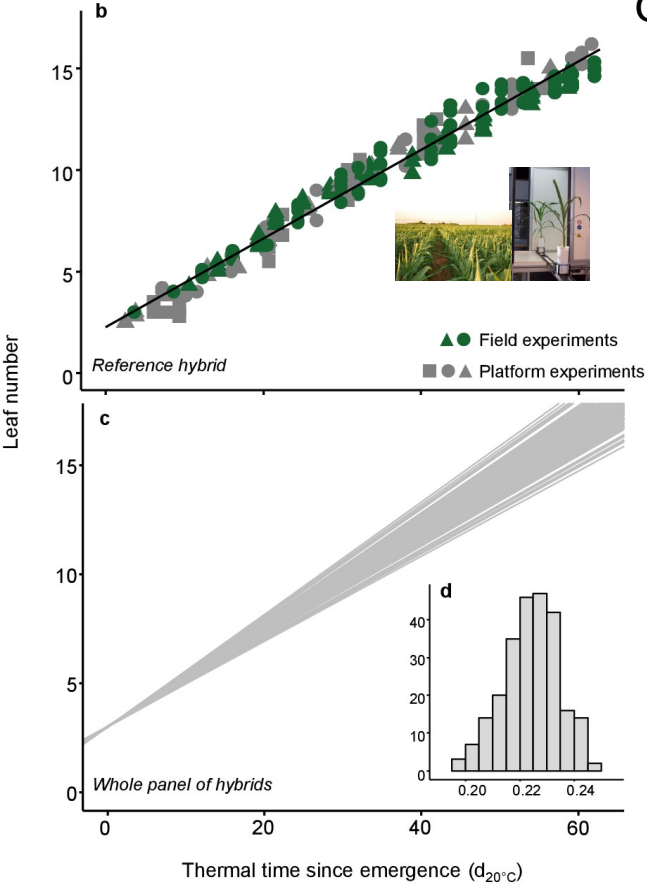
Also applicable in platforms for secondary traits that can also display G×E (environmental variability also in platform)

In field, we used variables around flowering time BUT the sensitivity of yield to environmental conditions largely varies with the timing of stressing periods linked to the plant phenology
=> simulation the progression of phenological stages



Dividing the crop cycle into phenological phases

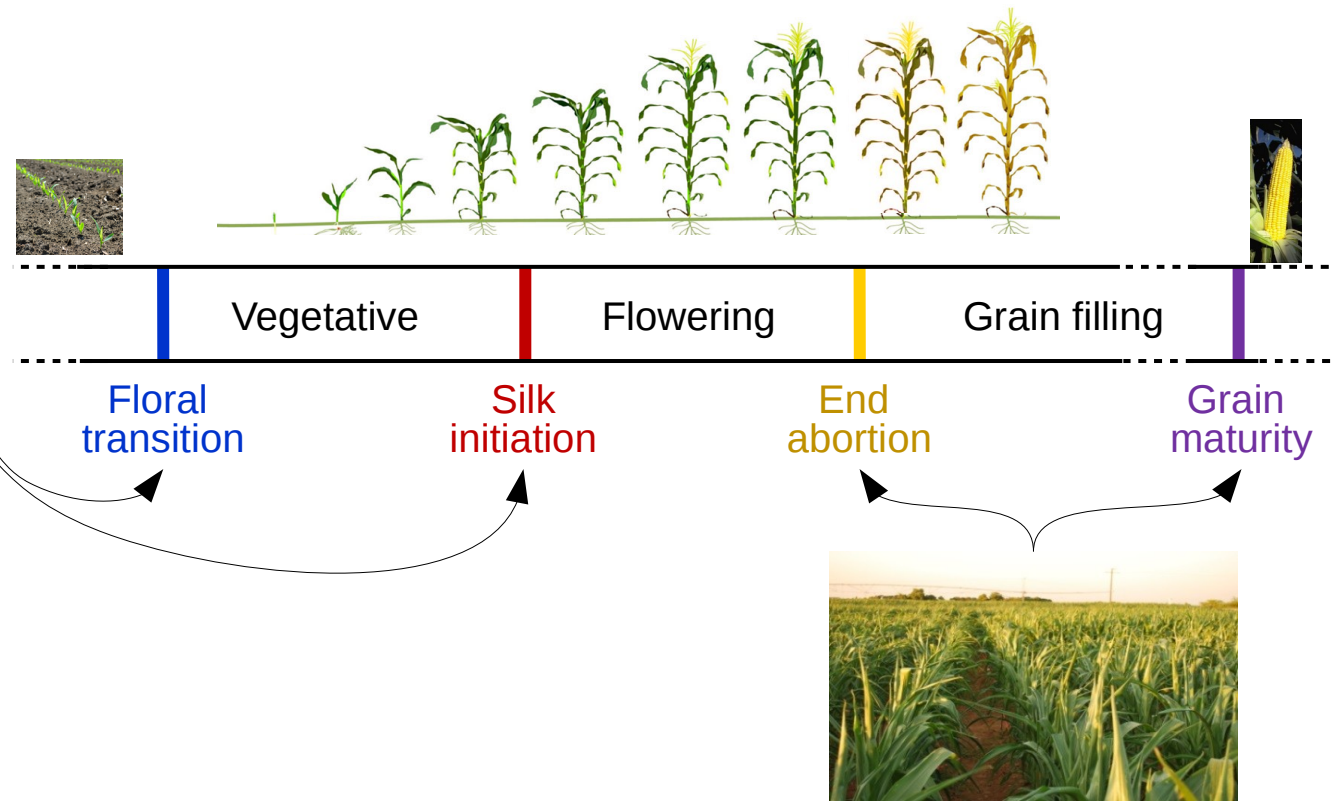
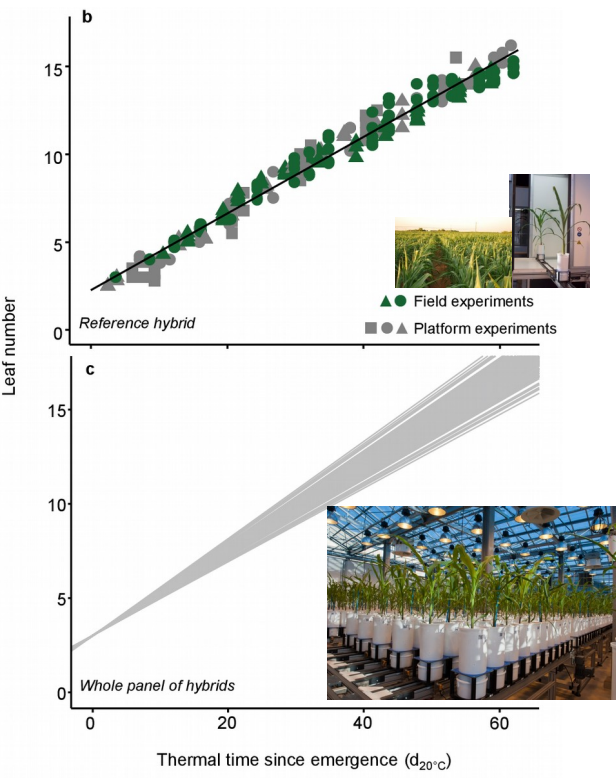
Common progression of stages in field and in platform (Phenoarch)



Alvarez Prado S.
Cabrera-Bosquet L.

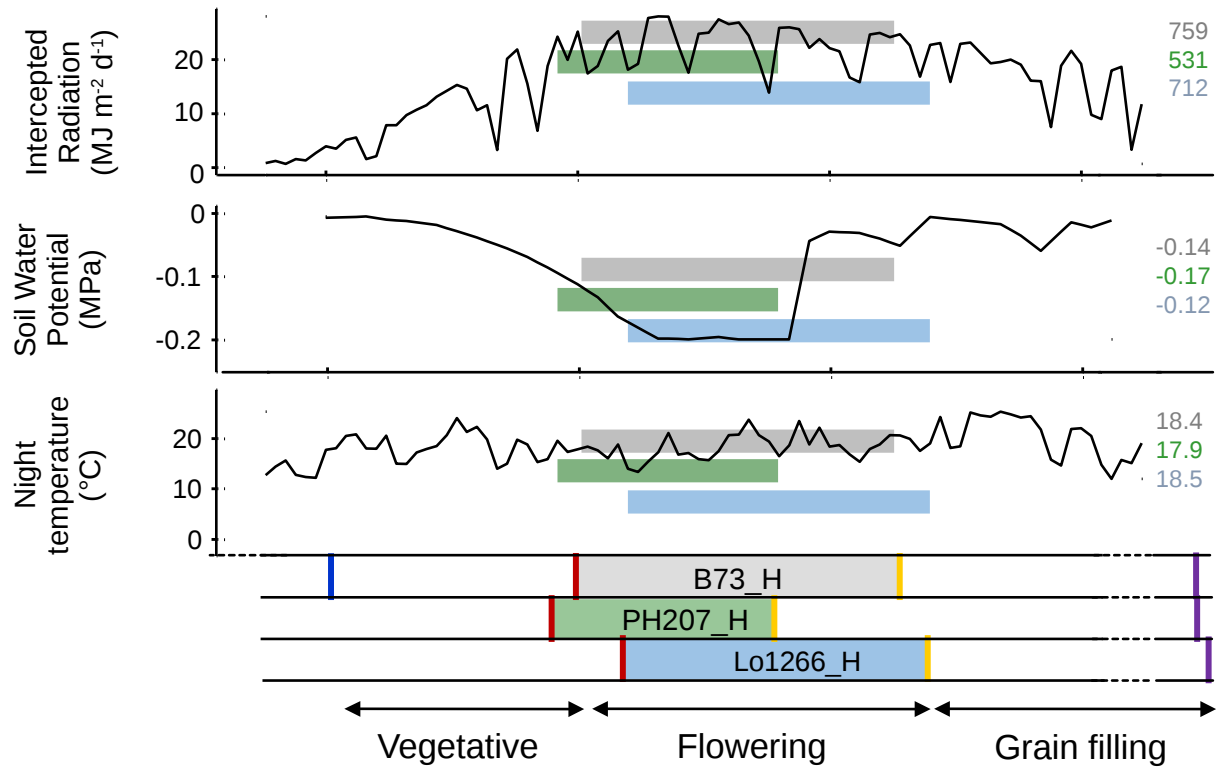
Dividing the crop cycle into phenological phases

Common progression of stages in field and in platform
Combined with stages measured in field = 3 phases



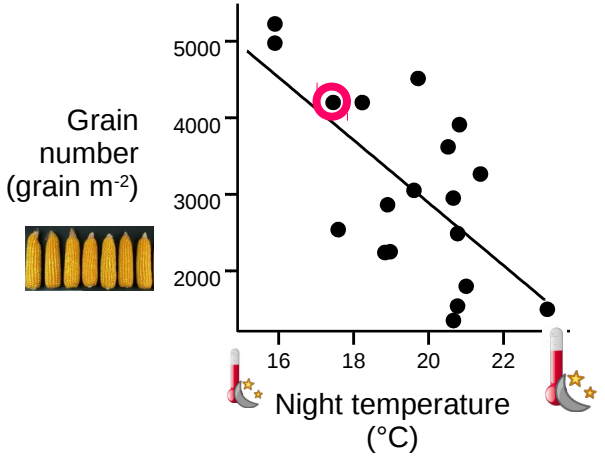
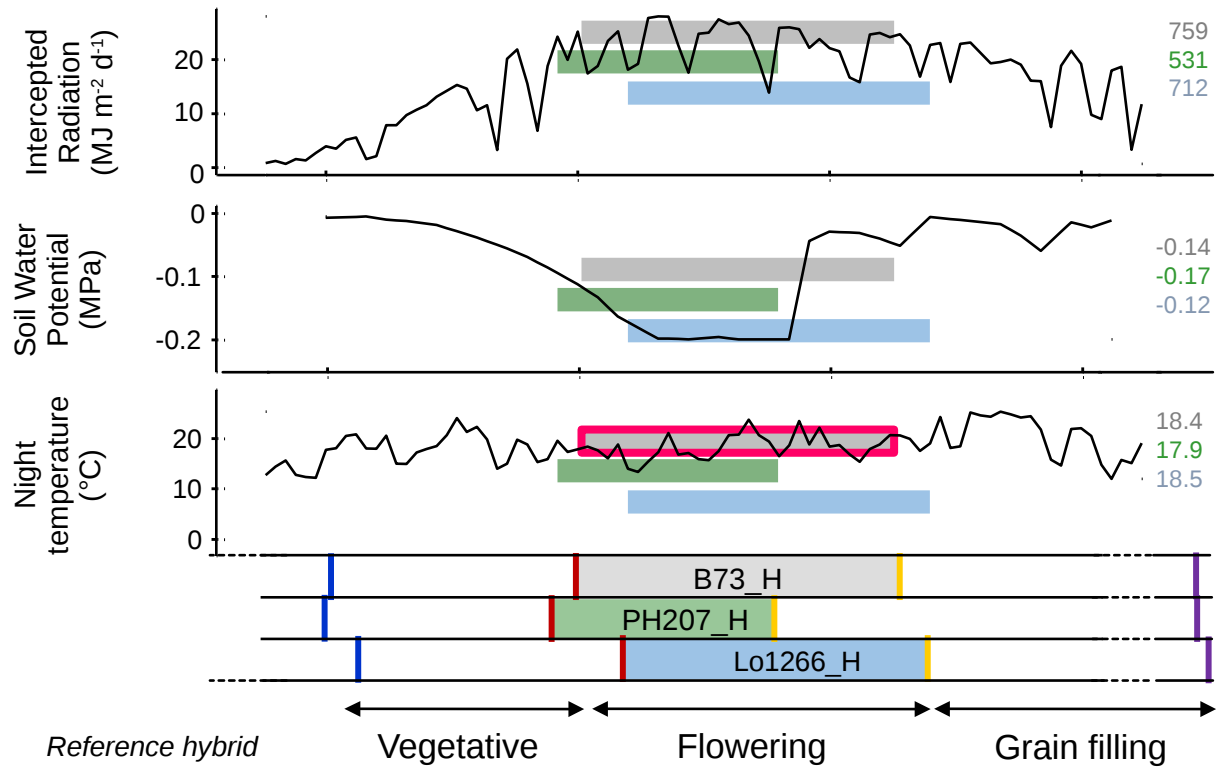
Different duration and position of the periods due to the differences in hybrids phenology

Different phenologies = different conditions sensed by the plants at the same phenological stage



Different duration and position of the periods due to the differences in hybrids phenology

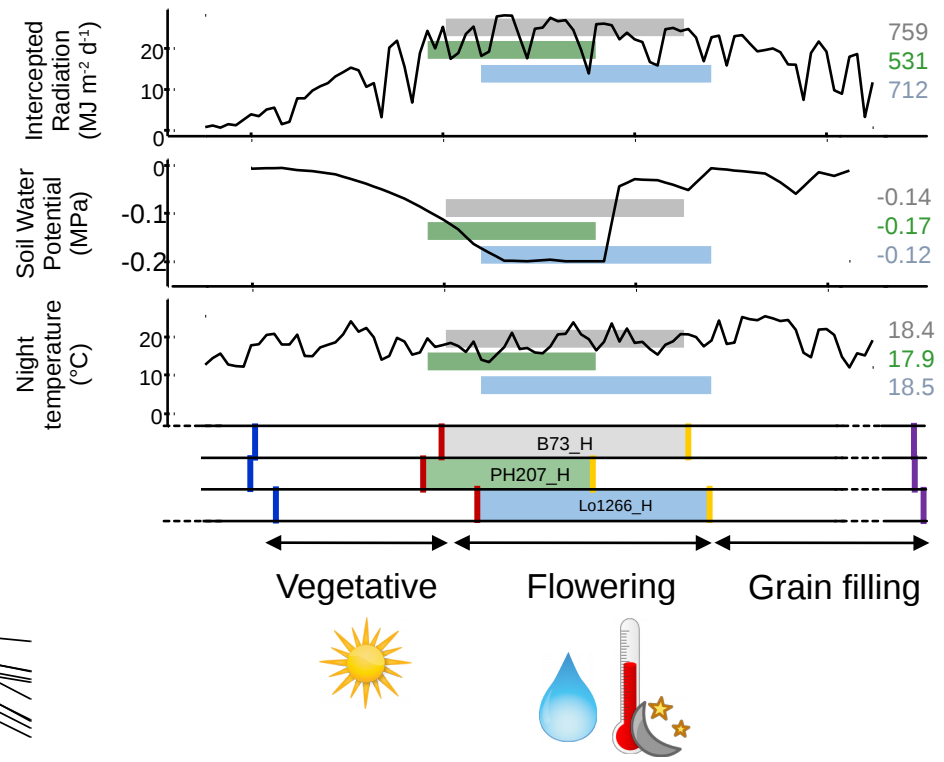
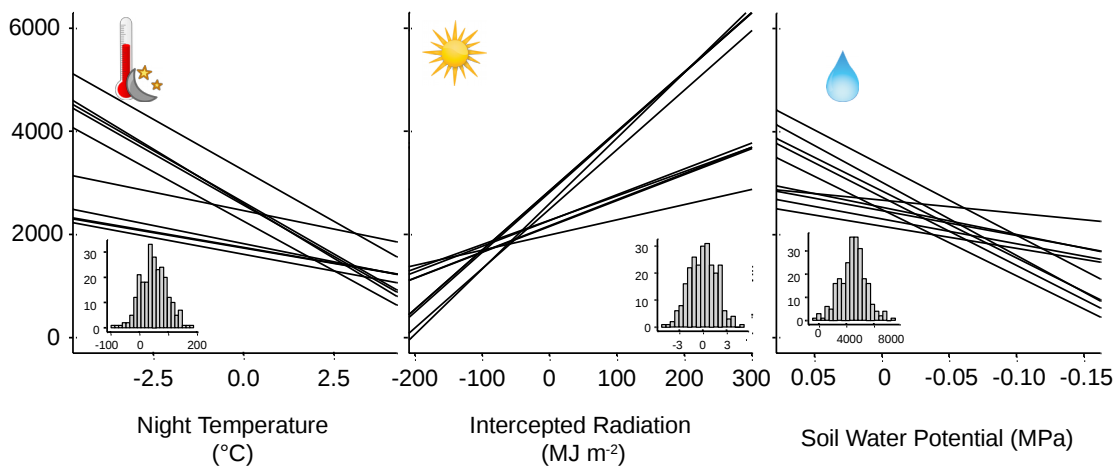
Different phenologies = different conditions sensed by the plants at the same phenological stage



⇒ Different sensitivities to environmental conditions

Dissection of grain number

$$\text{Grain Number}_{ij} = \mu + e_j + g_i + \sum_{l=1}^s \beta_{l,i} z_{l,j,i}$$



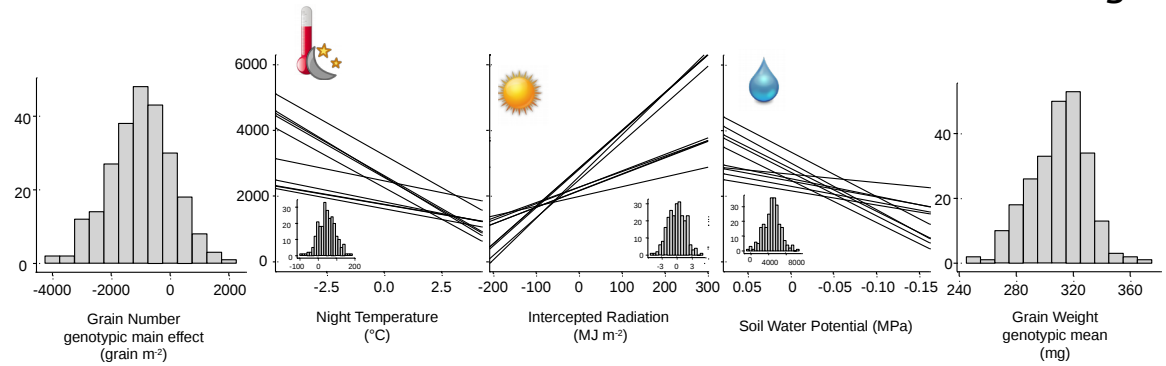
Establishing the model of grain yield dissection

Grain yield dissection into components and responses to environment (few parameters)

$$Grain Yield_{ij} = Grain Number_{ij} \times Grain Weight_i$$

$$Grain Yield_{ij} = (\mu + e_j + g_i + \sum_{l=1}^s \beta_{l,i} z_{l,j,i}) \times Grain Weight_i$$

environmental main effect genotypic main effect genotypic sensitivities environmental covariables genotypic grain weight



⇒ Can be predicted using marker profile and/or environmental indices



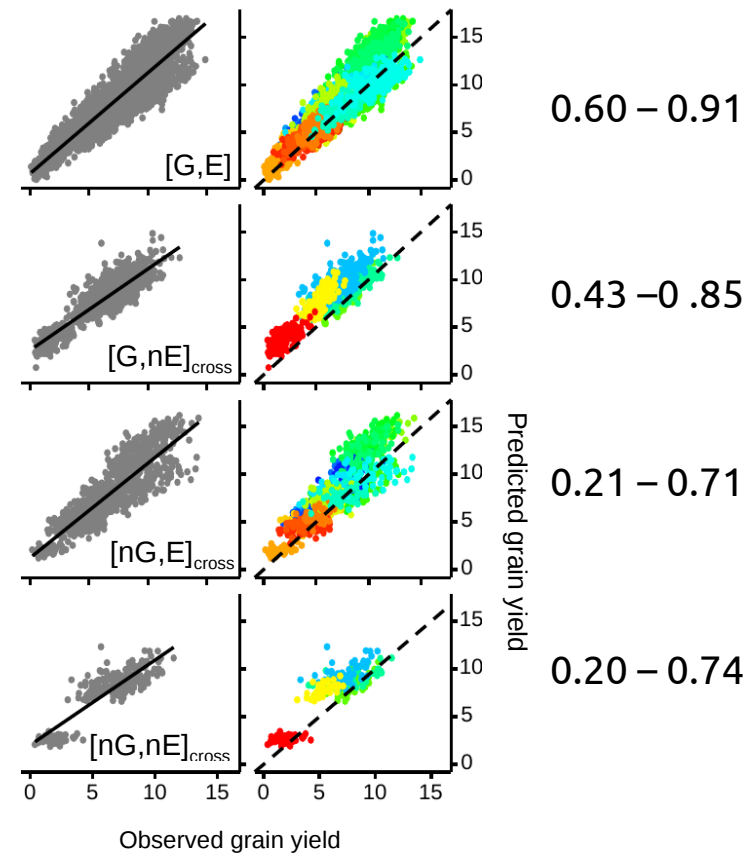
van Eeuwijk F. Kruijer W.

Whole genome regression with 50K SNPs and BayesR (Moser et al. 2015)

Prediction of grain yield in new experiments for new hybrids

Cross-validation and test of the model by sampling hybrids and experiments:
80% training – 20% test

	G (200)	nG (46)
E (20)	Training Estimation of model parameters	Test set Prediction of genotypic parameters using marker profile
nE (5)	Test set Prediction of main environmental effect using sensor data	Test set Prediction of genotypic and environmental parameters using marker profile and sensor data



⇒ A simple model allows a good estimation and prediction of grain yield

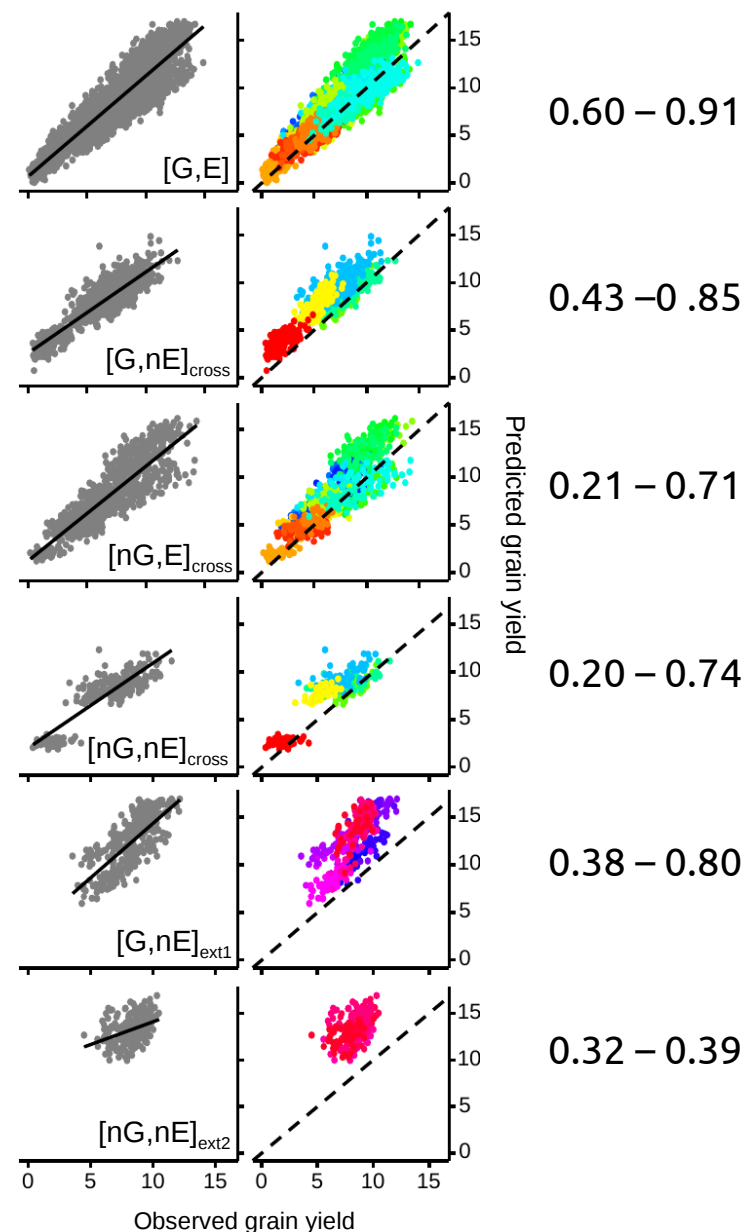
Prediction of grain yield in new experiments for new hybrids

Cross-validation and test of the model by sampling hybrids and experiments:
80% training – 20% test

	G (200)	nG (46)	nG _{ext} (56)
E (20)	Training Estimation of model parameters	Test set Prediction of genotypic parameters using marker profile	NA
nE (5)	Test set Prediction of main environmental effect using sensor data	Test set Prediction of genotypic and environmental parameters using marker profile and sensor data	NA
nE _{ext} (12)	Test set (subset of 32 Geno) Prediction of main environmental effect using sensor data	NA	Test set (subset of 4 Exp) Prediction of genotypic and environmental parameters using marker profile and sensor data

Cross-validation sets
 External validation sets

⇒ A simple model allows a good estimation and prediction of grain yield



Dissecting G×E by combining field and platform: a summary

Using phenomic **AND** sensor network (enviromic?) we could dissect the G×E in the field by using precise phenology of each hybrid

Despite a period of sensitivity at flowering time, early period also matters

Simple G2P model allows good prediction accuracies

What if we use other variable available at the plant level in the platform to predict the field trait?

Size input data	Modelling step	Input	Model / strategy	Output	Model dependence output
Large	Feature extraction	Multiple pixels/wavelengths for each plot, genotype, time point and environment (low level traits)	Segmentation Organ Tracking Indices (e.g. NDVI) Machine learning	Trait value for each plot, genotype, time point and environment	Small
	Correcting for design factors and spatial trends	Trait value for each plot, genotype, time point and environment	Mixed models: - AR@ AR - SpATS	Adjusted trait value for each genotype, time point and environment	
	Dynamical modelling	Trait value for each genotype, time point and environment	Standard mathematical functions (Logistic, Gompertz) Repeated measures Splines Crop growth models	Genotype specific parameters for each environment (intermediate level traits)	
	Modelling dependence on environmental gradients	Genotype specific parameters for each environment	Standard mathematical functions Splines Crop growth models	Genotypic sensitivities to environmental covariables (higher level traits)	
Small	Target trait prediction	Higher order traits and environmental characterizations	Mixed models (multi-trait, factorial regression) Crop growth models	Genotype specific yield predictions per environment	Large

Prediction of grain yield in field using metabolites in platform

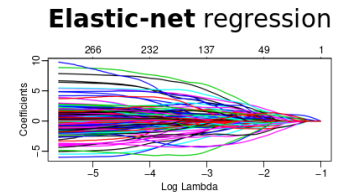
1 415 metabolic signatures + 11 identified metabolites
young plants in Phenoarch platform



Prigent S. Gibon Y.

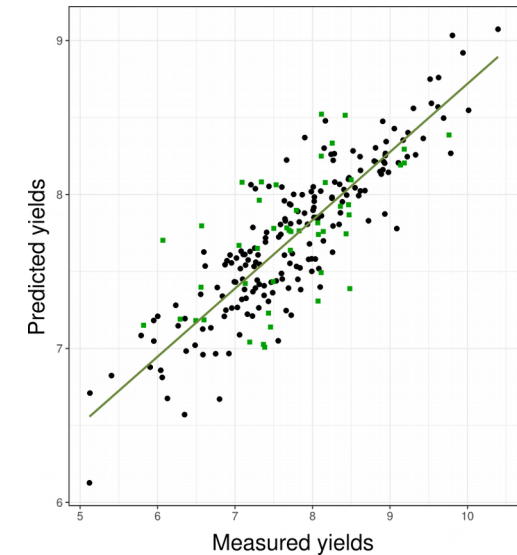
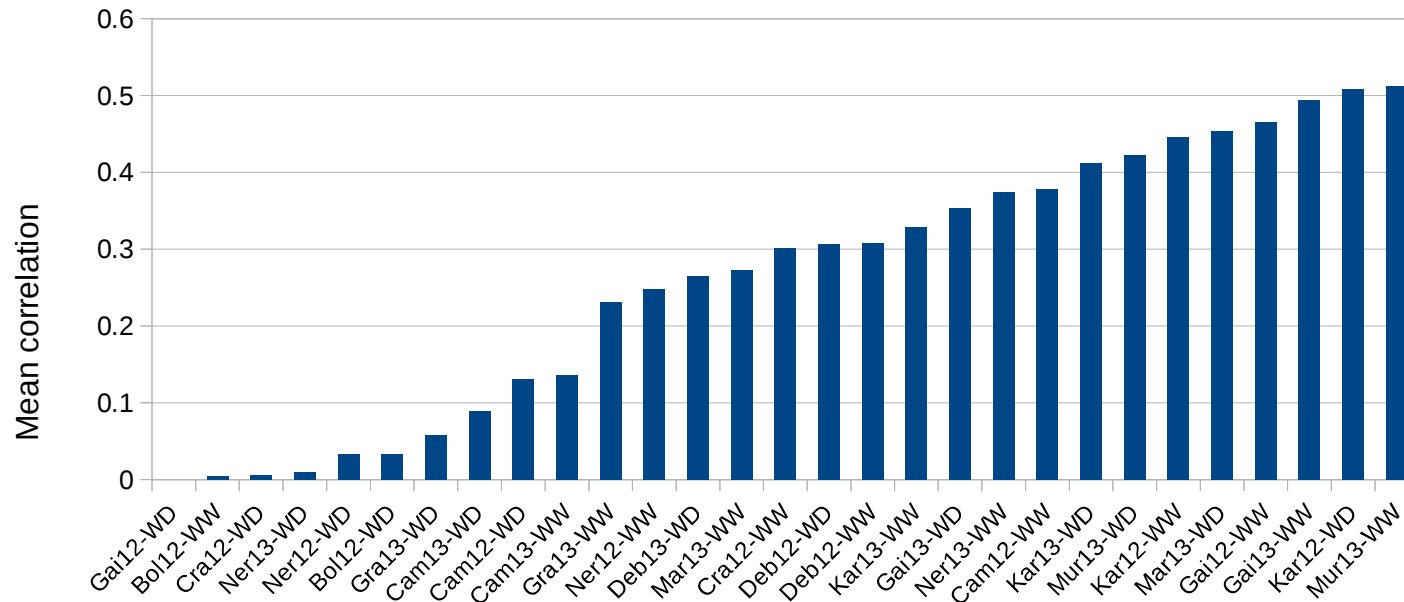
Creation of a linear model to link metabolic variables and yields: Generalized multi-linear models

$$GY = a_1 \text{metabo}_1 + \dots + a_n \text{metabo}_n$$



With cross-validation: using 20% of the genotypes to test the model, repeat 50 times

Mean prediction accuracy per env:

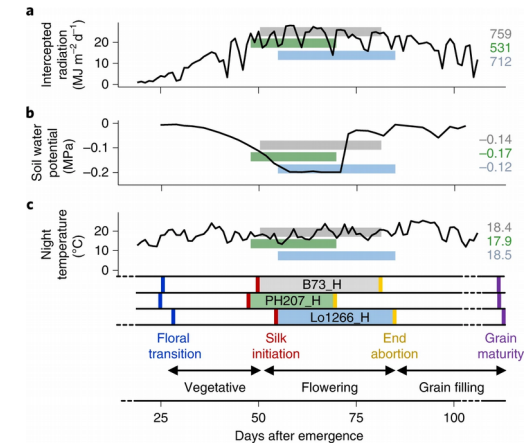
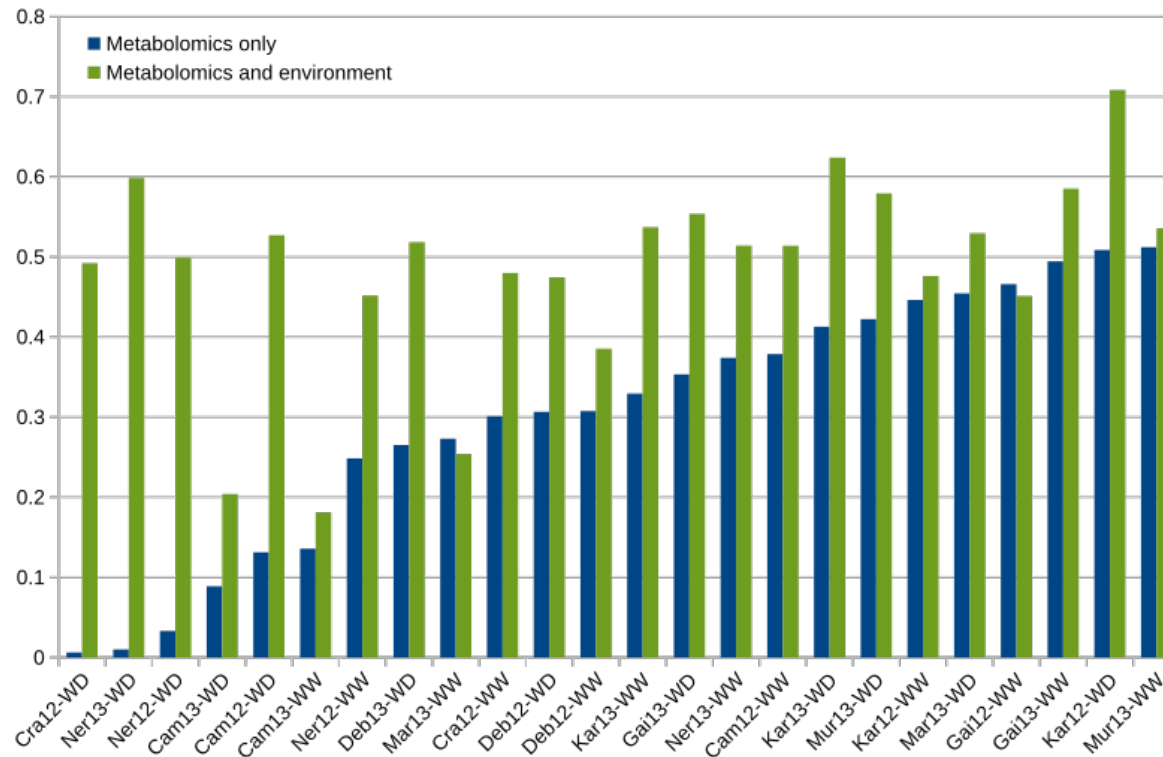


Combining metabolites in platform AND environmental covariates

Using field environmental covariates: 3 periods x 4 variables = 12 covariables:

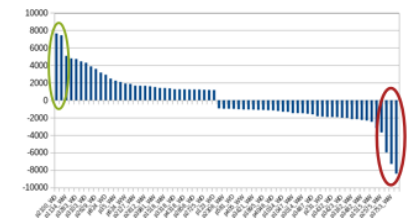
$$GY = a_1 \text{metabo}_1 + \dots + a_n \text{metabo}_n + b_1 \text{cov}_1 + \dots + b_l \text{cov}_l$$

With cross-validation: using 20% of the genotypes to test the model, 50 times
 Mean prediction accuracy per env:

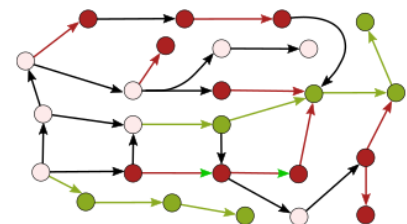


To do next:

Identification of biomarkers



Mapping biomarkers on metabolic maps



Original approach combining multiple sources of data and modelling methods

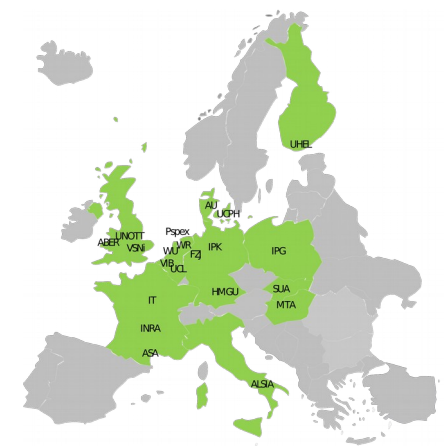
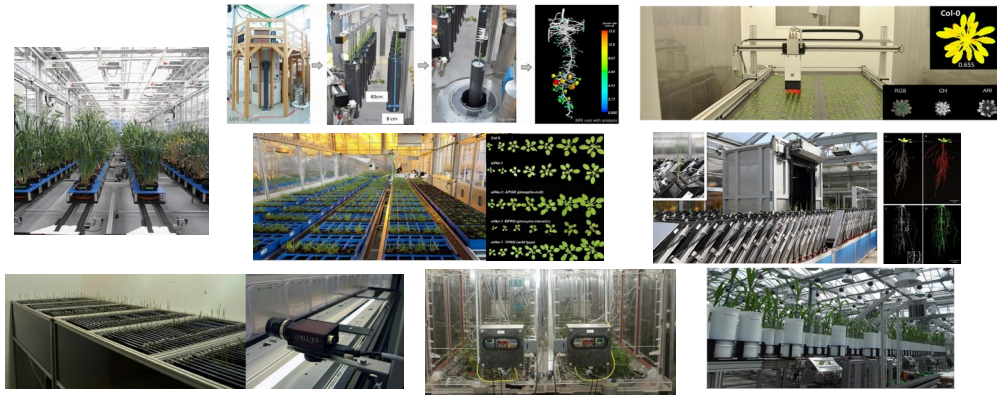
1. Using sensor network only we could classify QTLs and identify candidate genes (in field and in platform)
2. Combining traits measured in phenotyping platform and environmental characterization we could better dissect the G×E and predict the grain yield

Perspectives

- breeding programs in regions with contrasted environmental conditions
- relevant for climate change (night temp and soil water)

Ongoing work

- Validation of the genomic regions: NILs under test (field experiments, C. Welcker)
- Root traits in platform (coll. X. Draye, UCLouvain)



2017-2020 Access to 31 installations in Europe

<https://eppn2020.plant-phenotyping.eu/>



Based on a simple application procedure



Calls every 6 months (**7th call open in autumn 2019**)



Full cost of projects covered by the project, including travel



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T Spitkó
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