



HEALTHGRAIN Final Conference Enhancing health benefits of cereal foods - results, perspectives, challenges

Exploiting genomics and transgenesis for enhanced health benefits of wheat

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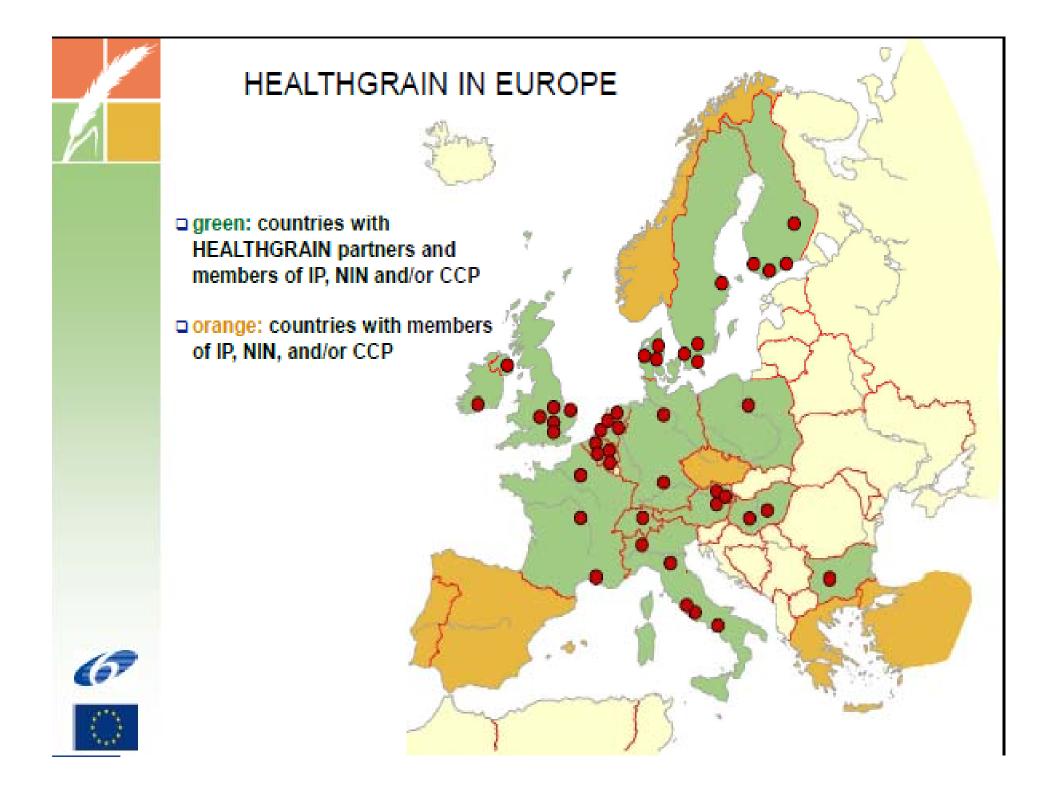


HEALTHGRAIN, very short history

- ECC Congress in Vienna March 2002: Working group "Nutrition and Health".
- In June 2002 an expression of interest was made to FP6 as one of the 1156 expressions in the area of food quality and safety: "Exploiting European cereal grains for human health"
- Working program appeared end 2002, with a call for project in this field in 2003.
- HEALTHGRAIN proposal was submitted on 5th February 2004.
- In June 2004 the proposal was selected as one of the 12 others considered for funding
- The project started 1st June 2005







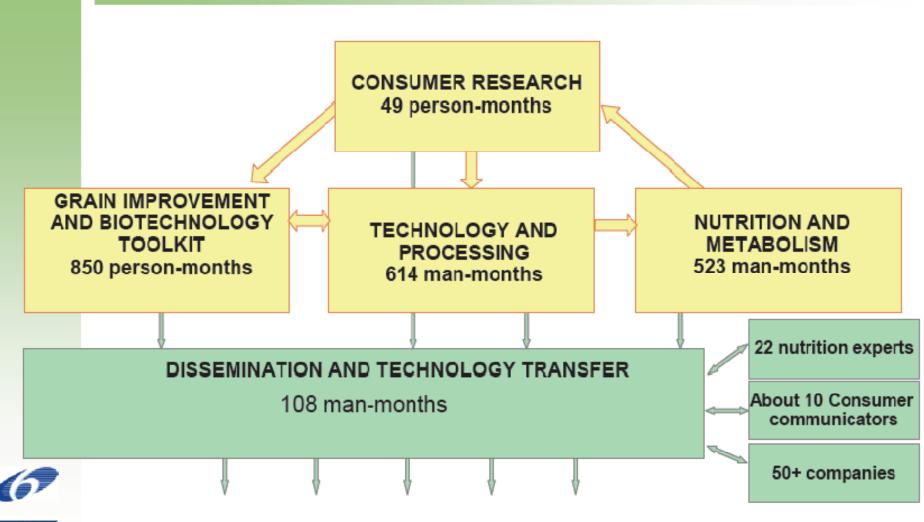
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Resources



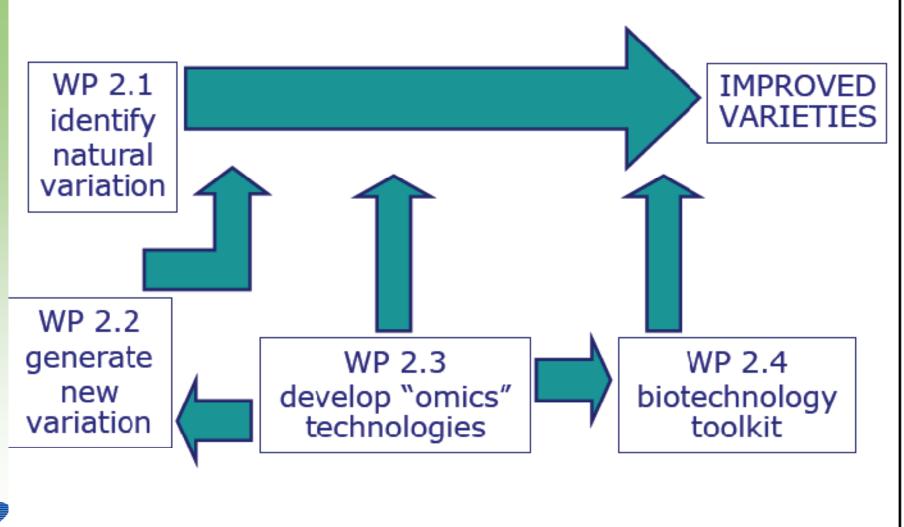
Breeders, food industry, trade, consumer organisations, authorities

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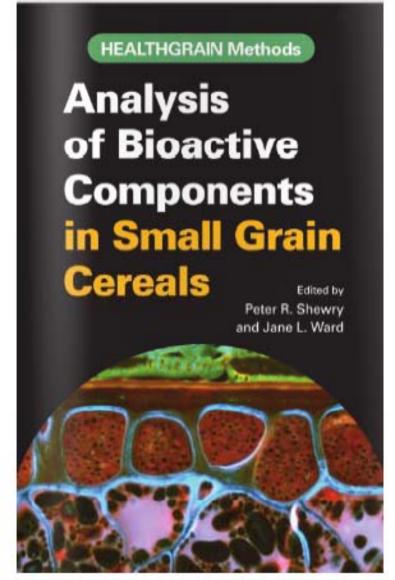
CROP IMPROVEMENT AND BIOTECHNOLOGY TOOL KIT Leader: Peter Shewry, Rothamsted Research, UK







Methods of Analysis



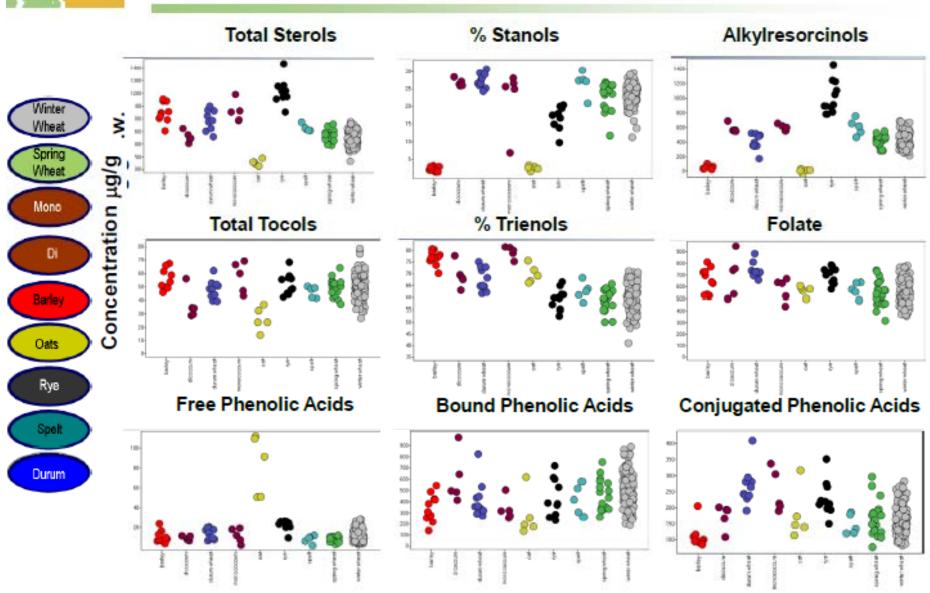
Analytical methods used for analysis of bioactive components have now been published by AACC

Easy to follow detailed protocols

Wide range of chemical analyses covered



Phytochemical Data from 200 line Diversity Screen – Comparison of Cereals





Assessing Stability with g x e experiment

- 1.150 wheat lines and 50 other cereals grown in Hungary in 2004-5.
- 2. 26 wheat and 5 ryes lines selected based on differences in composition grown again in Hungary in 2005-6

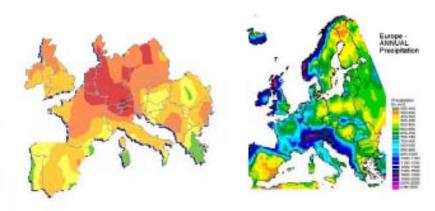
3. 26 lines grown on 4 sites in 2006-7 UK, France, Hungary, Poland



Martonvasar Hungary

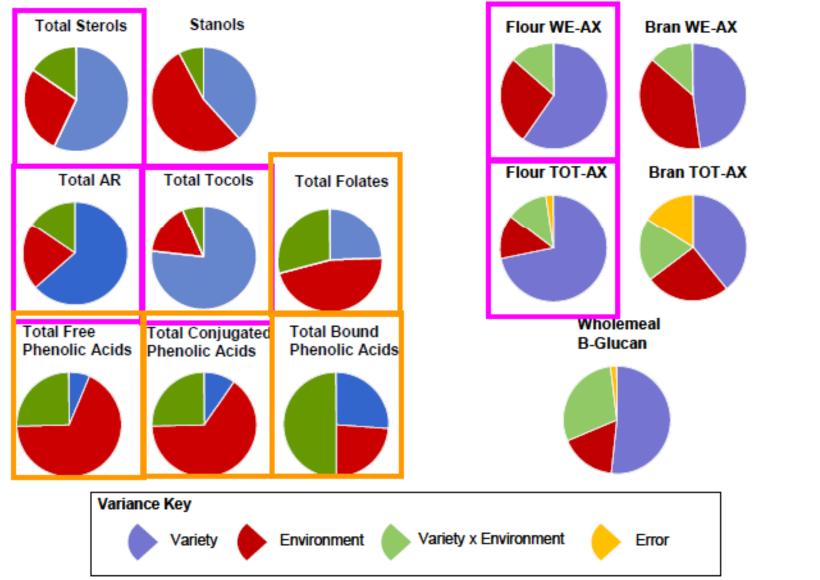


Correlation with environmental conditions





Assessment of Heritability Using data from multi site trials

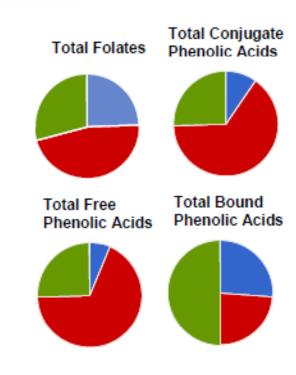




Correlations between bioactive components and weather measurements in wheat

	Average Temperature	Precipitation Heading to Harvest	Precipitation 3 months before heading	Precipitation 3 months before heading to harvest	
	R.	R	R	E	
Folates	0.690	-0.514	0.182	-0.354	
Sterols	0.551	-0.199	0.421	0.110	
% Stanols	0.870	-0.589	0.013	-0.562	
Tocols	0.563	-0.067	-0.159	-0.17	
Alkylresorcinols	0.140	0.041	-0.552	-0.35	
Bound Phenolic Acids	-0.126	0.181	-0.268	-0.019	
Conjugated Phenolic Acids	0.753	-0.744	0.694	-0.20	
Free Phenolic Acids	0.899	-0.706	0.194	-0.52	
Total phenolic Acids	0.317	-0.250	0.116	-0.15	
Bran Tot-AX	0.060	0.138	-0.407	-0.15	
Bran WE-AX	-0.889	0.737	0.190	0.82	
Flour Tot-AX	-0.516	0.259	0.446	0.559	
Flour WE-AX	-0.868	0.692	0.119	0.73	
Glucan	0.306	-0.684	0.728	-0.12	

Bioactive components which have lower heritable traits appear to have stronger negative correlations with precipitation between heading and harvest



WE-AX (bran and flour) shows a strong POSITIVE correlation with precipitation



I. From QTL to genes. A metagenomic approach: Example of dietary fibre

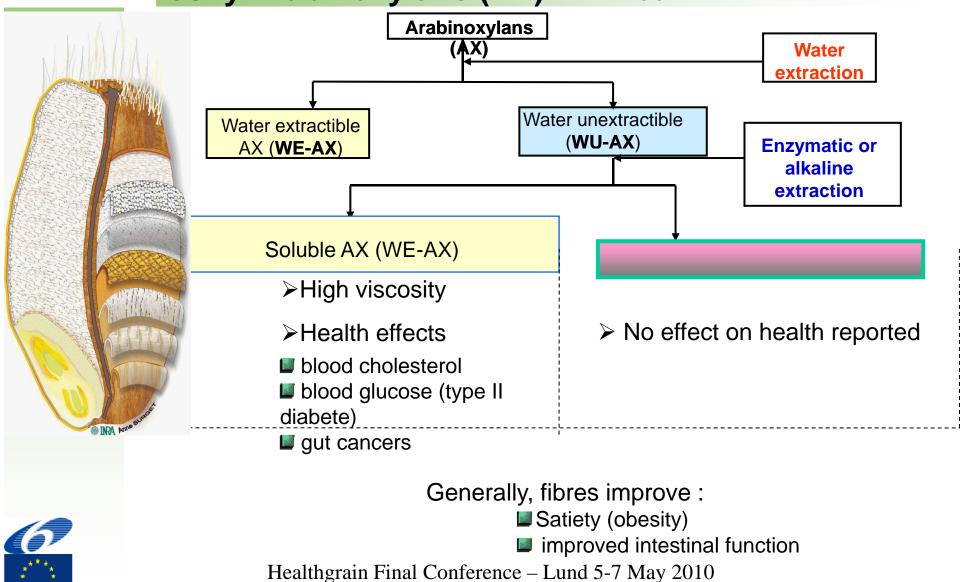






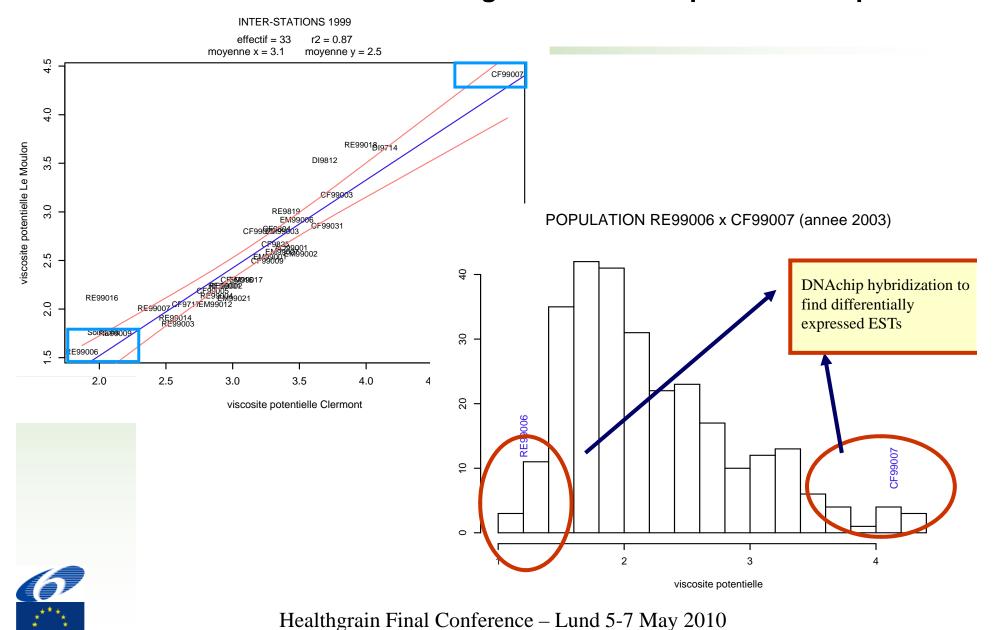


Dietary fibres are cell wall components, mostly Arabinoxylans (AX) in wheat



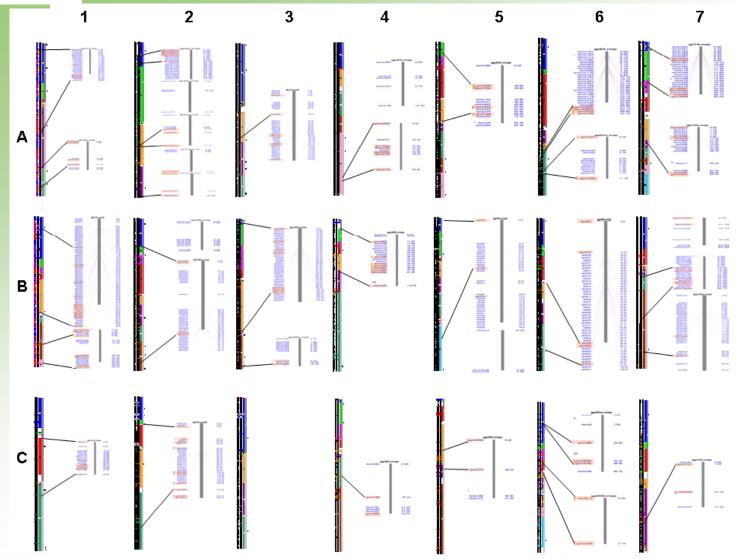


Genetic analysis of Flour WE-viscosity (predictor of WE-AX) Choice of two contrasted breeding lines to develop doubled haploids



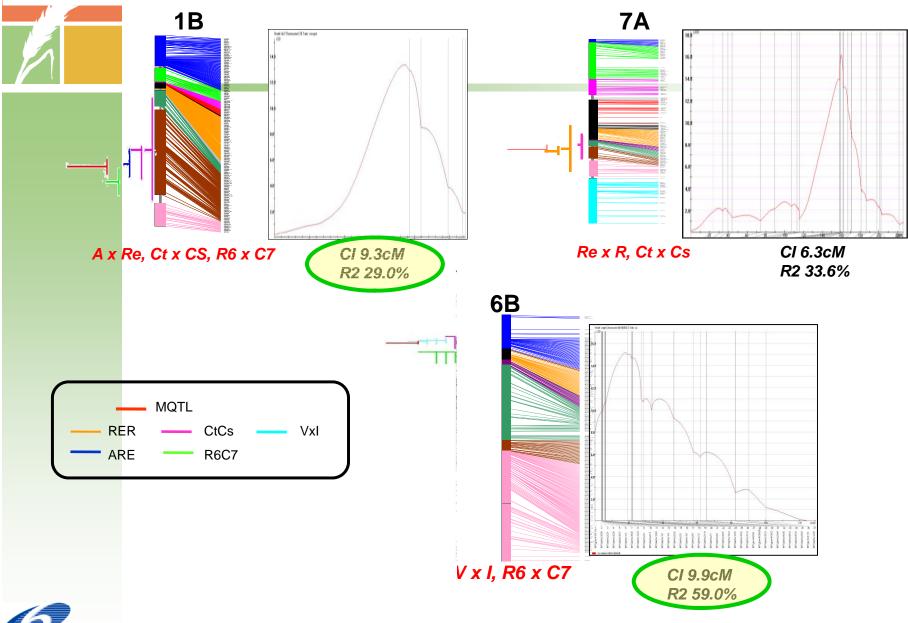


Construction of genetic maps with SSR and DArTs markers





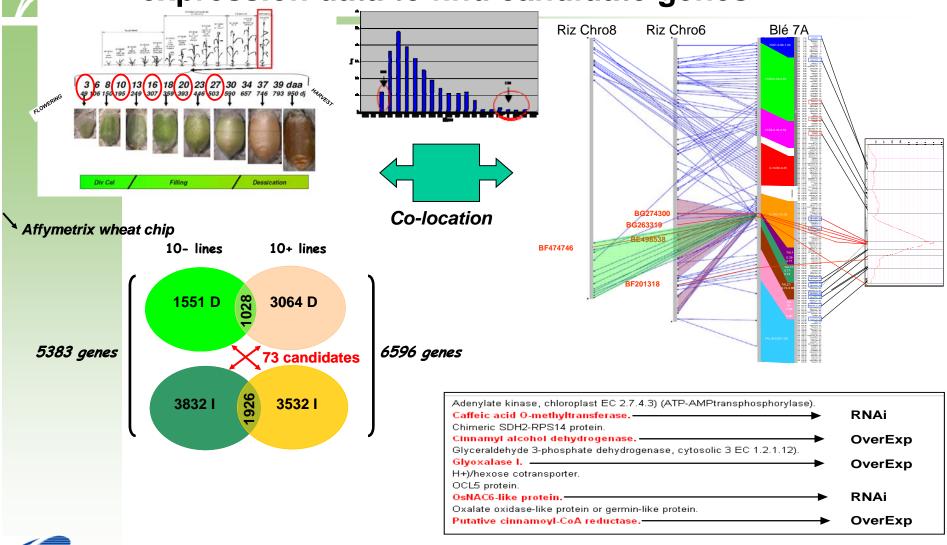
A total of 3 meta-QTL were found from literature and new experiments





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Metagenomic approach: combining mapping and expression data to find candidate genes



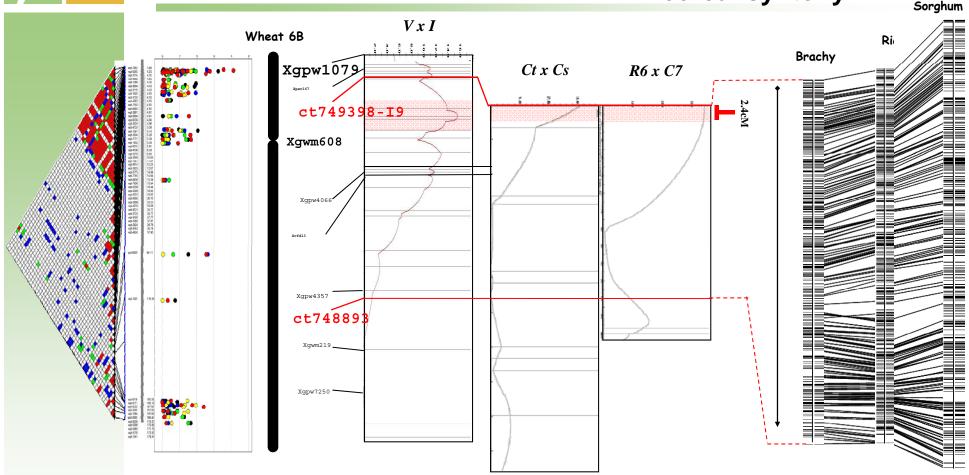


Candidate genes 6B



MQTL on chrom 6B

Candidate gene from cereal synteny



Fine mapping allowed identification of flanking markers

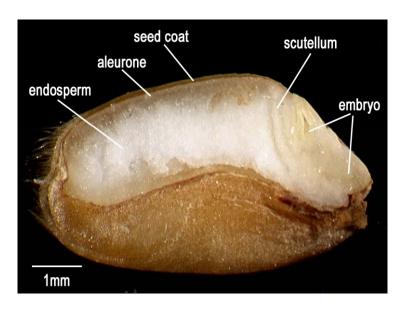








II. Proteomics of endosperm and aleurone layer



INRA, Clermont-Ferrand, France DTU, Copenhagen, Denmark







HEALTH GRAIN **Proteomics of aleurone layer proteins IPG** 10 343 proteins were identified These aleurone-specific spots are candidate genes for aleurone development, composition or mechanical properties (e.g. friability)



III. Candidate genes for phytochemicals: example of folates

Folic acid, or its naturally occurring form folate, is considered as a potentially health-protecting compound in the human diet.





Selection of candidate genes: folates

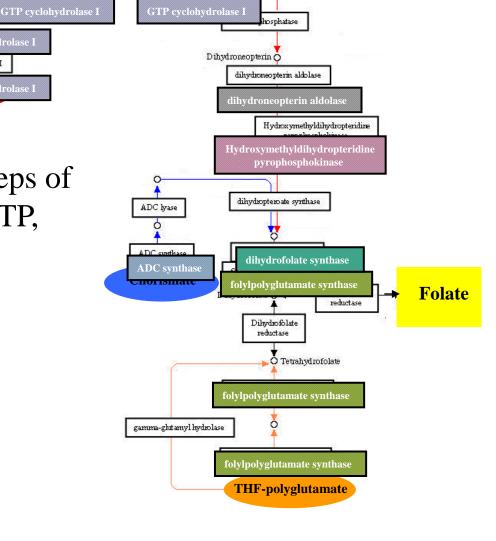
GTP cyclohydrolase I

GTP cyclohydrolase I

One enzyme for main steps of folate synthesis (from GTP, chorismate and THF

GTP cyclohydrolase

GTP cyclohydrolase I

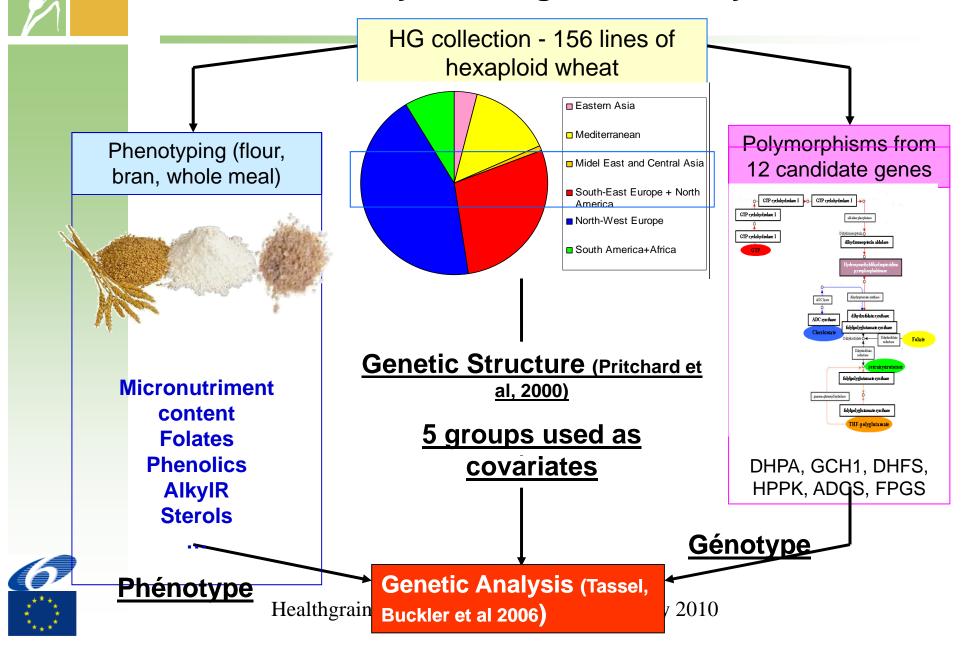




polyglutamate)



Association analysis using HD diversity screen data





GCH1 Genes

 Identification of the three homoeologous GCH1 genes

• Assignation on 2A 2B 2D GTP cyclohydrolase I

Dhydrofolate synthase

Ghylpolyglutamate synthase

Tetrahydrolase

Folate

THF-polyglutamate

THF-polyglutamate

• 2A copy: 1 SNP in a single line

2B copy: 1 SNP in a single line

2D copy: 13 SNPs

No association with folate content "

11 out of 13 associated with trienol (P-value from 0.0042 to 0.0362)

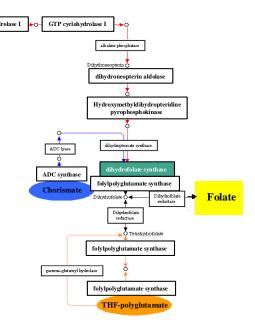






DHFS Genes

- 6 copies expected
- 3 copies assigned on 4B, 4D and 5A chromosomes



GTP cyclohydrolase I

GTP cyclohydrolase I

● 4B copy no SNP 4D copy 10 SNPs unbalanced 5A copy no SNP

No association with folate content !! but association with stanol (P-values = 0,000237)





Exploitation of Results: markers

Marker assisted selection using linked or gene-derived markers

Example of marker assisted back-crossing

Tranfer of high micronutrient alleles from exotic into adapted varieties

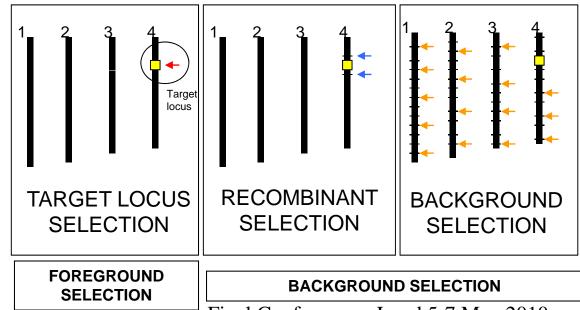






Marker-assisted backcrossing (MAB)

- MAB has several advantages over conventional backcrossing:
 - Effective selection of target loci
 - Minimize linkage drag
 - Accelerated recovery of recurrent parent



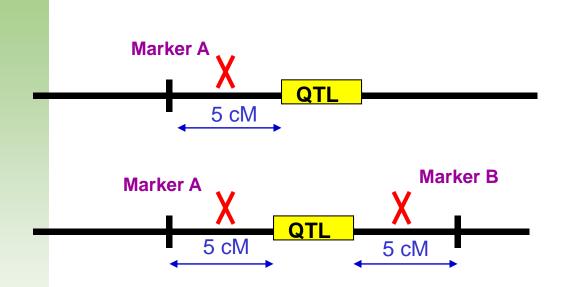


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Markers must be tightly-linked to target loci!

Ideally markers should be <5 cM from a gene or QTL



RELIABILITY FOR SELECTION

Using marker A only:

$$1 - r_A = ~95\%$$

Using markers A and B:

$$1 - 2 r_A r_B = ~99.5\%$$

- Using a pair of flanking markers can greatly improve reliability but increases time and cost
- Application to Valoris x Premio and Yumai34 x Premio



Exploitation of Results: Genes

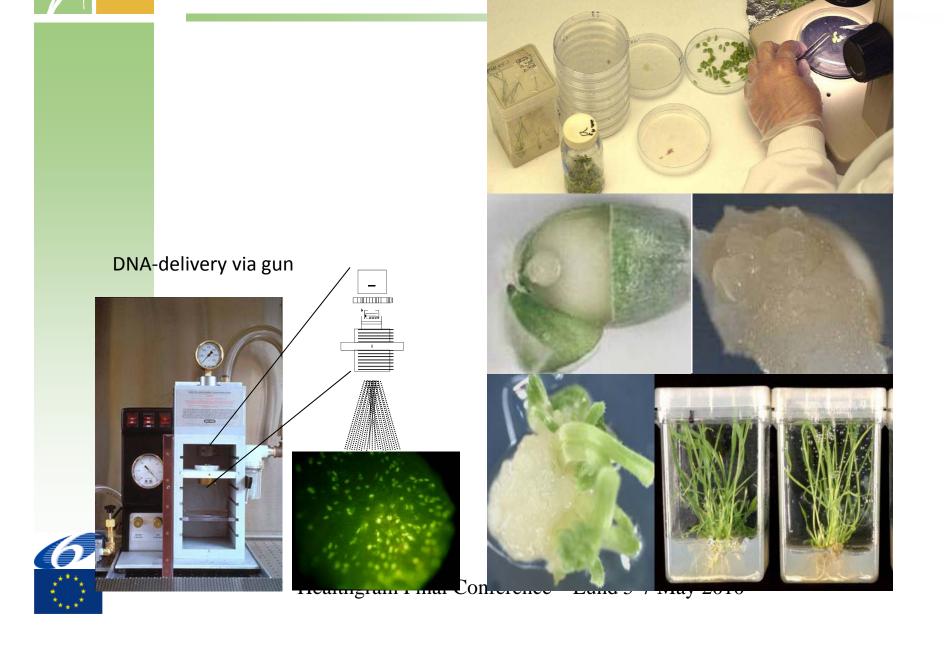
Biotechnology for modifying gene expression (beyond the range found in natural diversity)

Transgenesis of silencing or overexpression of dietary fibre genes



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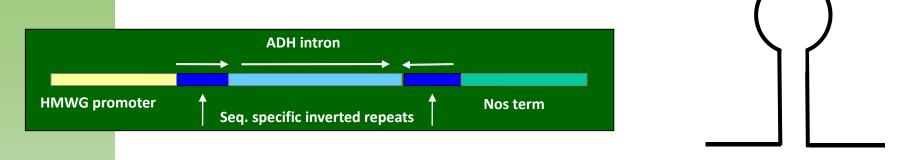
RNAi silencing of CSL6 gene in transgenic wheat







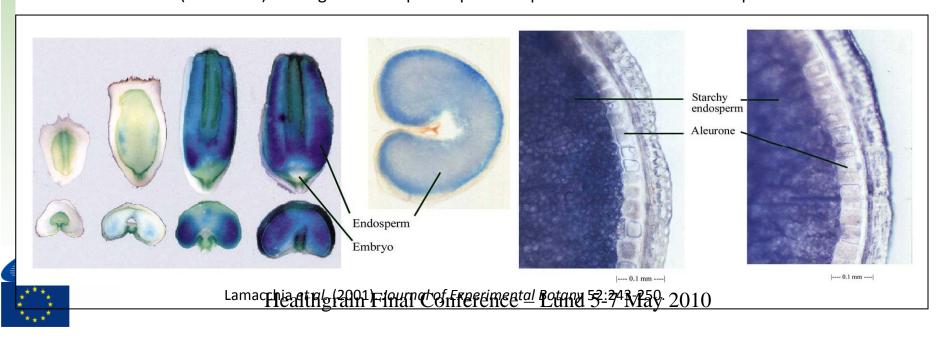
Endosperm-specific silencing in transgenic wheat



Hair-pin ds RNA structure

HMW Glutenin promoters

1Dx5 (-1141 +57) ::GUS gives endosperm-specific expression detectable 12-14 dpa



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308 T0 transgenic wheat lines See Huw Jones poster for more results

	ROTHAMSTED	
dv	RESEARCH	

Target Enzyme	Plasmid ID	No. GM plants generated	Totals per target enzyme	Status	Seed ready Date
Putative Glucan Synthase	pCSLD4 RNAi	8	. 35	Complete	July '07
	pCSLF6 RNAi	13		Complete	July '07
	pCSLD4 RNAi + pCSLF6 RNAi	8 (7*)		Complete	July '07
	pAHC1ESwithfullF6	6		Complete	Oct '09
	pGT61_1	12 (8*)	108	Ongoing	Aug '08
Putative Arabinosyl Transferase	pGT61+ pHMWAt13	6		Complete	July '08
Transiciase	pRNAi#55p113	21 (11*)		Complete	July '08
	pGT61_1	8		Complete	May '09
	pRNAi#13p113 (LS. INRA)	4*	1	Complete	May '09
	pRNAi#63p113 (LS. INRA)	9 (6*)	1	Complete	July '08
	pHMWGT61-2RNAi	48*	1	Complete	Oct '09
Putative Xylan Synthase	pHMWGT43RNAi	15 (12*)	53	Complete	Feb '09
	pHMWGT43-2 O/E	4		On-going	April 10
	pHMWAt13	20 (15*)	1	Complete	Nov '07
	pHMWGT47RNAi	14 (8*)	1	On-going	Dec '08
Putative Feryloyl Transferase	pHMW164RNAi	14 (12*)	. 57	Complete	Nov '09
	pHMW172RNAi	10 (8*)		On-going	Feb '10
	pHMWFT3RNAi	8*		On-going	Feb '10
	pUbi164RNAi	25 (21*)		Complete	July '09
	pAHC-UDPG-D	22 (21*)	55	Complete	Feb '09
UDP-Glucose dehydrogenase	pUDPG-RNAi	28 (27*)	. 55	Complete	April 09
acity at ogotiase	pUDPG-antisense	5 (4*)	1	Complete	March 09









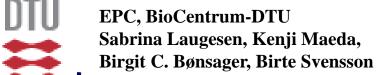
- 1. Identification of new sources of genetic diversity for fibre and bioactive compounds (WP2.1 Z Bedö, J Ward)
- 2. Identify markers for QTLs for WE-AX fibres: marker assisted transfer of favourable alleles (Valoris, Yumai?) into breeding germplasm
- 3. Functional validation of candidate genes for WEAX fibres
- 4. Map-based cloning of major QTL for WEAX fibre: Perfect gene-derived markers
- 5. Markers developped in candidate genes for folates may be helpful for improving... bioactive compounds in connected pathways (pholics, tocols...)
- 6. Proteomics can help targetting genes for aleurone development/fragility/expression
- 7. Transgenesis for manipulating gene expression: improving the biosynthetic pathway of dietary fibre
- 8. All presentations available on http://www.healthgrain.eu/pub/Final_conferencepresentations.php





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Contributions to this work



Peter Roepstorff Xumin Zhang

Nemeth C, Freeman J, Jones H, Mitchell RAC, J Ward, M Wilkinson, Shewry PR, Rothamsted Research,

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ROTHAMSTED RESEARCH



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I Romeuf, P Michaud,

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