Nitrogen use efficiency in bread wheat: breeding tools and recent genetic progress

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Nitrogen Use Efficiency in Bread Wheat: breeding tools and recent genetic progress

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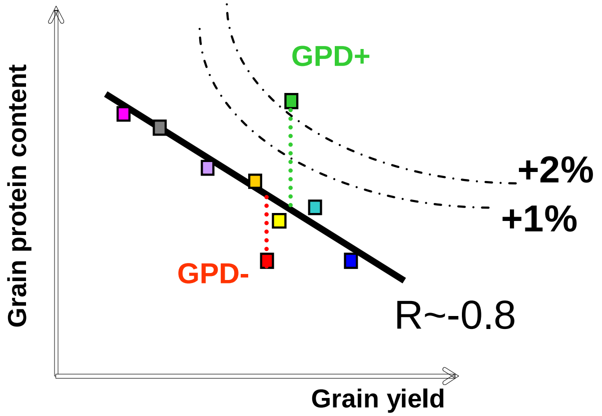
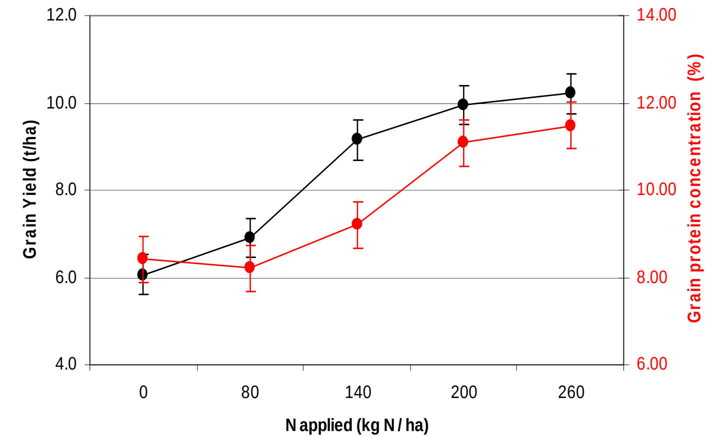
AAB Wheat Breeding Harpenden, 29-30 January 2014

What are the N traits to select for ?

- **GPD** = Grain Protein Deviation
  - Proposed by Monaghan et al (2001)
  - Bonus for GPD+ lines during registration in France (2007)



- **NUE** = Nitrogen Use Efficiency ?
  - First official trials at 3 N levels harvested in 2013
  - Identification of potential criteria after two experimental years
  - Bonus for « efficient » lines by 2016 ?



What is Nitrogen Use Efficiency?

- Two main components

  ✓ **N Uptake** = total plant N / available N

  ✓ **N Utilization** = grain yield / total plant N

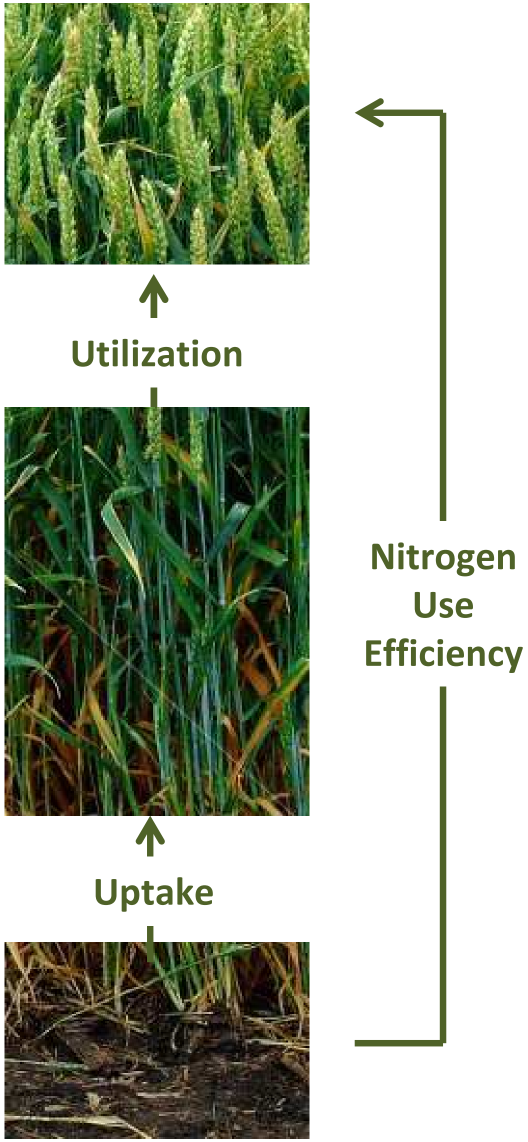
and sub-components : Straw N content, Grain N content, …

- Two main possible targets

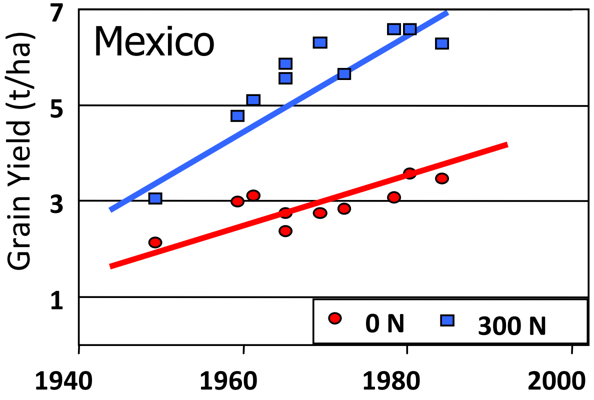
  ✓ **Sub-optimal** -> Maintain yield / quality

  ✓ **Optimal** - > Increase yield / quality

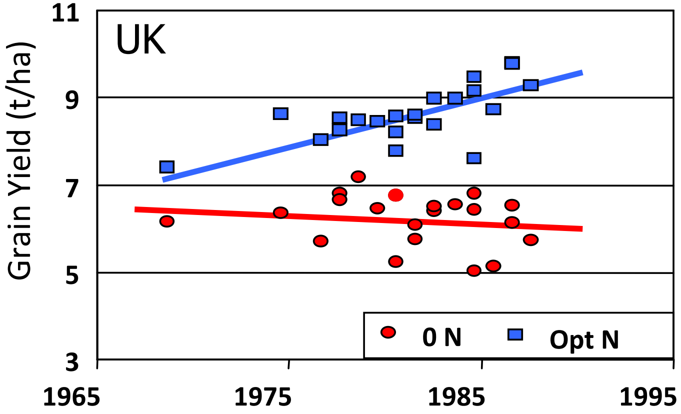
that will depend on Genotype x N level interactions



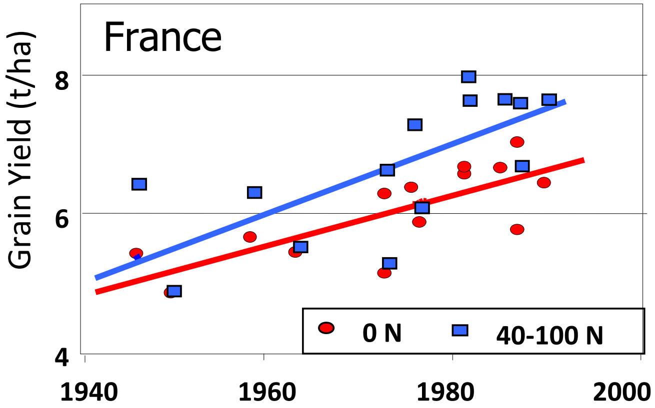
Can we improve NUE?



Ortiz-Monasterio et al, 1997



Foulkes et al, 1998



Brancourt et al, 2003

NUE = GY if we suppose Available N to be the same for all genotypes

What about recent breeding progress on NUE ?

Has NUE been increased ? How? For which N levels?

What are traits heritabilities?

Is there GxN interactions?

In which environment to select?

Is elite diversity sufficient?

A panel of registered lines

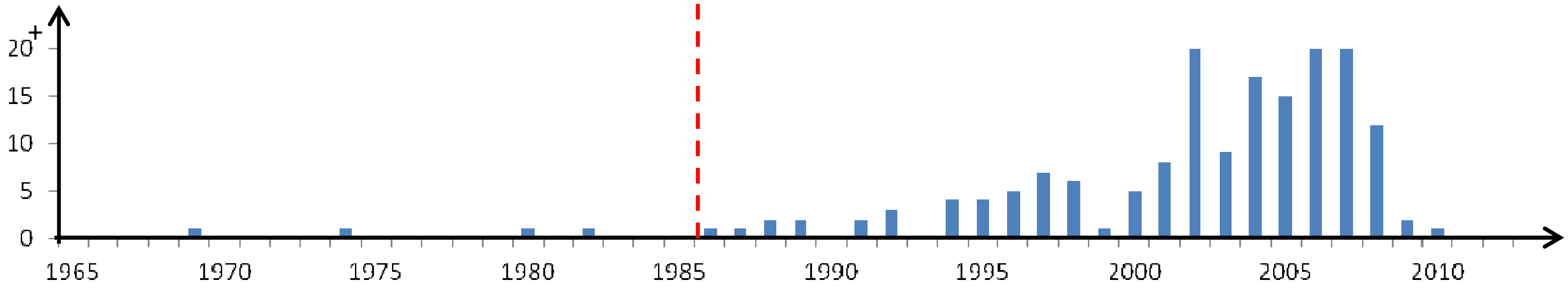
225 European elite varieties

160 “French” + 65 others

Registered from 1985 to 2010

Origin of non-French varieties

Distribution of year of registration



A network of field experiments

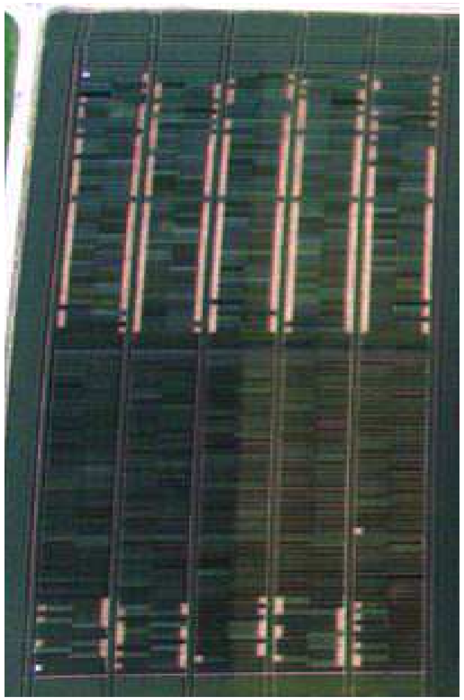
Site x Season	Years	Genotypes tested	Residual soil N (kg N ha^{-1})	N supply [1] (kg ha^{-1})	
				HN	**LN**
VB08	07/08	197	106	126	44
VR09	08/09	196	30	220	120
EM08	07/08	207	67	170	70
EM09	08/09	208	30	150	50

8 trials = 2 N x 4 environments
with environmental characterization (daily temperature, rain,…)

2865 plots - 10 measured traits

182 varieties (out of 225) tested in all trials

Controls: Apache, Orvantis, Caphorn, and Soissons (07/08) or Premio (08/09)



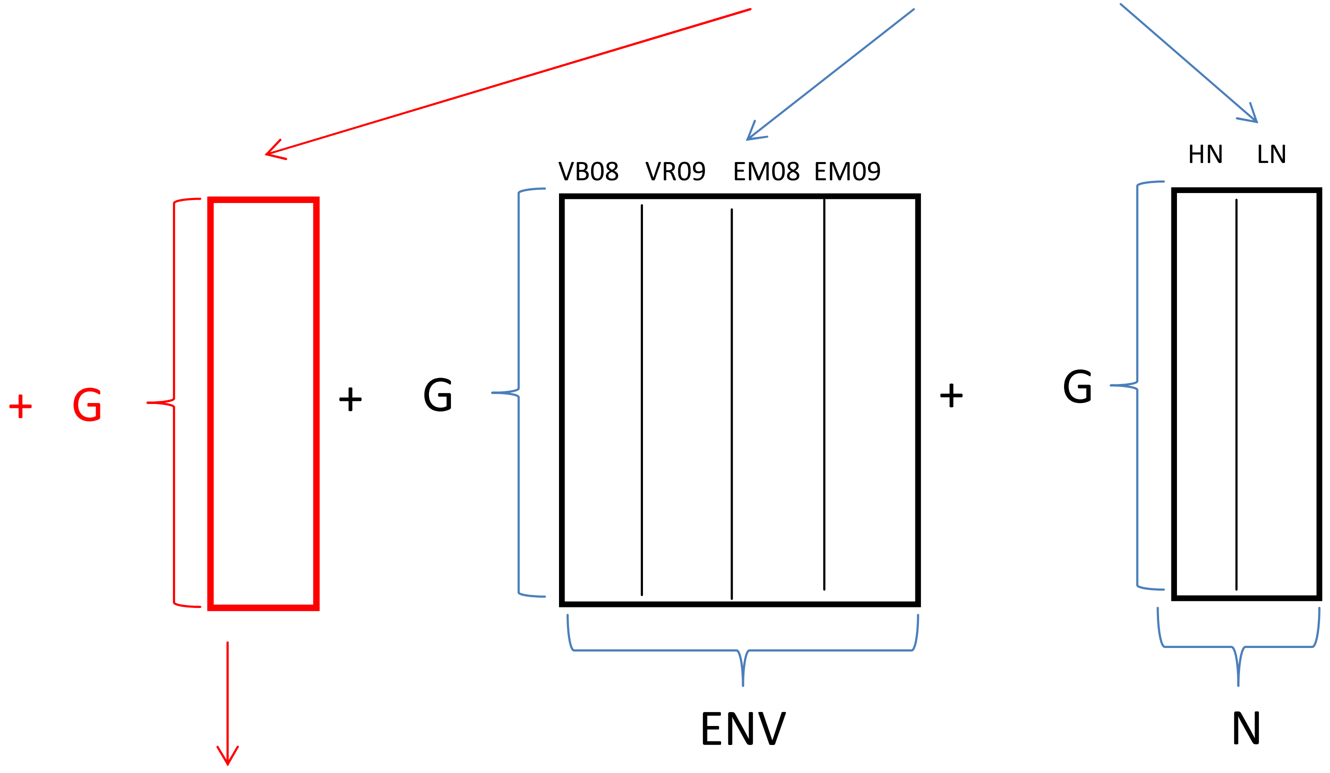
Aerial view of EM08

Location

Genetic progress estimation

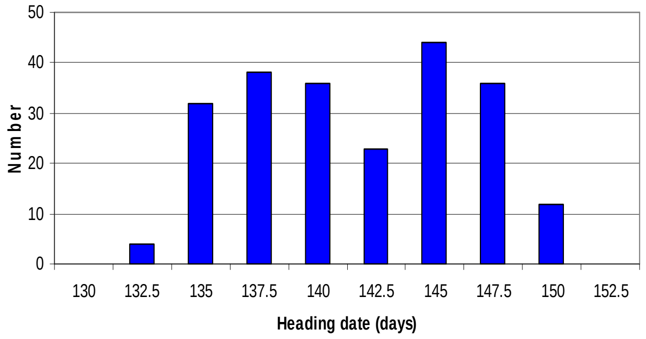
Additive effects

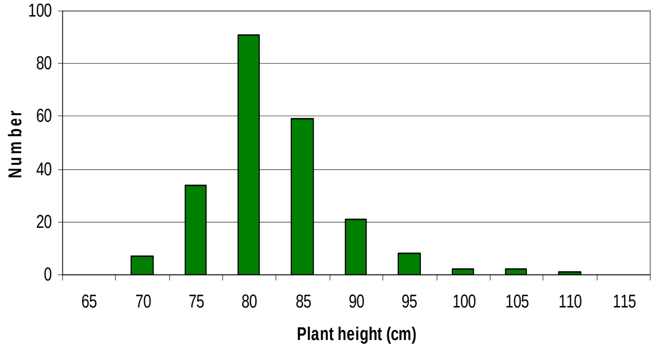
$Pijk = \mu + Nk + Ej + Ej \times Nk + Gi + Gi \times Ej + Gi \times Nk + \varepsilon ijk$



G = Quality + Precocity + Height + Year of Release

Quality classes	N°	YR means	GPC
High quality	104	2003 a	9.95 b
Good quality	50	2003 a	9.81 b
Biscuit quality	7	2001 ab	9.79 b
Other uses	7	2001 ab	9.20 c
Very high quality	12	1999 b	12.11 a

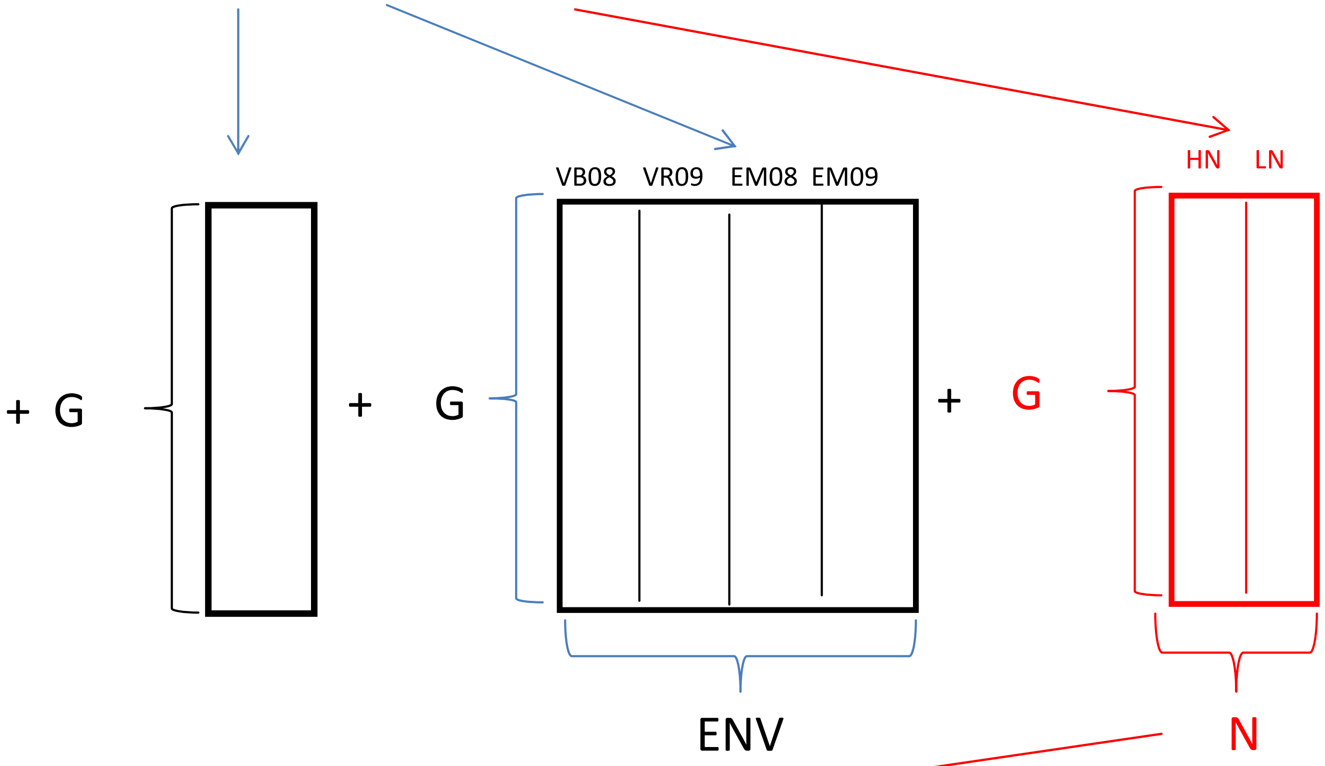




Genetic progress estimation

Interaction effect

$$P_{ijk} = \mu + N_k + E_j + E_j \times N_k + G_i + G_i \times E_j + G_i \times N_k + \varepsilon_{ijk}$$

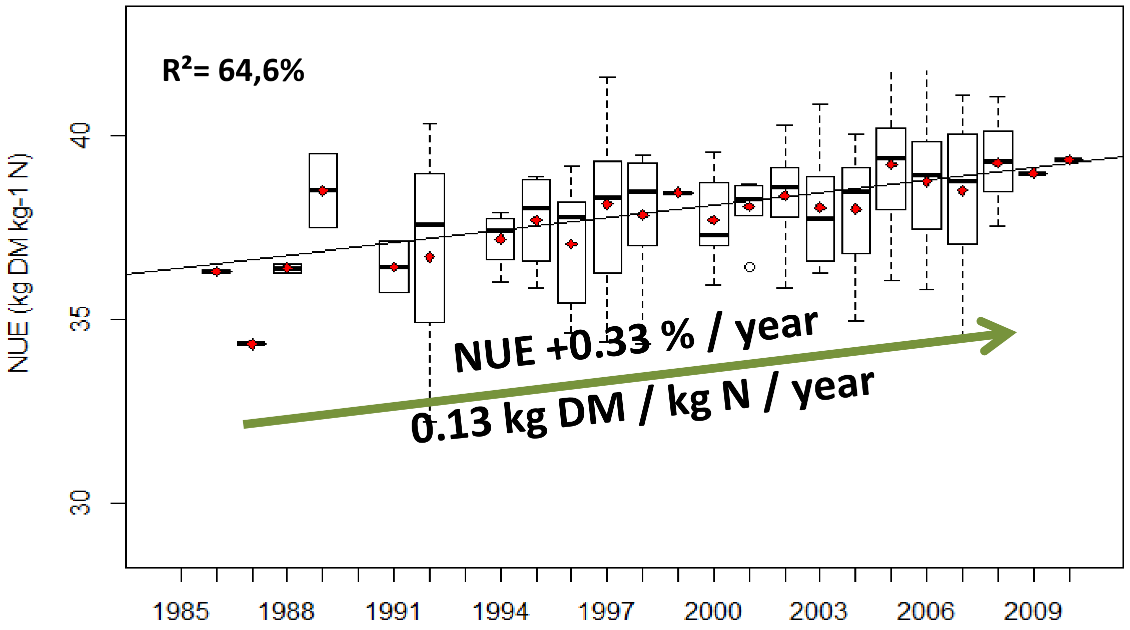


GxN = Quality + Precocity + Heigth + Year of Release

Genetic progress estimation

Variance components

Trait	**h^2**	**G**	**G × E**	**G × N**
NupE	0.00	**10% ns.**	77% ***	13% ns.
NutE	**0.79**	63% ***	30% ***	**7% *** **
NUE	**0.80**	69% ***	26% ***	**5% ***

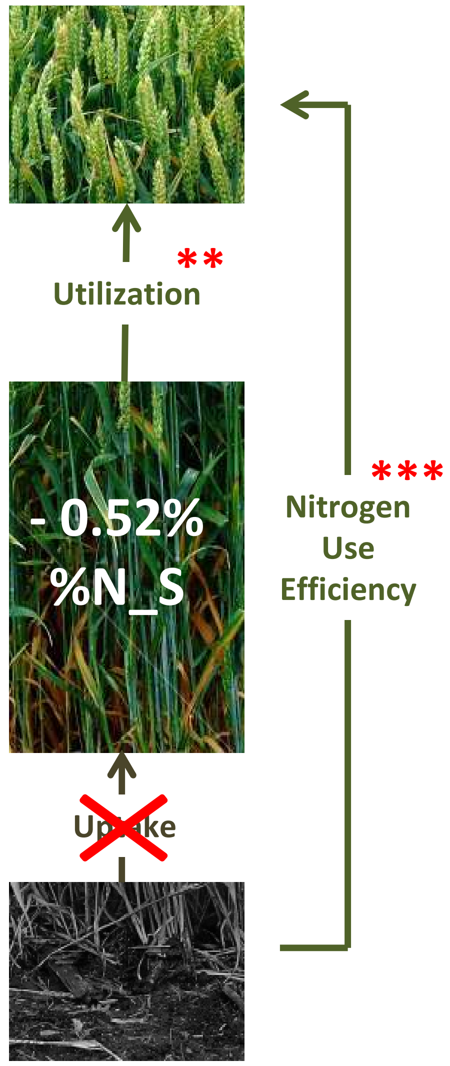


R²= 64,6%

NUE +0.33 % / year

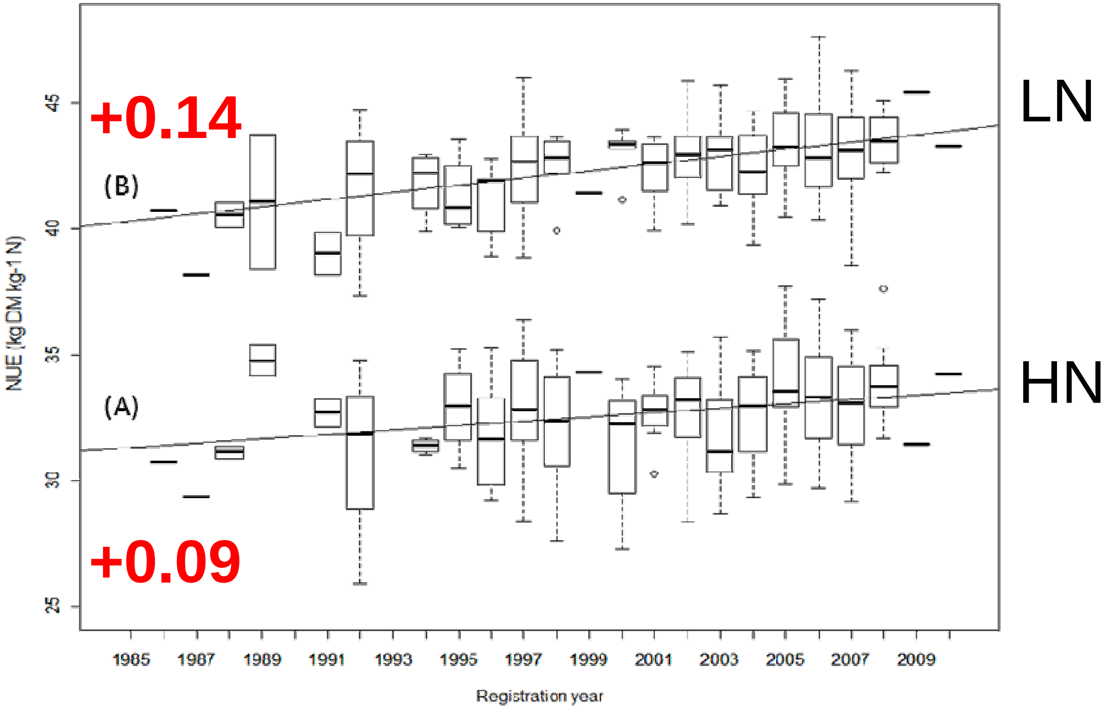
0.13 kg DM / kg N / year

NUE genetic values adjusted from quality, precocity and height in function of the YR



Genetic progress estimation

Interaction effects



Significant difference between HN and LN

Gain in yield stability

Based on heritabilities and genetic correlations:
Direct selection at LN is still the more efficient
Indirect Selection Efficiency ISE=0.78

How to maintain / accelerate this improvement?

✓Increase genetic diversity

- 2 new association panels (4600 INRA collection)
- 10 advanced backcross populations

✓Identify linked molecular markers

✓Develop phenotyping tools

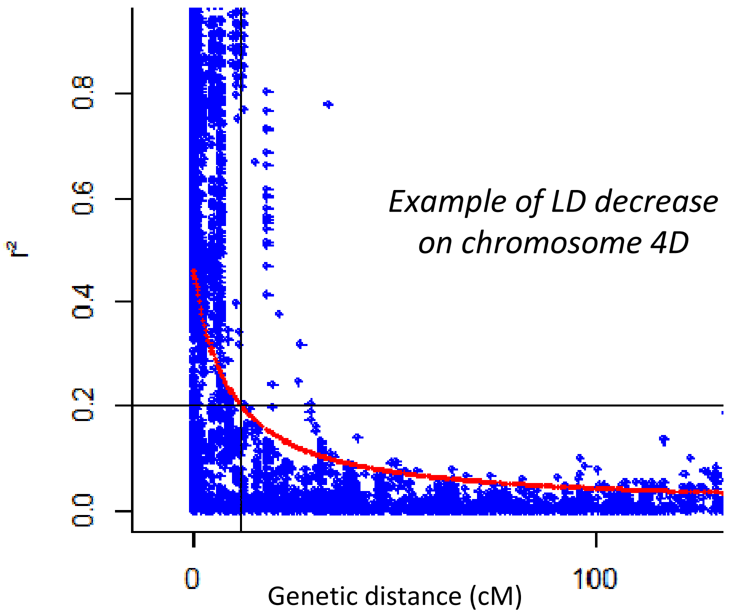
Association genetics parameters

214 genotyped varieties

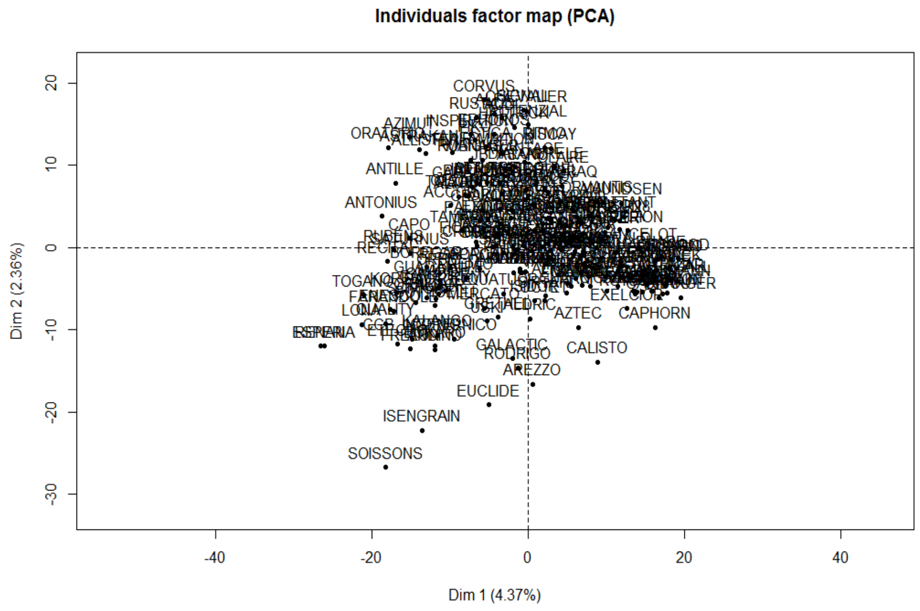
34 382 polymorphic SNP (Illumina 90K + Biogemma)

Mean Linkage Disequilibrium (LD) decay = 1.1 +/-1.3 cM

A poorly structured panel



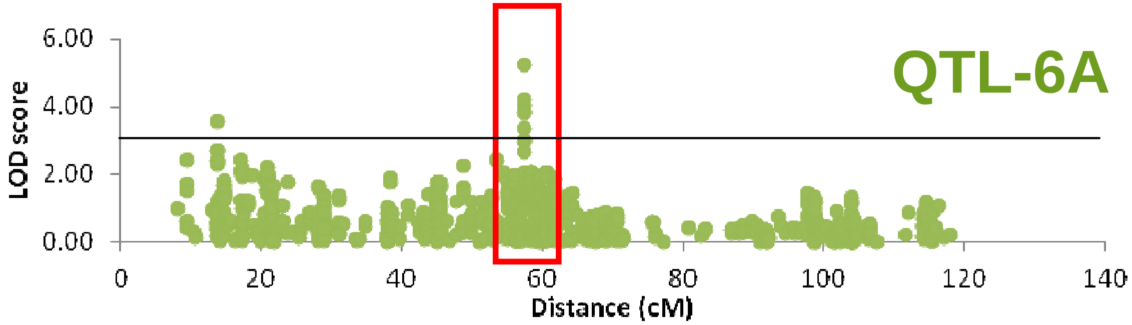
Example of LD decrease on chromosome 4D

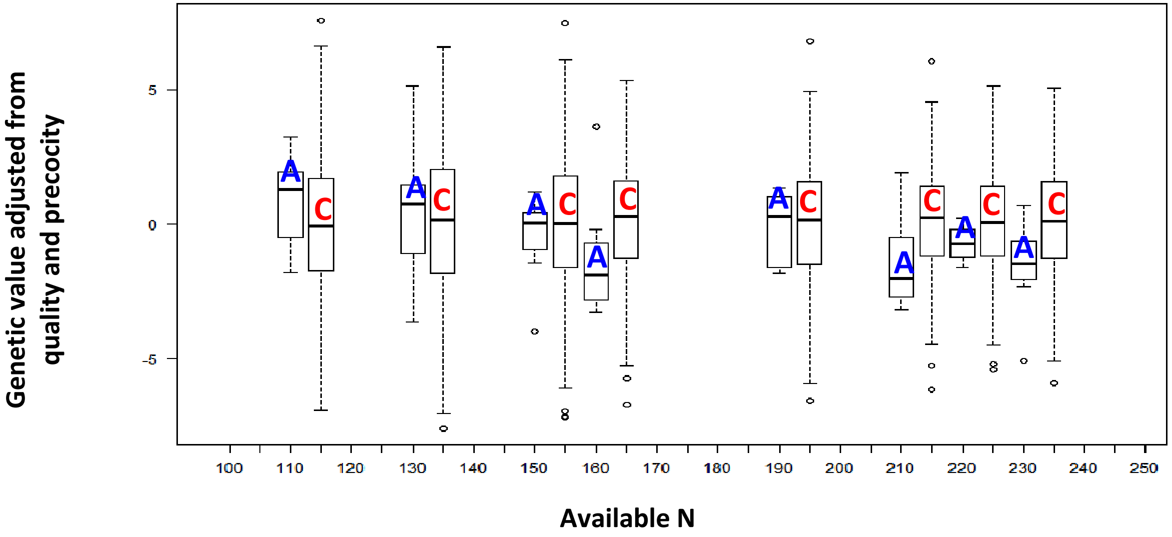


Two first axes of the PCA of varieties by 3 461 non-redondant SNP

Example of an associated region

NUE = ENV + Quality + Precocity + SNP + **SNP x N** + K





The most significant LOD score of interaction with available N

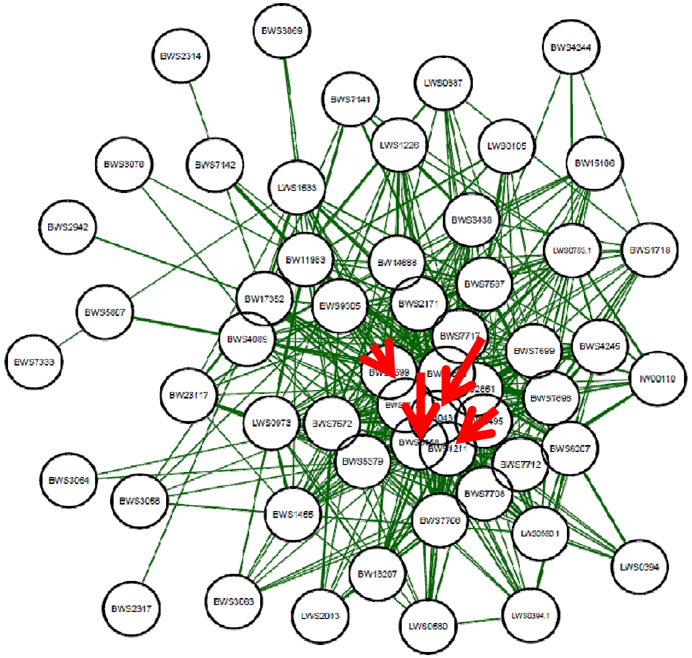
Effect on remobilization (NHI and %N in straw)

Region already identified in 2 independent yield GWAS (≠ GW2)

Epistasis and QTL6A

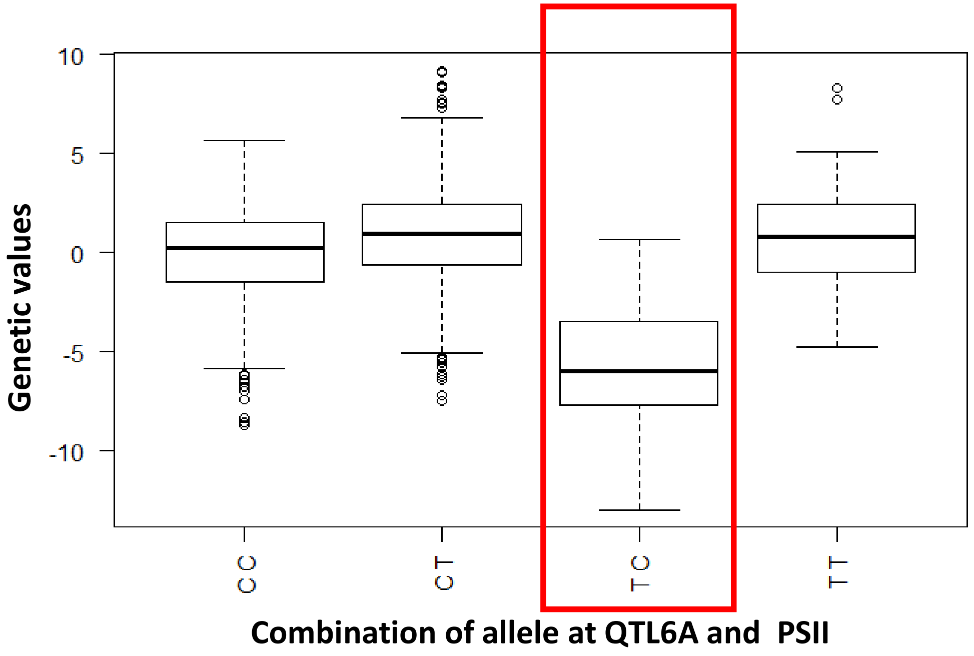
NUE = ENV + Quality + Precocity + **SNPi x SNPj** + K

The effect of this region is significantly conditionned by others



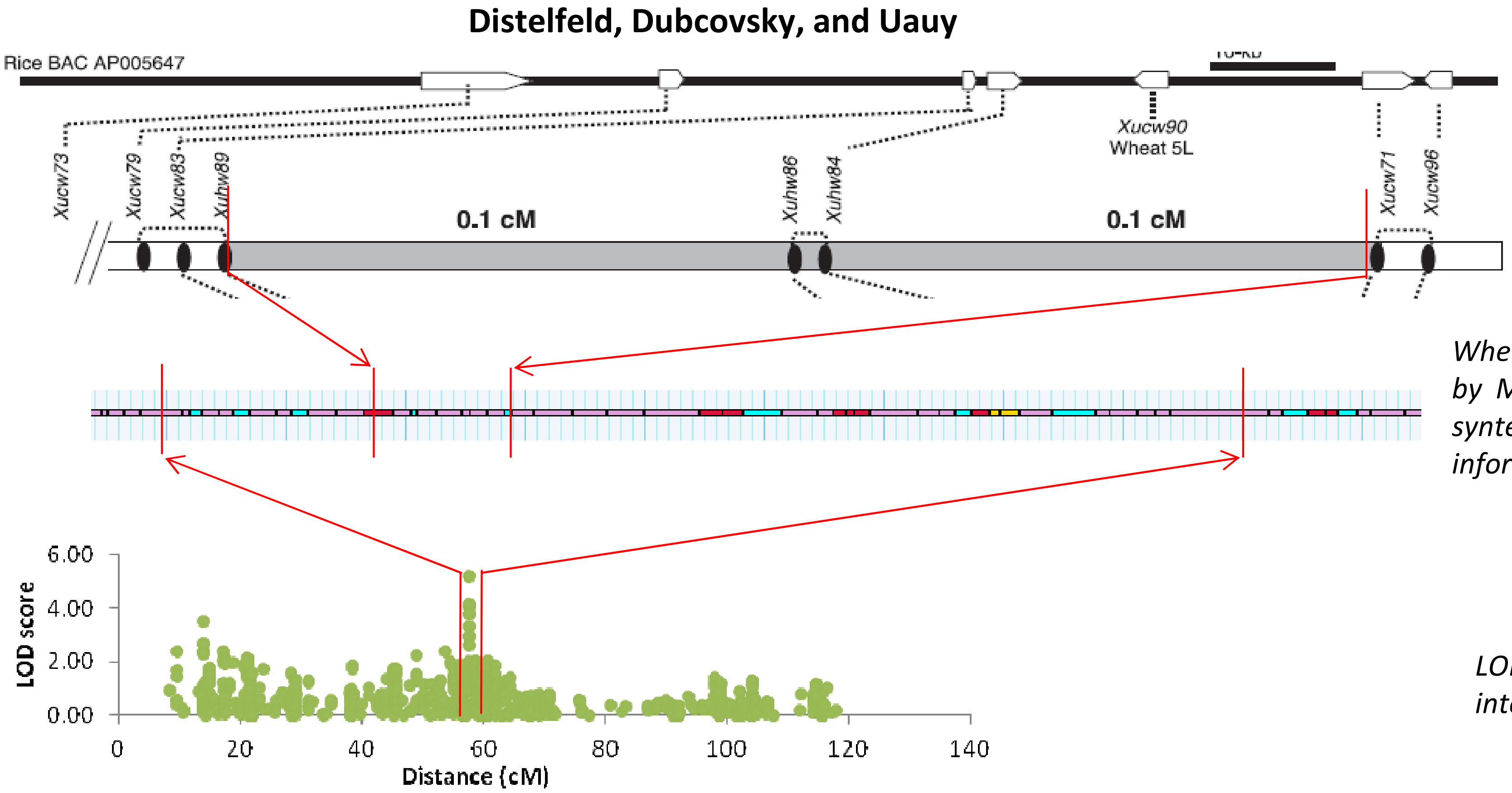
Interaction network based on significant epistatic interactions for NUE between SNP having a significant effect on NUE

20% of NUE genetic values can be explained by the interaction of QTL6A / Protein PSII



Boxplot of NUE genetic values as a function of alleles at QTL6A/PSII

A possible candidate gene



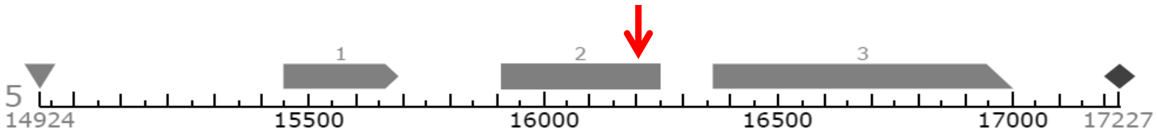
GPC-B1
Distelfeld et al, 2005

Wheat genome zipper inspired by Mayer et al (2011) mixing synteny and genetic map information (Biogemma)

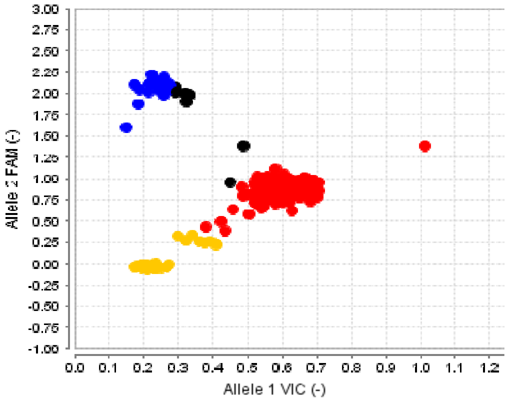
LOD score on 6A for the interaction with N

Looking for natural variants

Uauy et al. 2006 ***Tt*NAM-A1 = IWGSC 6A seq**

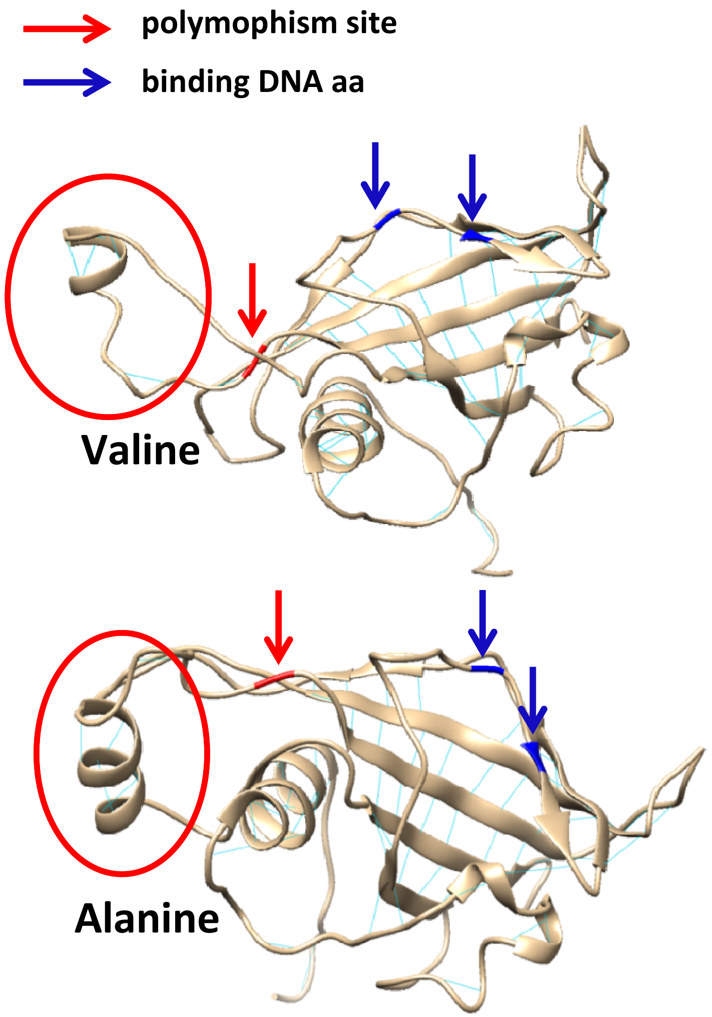


Genomic sequence of TaNAM-A1



Genotyping results of TaNAM-A1

GPC-A1 mapped in QTL6A confidence interval



Theoretical 3D structure of natural variant of TaNAM-A1 in European elite bread wheat (Chimera)

How to maintain / accelerate this improvement?

✓Increase genetic diversity

- 2 new association panels (4600 INRA collection)
- 10 advanced backcross populations

✓Identify linked molecular markers

✓Develop phenotyping tools

Development of high-throughput techniques

✓NUE is difficult to phenotype

- time-consuming (sampling, milling …)
- not repeatable (biomass, N content)

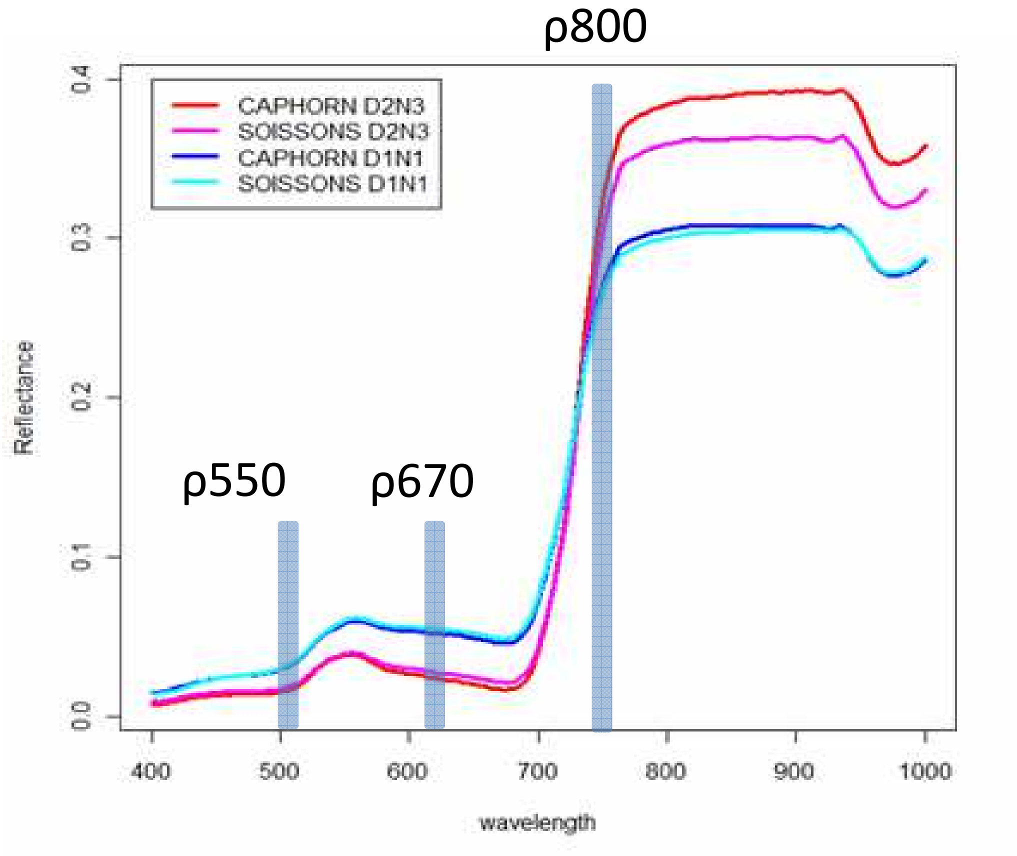
✓May explain that we detected no additive genetic diversity in the elite panel

✓The key trait is total plant N

- biomass and N content are difficult to estimate
- probably possible to approximate them estimating Leaf Area (LAI) and Chlorophyll Content (CC)

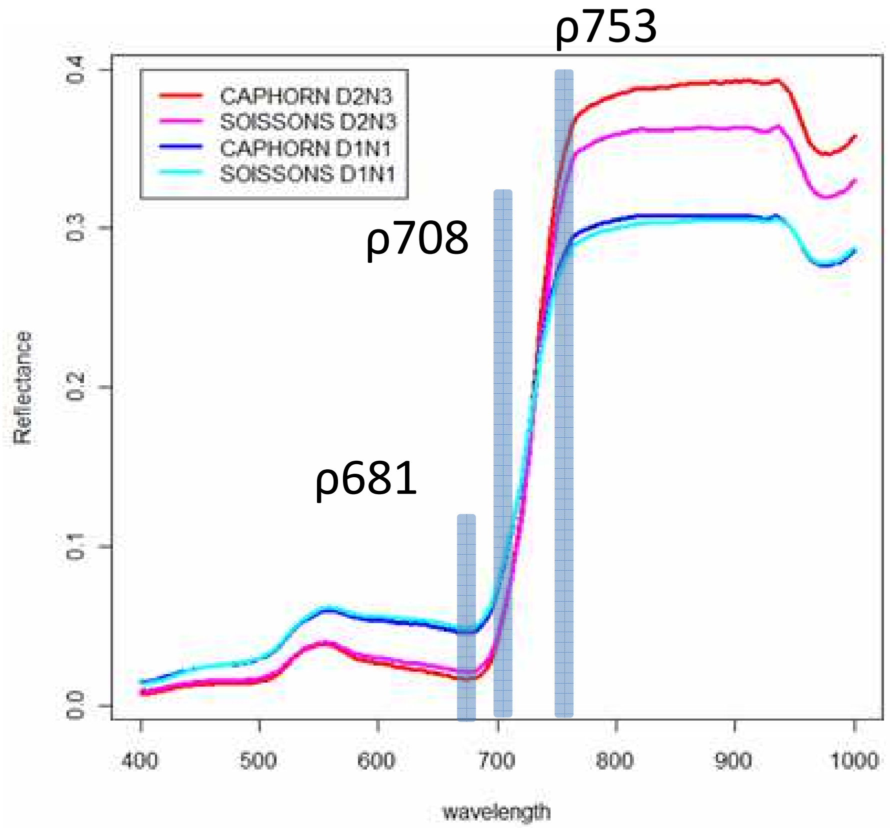
Based on indices using reflectance values

LAI: MCARI2 - Modified Chlorophyll Absorption Ratio Index 2



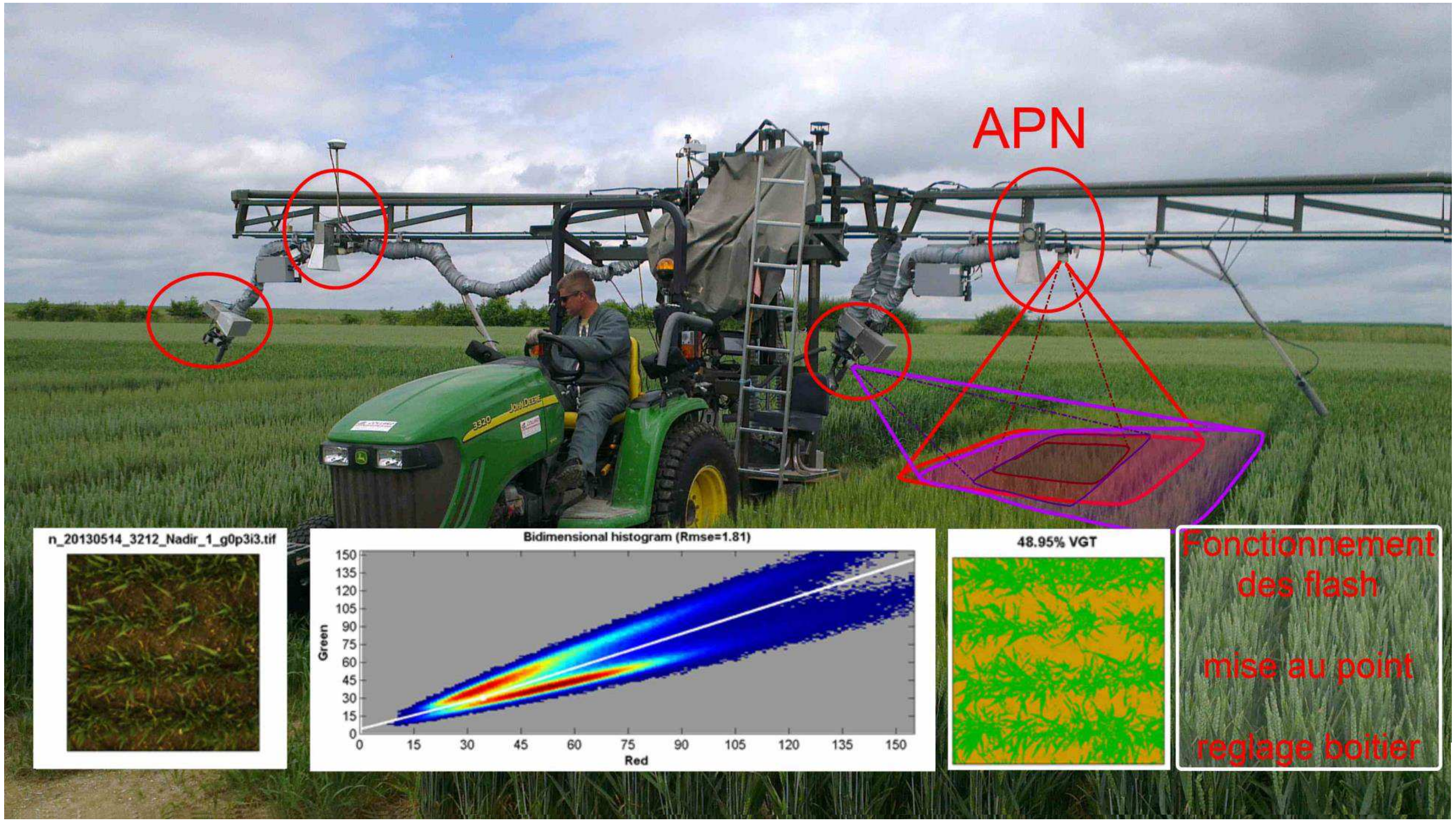
Haboudane et al., 2004

Chlorophyll: MTCI - MERIS Terrestrial Chlorophyll Index



Dash and Curran, 2004

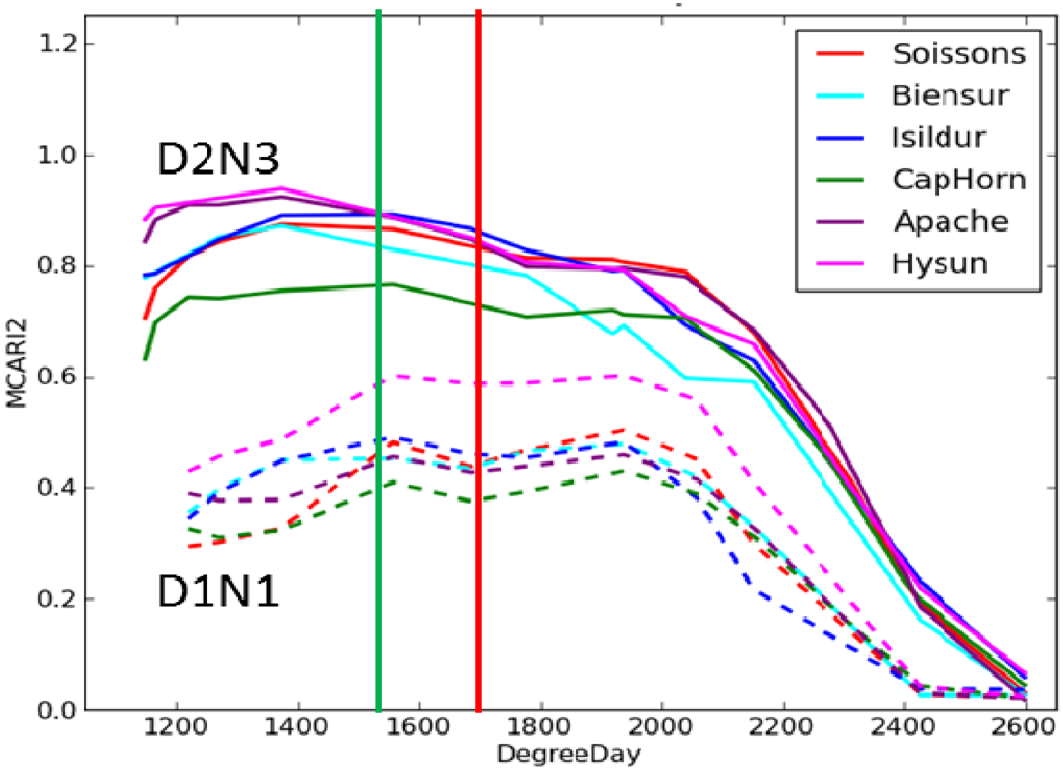
Developpement of a « PhenoMobile »



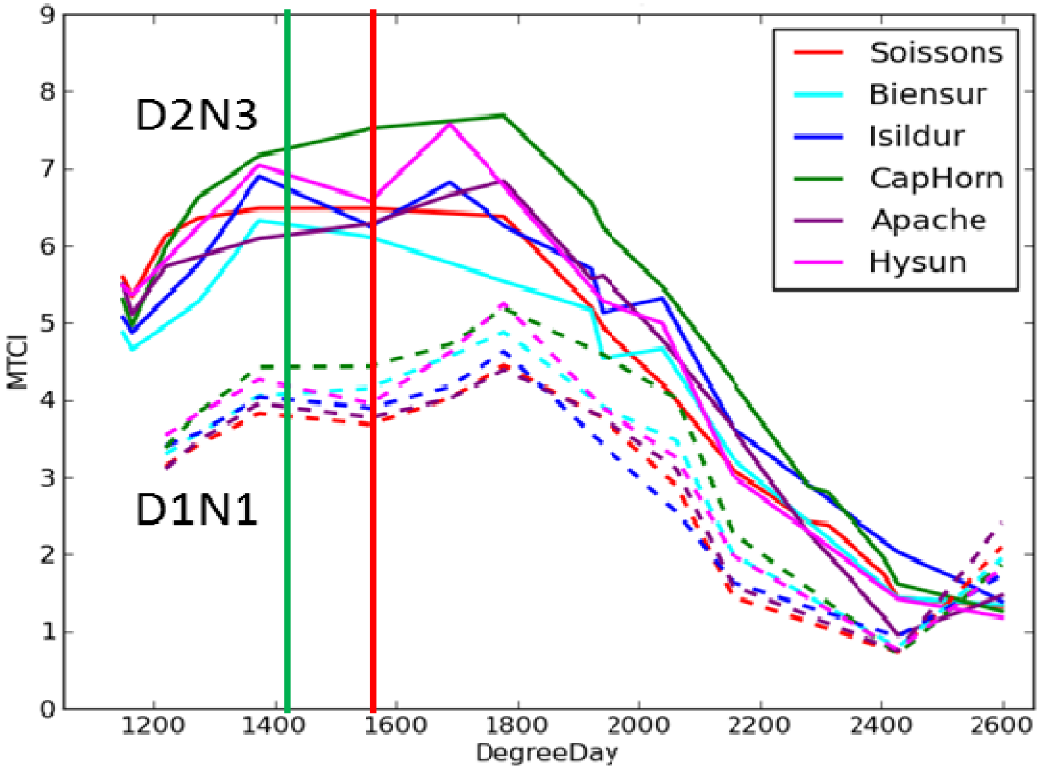
F. Baret, B. de Solan, P. Burger

Example of indices dynamics

Heading Flowering

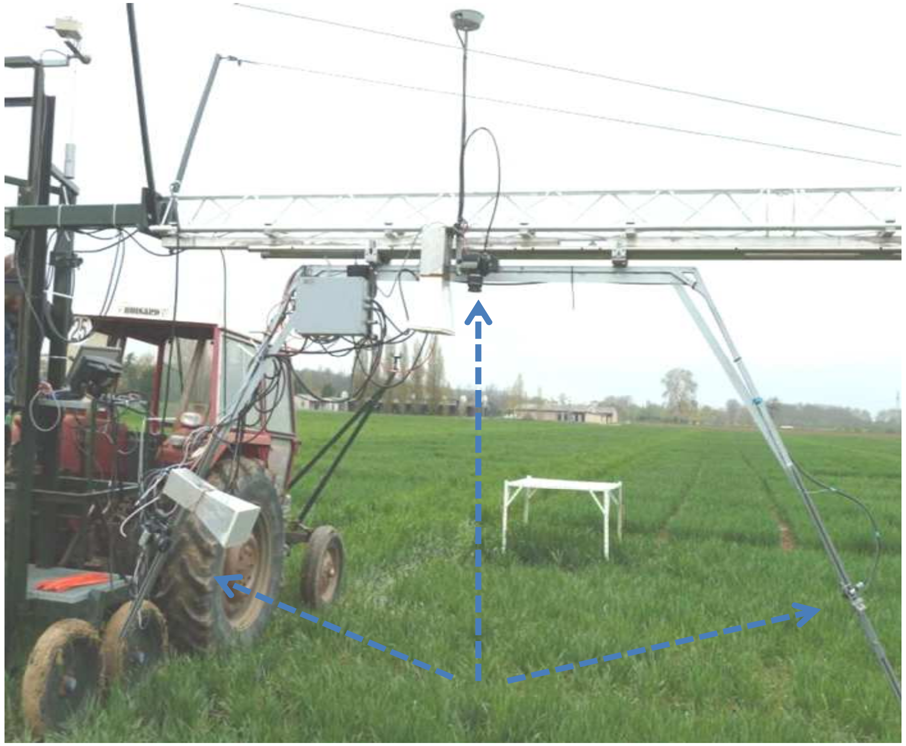


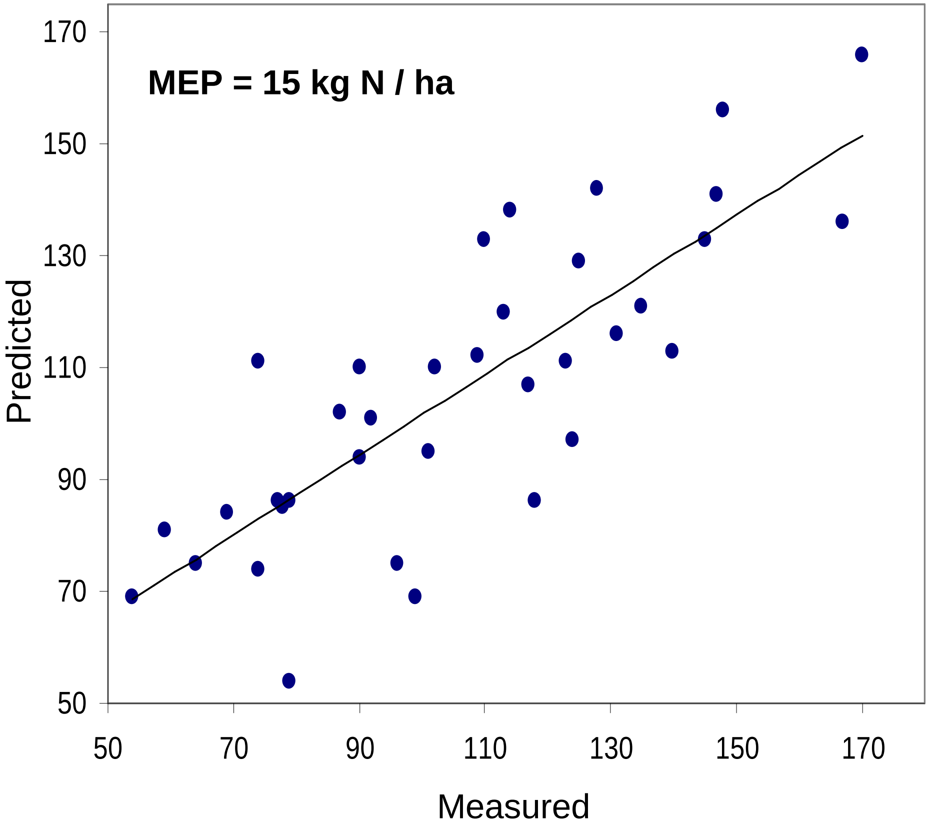
MCARI2 : LAI related



MTCI : Chlorophylle related

Estimation of absorbed N





Baret, Burger, et al

CONCLUSIONS

Estimation of genetic progress for NUE

- +0.33% / year
- significant G x N level interaction
- no significant genetic additive effect for N uptake

Association genetics in progress

- associated regions identified
- SNP x N level and SNP x SNP interactions detected

Phenotyping methods are currently developed

- LAI & Chlorophyll content dynamics

An second association panel was assembled (Breedwheat project)

- 220 elite lines, 100 common to the first panel
- genotyped (TaBW420k Affymetrix array, E. Paux et al)
- phenotyped
  - classical phenotyping (2012-2014)
  - high-throughput phenotyping (2012-2013)

Acknowlegments

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Emmanuel Heumez

Thank you for your attention