

**40 years of research on molecular biology
on plant genome
3-6th April Saint Petersburg**

INRA-VIR Collaboration and modern state wheat and barley grain proteins investigation at INRA

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INRA

Clermont Ferrand

FRANCE

Genetic determination of protein quality in wheat grain

Genetic aspects of wheat storage proteins

Wheat storage proteins and quality

Quantitative variations of wheat storage proteins

Proteomics of wheat kernel

Proteomics on developmental kernel

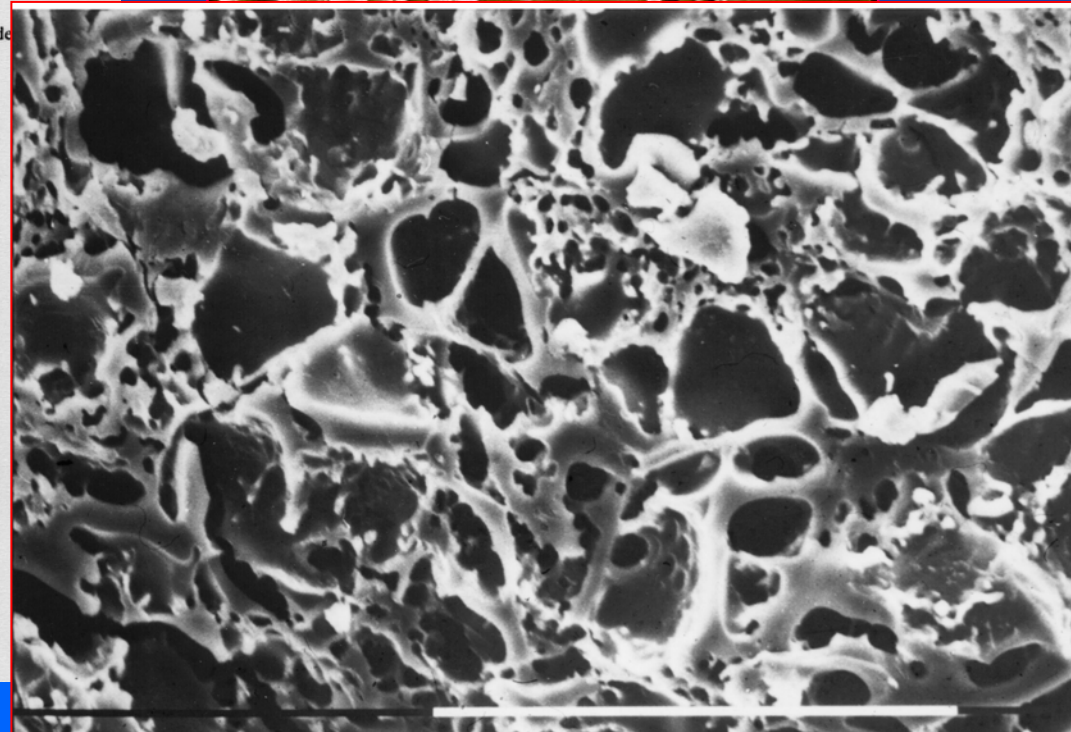
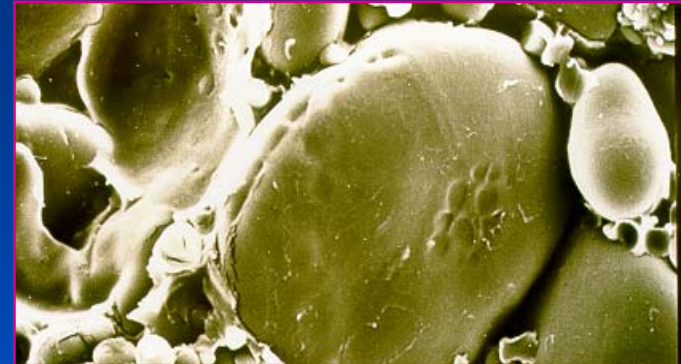
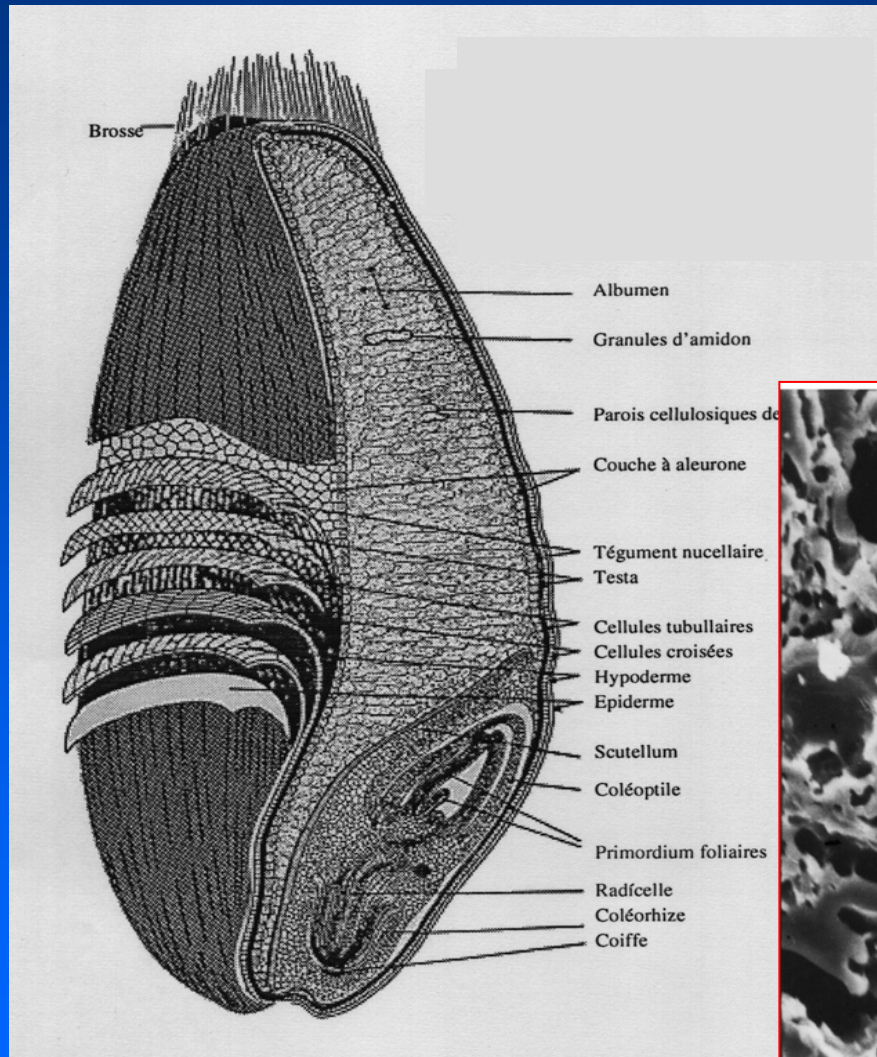
Endosperm responses to Heat stress

Some other proteins involved in quality

The Plate-forme for genotyping
at INRA Clermont Ferrand



Wheat endosperm and Protein matrix



Wheat Endosperm Proteins

Protein type	Solubility	% flour protein	Characteristics
Albumins	Water	10	Enzymes and cell structure
Globulins	NaCl 0.5M	10	MWs 5 – 100 kDa
Gliadins	Alcohol	35-45	Monomeric MWs 30 – 80 kDa
Glutenins	SDS		Polymeric
HMW-GS	+ R. A.	10-15	MWs 75 -120 kDa
LMW-GS		20-30	MWs 25 - 45 kDa

Soluble proteins

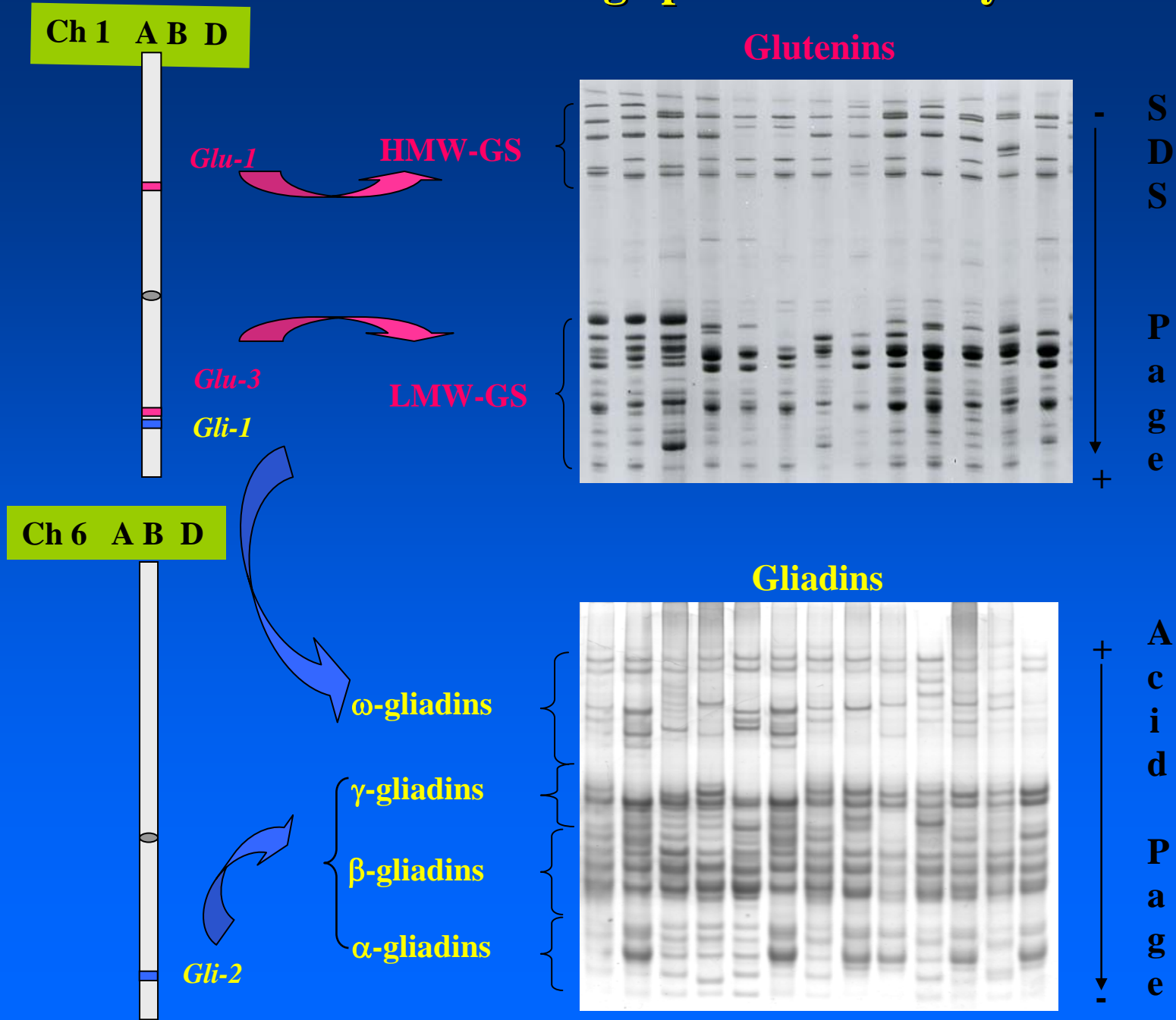
Storage proteins

Genetic determination of protein quality in wheat grain

Genetic aspects of wheat storage proteins



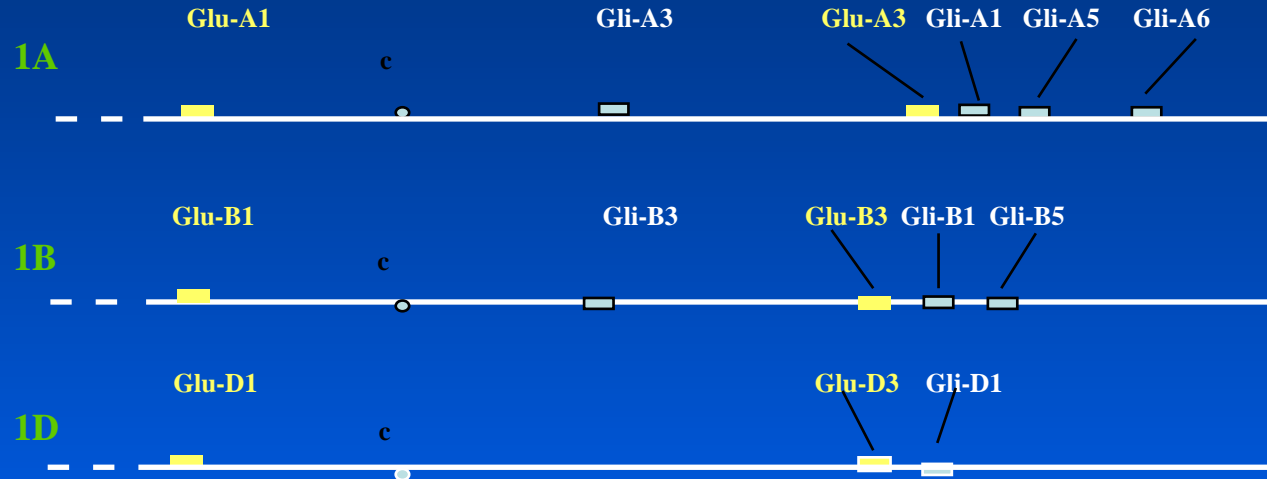
Wheat storage protein diversity



Main locus involved in synthesis of wheat endosperm storage proteins

Long arm

Short arm



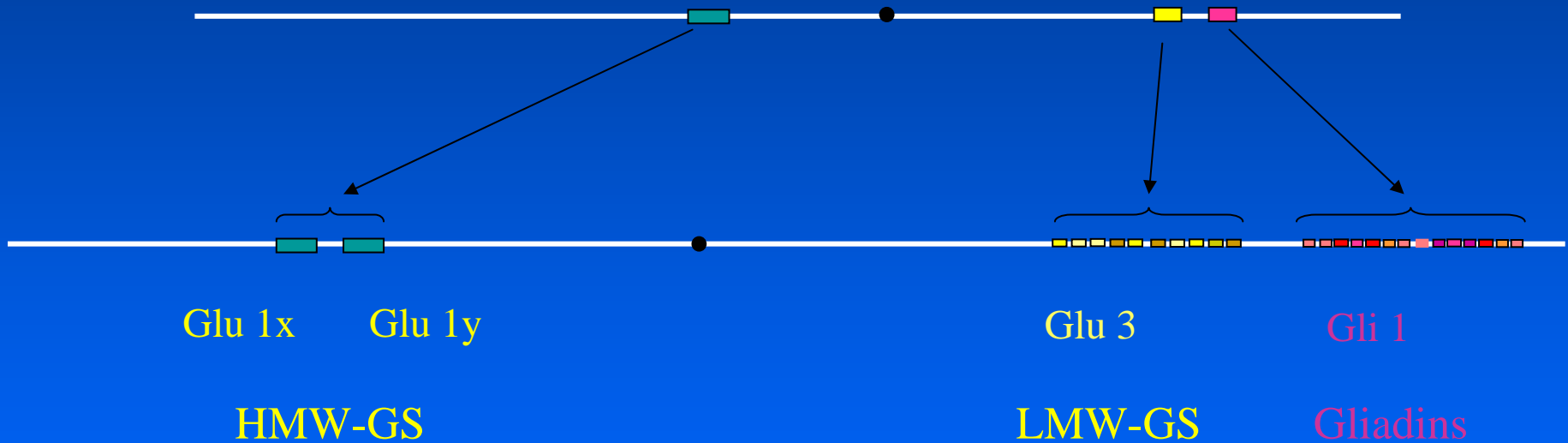
HMW GS

LMW GS ω -gliadins

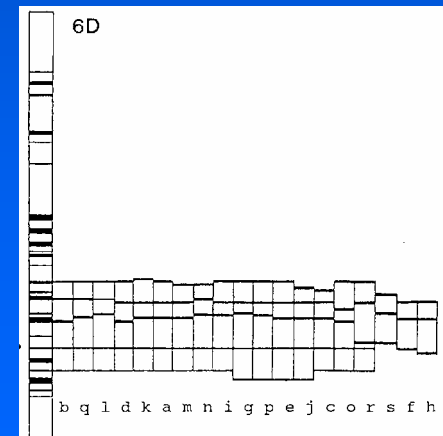
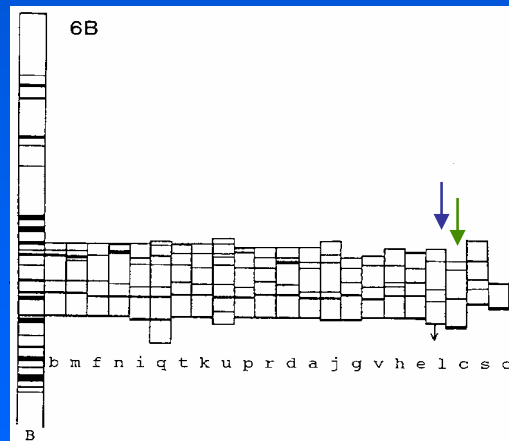
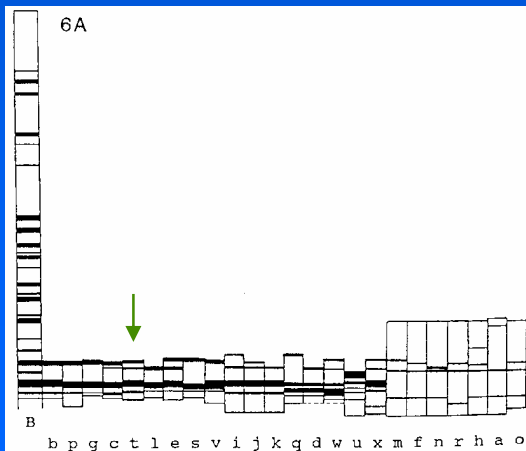
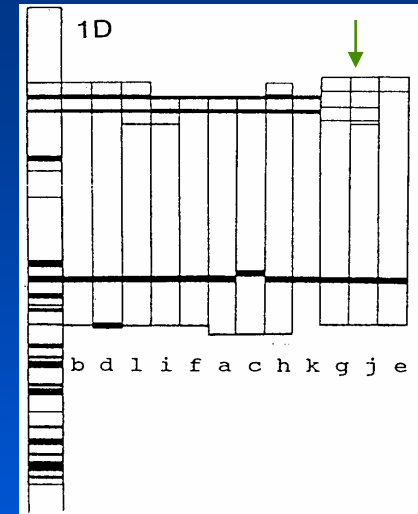
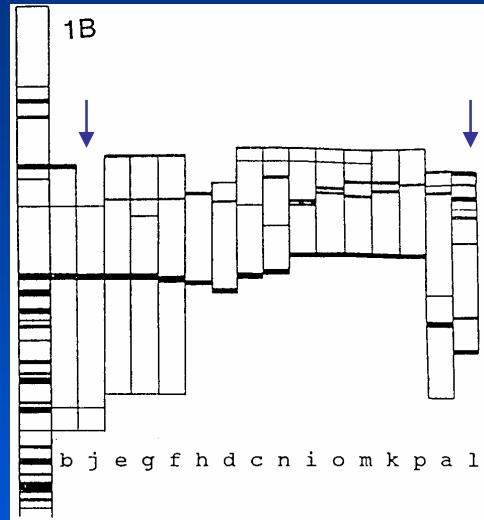
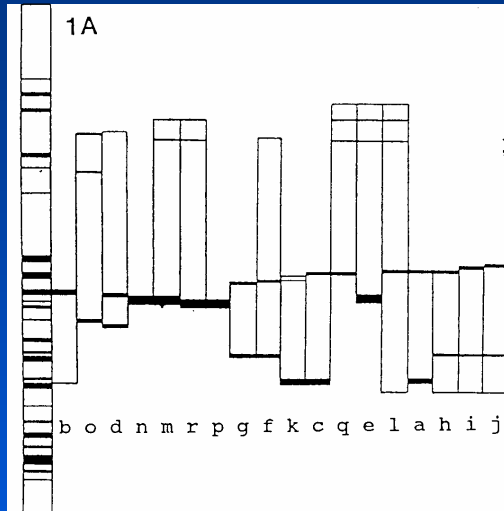


α , β , γ Gliadins

WSPs are encoded by clusters of genes

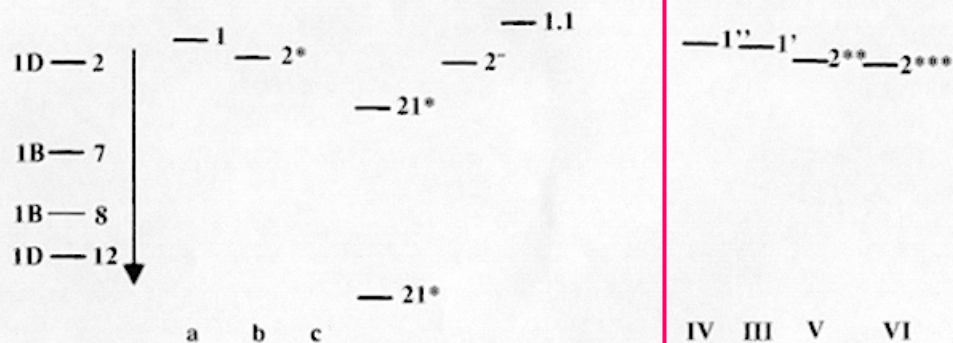


Allelic Diversity of Gliadins

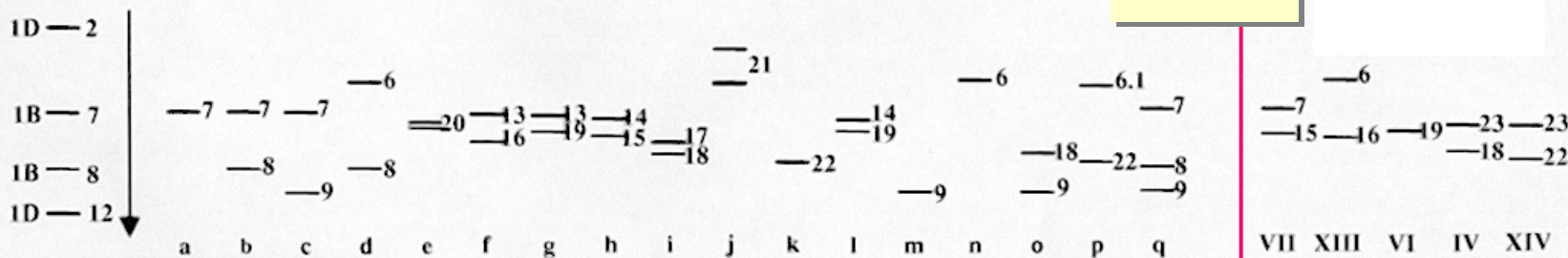


From Metakovsky 1994, J Genet.& Breeding

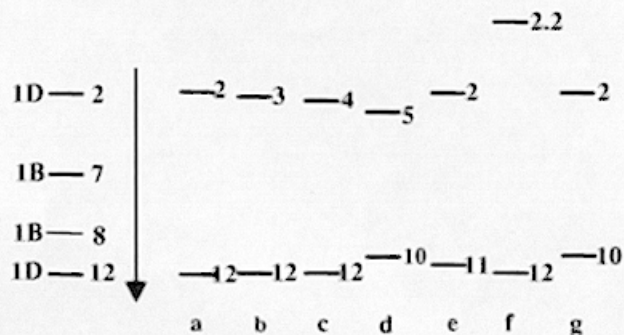
Main alleles encoding HMW-GS



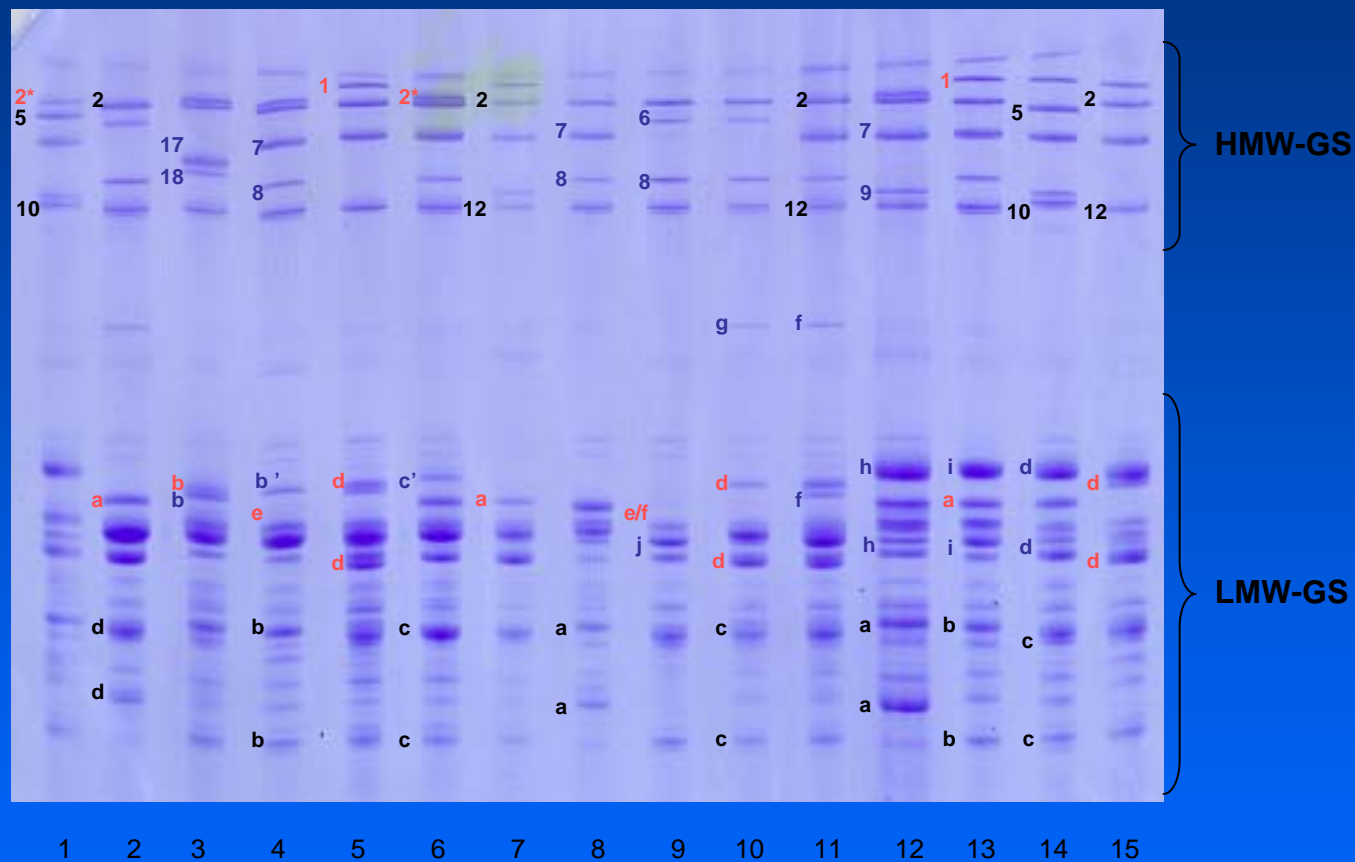
Glu-A1



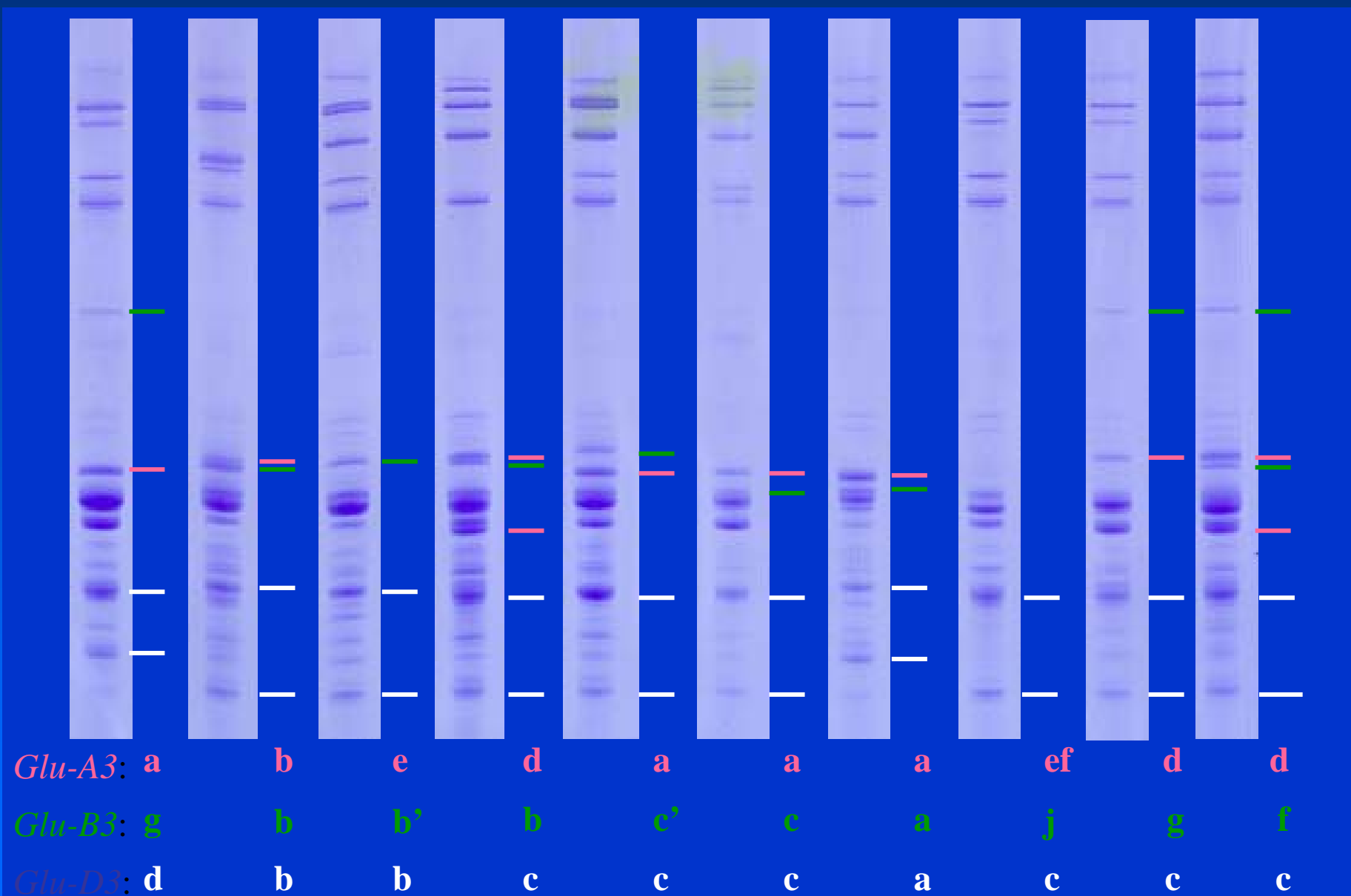
Glu-B1



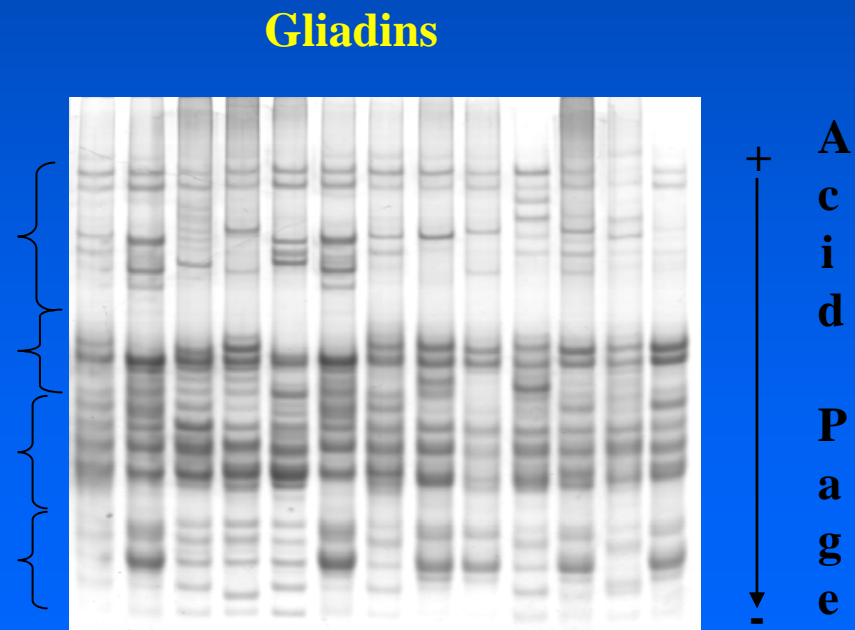
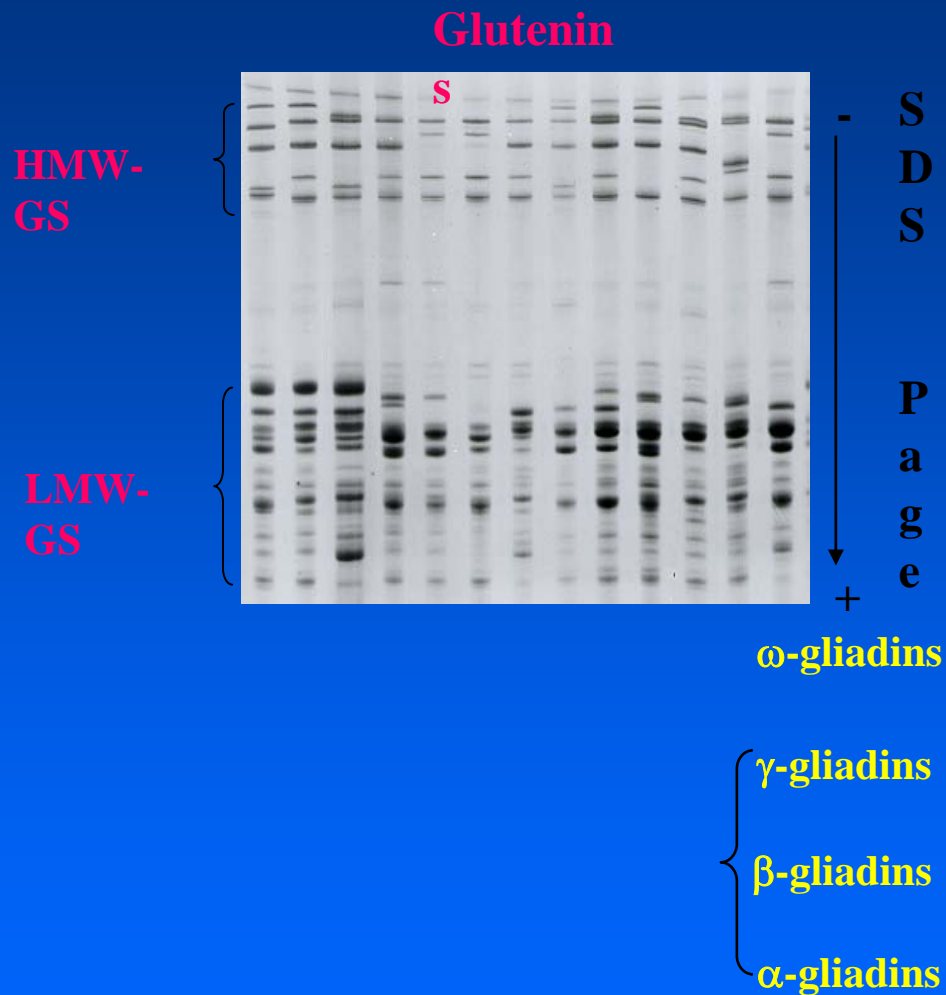
Some alleles of HMW-GS and LMW-GS



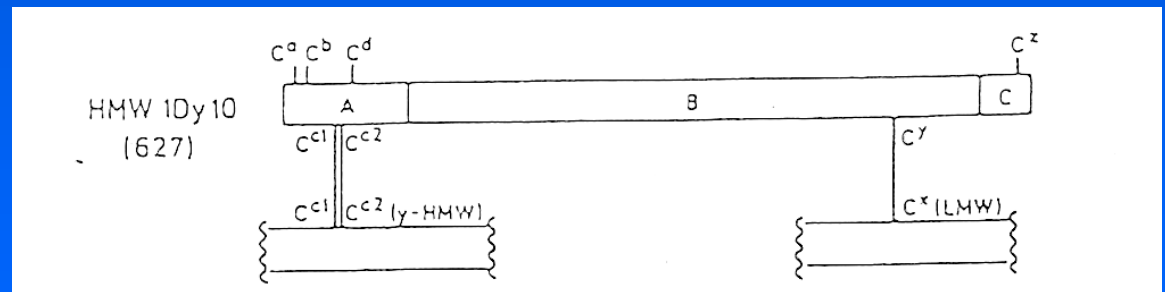
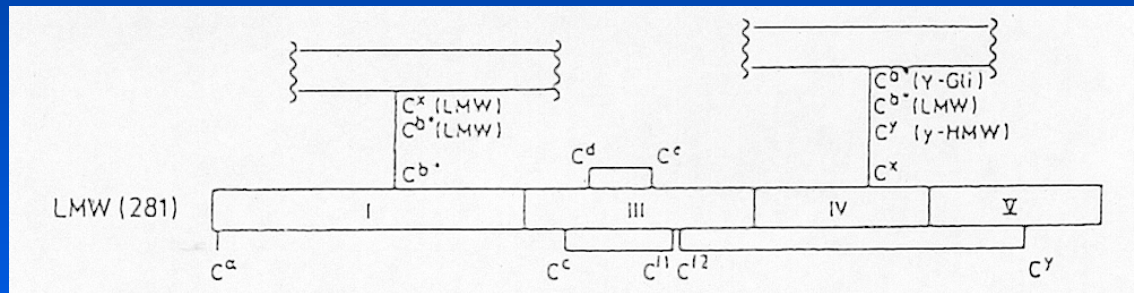
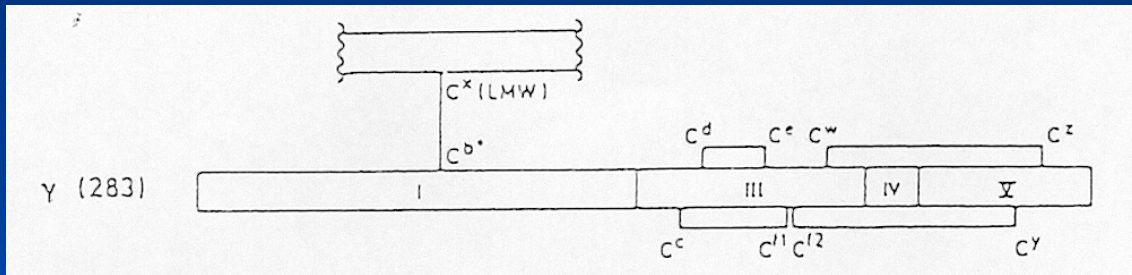
Identification of *Glu-A3*, *Glu-B3* and *Glu-D3* alleles



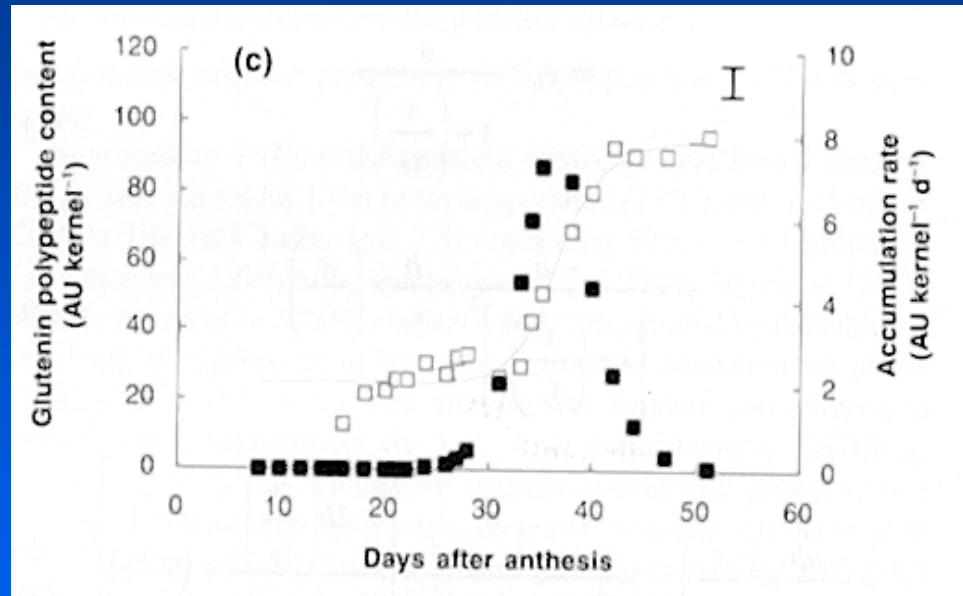
How these Wheat Storage Proteins are assembled ?



Covalent SS links between wheat storage proteins



SDS insoluble glutenin polymer formation in developing grains of wheat, (cv: Soissons)



From Carceller JL, Aussenac T., Aust. J. Plant Physiol 2001, 28; 193-201
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Wheat storage proteins and quality

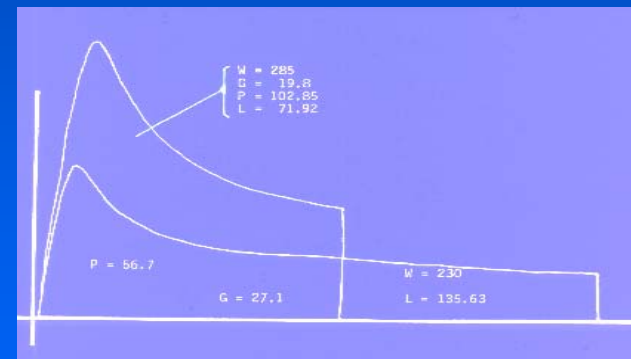


Wheat gluten proteins as part of the bread making quality



Comparison of alleles effects for phenotypic values of dough strength

Locus	Strength
<i>GluA1</i>	$2^* = 1 > \text{null}$
<i>GluB1</i>	$17-18 \geq 13-16 \geq 7-9 = 7-8 \geq 7 = 6-8$
<i>GluD1</i>	$5-10 \geq 3-12 = 2-12 \geq 4-12$
<i>GluA3</i>	$a = d = f \geq e$
<i>GluB3</i>	$b' \geq d = c = c' = b = g > i > f \geq j$
<i>GluD3</i>	$a \geq b = d = c$
<i>GliA2</i>	$t \geq k = r = f = g = j \geq l = b = p$
<i>GliB2</i>	$m > b \geq r \geq h = o = g \geq ae = l = ac$
<i>GliD2</i>	$m = e \geq a = h = v = g = n$



From: Branlard G., Dardevet M., Saccomano R., Lagoutte F., Gourdon J.
Euphytica, 2001, 119, 59-67

Comparison of alleles effects for phenotypic values of dough extensibility

Locus	Extensibility
<i>GluA1</i>	nsd
<i>GluB1</i>	$13-16 \geq 7-8 = 7-9 = 17-18 \geq 7 \geq 6-8$
<i>GluD1</i>	nsd
<i>GluA3</i>	$d = a = f \geq e$
<i>GluB3</i>	$i \geq b' \geq c = c' = g > b = f = d > j$
<i>GluD3</i>	nsd
<i>GliA2</i>	$b = t \geq k = g = l \geq p = r = f = j$
<i>GliB2</i>	$ae \geq m \geq g = o = h = ac \geq b = r = l$
<i>GliD2</i>	nsd

(nsd: not significantly different)

From: Branlard G., Dardevet M., Saccomano R., Lagoutte F., Gourdon J.
Euphytica, 2001, 119, 59-67

Comparison of loci effects on quality parameters

HMW Glutenins

GluB1 \geq GluD1 > GluA1

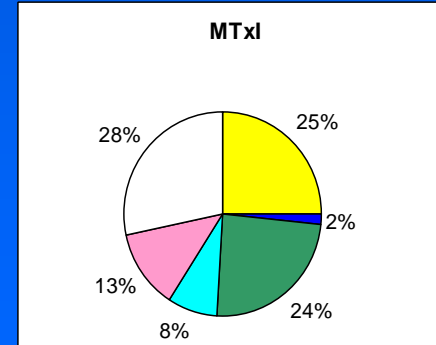
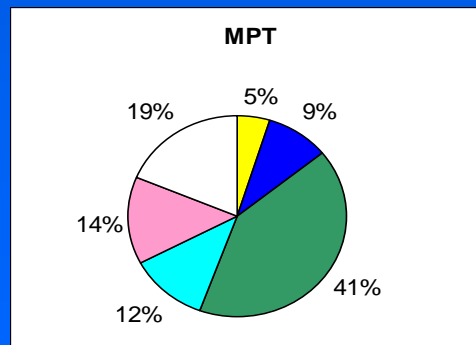
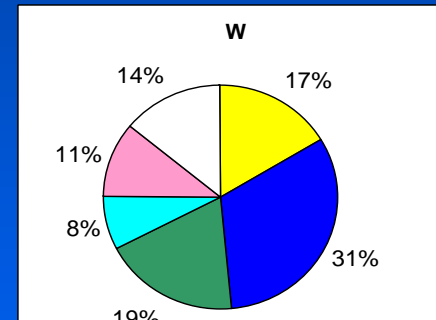
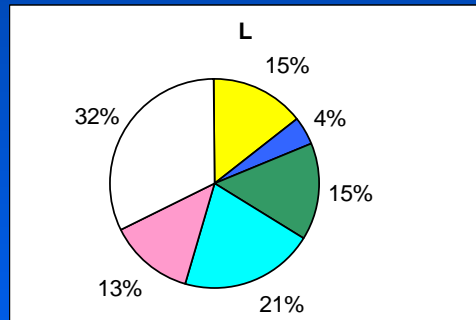
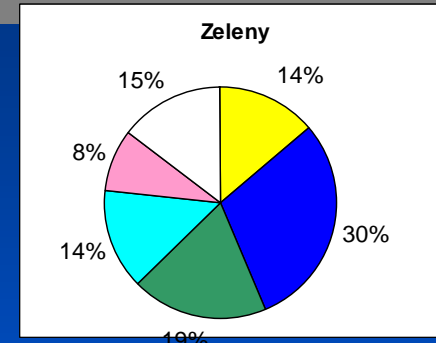
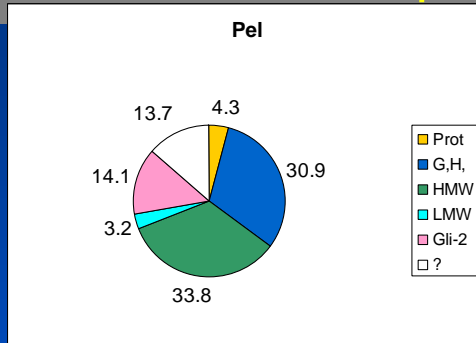
LMW Glutenins

GluB3 > GluA3 > GluD3

α , β , γ -gliadins

GliA2 > GliB2 > GliD2

Part (R^2) of Protein content, G. Hardness, HMW, LMW GS and α , β , γ -gliadins in the genotypic variations of six bread wheat quality parameters



From: Branlard G., Dardevet M., Saccomano R., Lagoutte F., Gourdon J.

Euphytica, 2001, 119, 59-67

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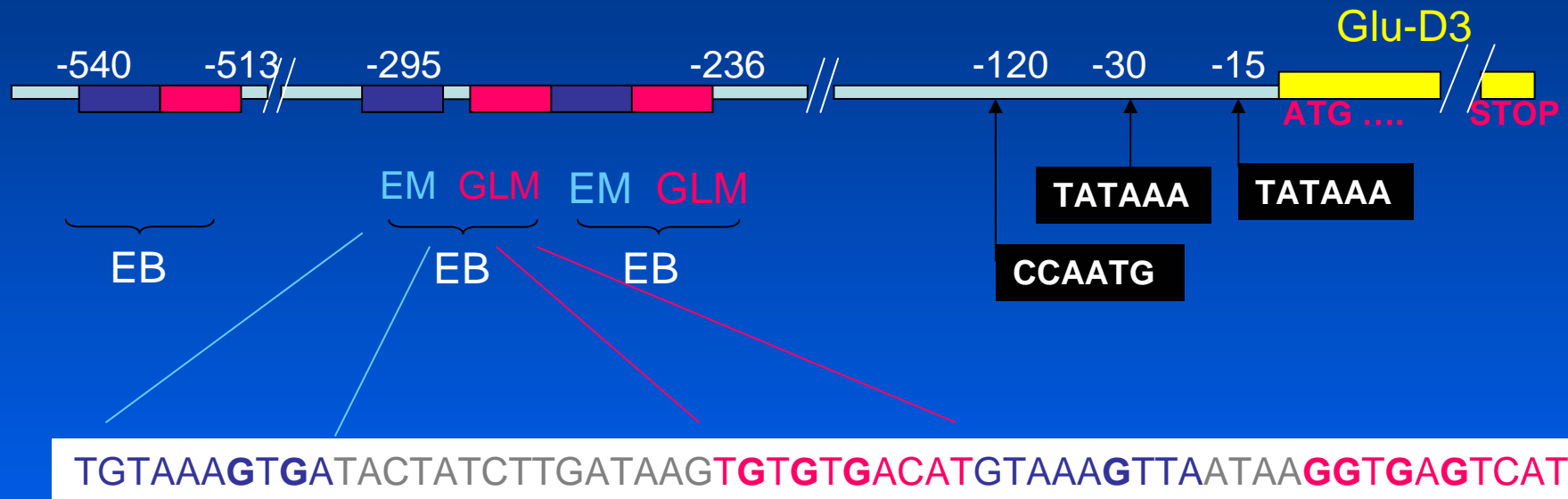
Wheat storage proteins and quality

Quantitative variations of wheat storage proteins



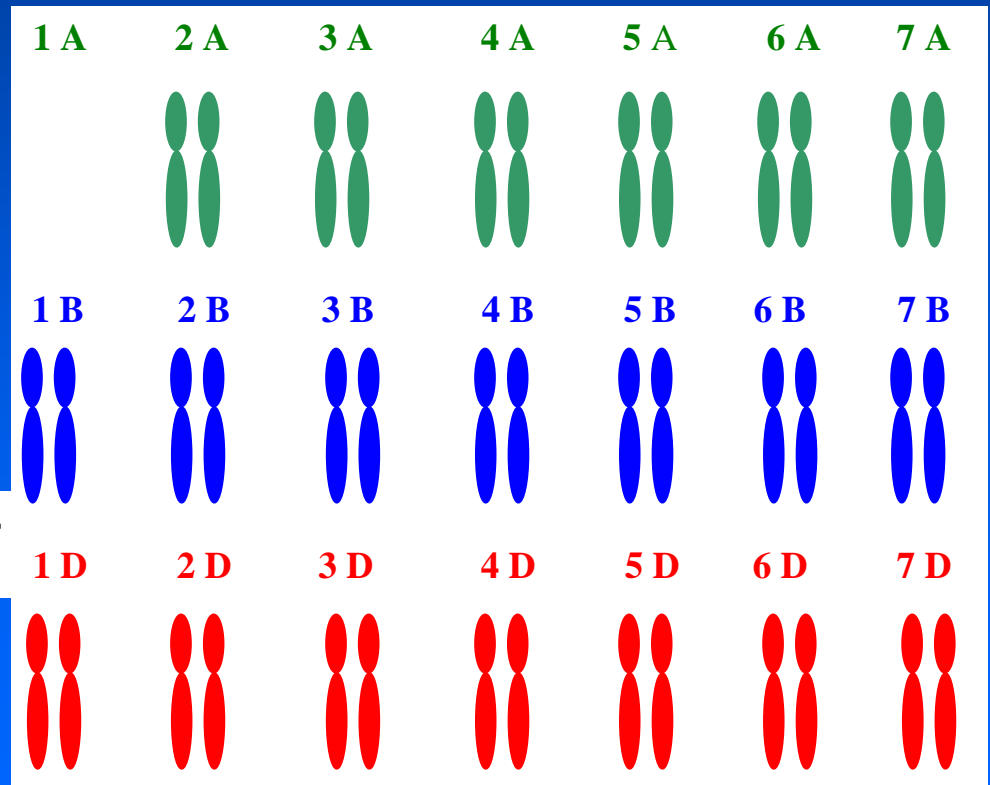
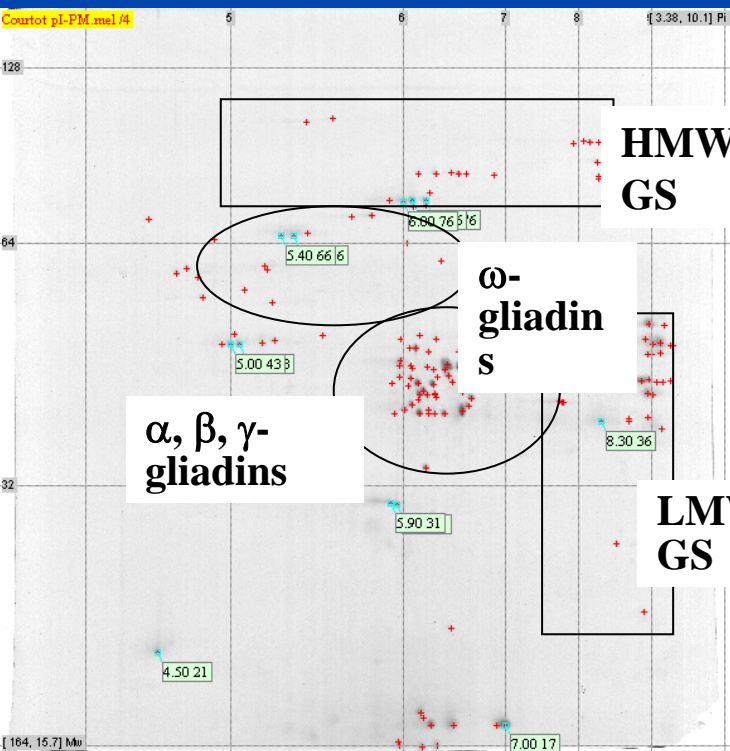
Regulation of the expression

Promoter region of the LMW-GS Glu-3D

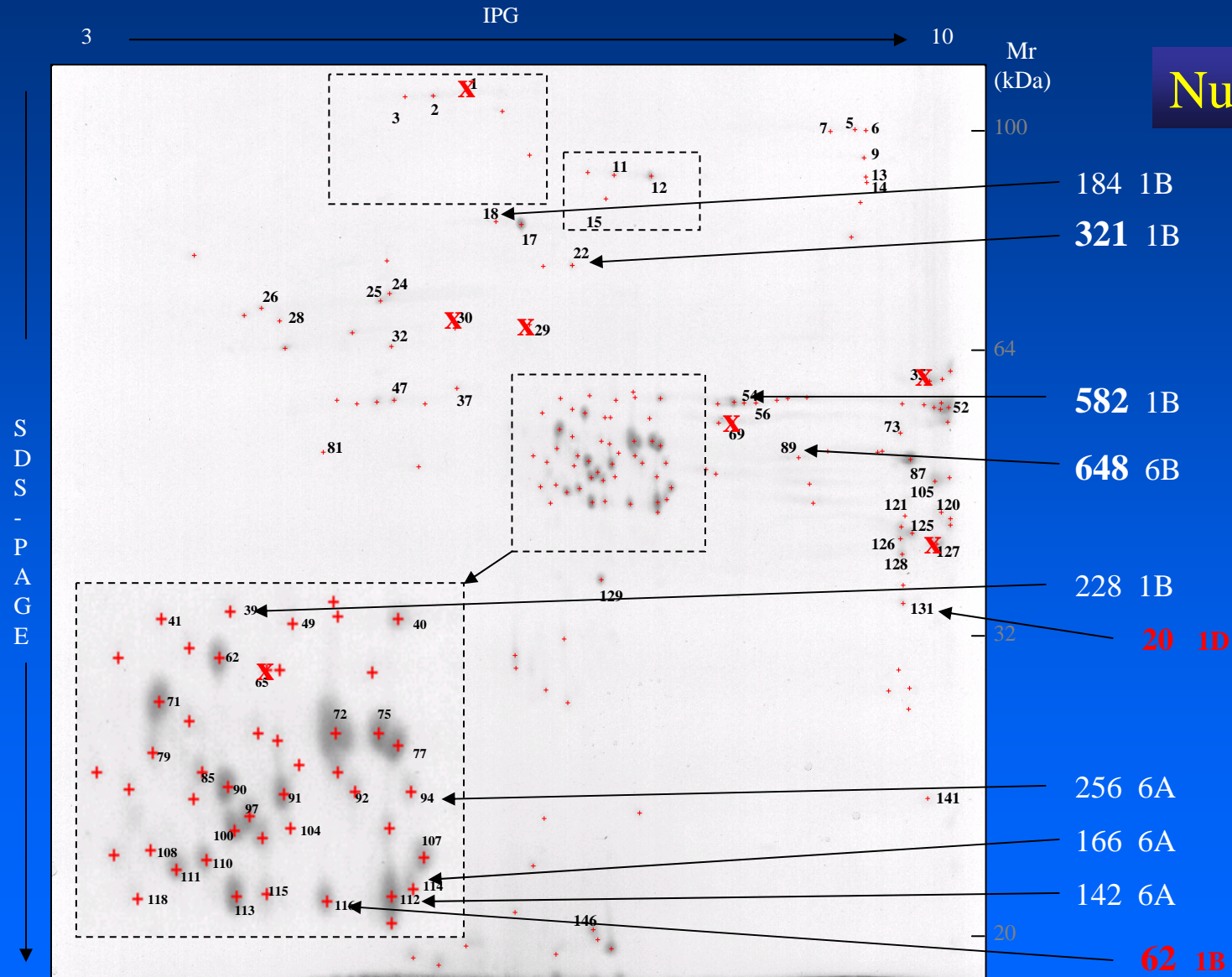


Regulation of the quantitative expression of the different loci

interactions between chromosomes (homologous and homeologous)



Regulation of the quantitative expression of the different loci interactions between homeologous chromosomes. cv Courtot



Regulation of the quantitative expression of the different loci interactions between homologous chr and homeologous chr.

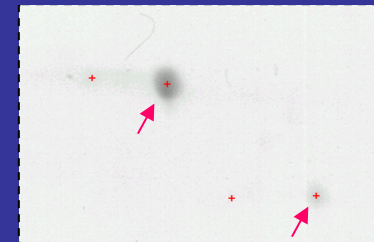
IPG

(a)

Quantitative differences



Courtot Null1D

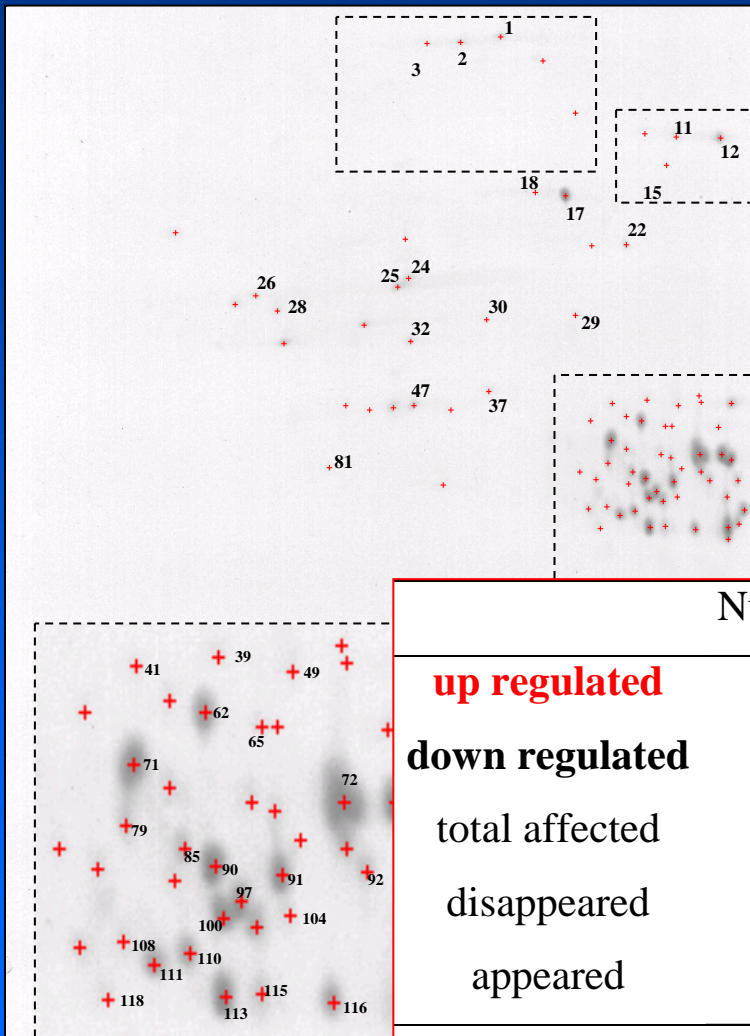


Courtot Normal

Qualitative differences



S
D
S
-
P
A
G
E



	Null-1A	Null-1B	Null-1D	M-1A	M-1B	M-1D
up regulated	8	15	14	17	16	26
down regulated	2	10	5	17	12	19
total affected	10	25	19	34	28	45
disappeared	13	32	24	0	0	0
appeared	0	0	13	0	0	0

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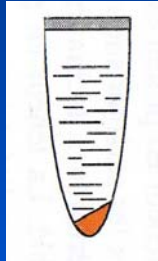
Quantitative variations of wheat storage proteins

Proteomics of wheat kernel

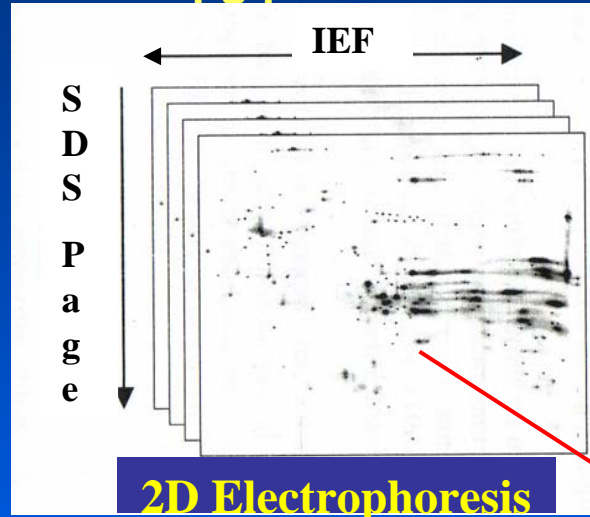


Methods: The main steps of proteomic

100-300 μ g proteins loaded



Protein extraction



2D Electrophoresis

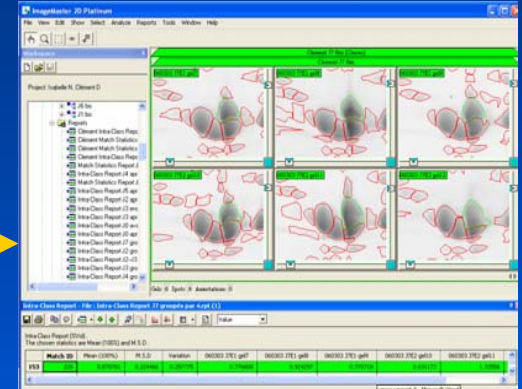
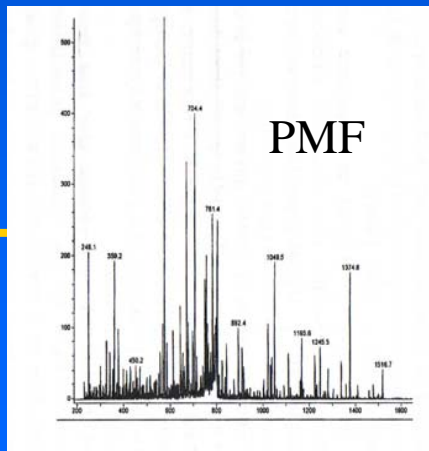


Image Analysis
Melanie 3/4
2D Platinum v 6.0

Swiss Prot
NCBI

Data Base
Interrogation



MALDI-TOF
ESI MS/MS

Mass Spectrometry



Trypsin Dig.

Data Base interrogations

Main softwares used

Profound

Mascot

Msfit

Main Data bases used

SWISSPROT

NCBI

TrEMBL

ProFound - Peptide Mapping [Short Form] Version 4.10.5 The Rockefeller University Edition

General

Sample ID:

Database: SWISS-PROT in nr

Taxonomic Category: All taxa

Search for: single protein only

Protein Mass: 0 - 3000 kDa

Protein pI: 0 - 14

Report Top: 10 Candidates

Questions? Please write to [ProFound](#)

What's new [about ProFound?](#)

Digestion

Allow maximum: 1 missed cleavages

Enzyme: Trypsin

For user-defined cleavage, please click [here](#).

Modifications

Complete Modification(s): Unmodified, 4-vinyl-pyridine (Cys), Acrylamide (Cys), Iodoacetamide (Cys), Iodoacetic acid (Cys)

Partial Modification: ☐ Methionine oxidation

For more partial modifications, please click [here](#).

Masses

Average Masses:

Mass tolerance for average data: +/- 1

Tolerance unit: ☐ Da ☐ % ☐ ppm

Monoisotopic Masses:

Mass tolerance for monoisotopic data: +/- 0.1

Charge state: ☐ M ☐ MH+

Identify Protein Extra Settings Example Reset Form

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Wheat kernel sampling and 2DE

Bread wheat cultivar : Récital

Day / night temperature 18°C

Accurate notation of anthesis for each ears

0	1	3	6	9	12	15	18	← Day after Anthesis
J0	J1	J2	J3	J4	J5	J6	J7	← named stage

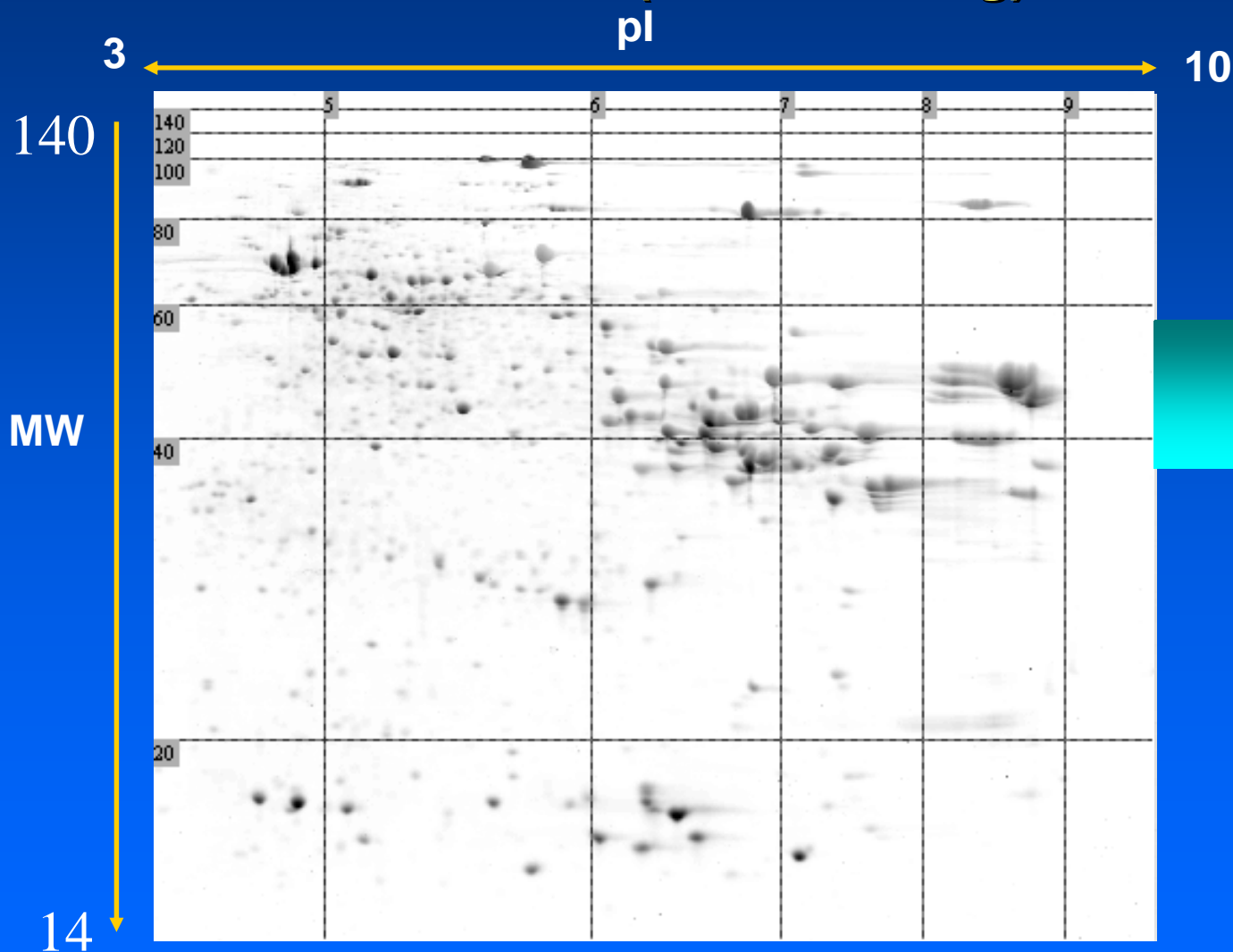


0	20	50	100	150	200	250	300	°C Day (Cumulative Day temperature.)
---	----	----	-----	-----	-----	-----	-----	--------------------------------------

Total protein extraction from whole developing seed

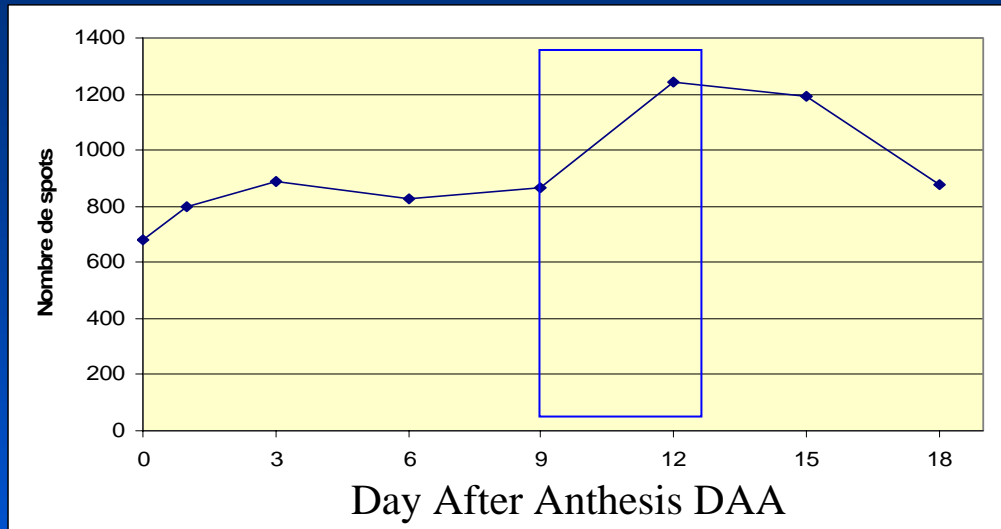
6 2DE (IPG pH 3-10 x SDS PAGE) for each stage

Typical 2DE IPG x SDS PAGE of the Albumins-Globulins of developing wheat kernel (CBB staining)

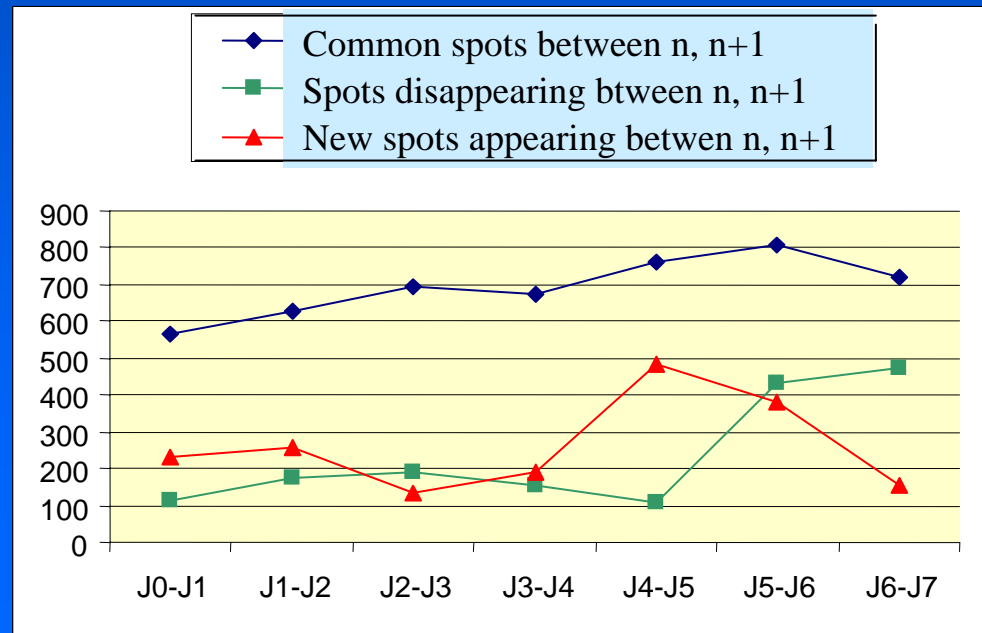


875 spots
DAA 18

Evolution of spots number in cours of time



The number of spots increased of 43% between 9 and 12 DAA

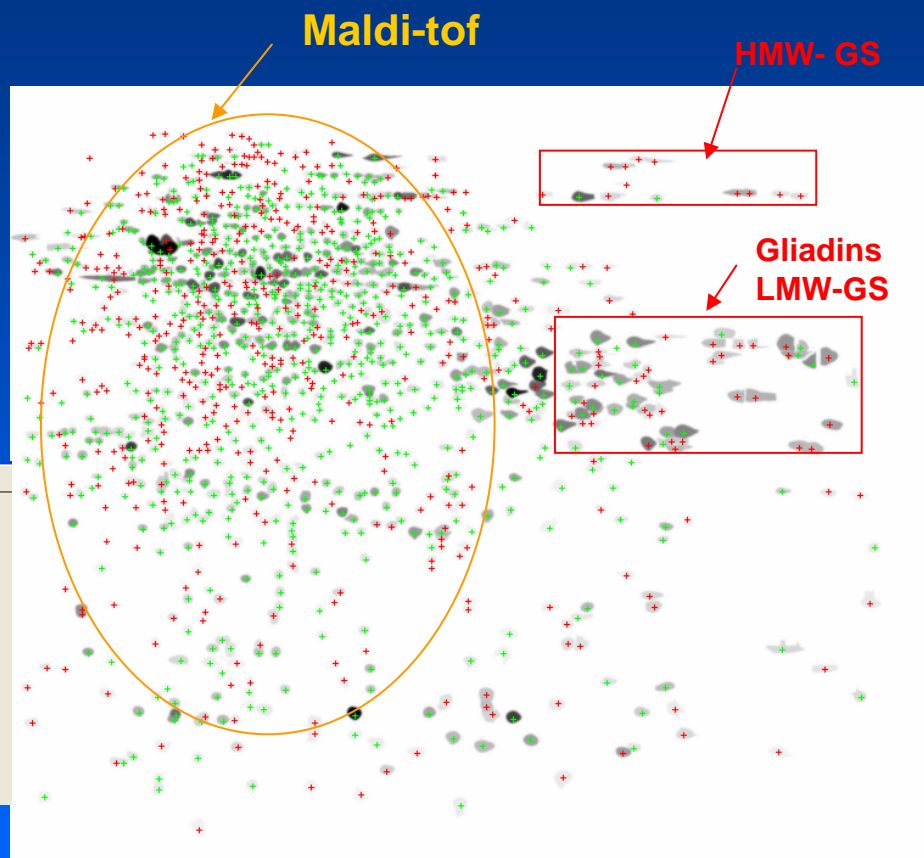
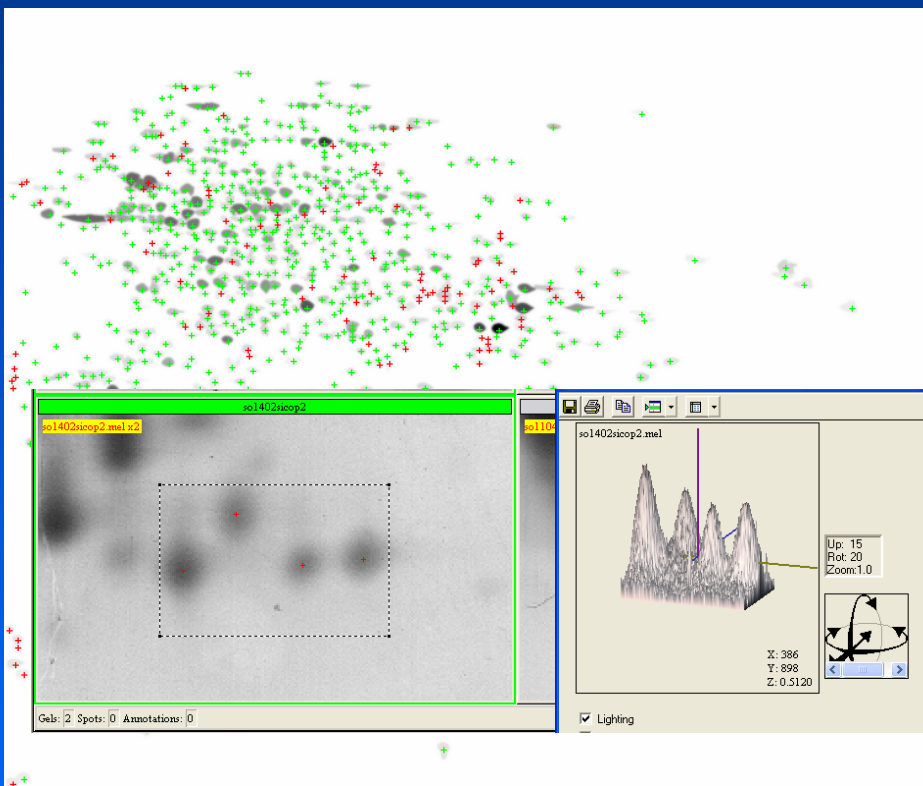


Parallele evolution of the number of new spots and spots disappearing

Proteomic differences between two consecutive stages

For example

DAA 9 - DAA 12



DAA 9 : 865 Proteins

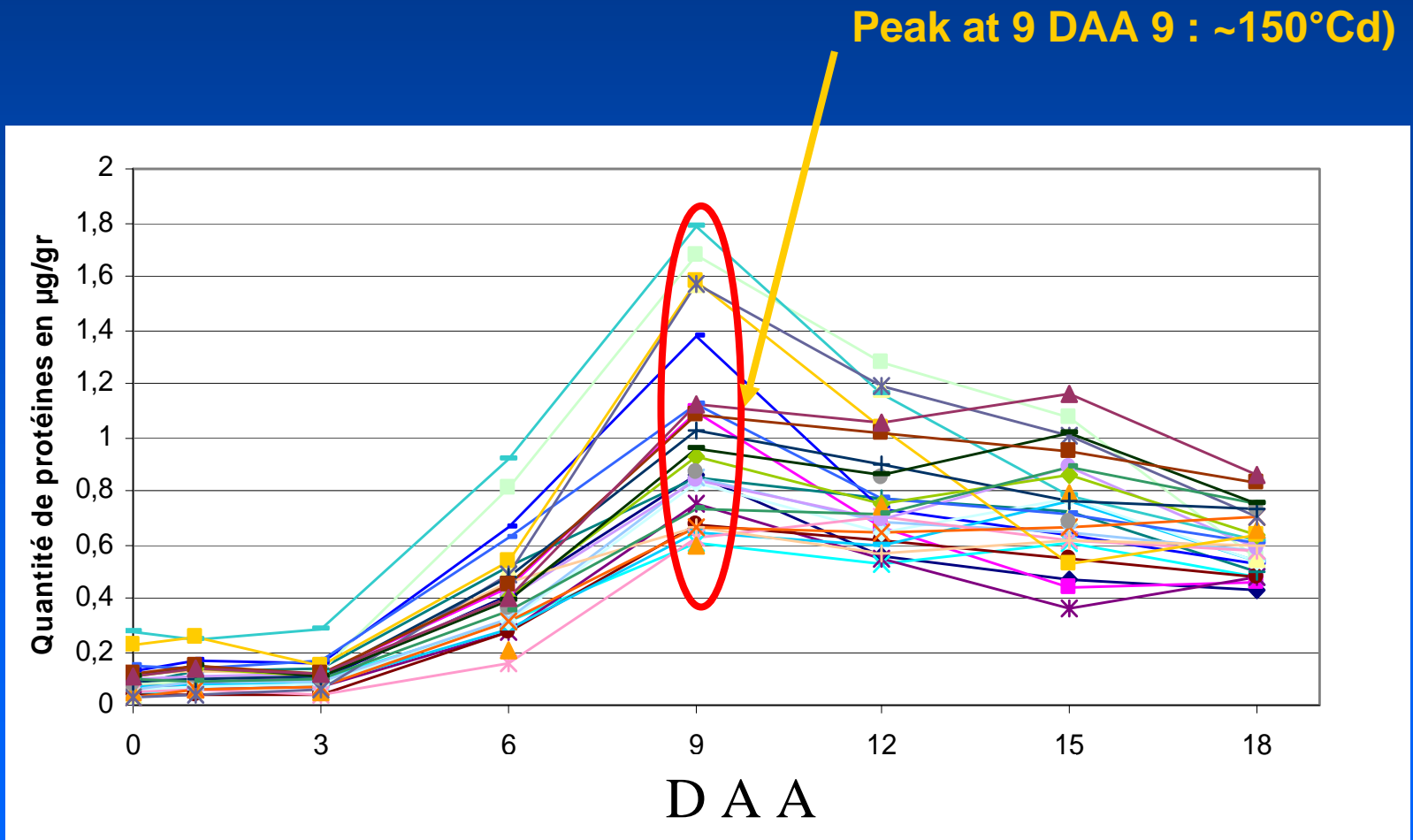
106 Disappearing proteins

DAA 12 : 1242 proteins

483 New proteins

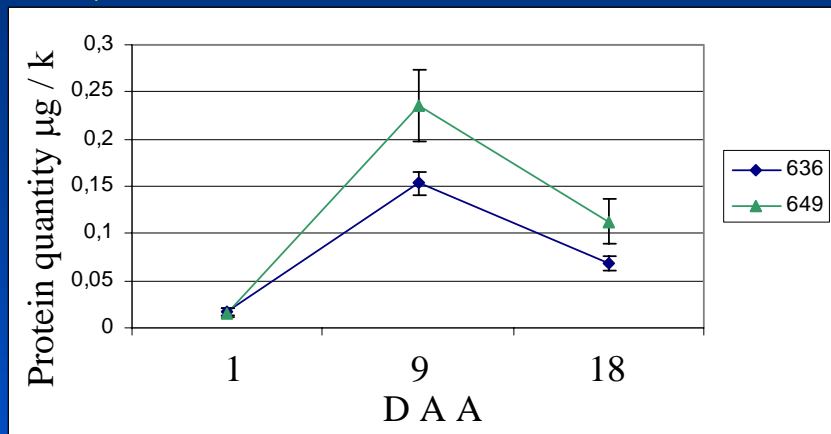
759 commun proteins

Evolution of the amount of protein per kernel ($\mu\text{g}/\text{kernel}$) for 285 spots commun to all stages (0 to 18 DAA)



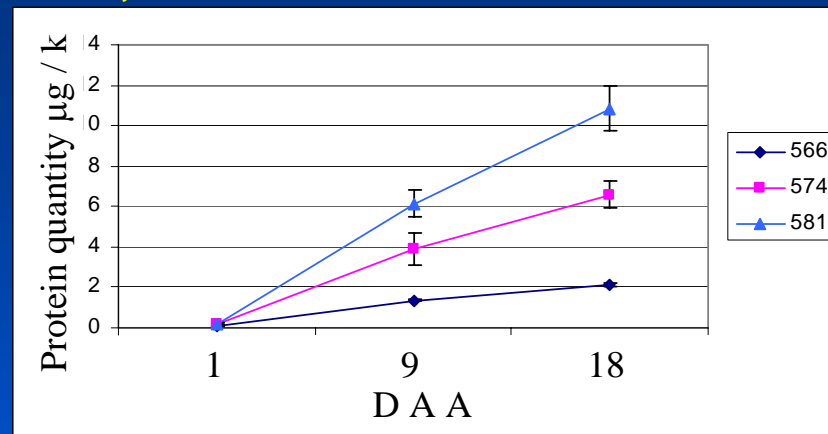
Main profiles found for the amount of protein ($\mu\text{g}/\text{kernel}$) accumulated, for the commun spots

78,2 %



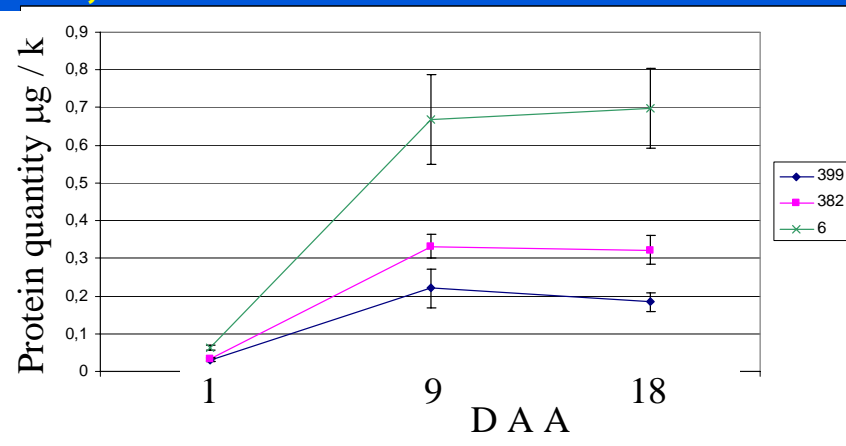
Cell division and cell structure

11,2 %



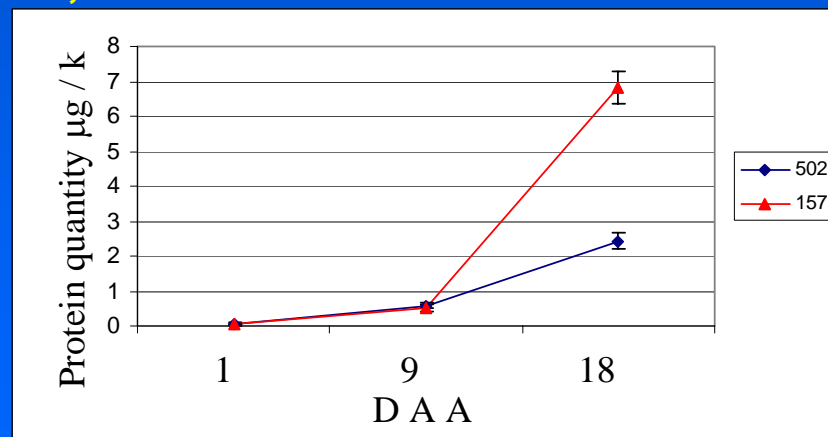
Enzymes for storage proteins and starch accumulation

8,8 %



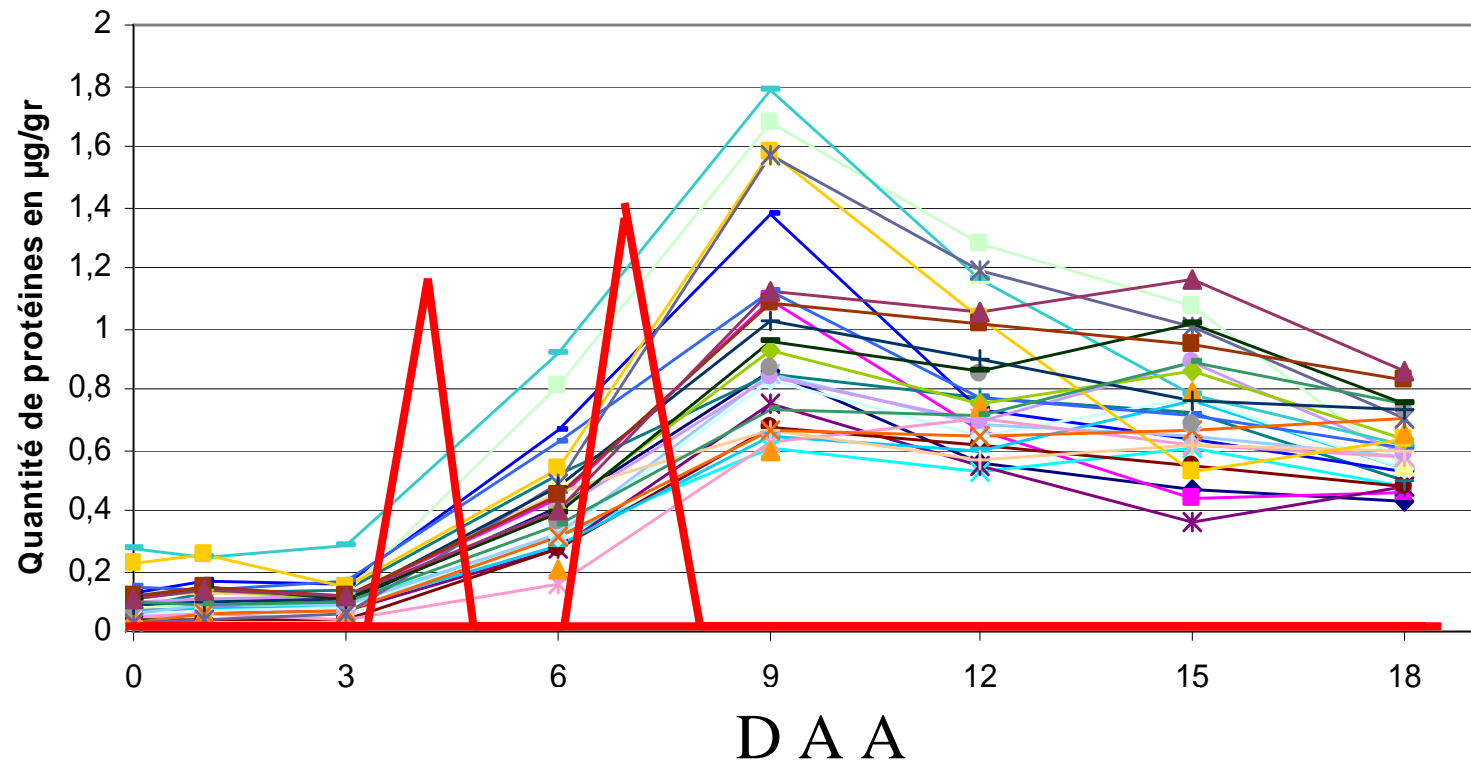
Keeping house proteins

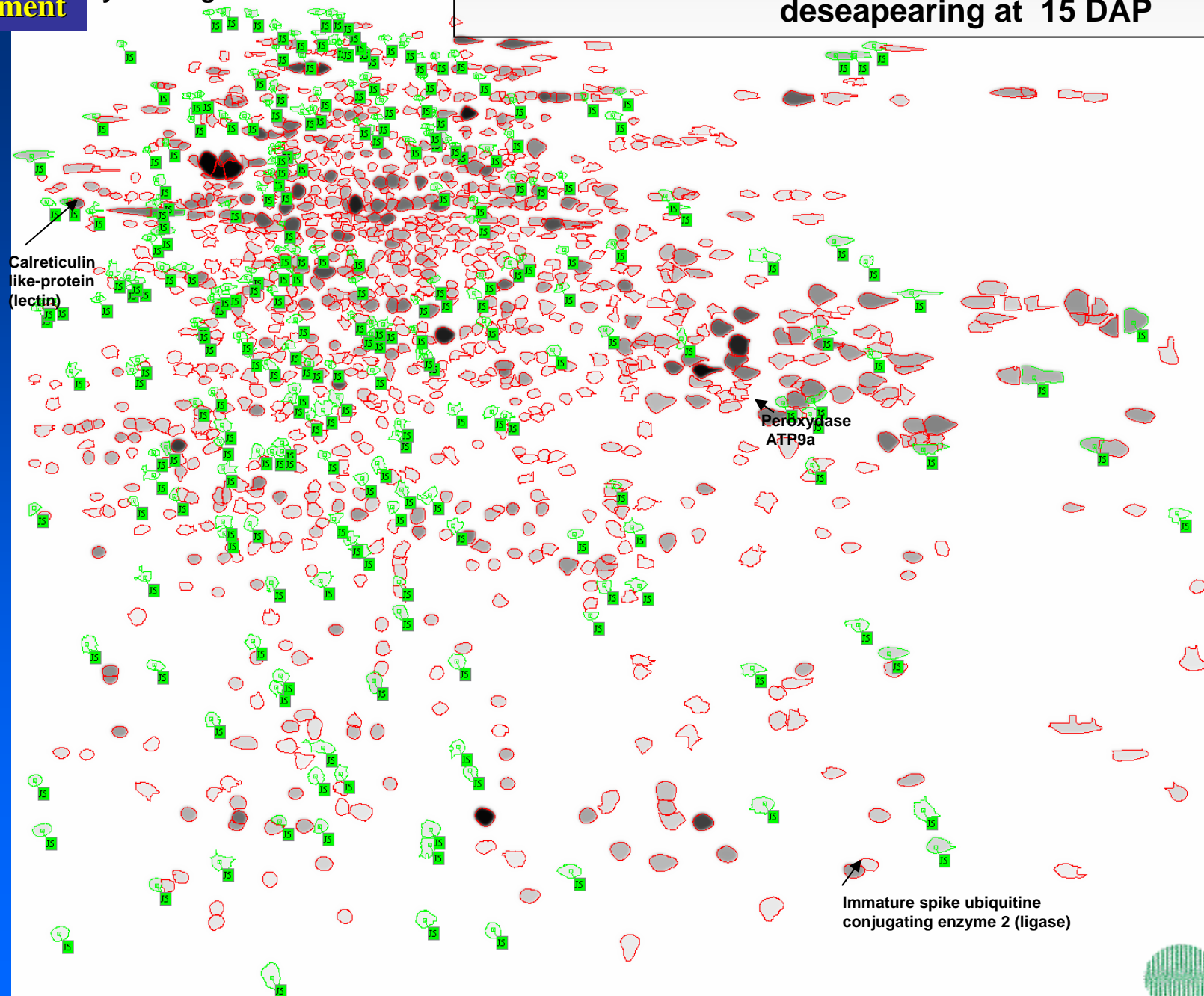
1,8 %



Enzymes for starch and storage protein polymerisation

Another group of proteins





Example of data collected from data bases and bio analysis

Pathway	Putative fonction	Biological process	Family protein	Developmental stages	Protein name	Organism	cell localization	Tissue	N° accession Swiss Prot	N° spot
Environmental Information Processing	Signal transduction	Coleoptile phototropism	NPH3 family	0 to 18 DAP	Root phototropism protein 2 (RPT2)	Arabidopsis thaliana	hypocotyl, guard cells, mesophyll cells		Q682S0	2626
Environmental Information Processing	Signal transduction	Protein synthesis	ribosomal protein	0 to 18 DAP	40S ribosomal protein SA, putative,	Oryza sativa	reticulum endoplasmic		ABF94326	2253
Environmental Information Processing	Signal transduction	Protein synthesis	ribosomal protein	0 to 18 DAP	putative 40S ribosomal protein	Oryza sativa			XP_479167	2275
Genetic Information Processing	Folding, Sorting and Degradation	Catalysis of the rearrangement of both intrachain and	isomerase	0 to 18 DAP	protein disulfide isomerase precursor	Triticum aestivum	reticulum endoplasmic	endosperm	P52589	1901
Metabolism	Carbohydrate metabolism	Calvin cycle	kinase	0 to 18 DAP	phosphoglycerate kinase	Triticum aestivum	Plastid; chloroplast	leaf	CAA51931	2267
Metabolism	Carbohydrate metabolism	Galactose metabolism	hydrolase	0 to 18 DAP	Alpha-Galactosidase	Oryza sativa	Endoplasmic reticulum		1UAS_A	2344
Metabolism	Carbohydrate metabolism	Glucose catabolism	phosphoglycerate mutase	0 to 18 DAP	phosphoglycerate mutase	Triticum aestivum	cytoplasm		AAP80633	1868
Metabolism	Carbohydrate metabolism	Starch synthesis	synthase	0 to 18 DAP	starch synthase I	Hordeum vulgare			AAF37876	1767
Metabolism	Carbohydrate metabolism	Xylose metabolism	xylose isomerase family	0 to 18 DAP	Xylose isomerase	Hordeum vulgare			Q40082	1970
Metabolism	Carbon utilization	alcohol metabolism	oxidoreductase	0 to 18 DAP	alcohol dehydrogenase	Hordeum vulgare	cytoplasm		AAC19351	2276
Metabolism	Carbon utilization	Regulation of photosystem	decarboxylase	0 to 18 DAP	isocitrate dehydrogenase	Medicago sativa	chloroplast		Q40345	2284

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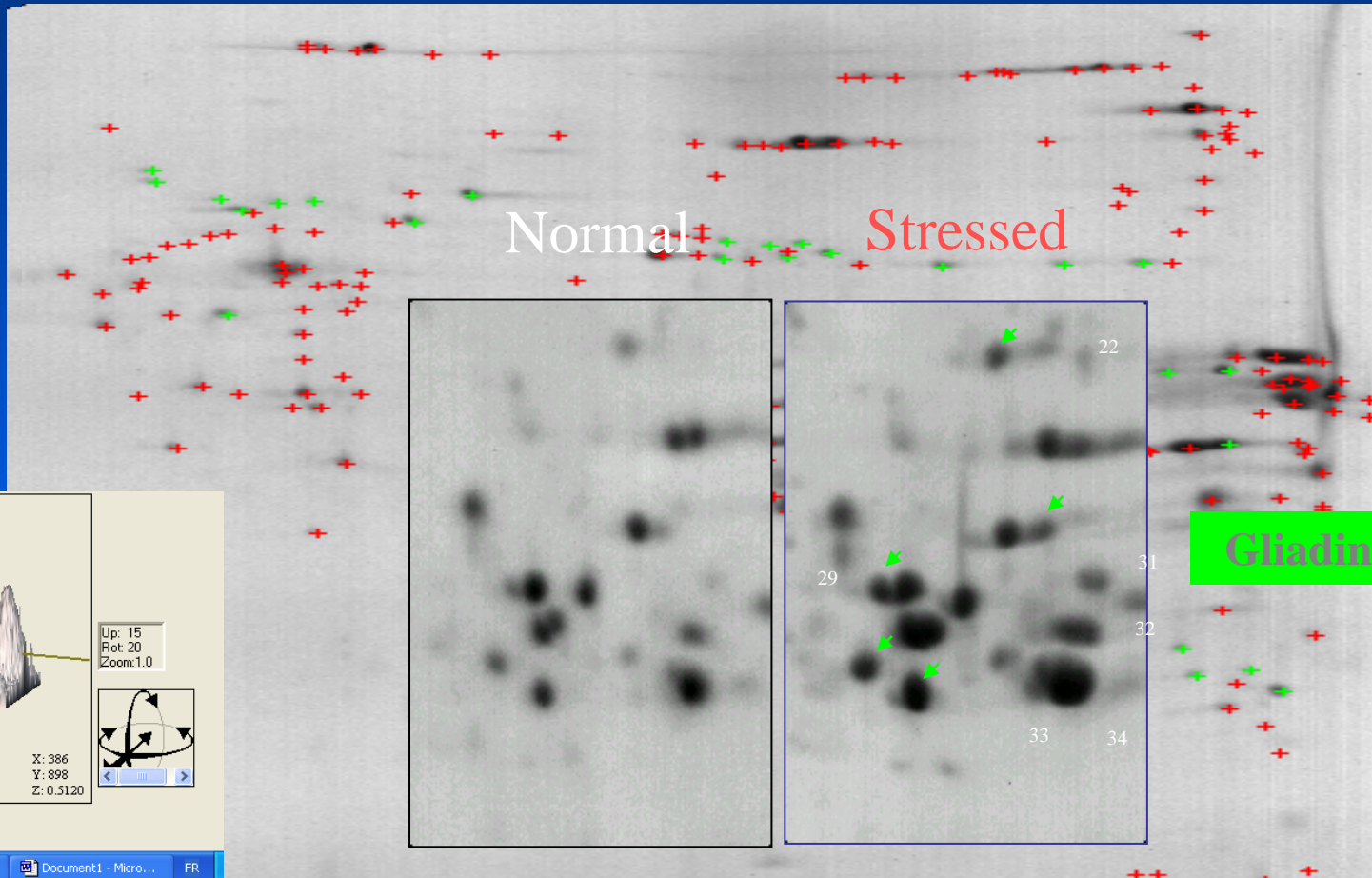
Endosperm responses to Heat stress



Differential proteomics : quantitative analysis between two types of samples

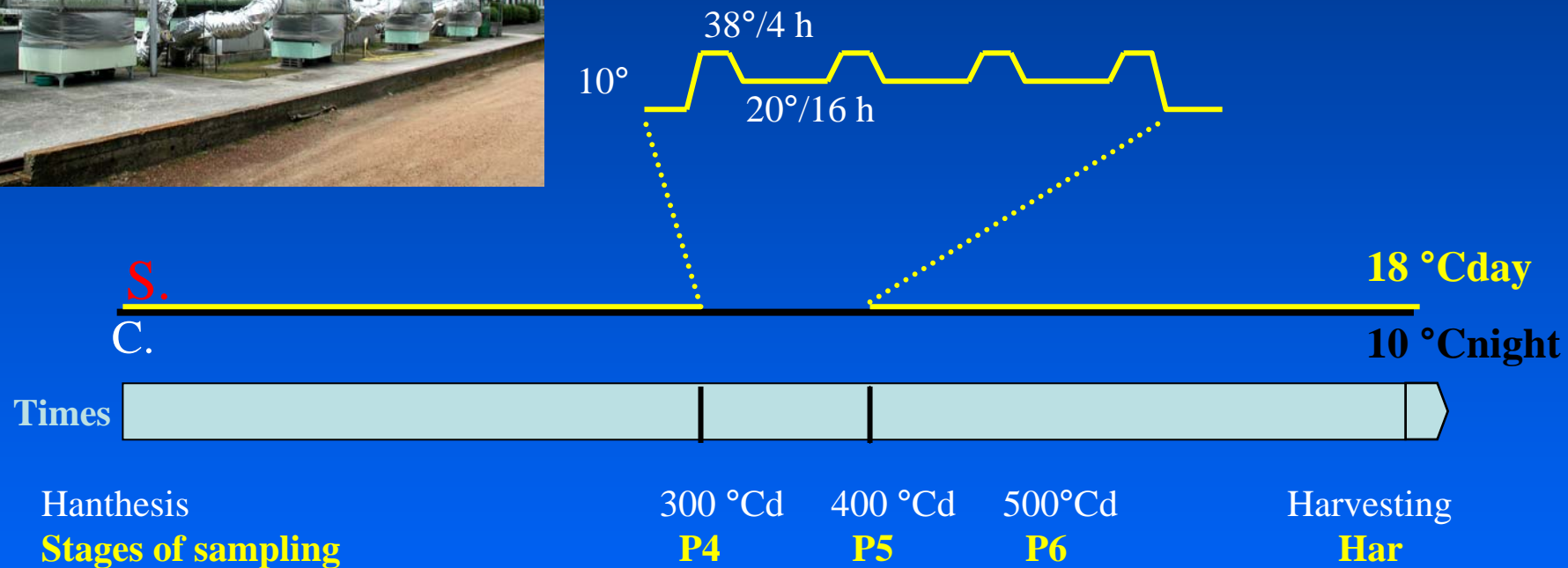
Effect of warm temperature on wheat proteome at kernel maturity on cv Thésée

3 ← IPG → 10

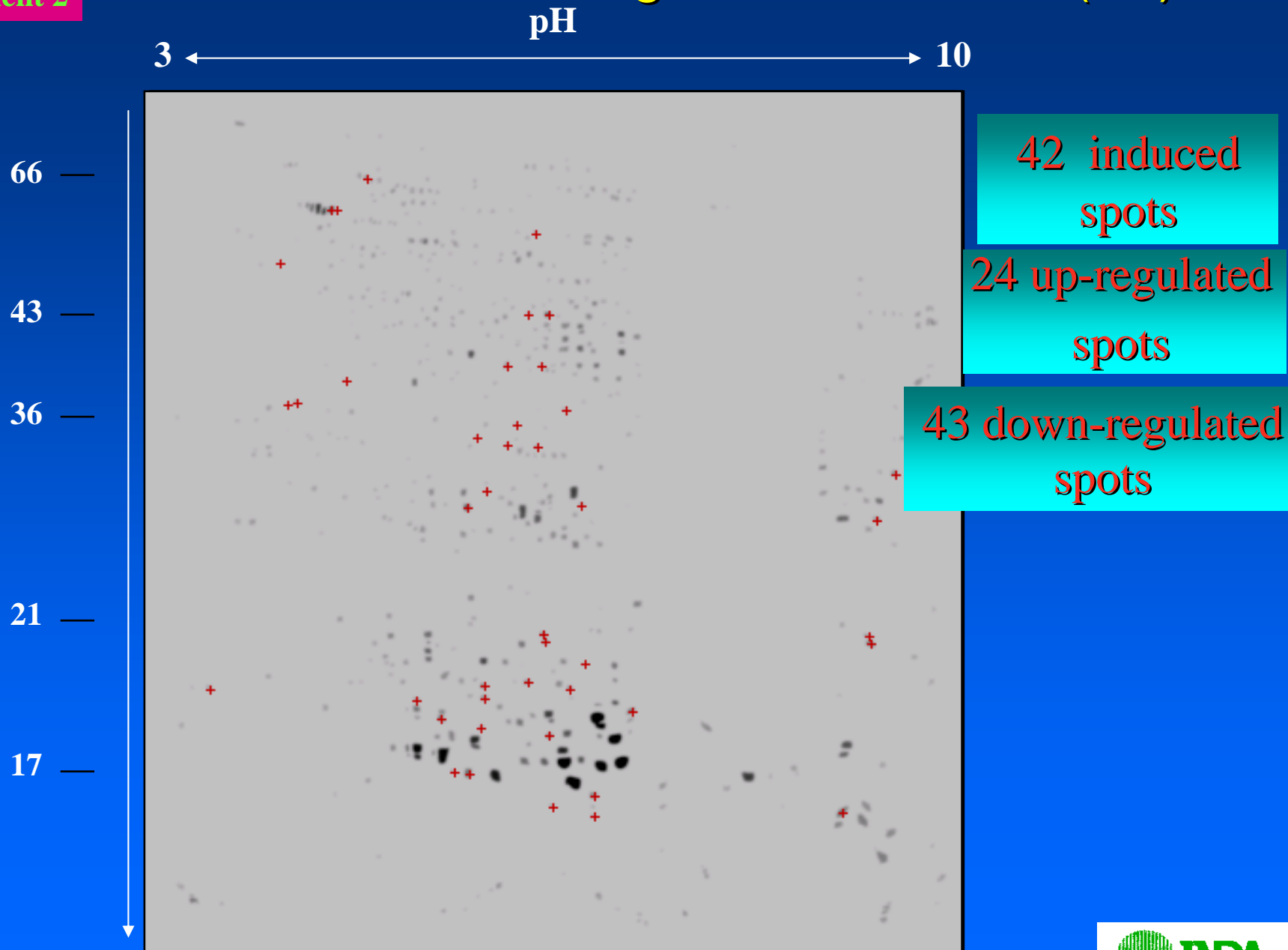


Common Spots of Higher amount at 34/10 ($p < 0.005$)

Thermal conditions for control and stressed wheat : cv Récital



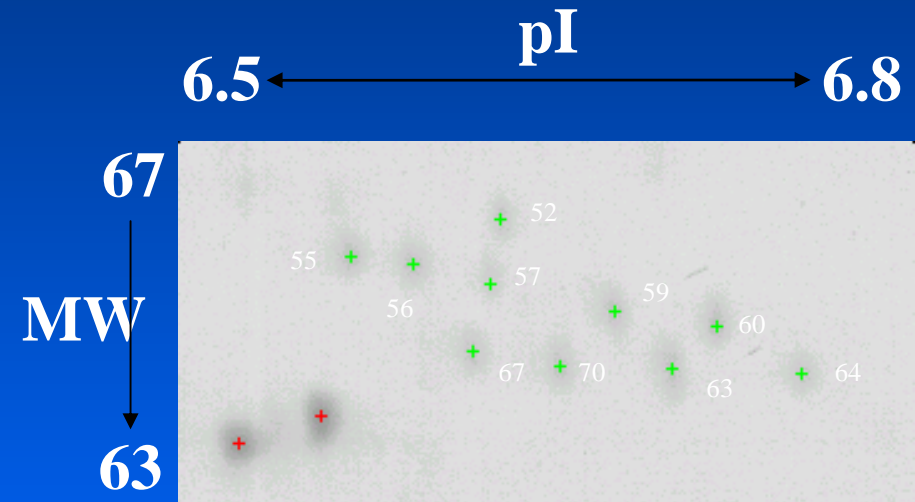
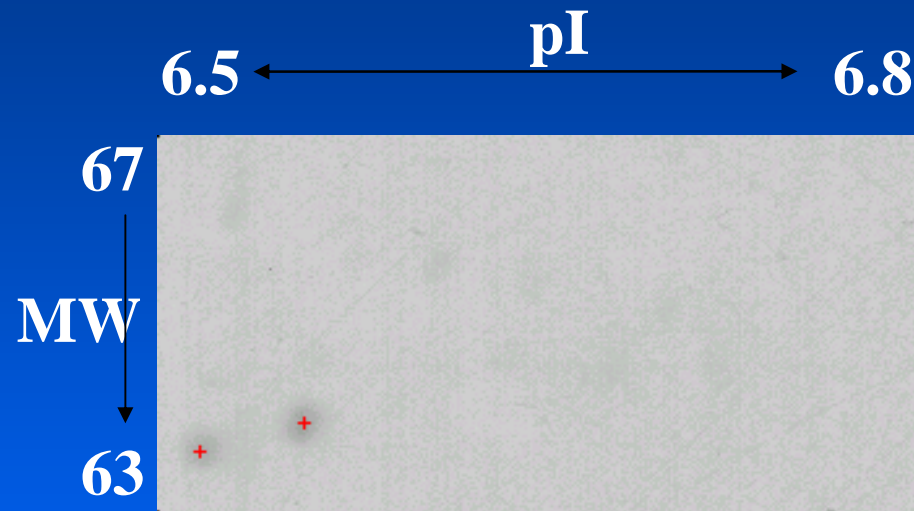
2DE of the Albumins-globulins Récital (P5)



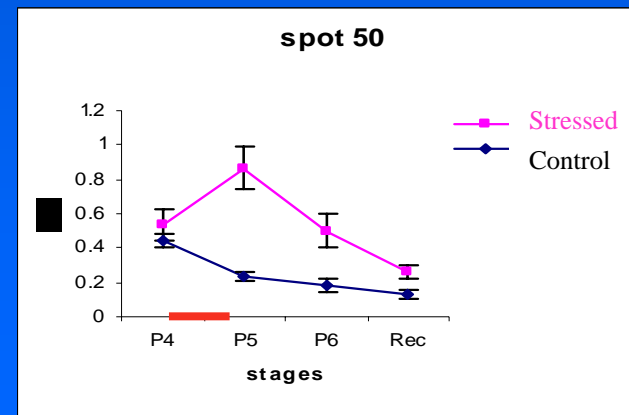
Qualitative variations (presence/absence) of endosperm proteins at stage P5 (after 4 days of heat stress)

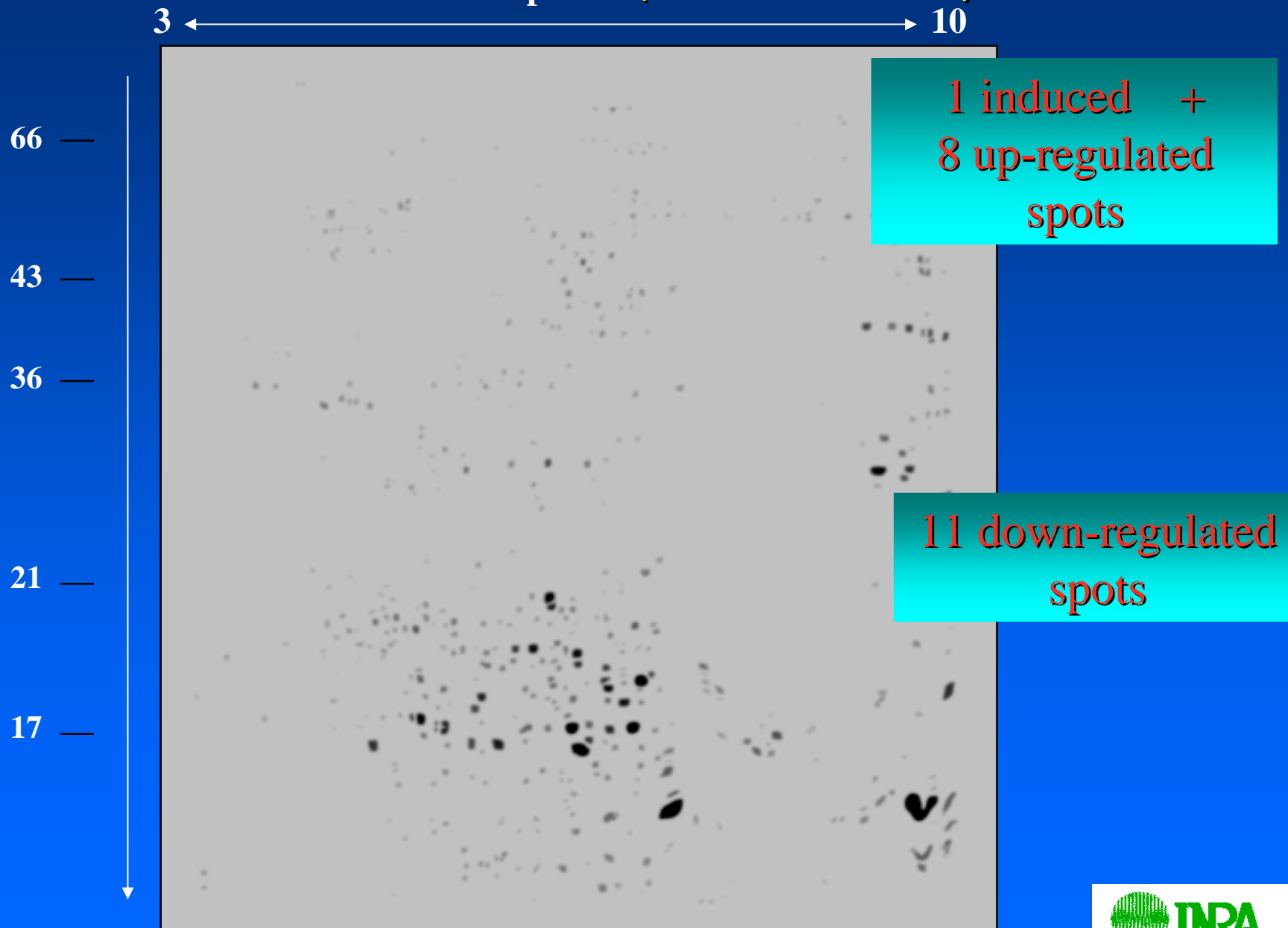
Control

Stressed



HSP70 : Bind ATP. Also involved in the folding and oligomerization of newly synthesized polypeptides, involved in the assembly disassembly of multimeric structures.



2DE of the Albumins-globulins Récital
(Harvest time)

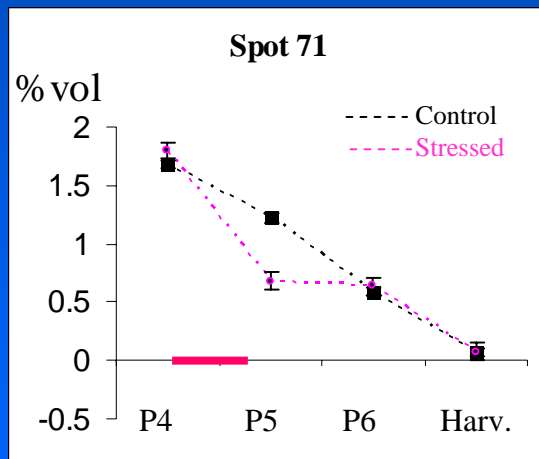
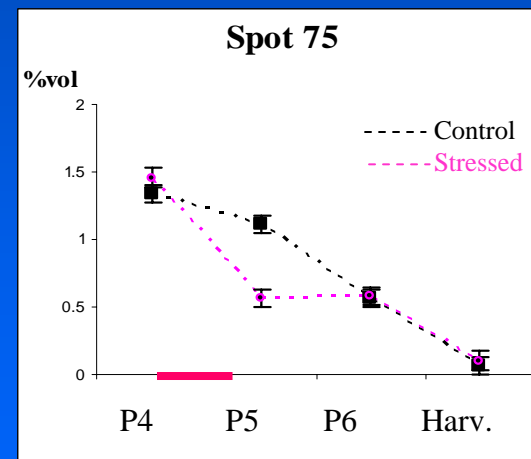
Identification of some proteins and variation during grain formation

(Continuation)

Glutathion synthase } oxydo-reduction, polymerisation

Glutathion transferase } of proteins, detoxication etc...

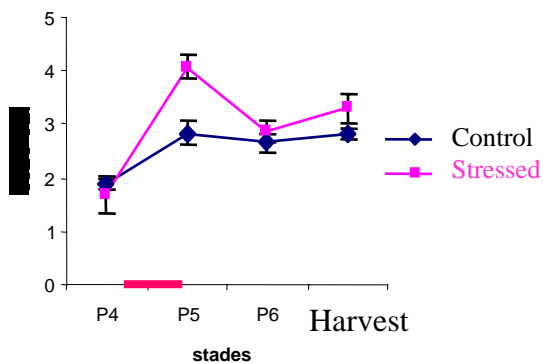
Protein disulfite isomerase: Binding proteins, protein folding, chaperone

**PDI**

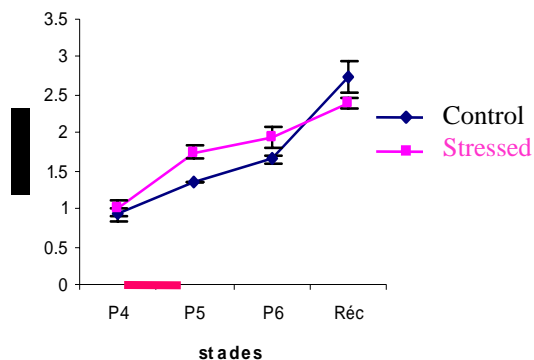
Identification of some proteins and variation during grain formation

α -Gliadins

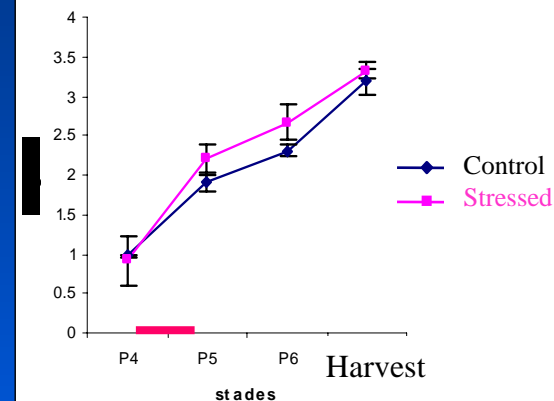
Gli 6



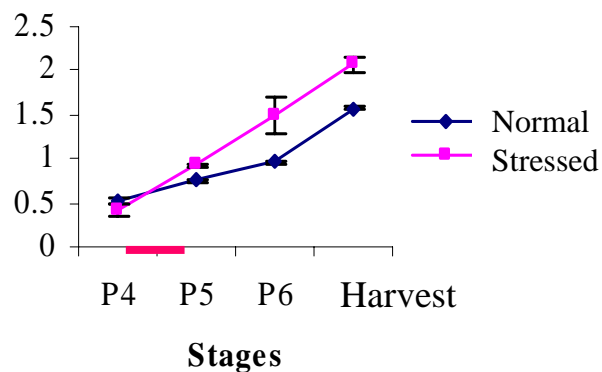
Gli 7



Gli 8



glu 1



HMW-GS

Genetic determination of protein quality in wheat grain

Genetic aspects of wheat storage proteins

Wheat storage proteins and quality

Quantitative variations of wheat storage proteins

Proteomics of wheat kernel

Proteomics on developmental kernel

Endosperm responses to Heat stress

Some other proteins involved in quality

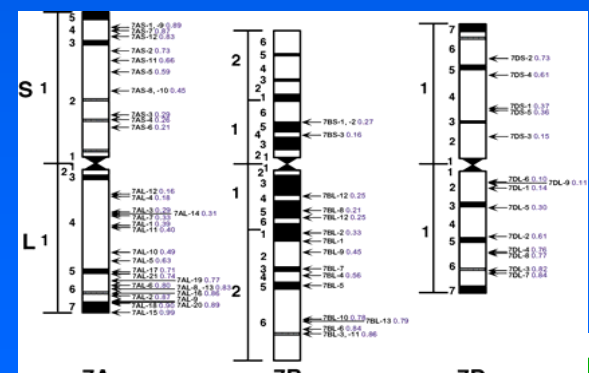
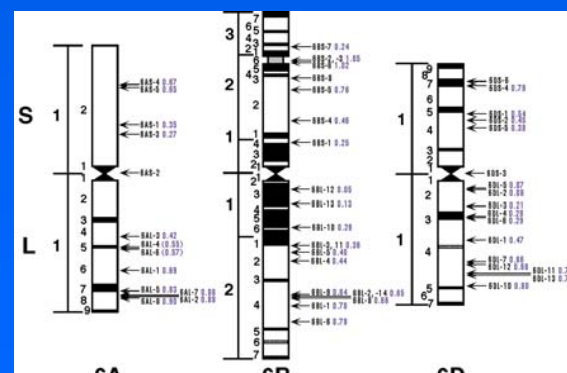
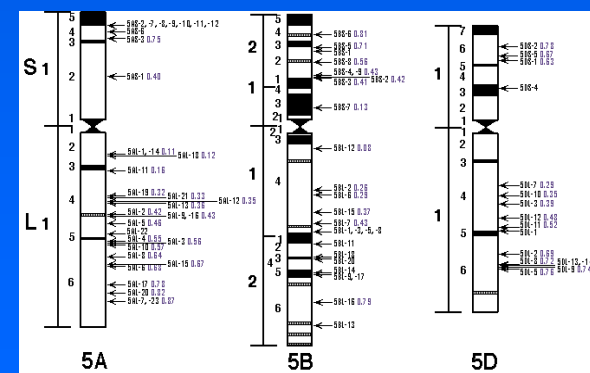
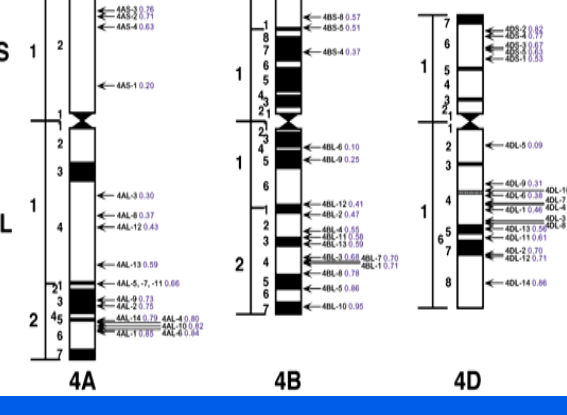
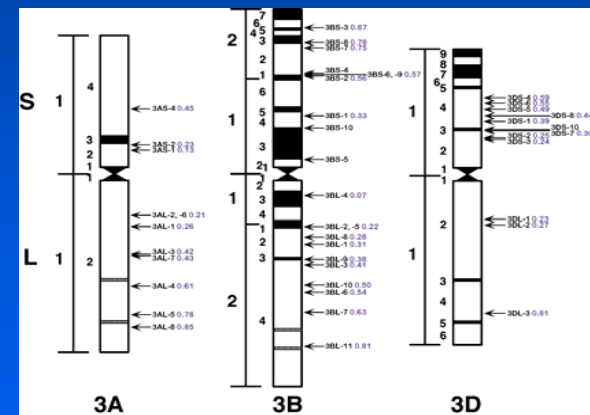
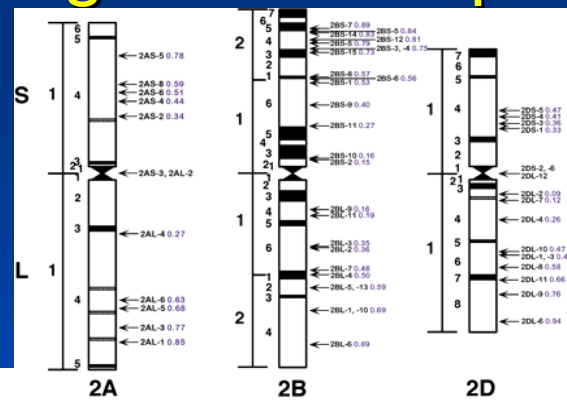
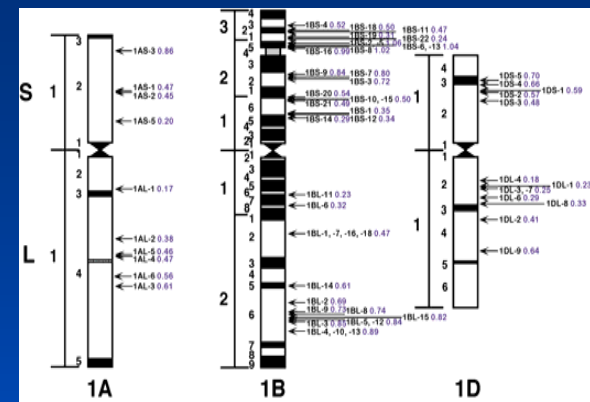


Current mapping of tissue specific proteins using Chinese Spring deletion lines

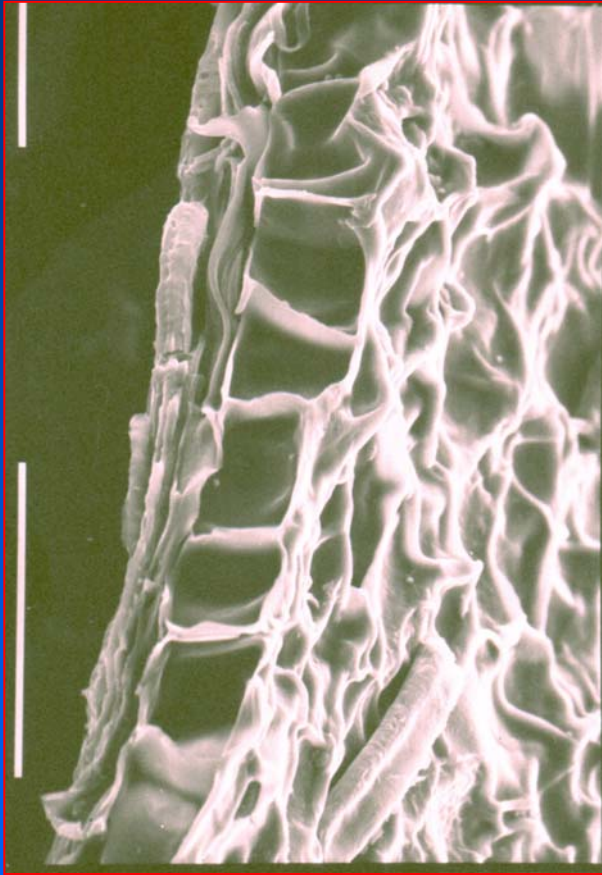
From B. Gill KSU, USA

Proteins of the aleurone layer

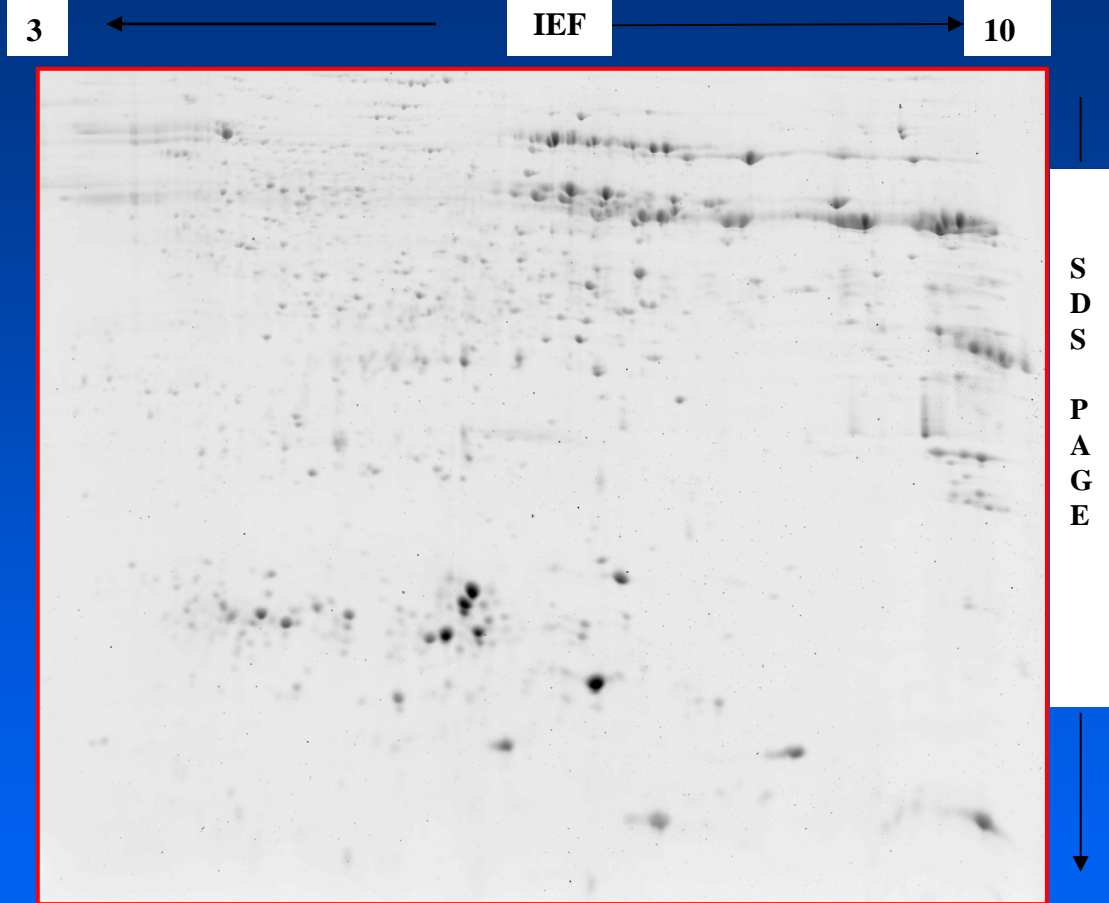
Albumins-Globulins of the endosperm



Proteomics of aleurone layer

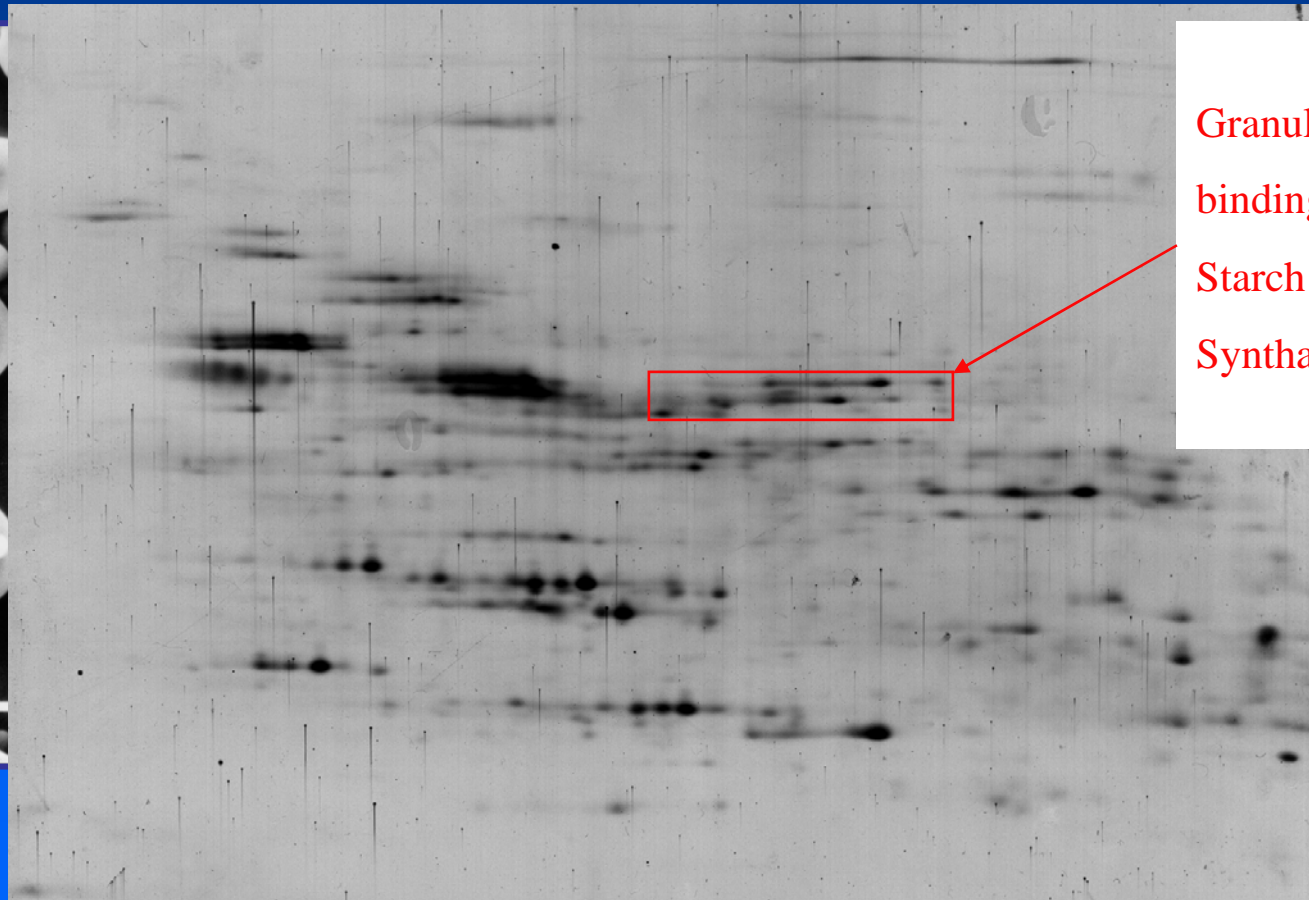
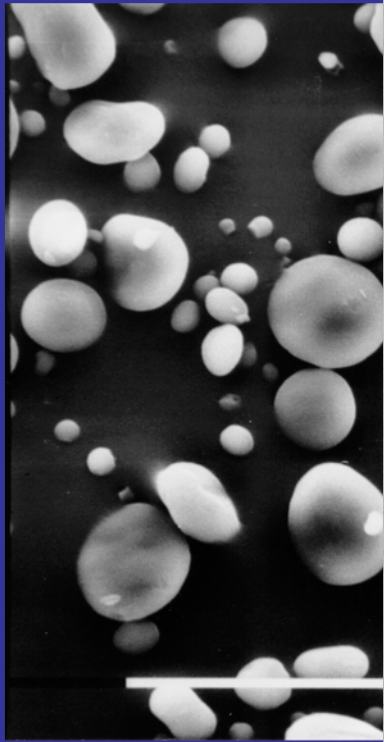


(+ nucelus): e = 100 microns



Proteomics of wheat starch granules: Diversity of the inner or strongly attached proteins to starch granules

+ 5 ← IPG → 7 -



Granule
binding
Starch
Synthase

S
D
S
P
a
g
e
↓
+

From: Branlard G. 2000, IAA, 5, 91-97

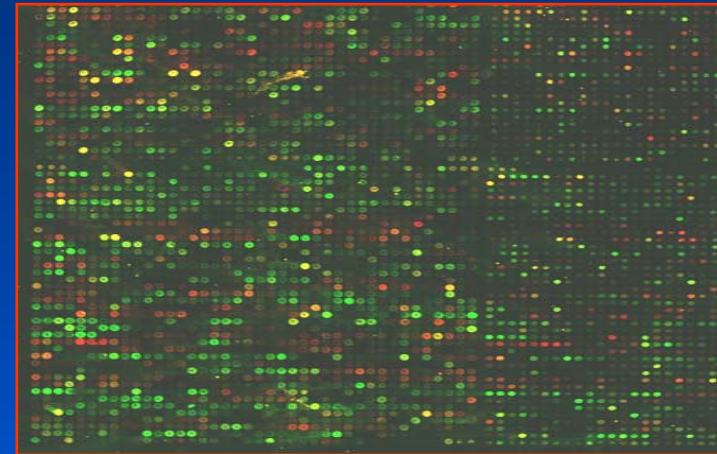
Conclusion

- Proteomic analysis of soluble proteins allowed to identify in total approx 400 soluble proteins and genes coding 260 spots have already been located on 21 Chr.
- Proteomic approach will be an unavoidable tool for studies on:
 - gene expression
 - functional genomic (assoc. with transcriptome)
 - gene regulations
 - genome interactions
 - relations between genotype and phenotype
 - plant physiology and environmental influence
 - etc...
- Proteomic can be carried out on different cell components or specific tissues. A proteomic DB is currently in preparation

Question: How to find-out the key genes that govern the kernel protein content for future quality wheat ?

Micro-array provides a complex picture of the numerous DNA sequences which could be directly or not associated to the character

Micro-array is a **bottom-up** approach for studying gene expression



Proteomic approach is an unavoidable tool for studies on:

- gene expression, functional genomic, gene regulations
- relation between genotype and phenotype
- etc...

Proteomic is the **top-down** approach particularly useful for studies on plant physiology and environmental influence

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**The Plate-forme for genotyping
at INRA Clermont Ferrand**



Specific rooms were setting – up

210 m² of laboratories, Inaugurated in june 2006

- Cold room
- room DNA-Extractions
- room pre-PCR 1 (ADN)
- room pre-PCR 2 (Mix)
- room post-PCR
- room RT-PCR
- room Developement Technology
- Room Informatique – Data analysis
- Office

Tools on the plate-forme

- **1 LIMS (Laboratory Information Management System)**
([SQL-LIMS APPLIED BIOSYSTEMS](#) - installation in progress)
- **3 Computers:** 2 Linux (HP Bi processeurs 2.4 GHz);
1 Windows (Dell Bi processeurs 3 GHz)
- **3 capillary sequencers** [ABI 3100](#)
(APPLIED BIOSYSTEMS)
- **1 plateforme RT-PCR** [ABI PRISM 7900HT-384](#) wells
(APPLIED BIOSYSTEMS)
- **1 plate-forme for automatic pipeting** [Genesis 150](#) (TECAN)
- **3 plate-forme for automatic pipeting heads 96** [BiomekFX](#) /
[BiomekNX](#) / [Multimek](#) (BECKMAN)
- **1 robot for pipeting** [Biomek2000](#) (BECKMAN)
- **3 thermocyclers** [PTC-225](#) : **12 blocs 384** (MJ RESEARCH)

Other researches carried out at Inra Clermont-Ferrand

Wheat Genetic resources : characterization, evolution : F Balfourier

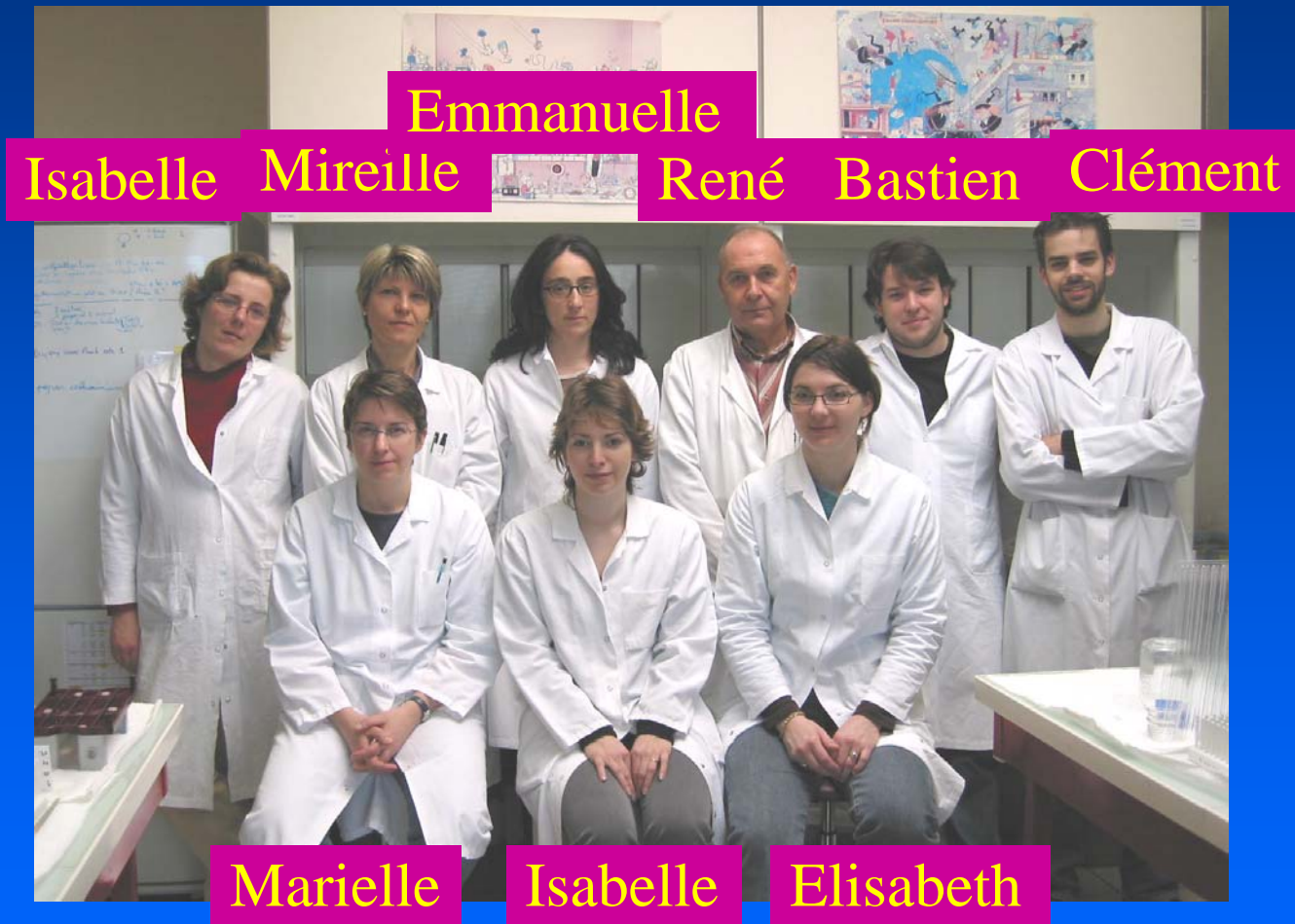
Stability of wheat quality : Nitrogen use efficiency : J Legouis

Identification of genes involved in wheat quality

- **SNP and Transcriptional Factors : C Ravel**
- **Syntenic, transcriptional genetics : J Salse**

Genomics and physical mapping of Chr 3B : C. Feuillet

Aknowlegements



Thank you