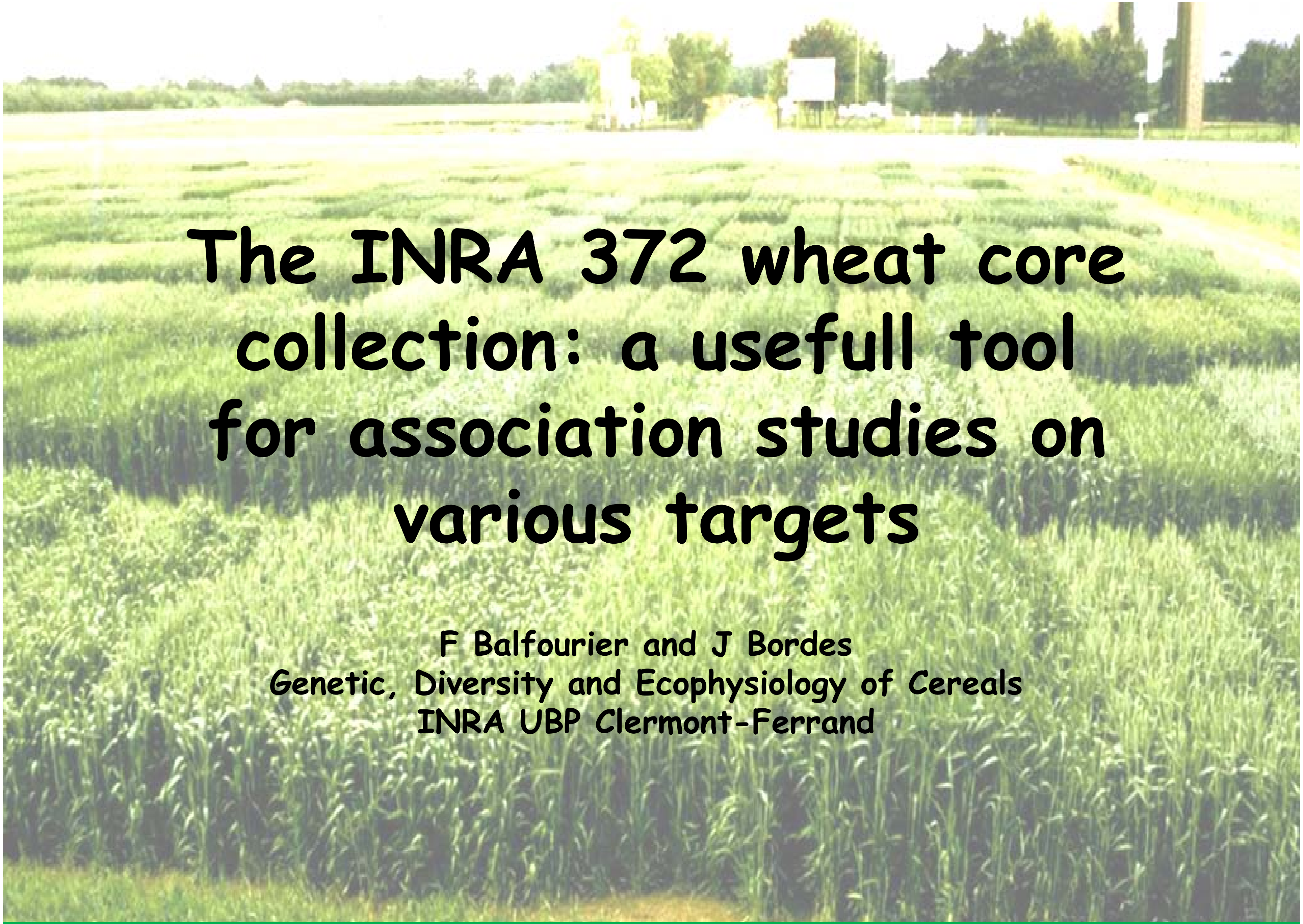


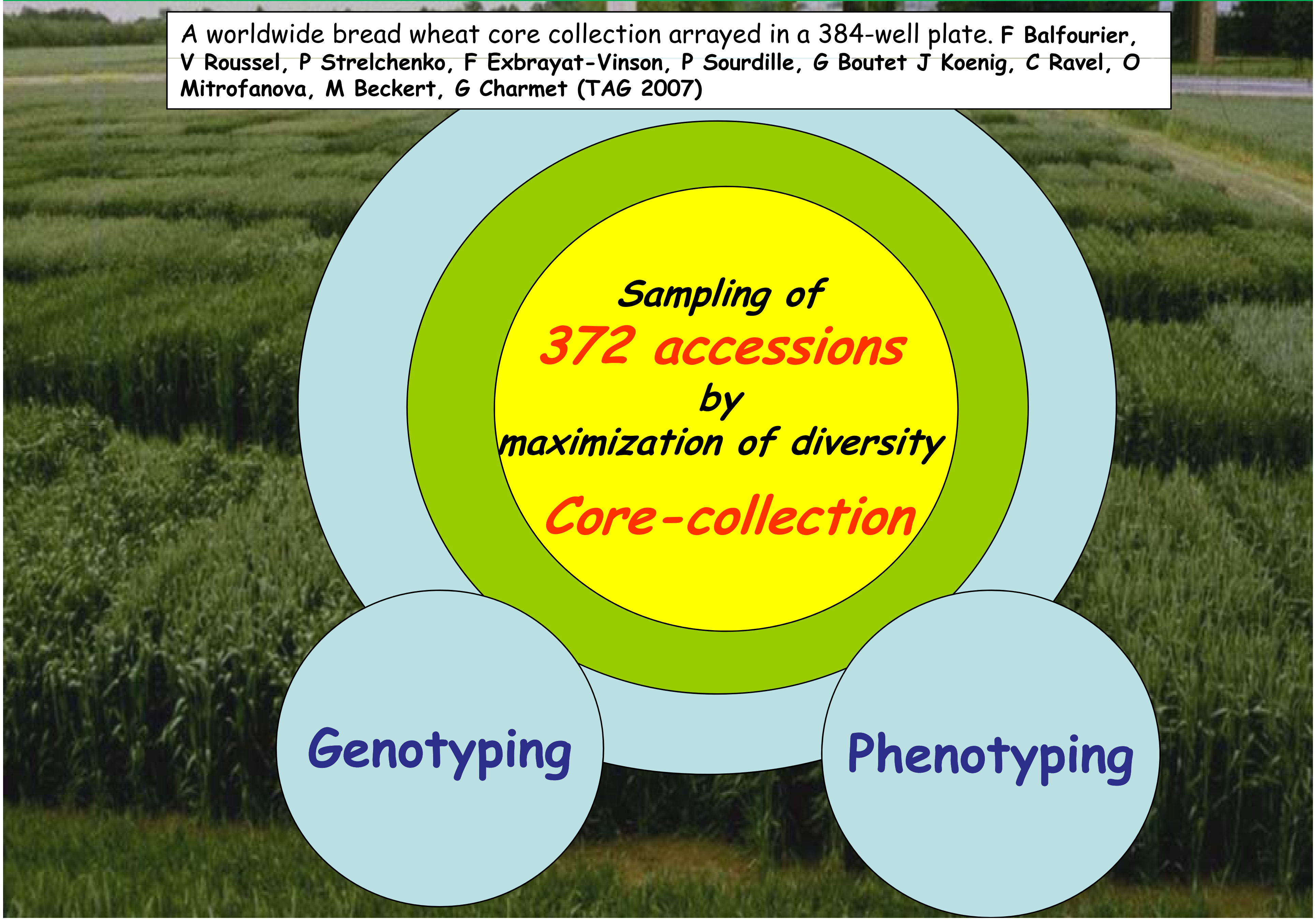
The INRA 372 wheat core collection: a usefull tool for association studies on various targets

F Balfourier and J Bordes
Genetic, Diversity and Ecophysiology of Cereals
INRA UBP Clermont-Ferrand

Groupe Céréales à pailles 29-30 Mars 2011-Changins

Worldwide wheat core collection 372CC

A worldwide bread wheat core collection arrayed in a 384-well plate. **F Balfourier, V Roussel, P Strelchenko, F Exbrayat-Vinson, P Sourdille, G Boutet J Koenig, C Ravel, O Mitrofanova, M Beckert, G Charmet (TAG 2007)**



Sampling of
372 accessions
by
maximization of diversity

Core-collection

Genotyping

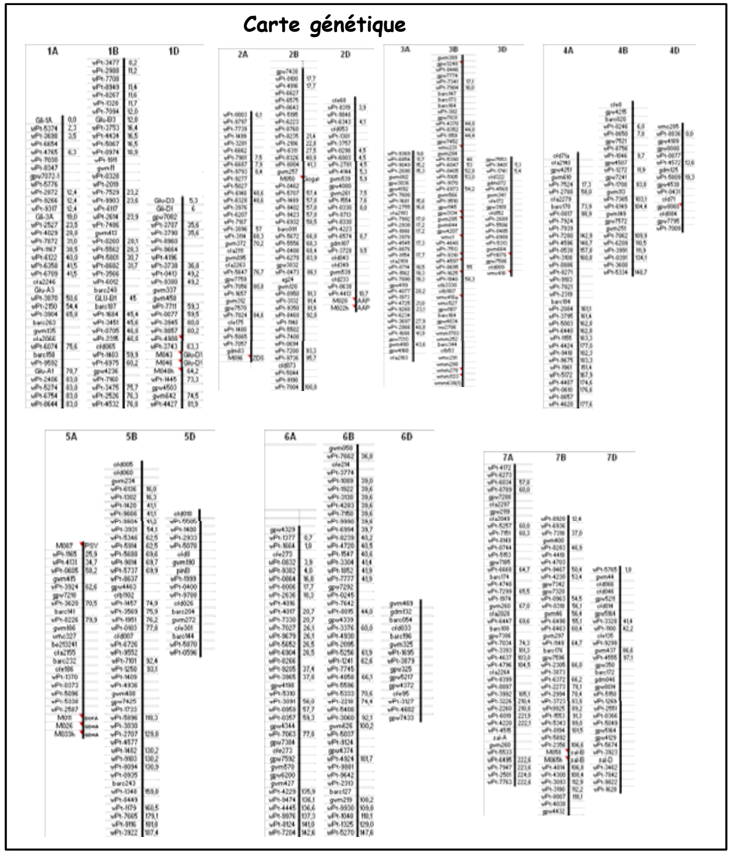
Phenotyping

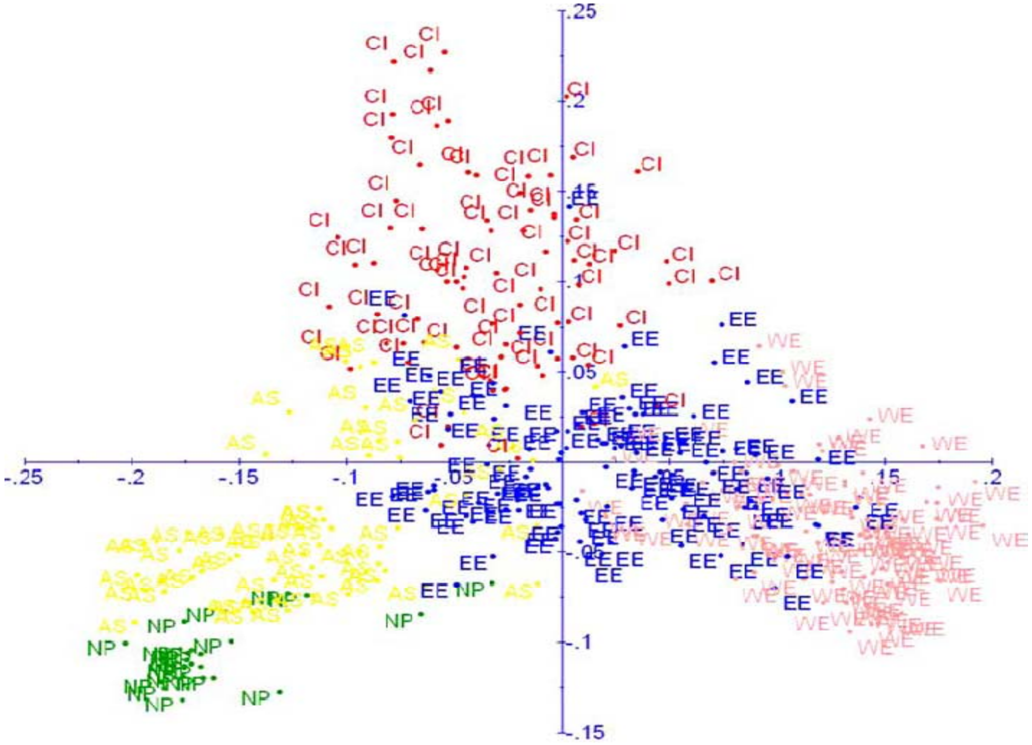
372 CC Genotyping

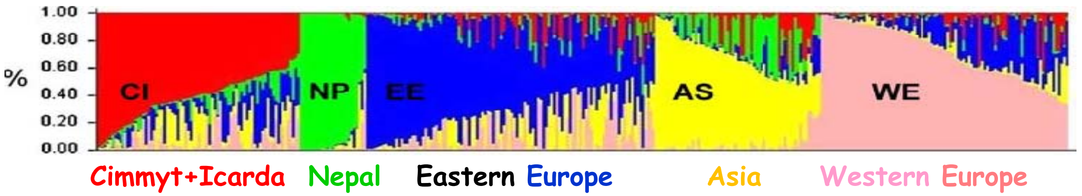
Analysis of diversity and linkage disequilibrium along chromosome 3B of bread wheat (Triticum aestivum L.). **Horvath A, A Didier, J Koenig, F Exbrayat, G Charmet, F Balfourier (TAG 2009)**

Genotyping:

- 570 DARTs
- 271 SSRs
- 400 SNPs







Genetic Structure analysis: 5 funding populations related to the geographical origins of accessions

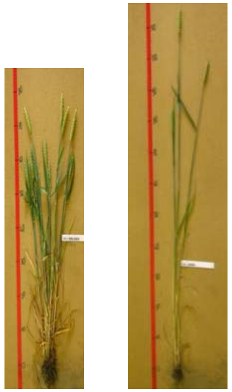
372 CC Phenotyping

Agronomic characteristics, grain quality and flour rheology of 372 bread wheats in a worldwide core collection. **Bordes J, Branlard G, Oury F-X, Charmet G, Balfourier F. (JCS 2008)**

372 CC deeply phenotyped for:
- agronomical and morphological traits
- biochemical and rehological characteristics


Plant height

Ear characteristics



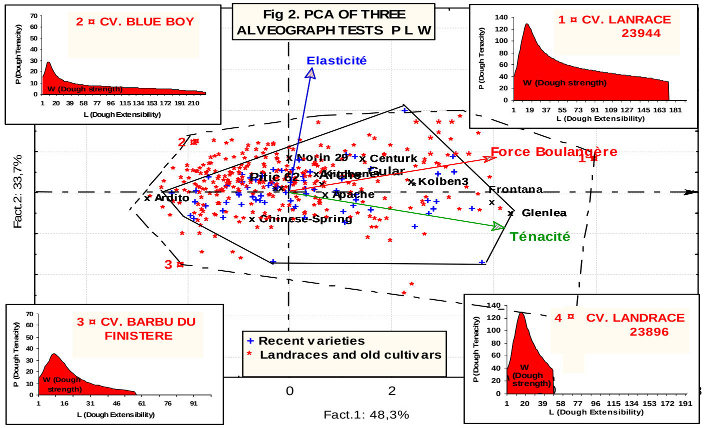

Pre-harvest Sprouting

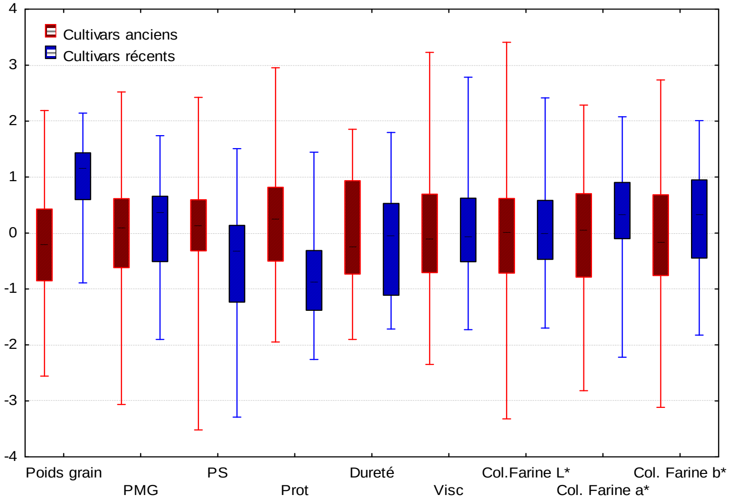
Septoriose


Grain color

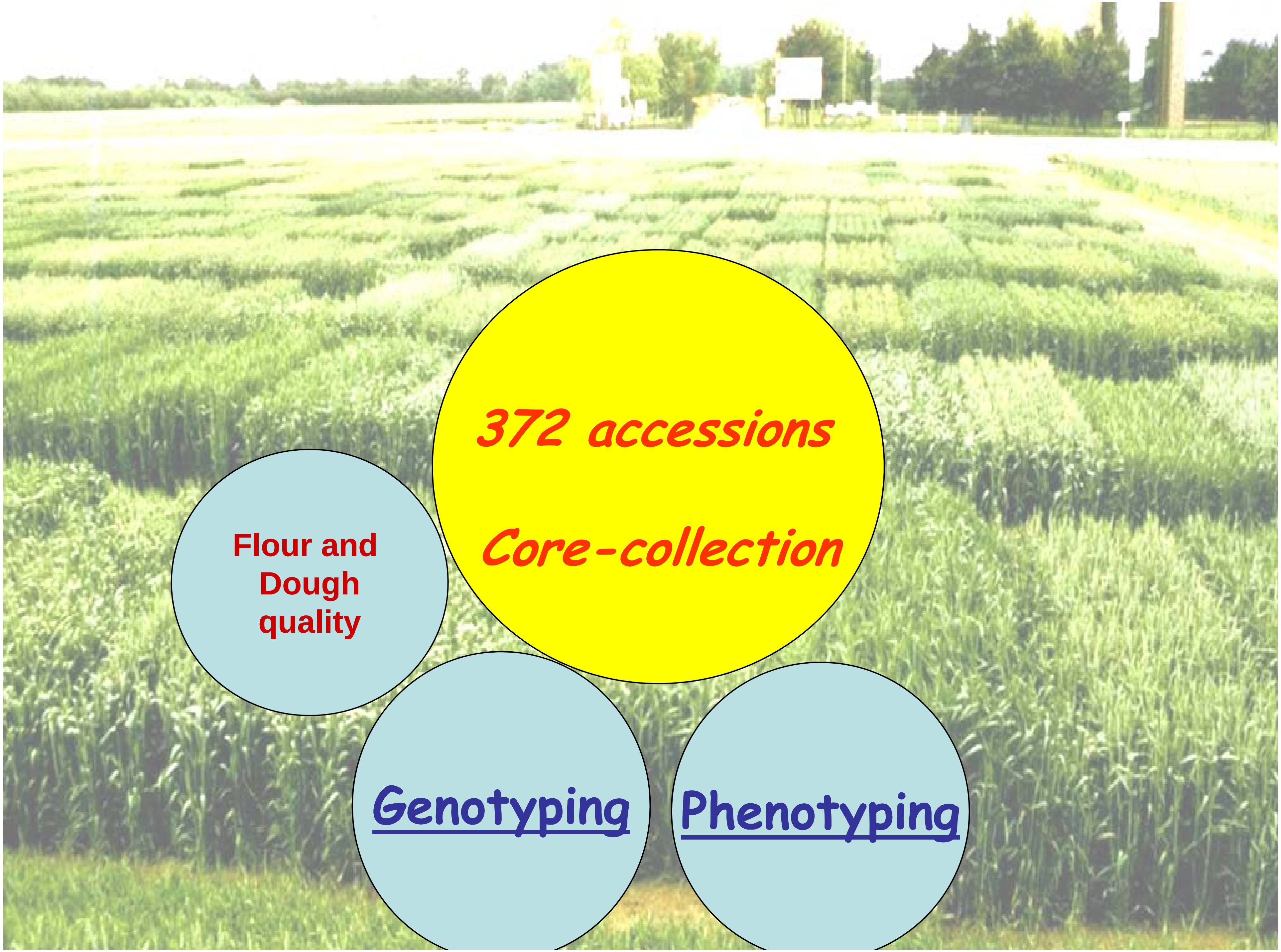

Grain hardness

ALVEOGRAPH TEST





Large phenotypic variability observed for the whole measured traits



372 accessions

Core-collection

Flour and Dough quality

Genotyping

Phenotyping

Flour and dough quality: association study

Use of a worldwide wheat core collection for association analysis of flour and dough quality traits. **J Bordes, C Ravel, J Le Gouis, G Charmet and F Balfourier . (JCS 2011, in press)**

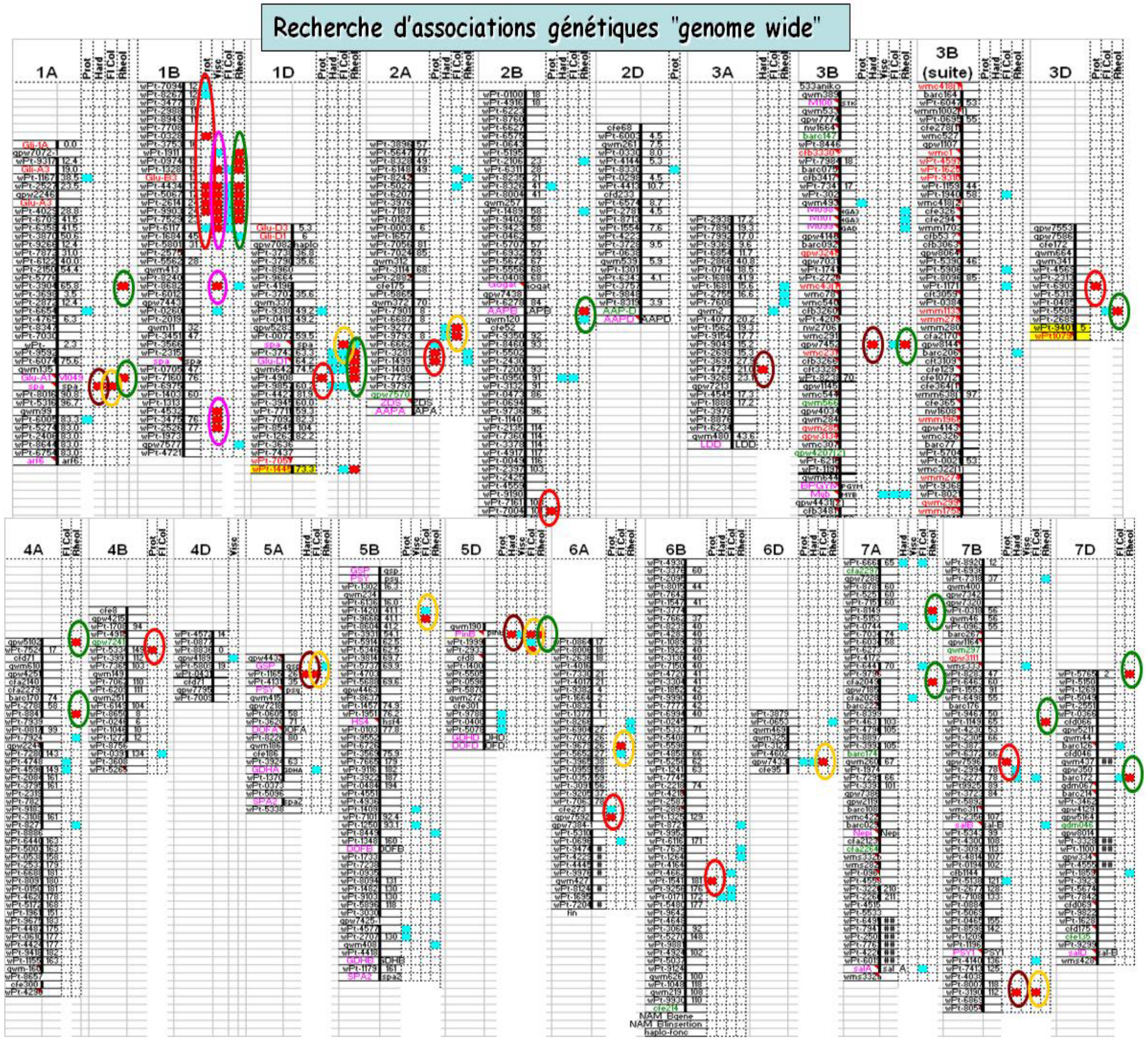
Observed traits in 372CC

- **proteins content** ○
- viscosity ○
- **hardness** ○
- florr color ○

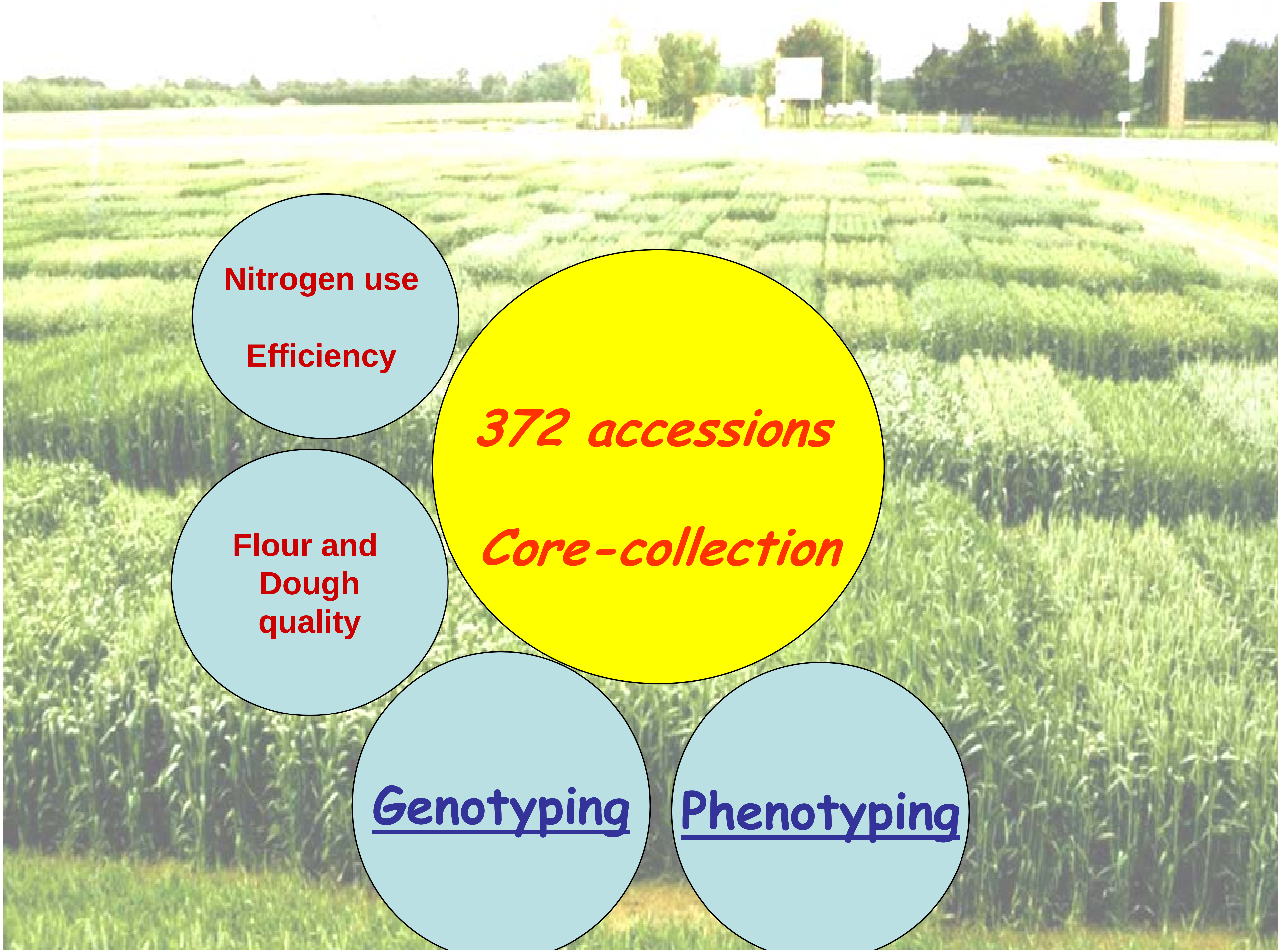
  L*, a* et b*
- **Rehological values** ○

  Mixograph and Alveograph

ALVEOGRAPH TEST


Recherche d'associations génétiques "genome wide"

Great number of significant associations at the whole genome scale



Nitrogen use

Efficiency

372 accessions

Core-collection

Flour and
Dough
quality

Genotyping

Phenotyping

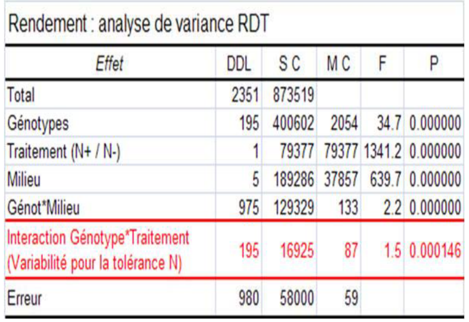
Research of new specific alleles for low-inputs tolerance

(Support: FUI SDD)

Use of a worldwide wheat core collection for association analysis of tolerance to less nitrogen fertilizer. (In prep).

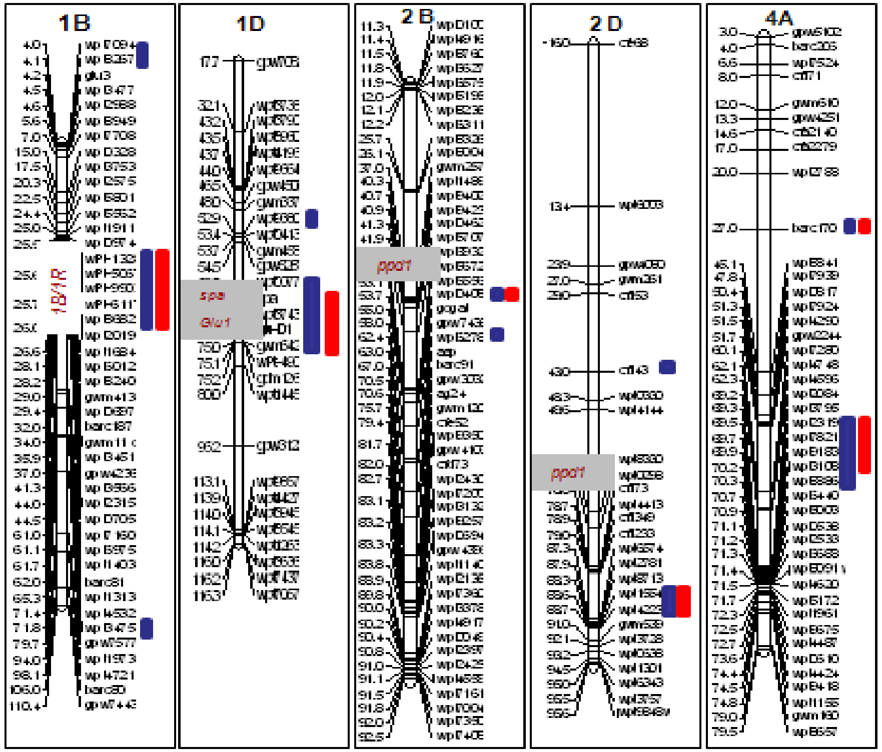
372 CC Yield and its components observed in 3 locations x 2 level of Nitrogen :

- high level **(N^+)**
- **Low level (N^-)**



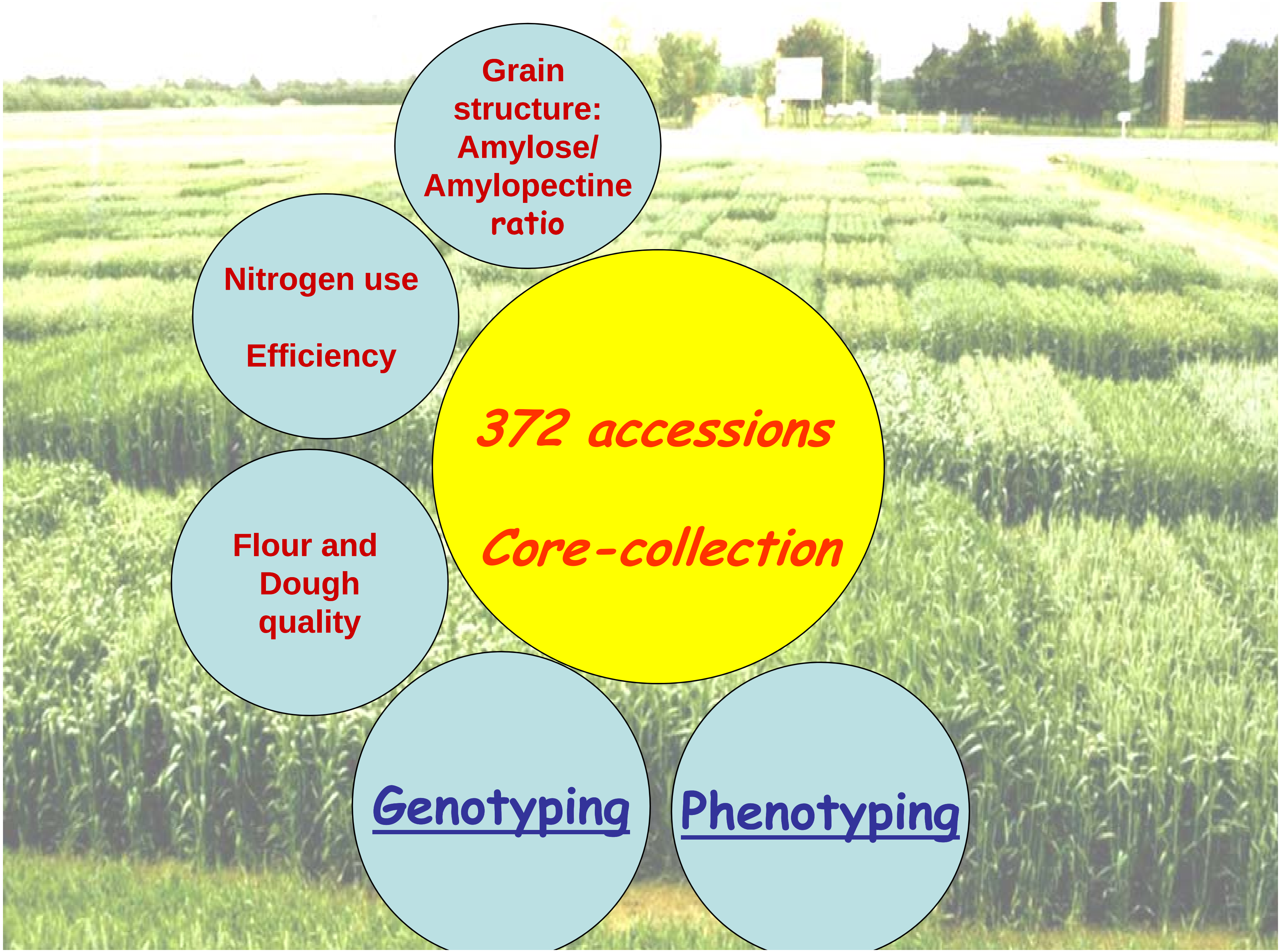
Rendement : analyse de variance RDT

Effet	DDL	S C	M C	F	P
Total	2351	873519			
Génotypes	195	400602	2054	34.7	0.000000
Traitement (N+ / N-)	1	79377	79377	1341.2	0.000000
Milieu	5	189286	37857	639.7	0.000000
Génot*Milieu	975	129329	133	2.2	0.000000
Interaction Génotype*Traitement (Variabilité pour la tolérance N)	195	16925	87	1.5	0.000146
Erreur	980	58000	59		



🟦 yield 🟥 Low input tolerance

Clear variability for tolerance to less nitrogen fertilizer
Several significant genetic associations observed for this trait



Grain structure: Amylose/ Amylopectine ratio

Nitrogen use

Efficiency

372 accessions

Core-collection

Flour and Dough quality

Genotyping

Phenotyping

Grain structure : amylose/amylopectine ratio (B, Jallais)

(Support: ANR NOMAC – coll. BIA Nantes)

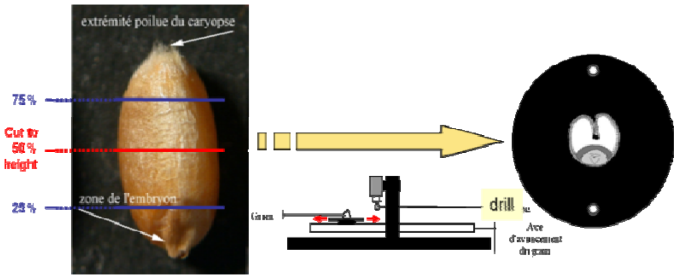
Sub-sample of 372CC maximized for amylose/amylopectine ratio
- NIRS approach
- molecular approach

Diversity Maximisation at 63 SSR locus

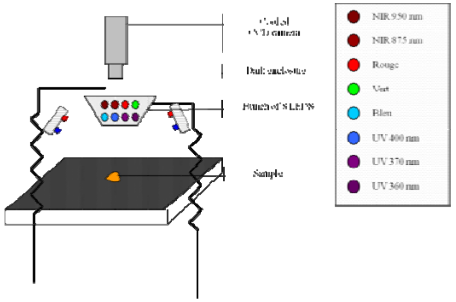
Wx: Waxy
SS: Starch Synthase
BE: Branching Enzyme
AGPase : ADP Glucose Pyrophosphorylase
α et β-amy: α et β-amylases

Multispectral imagery to predict grain amylose content

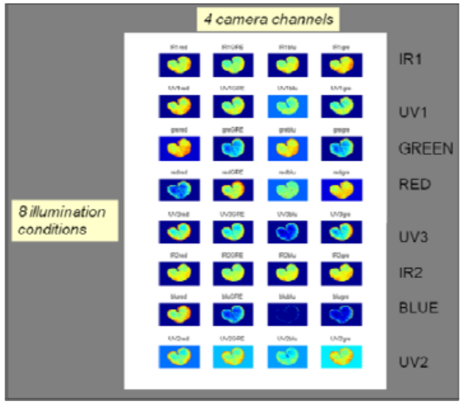
8 illumination conditions x 4 channels RGB = 32 channels



Wheat kernel cutting

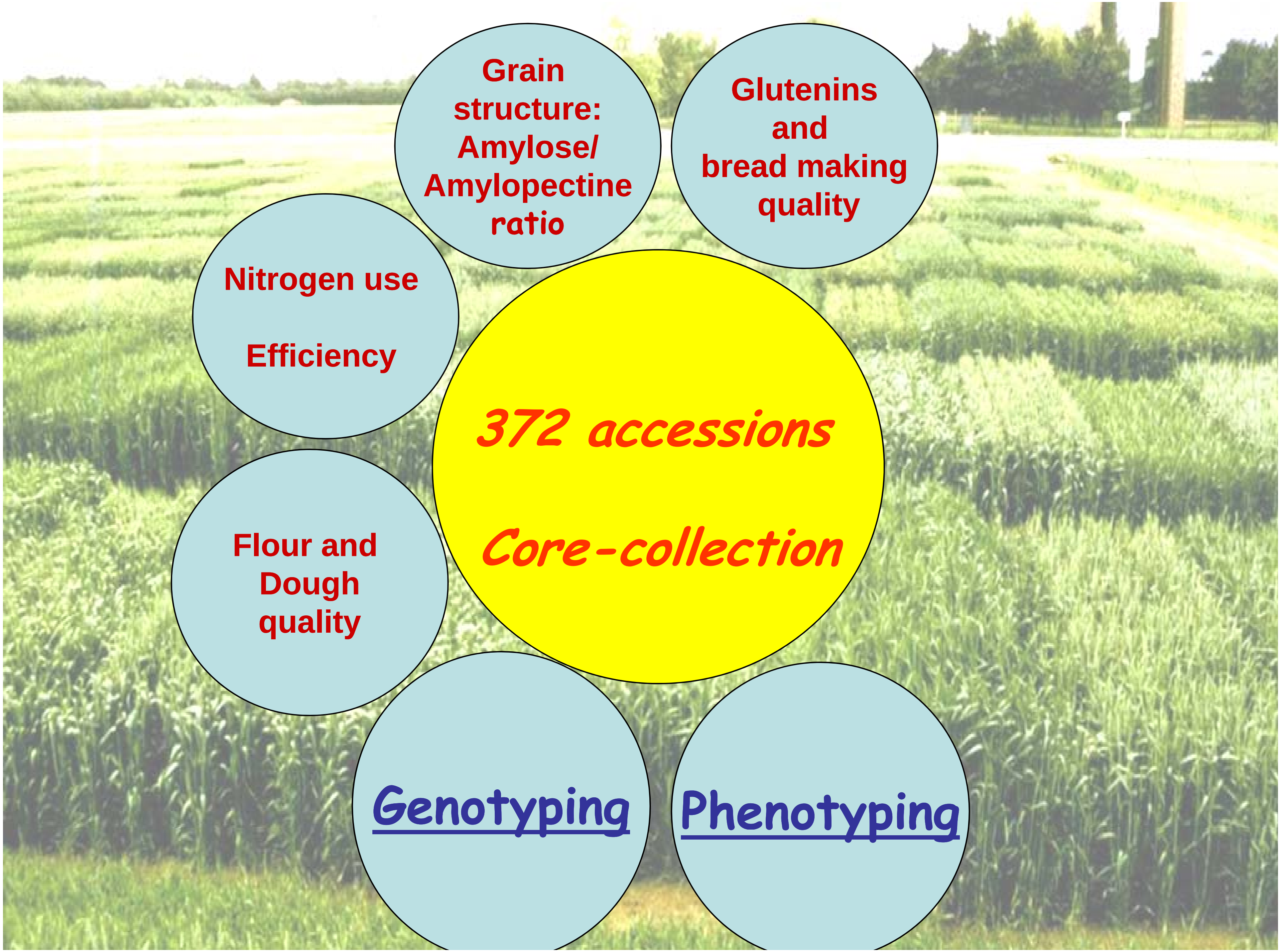


Multiway imaging



Multivariate image analysis

Outcome: new phenotyping technology – bread with low glycemic index



372 accessions

Core-collection

Grain structure: Amylose/ Amylopectine ratio

Glutenins and bread making quality

Nitrogen use Efficiency

Flour and Dough quality

Genotyping

Phenotyping

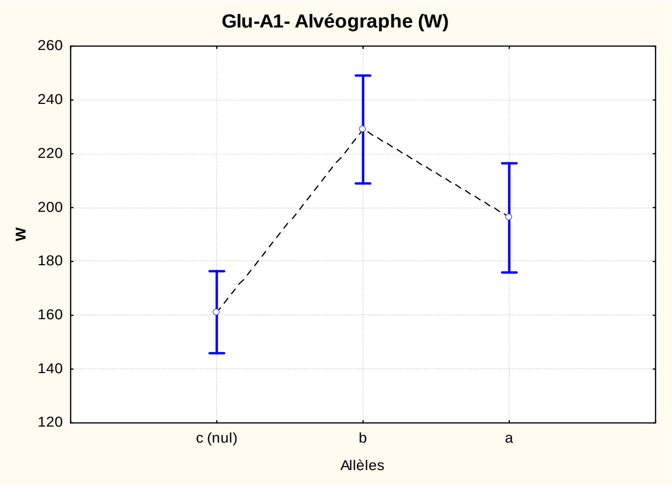
Genetic components of bread wheat quality (C Ravel, S Lafarge)

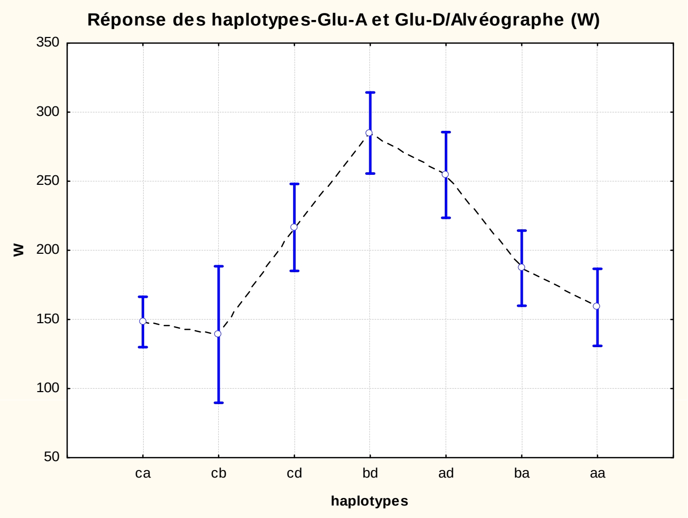
(Support: FUI QualitNblé)

372 CC description for les High molecular weight glutenins

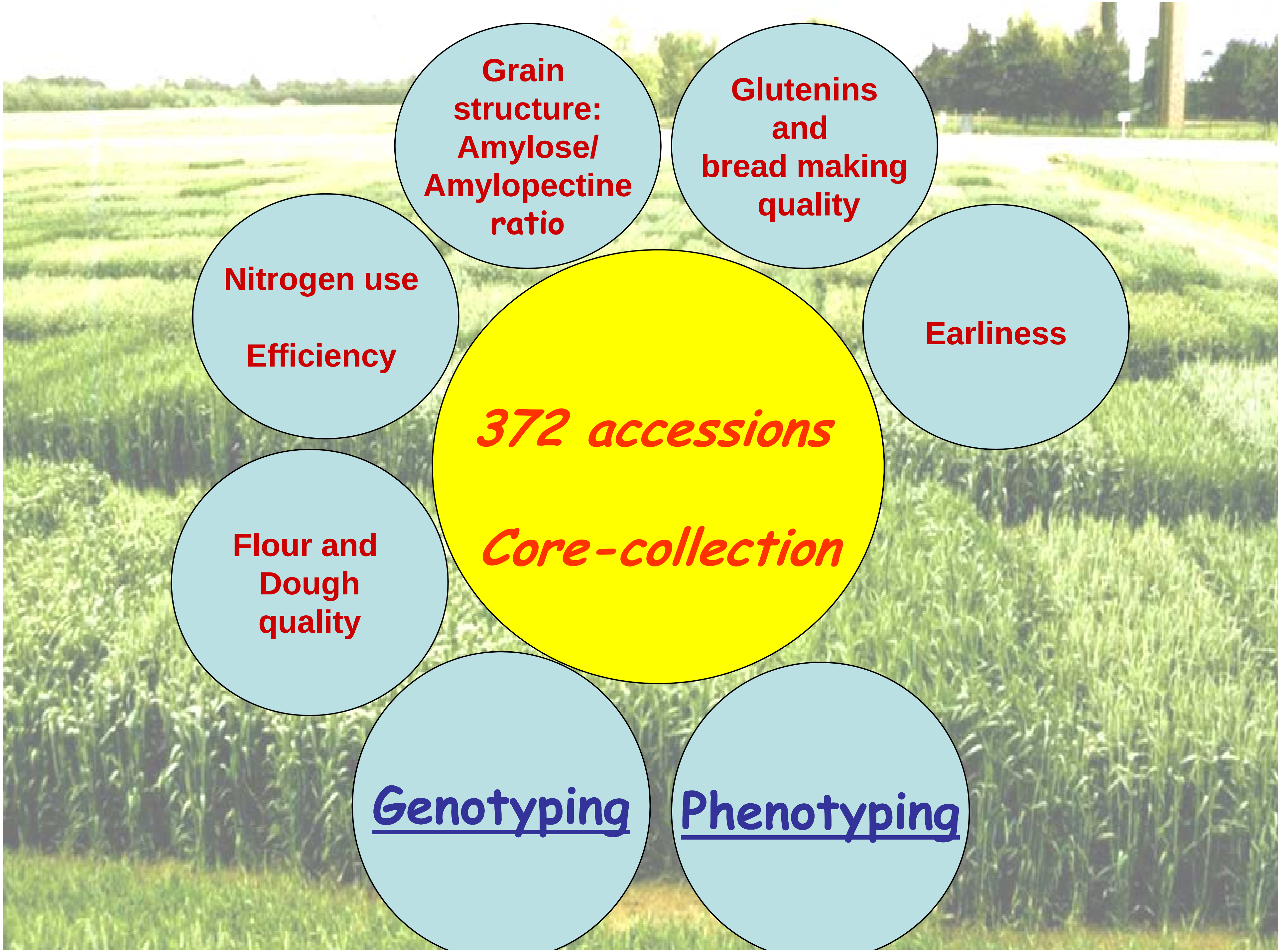
Allèles des genes des HMWG de la Core-collection

Locus Glu-A1			Locus Glu-B1			Locus Glu-D1		
Allèles	Nb	%	Allèles	Nb	%	Allèles	Nb	%
c (0)	154	46,7	*b (7+8)*	128	39,9	*a (2+12)*	179	54,7
b (2)*	89	27,0	*c (7+9)*	63	19,6	*d (5+10)*	102	31,2
a (1)	87	26,4	*d (6+8)*	42	13,1	*b (3+12)*	20	6,1
			a (7)	30	9,3	*c (4+12)*	18	5,5
			e (20)	17	5,3	*f (2.2+12)*	4	1,2
			i (17+18)	17	5,3	*x (2)*	1	0,3
			f (13+16)	11	3,4	*y (12)*	1	0,3
			h (14+15)	4	1,2	*z (12)*	1	0,3
			p (6.1-22)	4	1,2	*g (2+10)*	1	0,3
			8	1	0,3			
			18	1	0,3			
			g (13+19)	1	0,3			
			k (22)	1	0,3			
			iv (23+18)	1	0,3			





Important allelic diversity related to dough quality



372 accessions

Core-collection

Grain structure: Amylose/ Amylopectine ratio

Glutenins and bread making quality

Nitrogen use

Efficiency

Earliness

Flour and Dough quality

Genotyping

Phenotyping

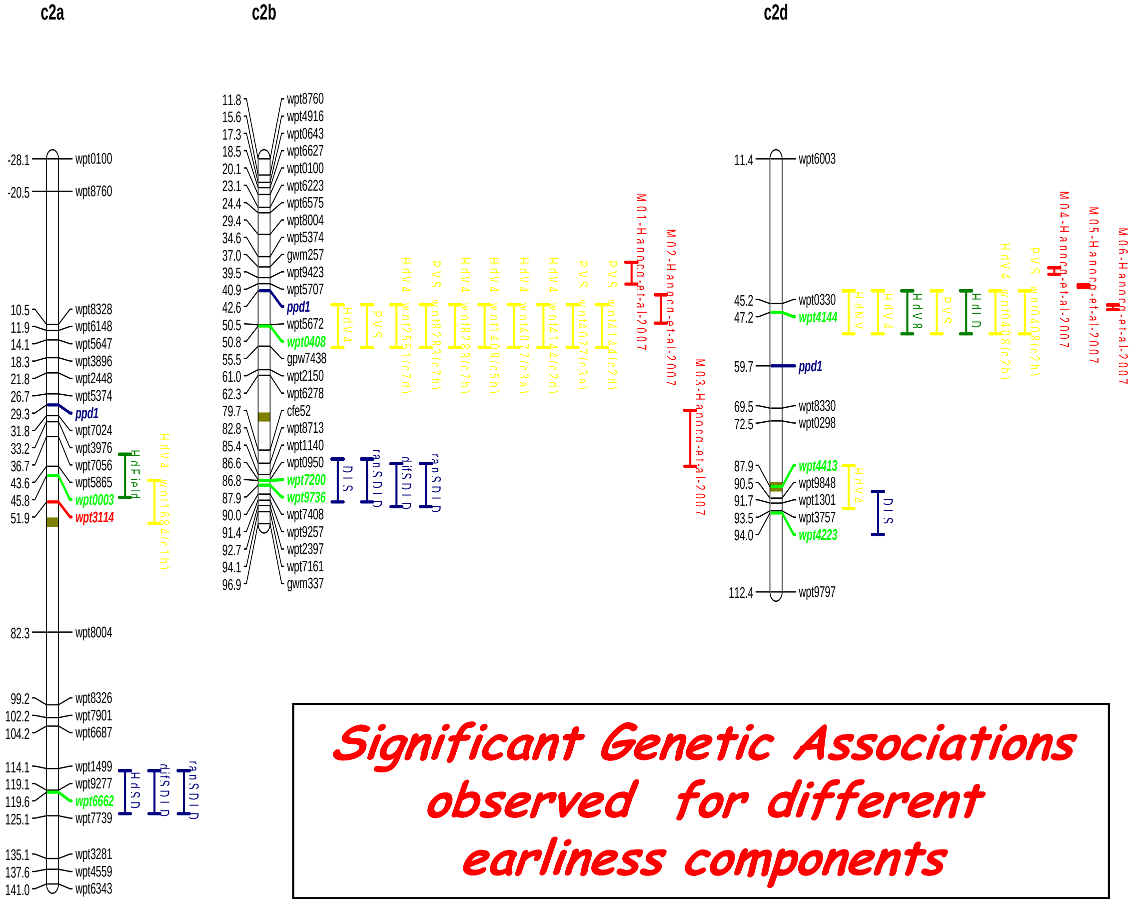
Earliness components (J Legouis, M Rousset)

A genome wide association analysis enabled to identify the main chromosomal regions determining components of earliness in wheat. **J Le Gouis, Bordes J, Ravel C, Heumez E, Faure S, Praud S, Balfourier F, Allard V, Rousset M (TAG, submitted)**

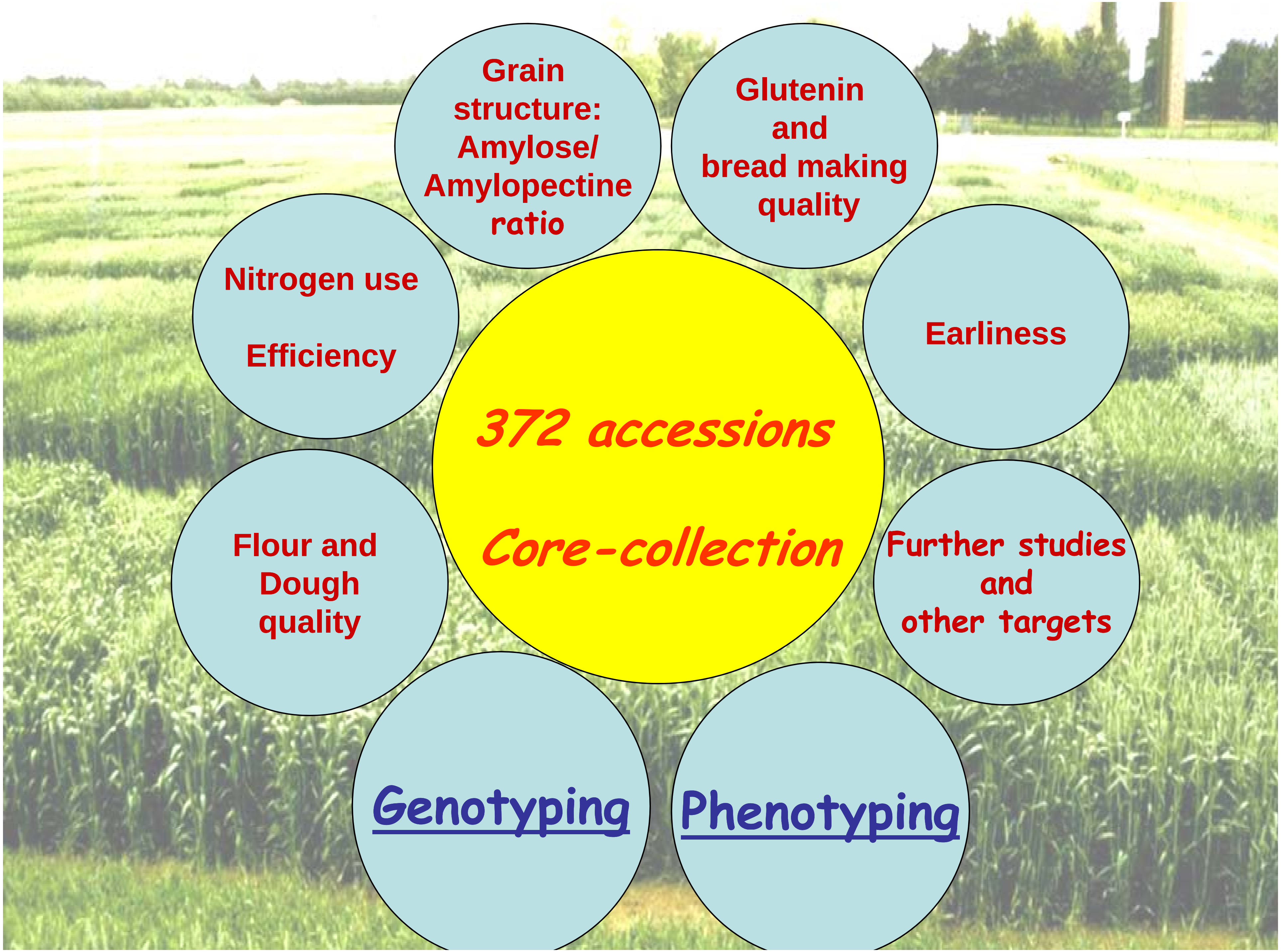
(Support: ANR Wheatperformance)

Field and glasshouse characterisation of a part of 372CC for earliness components :

- vernalisation requirement
- photoperiod sensitivity
- narrow sense earliness



Significant Genetic Associations observed for different earliness components



372 accessions

Core-collection

Grain structure: Amylose/ Amylopectine ratio

Glutenin and bread making quality

Earliness

Further studies and other targets

Phenotyping

Genotyping

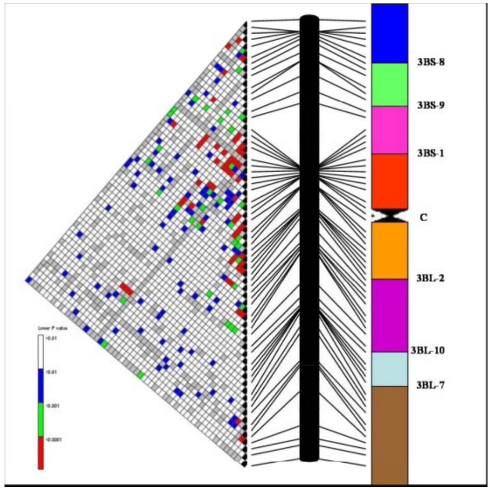
Flour and Dough quality

Nitrogen use Efficiency

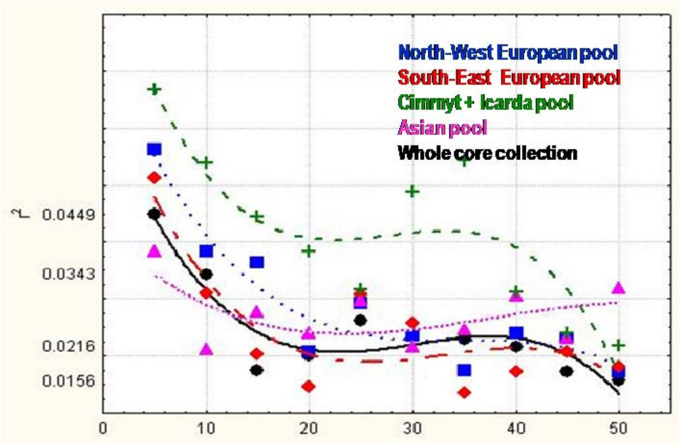
Linkage disequilibrium studies (C. Feuillet, C. Ravel)

(Supports: ANR Exegese Blé, FUI SDD, PRA)

LD at the 3B chromosome level in 372 CC



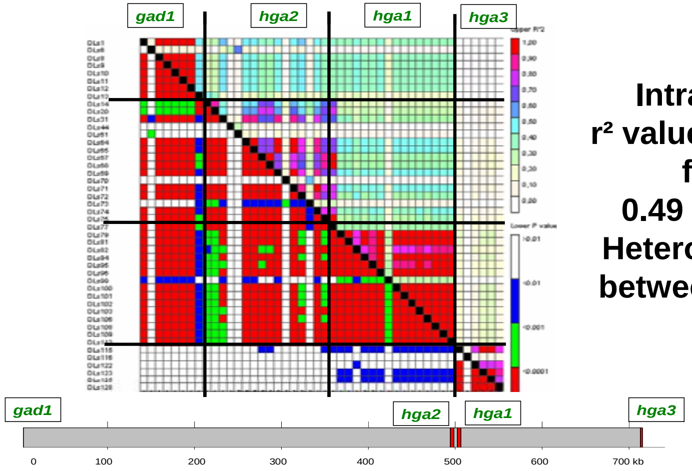
Low but significant LD in centromeric and telomeric (3BS) regions



Decrease of r² ~20cM, with differences between geographical genepools

(TAG, 2009, 119:1523-1537)

LD at the gene level along *Rph7*

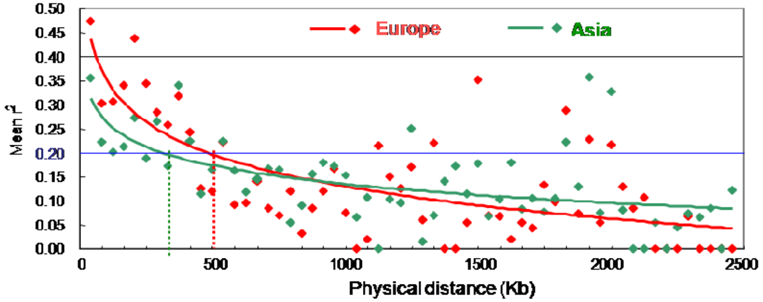


Intra-gene r² values ranges from 0.49 to 0.81; Heterogeneity between genes

(Chromosoma, 2010, in press)

LD at the R locus (*Rph7-Fhb1) level*

(3.2 Mb on 3BS8 deletion bin)



LD within 600 Kb, differences between geographic
origins: Europe (600 Kb) vs Asia (400 Kb)

(TAG, 2010, 121:1209-1225)

Further studies and targets

- **Dwarf genes** Coll INRA-JIC/NIAB (E Wilhem) *Rht genes diversity*
- **NAM B1/ GPC – Grain proteins content** Coll Uppsala University – Suède (J. Hagenblad, M. Leino, C. Ravel, J. Le gouis)
- **SKR – wheat x rye crossability** (C. Feuillet, S. Hofmann, T. Gerjets, P. Sourdille, A. Bouguennec)
- **SNPs diversity** (C Ravel, P Martre -QualitNblé)
  Influence of Transcriptional Activator *Spa* on Grain Protein Composition, dough viscoelasticity and grain hardness. **Ravel C, P Martre, I Romeuf, M Dardevet, R El-Malki1, JBordes, N Duchateau, D Brunel, F Balfourier, G Charmet (Plant Physiology 2009)**
- **Extend of LD at different genome scales** (E. Paux – 3BSeq, Digital)
- **Starch granules size** – (G. Branlard) **Analysis and identification of starch granules size related to grain composition**
- **Metabolites and nutrition value**- (G. Branlard) **Genetic and environmental factors associated to human nutrition value**

Conclusions

Core collection = Population of managable size……

1) Widely genotyped on the whole genome size
and showing a great genotypic variability

2) phenotyped for a large number of traits
and exhibiting an important phenotypic diversity for these traits

…usefull for association genetic studies…

…offering avantages compared to biparental populations

…polymorphic on a wider part of the genome

….for a larger numbre of traits

….well adapted to the study of numerous targeted traits

……and implied in diverse scientific projects

Ont participé à ce travail :

F Balfourier
J Koenig
J Bordes
A Didier
A Lapierre
F Exbrayat
L Bardy

C Ravel
A Besson (CDD)
A L Pissavy (CDD)
E Boulat (CDD)