Targeting wheat quality attributes in plant breeding

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Background to project

- UK trading system based on named varieties for quality wheat
- Advances in plant breeding facilitated the move to high levels of home-grown wheat being used following UK's entry to EU

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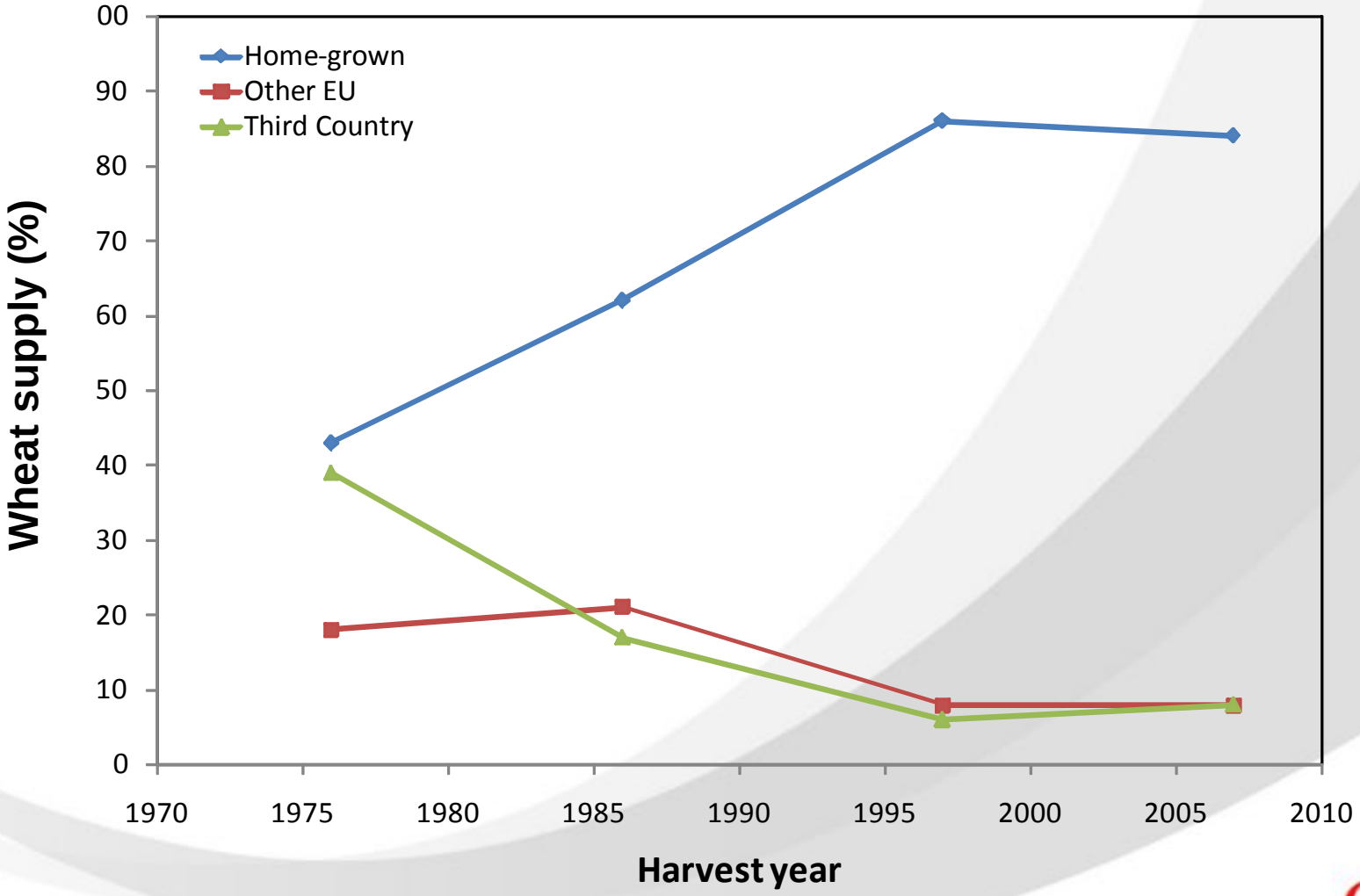
Changes in UK wheat supply



Figures from Defra/HGCA/**nabim**

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Background to project

- UK trading system based on named varieties for quality wheat
- Advances in plant breeding facilitated the move to high levels of home-grown wheat being used following UK's entry to EU
- Further developments in genetic approaches have generated more targeted breeding approaches
- Opportunity recognised to apply these developments to end use quality rather than agronomy or plant physiology alone

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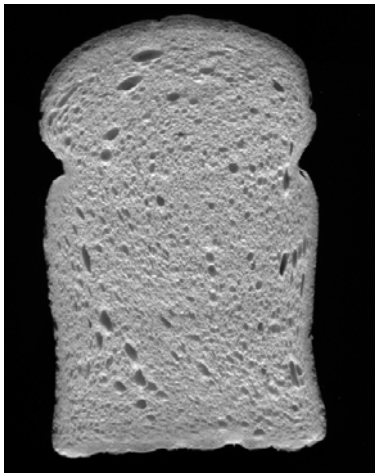
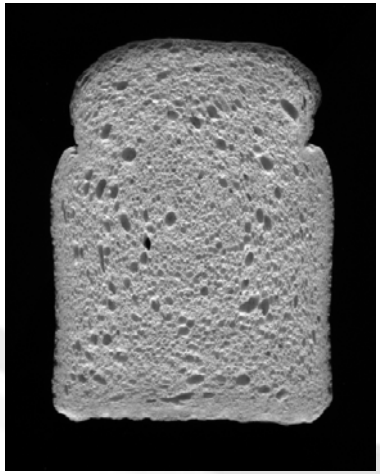
Overall project aim

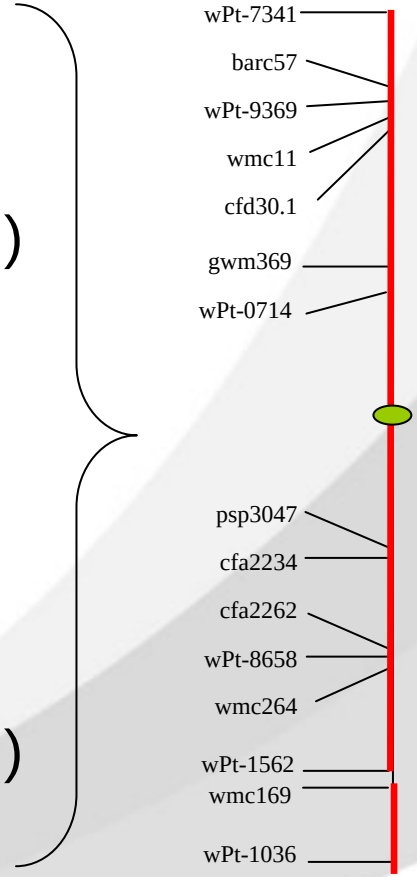
Determine genetic control of wheat baking quality



Breeding line with good performance (objectively assessed)



Breeding line with poor performance (objectively assessed)



Locate genes on genetic map

800g loaves produced using a Spiral mixer

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Project objectives

- Develop and use doubled haploid (DH) populations to determine the genetic control of end-use quality
- Agree and apply objective measures of final product quality for UK bread and puff pastry
- Improve the understanding of raw material functionality and processing for the production of high value baked goods
- Identify relationships between processing quality and composition

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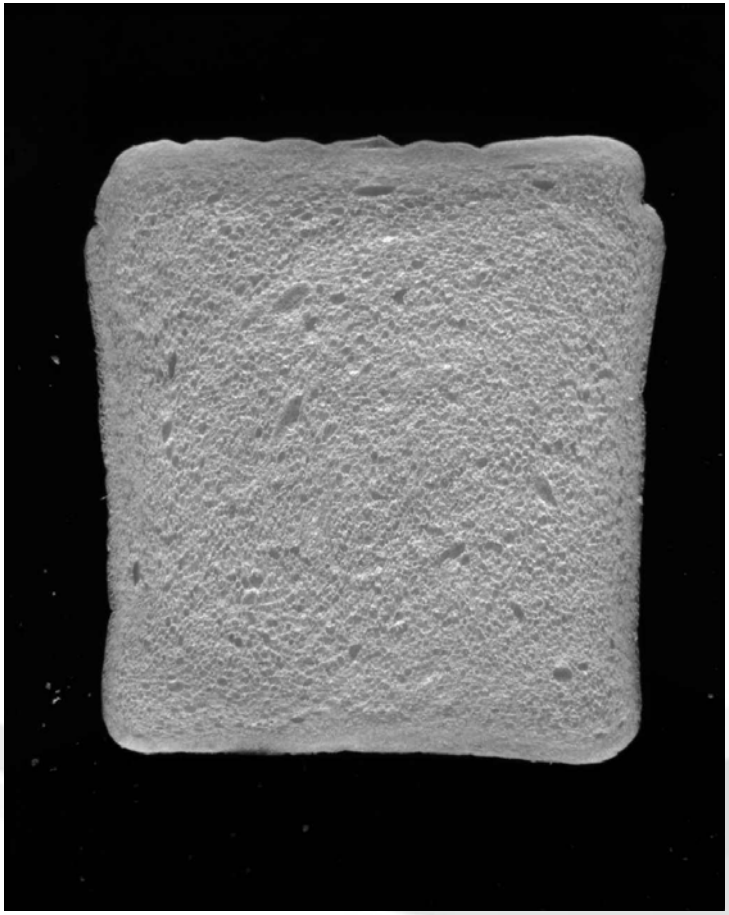
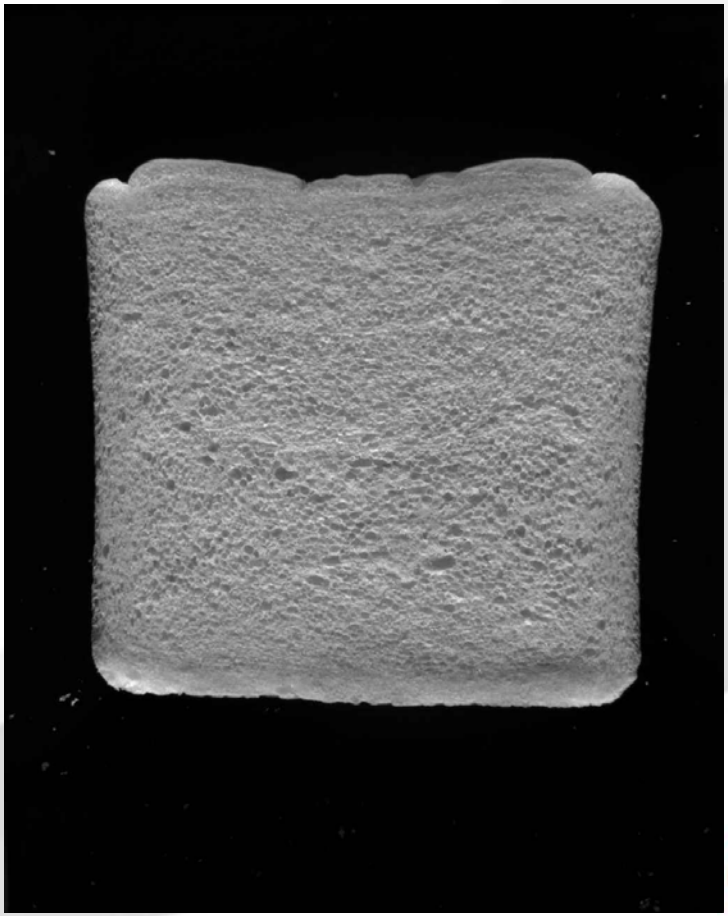
End use quality – examples of product variation for CBP bread

Good performance



Poor performance



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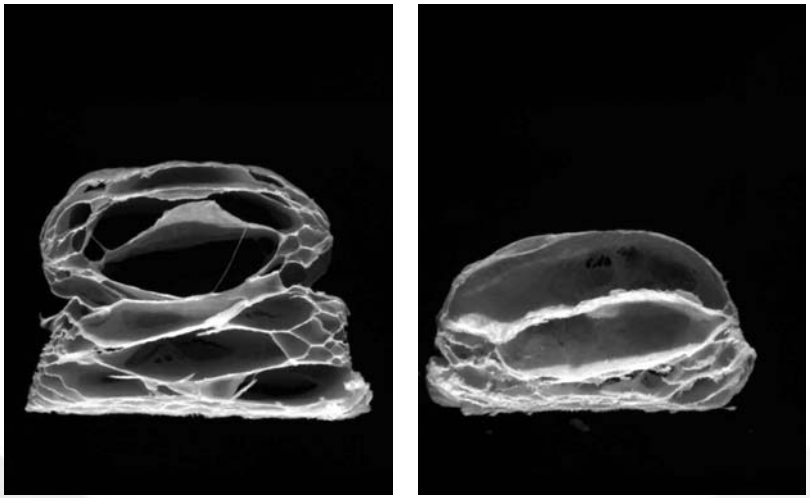
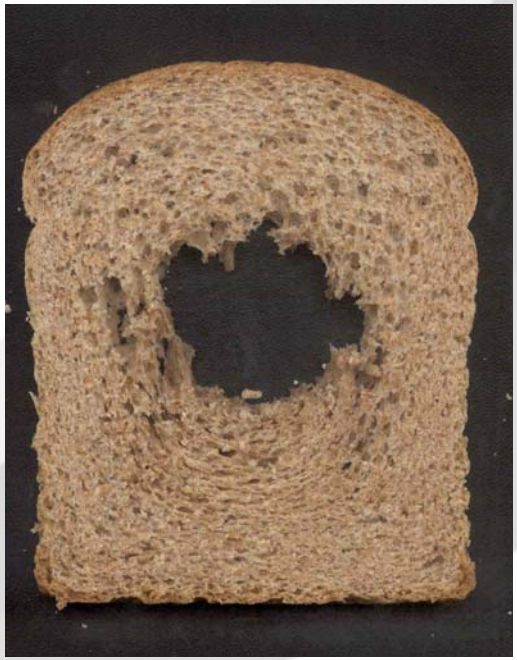
End use quality – examples of variability in other products assessed

Wide variation in lift, structure and tenderness for puff pastry



Occasional appearance of holes in wholemeal bread



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End use quality – examples of relationships between loaf volume and crumb structure

Loaf volume = 4033ml
Cell diameter = 14.2pixels
Number of cells = 10479

Loaf volume = 3869ml
Cell diameter = 12.4pixels
Number of cells = 11576

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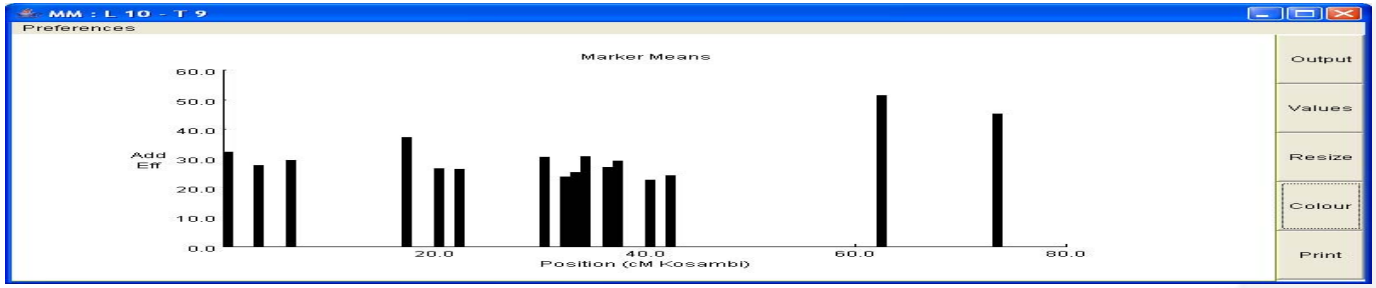
Tools for targeted wheat breeding

- Key area of development is the use of molecular markers
- These markers represent small sequences of wheat DNA located in specific regions on the chromosomes
- Where these markers are linked to specific properties (e.g. dwarfing genes, grain hardness, protein subunits) they give breeders a rapid means of assessing lines from an early stage using DNA fingerprinting
- Marker technology is expensive but extremely powerful
- Marker approaches often used with specific quantitative trait loci (QTL), regions of the chromosomes which correlate with specific characteristics (e.g. milling performance, protein content, baking performance)

Developing links between genetic and end use data – QTL analysis

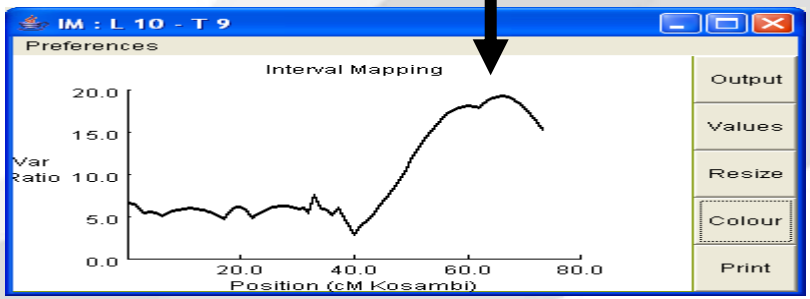


QTL Mapping by Interval mapping

QTL Mapping by Interval Mapping: Result 1 QTL
Linkage Group: 10
Trait: 9
QTL located at 66 cM
Test Statistics : F 19.3566 LR 18.0006

Res. SS - Full Model	1154373.6	d.f.	96
Res. SS - Red. Model	1387131.1	d.f.	97
Mean	3103.163		
Add Eff.	53.2465		

QTL location



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Summary of overall method used in project

- Three populations of quality wheat were produced by plant breeders based on Malacca×Charger, Shango×Shamrock and Hereward×Malacca
- Lines (~100) were selected from each population with a view to having a range of baking characteristics represented in the final sample sets
- Genetic markers for each population were applied to develop genetic maps for QTL analysis
- Seed from each population was bulked up over several years to give 2 harvest years in which suitable (~25kg) quantities for quality testing were produced.

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Summary of overall method used in project

- Over the 2005 and 2006 harvest years, each population was milled, quality tested and baked for four bakery products : CBP white bread, wholemeal bread, Spiral white bread and puff pastry
- Objective methods of assessing product quality were developed and used to assess each sample
- Quantitative trait loci (QTL) were identified for each of the objectively assessed parameters

End use assessment of 2005 and 2006 harvest material – basic grain quality

	Protein (%) dmb		Hardness		HFN (s)	
	Mean	Range	Mean	Range	Mean	Range
			2005			
H×M	14.4	13.5-15.2	72	56-83	322	169-418
M×C	13.1	11.8-14.8	60	45-70	351	236-440
S×S	12.8	12.1-13.8	70	44-93	211	98-302
			2006			
H×M	14.6	13.5-15.7	65	57-74	405	352-443
M×C	13.4	12.2-14.4	65	47-81	417	288-492
S×S	15.1	13.9-16.9	77	61-93	385	312-450

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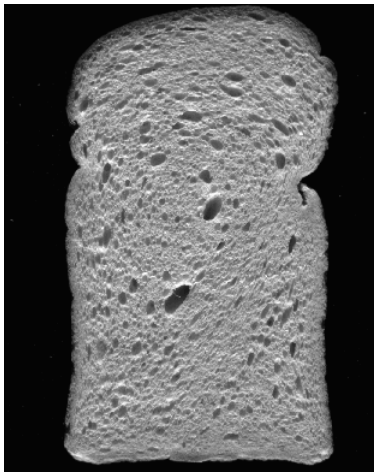
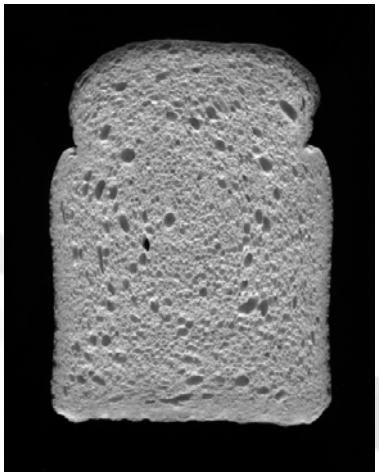
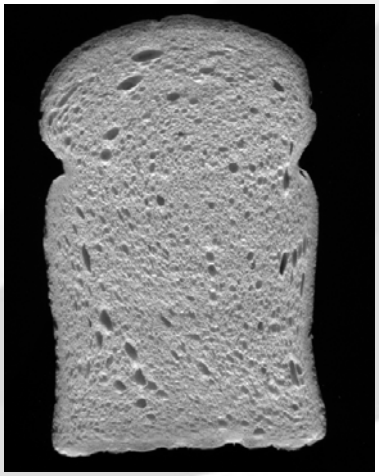
Ranking of samples for one population

Worst	Middle	Best	
			2006
			2005

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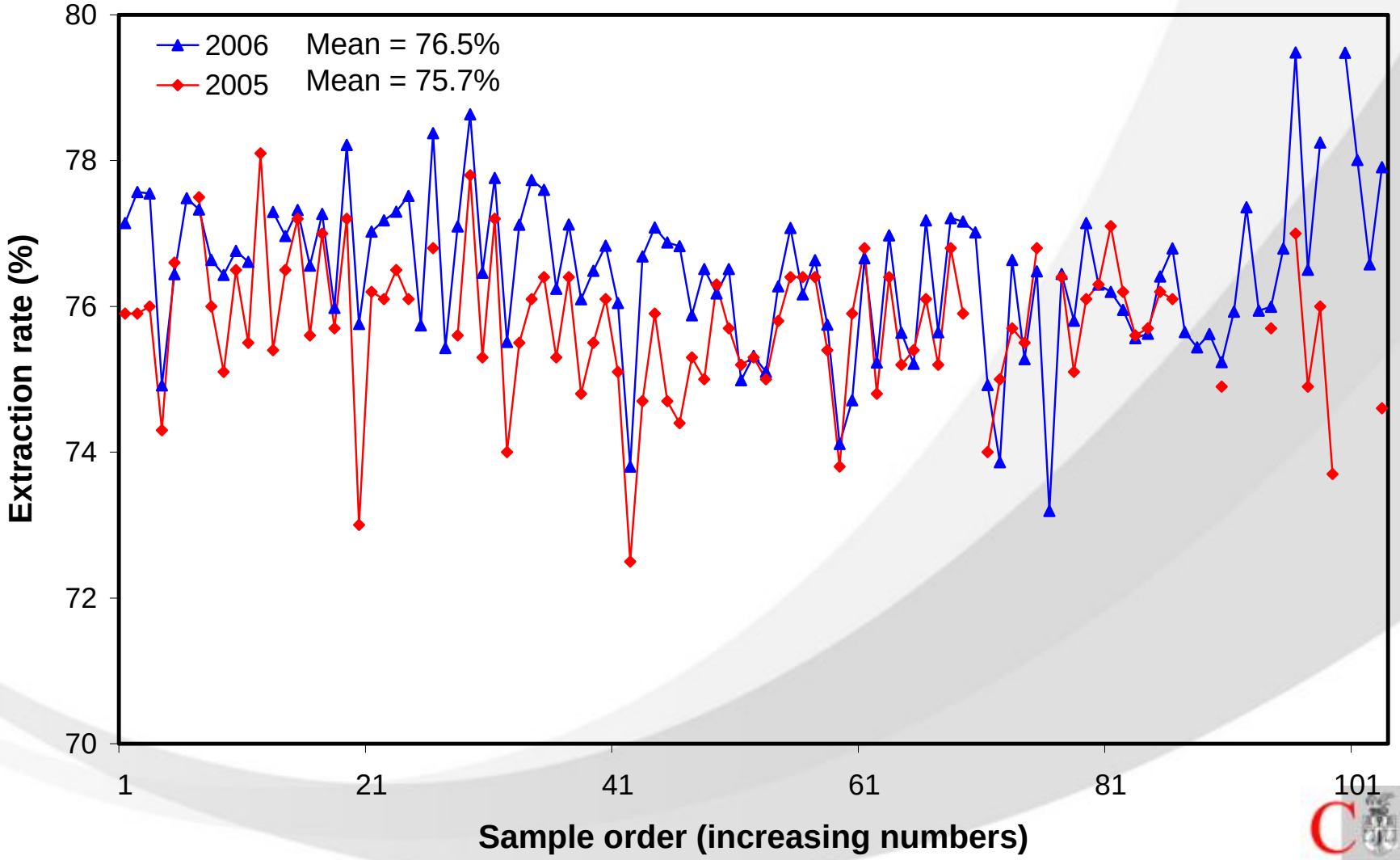
Milling extraction for H×M showing transgressive segregation



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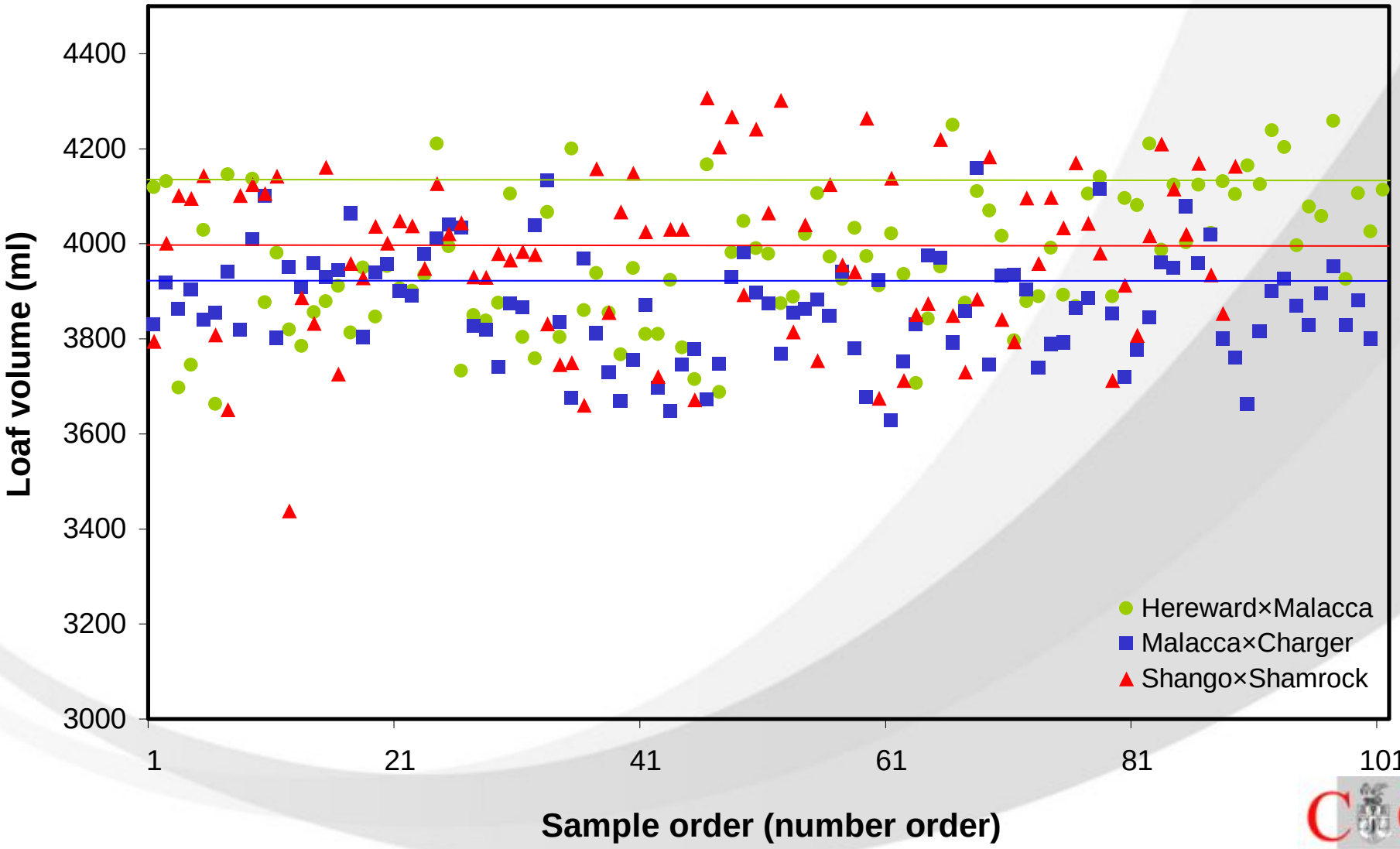
Loaf volume for Spiral white bread for all populations from 2006 harvest – lines represent upper parent



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Identifying molecular markers (mapping) each population – final genotype file

DH lines (~100) →

Markers (274) ↓

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Example QTL summary showing common responses across years

End use response →

Linkage group ↓

	2006	2005		2006	2005		2006	2005		2006	2005		2006	2005		2006	2005		2006	2005		2006	2005
linkage group	Loaf volume, ml	Loaf volume, ml		L*	L*		Firmness @25% compression (Day 1), N	Firmness @25% compression (Day 1), N		Firmness @25% compression (Day 3), N	Firmness @25% compression (Day 3), N		Average Height_Max	Average Height_Max		Number_of_Cells	Number_of_Cells		Wall_Thickness	Wall_Thickness		Cell_Diameter	Cell_Diameter
1				** G	* G			** G			* G		* R	** R			* RG		* R	* R		* R	** R
2	* G	** G		*** G	** G		* R			* R			*** G	*** G		*** G	*** G			*** R			*** R
3											* G									* R			* R
4							* R						* G	* G		** G	* G		** R	* R		** R	* R
5										* R	* R						* G			* R			* R
6					** R		* G			* G				* G		** G	* G		* R			* R	* R
7		* R		* G			*** G			** G	* G						* R		** G	*** G		* G	*** G
8																			*** R			** R	
9													* G				* G						
10					* G																		
11																							
12																							
13																* G							
14							* G			* G													
15														* G									
16																						* R	
17																							
18																			** G			*** G	
19		* G			* G			** R		* R	** R			** G			* G		* G				
20		** R			* R								*** R	* RG			* R					** R	
21																							
22				** G				* R			* R			* G		* G							
23		** G												* G									
24																	* R			* G			* G
25		** G			*** G									* G			** G						
26		* G		* R									* G			** G			* R			* R	
27					* R		** G			* G			** R	** R		** R	*** R			** G			* G
28		** R			* R									** R			* R						
29		** G						* R			* R		* G	** G									
30				* R			* G			* G							* R						* G
31		** R			* R		* G			* G				** R			** R			* G			* G
32				* G	* G											** G	* G		** R	* R		* R	
33				* G												* G							
34																							
35					* R																		

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QTL linking loaf volume and protein content for Spiral white

	Protein	Protein		SKCS	SKCS		WAB	WAB		DDT	DDT
linkage	1	1		3	3		10	10		11	11
1		*** R									
2	* G			* R	* R			* R			
3											
4	*** R/G										
5								* G			
6		** G			** G			*** G			* G
7	** R	* R		*** R	* R		*** R	* R		*** R	*** R
8		* R									

QTL in linkage group 7 for S×S. Shamrock gives higher protein content and water absorption

	2006	2005			2006	2005		2006	2005		2006	2005		2006	2005		2006	2005
	1	2			3	10		4	17		5	32		8	62		9	69
linkage	Loaf volume (ml)	Loaf volume (ml)			Day 1 TPA firmness(g)	Day 1 TPA firmness(g)		Day 3 TPA firmness(g)	Day 3 TPA firmness(g)		Height (max) / px	Height (max) / px		Cell Diameter / px	Cell Diameter / px		Coarse Cell Volume	Coarse Cell Volume
1	* R	* R			* G						* R	* R		* G	* G		* G	* G
2	* G								* G		* G			* R				
3																		
4					* R										** G			** G
5								* R										
6						* R			* R						** G			** G
7	*** R	*** R			*** G	*** G		*** G	*** G		*** R	*** R		*** R	** R		*** R	** R
8																		

QTL in linkage group 7 for S×S. Shamrock gives greater loaf volume, softer crumb and larger cells

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QTL linking loaf volume to greater numbers of cells in bread products

linkage	2006 Loaf volume, ml	2005 Loaf volume, ml	2006 L*	2005 L*	2006 Average Height_Max	2005 Average Height_Max	2006 Number_of_Cells	2005 Number_of_Cells
1			** G	* G	* R	** R		* RG
2	* G	** G	*** G	** G	*** G	*** G	*** G	*** G
3								

QTL in linkage group 2 for S×S CBP. Shango gives greater loaf volume and more cells

linkage	2006 9 Loaf Volume ml	2005 9 Loaf volume, ml	2006 10 L*	2005 10 L*	2006 20 Number_of_Cells	2005 44 Number_of_Cells
1						
2						
3			* C			
4						
5	* C	* C				* C
6						
7	* C		** M	* M	** C	
8			* M	* M		
9	* M	** M	** M		** M	* M
10	** M	*** M	* M	*** M	*** M	*** M
11					* M	
12	** M	** M		*** M	* M	** M
13				*** C		

QTL in linkage group 10 for M×C wholemeal. Malacca gives greater loaf volume and more cells

linkage	2006 1 Loaf volume (ml)	2005 2 Loaf volume (ml)	2006 5 Height (max) / px	2005 32 Height (max) / px	2006 6 Number of Cells	2005 56 Number of Cells
1						
2	*** H		* H		*** H	** H
3	* H		* H			

QTL in linkage group 2 for H×M Spiral white. Hereward gives more cells but loaf volume is inconsistent

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QTL for baking effects with no milling background

/holemeal		2006	2005		2006	2005
		9	9		20	44
linkage		Loaf Volume ml	Loaf volume, ml		Number_of_Cells	Number_of_Cells
6						
7		* C			** C	
8						
9		* M	** M		** M	* M
10		** M	*** M		*** M	*** M
11					* M	
12		** M	** M		* M	** M
13						

QTL in linkage group 12 for M×C wholemeal. Malacca gives greater loaf volume and more cells with no consistent milling effects

illing	2006	2005	2006	2005		2006	2005		2006	2005		2006	2005
	3	3	7	7		8			9	8		11	9
linkage	Hardness Index (NIR),	Hardness Index (NIR),	Protein content, % (N x5.7) @14%mc	Protein content, % (N x5.7) @14%mc		Protein content, % (N x5.7) dmb			Water absorption (600 line), %	Water absorption (600 line), %		Development time, min	Development time, min
6													
7		* M							* M				
8	* C	* C	* C	* C		* C			** C	* C			
9	* M		* M			* M							
10	* M		* M	* M		* M							
11				* M									* M
12	* C								* C			* M	
13			*** M	*** C		*** M						*** M	* M

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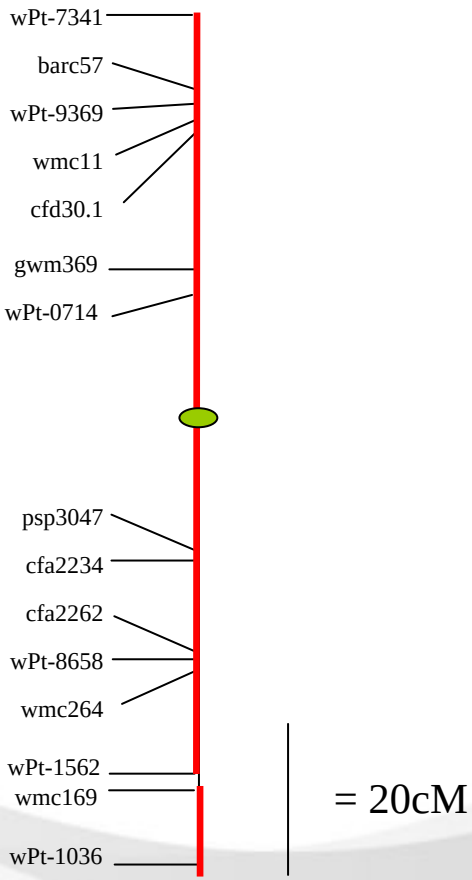
Developing links between genetic and end use data – output for plant breeders



- Objective measures of product performance mapped to markers on individual chromosomes
- Positions identified compared across products and populations
- Robust QTL across seasons then available for further development in breeding programmes

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Summary of project findings

- Significant variation in processing performance was seen over both years indicating that lines were well-selected during population development
- Objective methods used for product assessment were consistent in response and gave a solid platform for QTL analysis
- Output from both years of assessment was used to identify a number of robust QTL which control important aspects of wheat processing during baking
- These QTL will form the basis of new breeding initiatives to further improve the quality of UK wheat

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Conclusions

- The project has been a ‘once in a lifetime’ opportunity to make a step change in UK breeding for quality wheat
- The project is at the forefront of similar work globally and compares favourably with Australian and French initiatives
- The project has been a large undertaking (both financially and in timescale) but has achieved a very high measure of success
- The outputs from the project have considerable value both in terms of short to mid-term breeding exploitation as well as through the resource created for future work

Acknowledgements

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