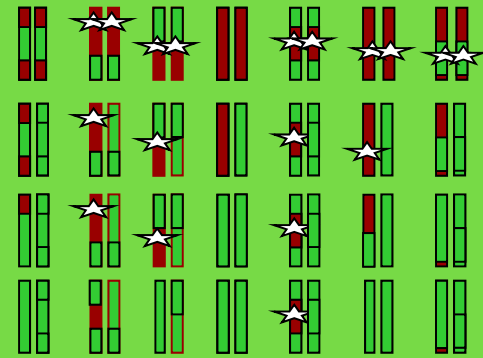
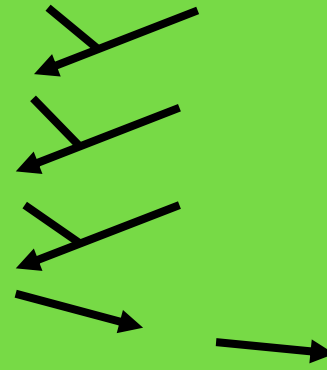


WGIN2 JIC Update

Development of Near Isogenic Lines

Near Isogenic Line development

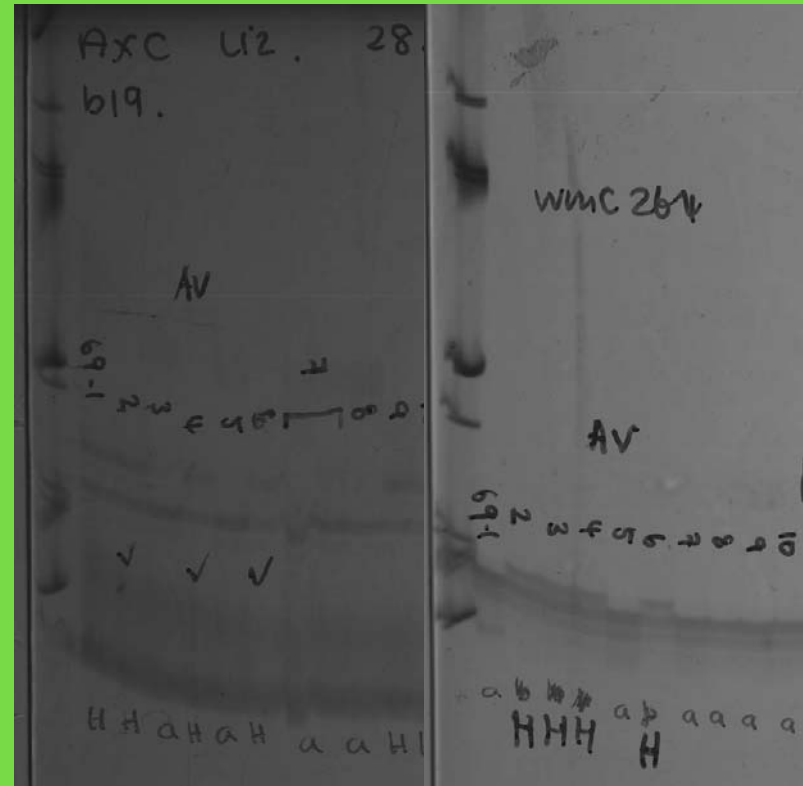
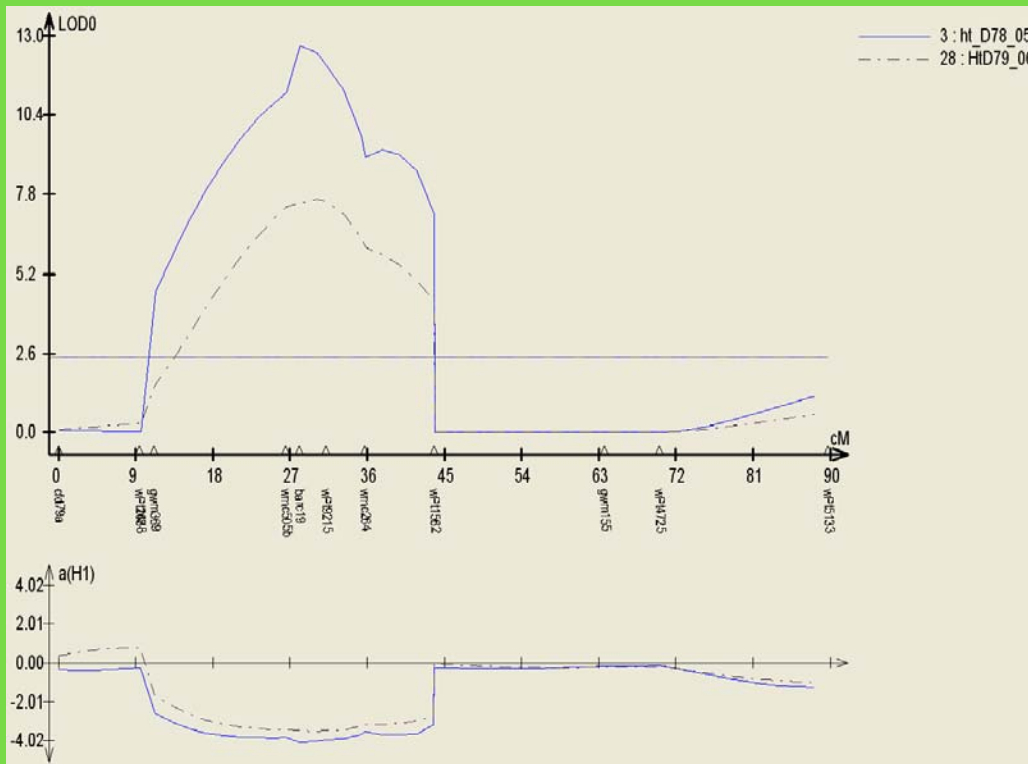
-Example of strategy for 3A height



WGIN1



WGIN2



Near isogenic line development- Yield

QTL	F ₁	BC ₁	BC ₂	Homozygotes
2D				
3B				
5A				
7B				
7D				

DNA for heterozygotes (BC₂) and homozygotes BC₂F₂ now extracted ready for MAS

Near isogenic line development- Crop height

QTL	F ₁	BC ₁	BC ₂	Homozygotes
2A	Dark Blue	Dark Blue	Dark Blue	Light Blue
2D	Dark Blue	Dark Blue	Diagonal Lines	Light Blue
3A	Dark Blue	Dark Blue	Dark Blue	Dark Blue
3B	Dark Blue	Dark Blue	Diagonal Lines	Light Blue
6A	Dark Blue	Dark Blue	Dark Blue	Light Blue
6B	Dark Blue	Dark Blue	Dark Blue	Light Blue

DNA for heterozygotes (BC₂) and homozygotes BC₂F₂ now extracted ready for MAS

Near isogenic line development- Ear emergence

QTL	F ₁	BC ₁	BC ₂	Homozygotes
1B	Dark Blue	Dark Blue	Diagonal Lines	Diagonal Lines
1D	Dark Blue	Dark Blue	Diagonal Lines	Light Blue
6B	Dark Blue	Dark Blue	Dark Blue	Light Blue

DNA for heterozygotes (BC₂) and homozygotes BC₂F₂ now extracted ready for MAS

Gamma mutagenesis



Gamma M_1 mutants:
CS bagged left (2500 sown). Paragon (2000 sown) currently bagging right
50% fertility rate expected

Now harvested M_2 seed- for sowing in spring 2010
Scope for a further 4000

Taking Paragon EMS alleles
forward

Leaf senescence segregating

Tagging plants by visiting students for
DNA collection and trait scoring



Mutant x Spring cultivars: F_2 families

12 families – segregations of mutant types height, flowering, leaf senescence and biomass



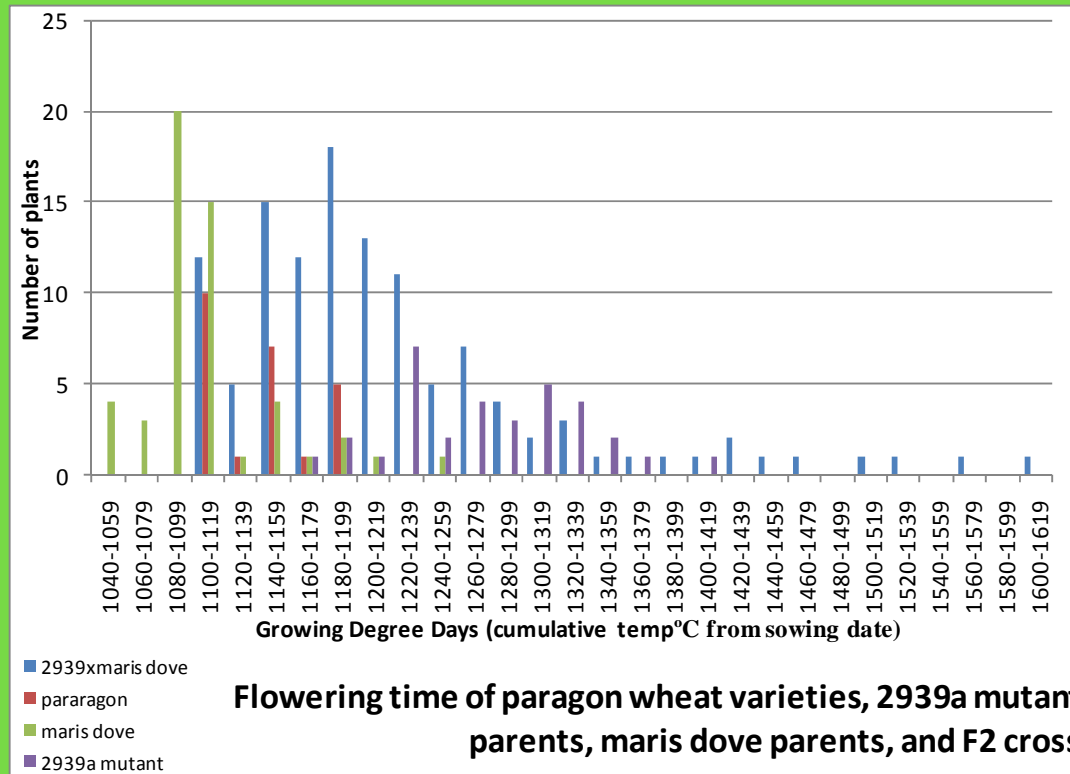
Paragon mutants in Hege 80s

Left – flowering time differences (first two plots) Right – leaf senescence

Heading date DArT data returned for heading date

- 2939a mutant was crossed with Maris Dove
- 2939a mutant was crossed with Wembley
- 423a mutant was crossed with White Fife
- 423a mutant was crossed with Koga

Segregation of ear emergence for 2939a



'Late late' 423a



Koga 7A nullisomics



AE Watkins and population development

Ten AE Watkins x Paragon SSD populations- now at F₃

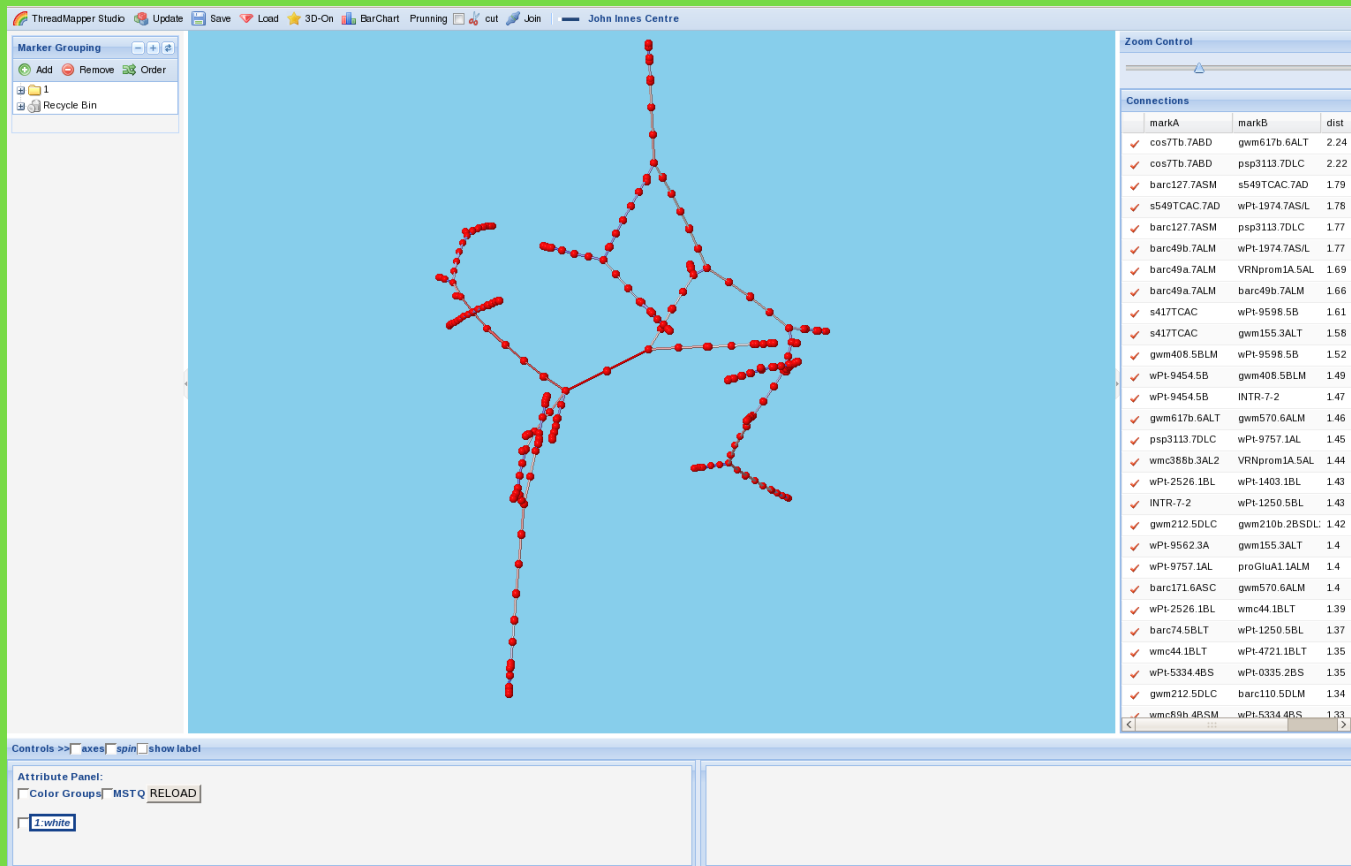
- Extremes- height and ear emergence. Ten SSD populations up to F₃ plants, therefore F₅ seed in June '10.
- More to come eg- Thousand grain weight, grain length and grain width measured on 1100 Watkins lines. Done, data ready for website now and lines sown for crossing to Paragon.
- Also 2 SSDs Paragon X CS and JIC synthetic up to F₄. F₅ seed now sown and DNA extracted.
- 1071 Watkins accessions in soil house and field (Hege 90, 1m²) Autumn '09.
- DNA extraction of soil house material (bagged) and minimum 800g of Watkins seed for further work.

Avalon x Cadenza

- Workshop When? 3rd Nov
- Where? JIC- Genome Centre Seminar Room
- JIC continues to maintain stocks

Improving A x C map

- <http://cbr.jic.ac.uk/threadmapper>



Handling data

- Development of relational database as core resource at JIC
- Propose to link version containing WGIN data to WGIN website



Navigation

- [Home](#)
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- [Map Data](#)
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- [Phenotype Data](#)

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- [Credits](#)

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View Map Definitions

The following maps were found in this version of Germinate.

To view markers contained on a map choose a map from the table below and click on its description.

Description	Created On	Updated On
JIC 2007 Savannah X Rialto map (SaXRi or RxS)	2009-05-28 16:47:21	
JIC 2007 Malacca X Charger map (MaXCh or MxC)	2009-05-28 17:10:00	
JIC 2006 Charger X Badger map (ChXBa or CxB)	2009-05-28 17:13:48	
JIC 2006 Beaver X Soisson map (BeXSo or BxS)	2009-05-28 17:31:43	
JIC 2009 Avalon X Cadenza map (AvXCa or AxC)	2009-05-28 17:43:59	

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JIC 2006 Beaver X Soisson map (BeXSo or BxS)	2009-05-28 17:31:43	
JIC 2009 Avalon X Cadenza map (AvXCa or AxC)	2009-05-28 17:43:59	

Retrieving map data for map : JIC 2009 Avalon X Cadenza map (AvXCa or AxC)

The table below contains further information about markers contained on your selected map. Clicking the marker name will take you to further information about that particular marker while clicking the 'MapChart Format' button will allow you to export the map in MapChart format. For further information about MapChart please visit <http://www.biometris.wur.nl/uk/Software/MapChart/>

[Export to MapChart Format](#)

[Show Marker Data](#)

Marker Name	Close Index	Map Feature Description	Chromosome	Feature Start	Feature End
Tagluten	1A	Gene	1A	0.00	0.00
wmc336a	1AS	SSR	1A	3.00	3.00
I102W1		Gene	1A	4.00	4.00
psp3027	1A	SSR	1A	6.00	6.00
gwm164	1A	SSR	1A	7.00	7.00
gwm498	1A	SSR	1A	8.00	8.00
GluA1		Gene	1A	9.00	9.00
wPt9757		DArT	1A	10.00	10.00
wmc93		SSR	1A	11.00	11.00
gwm99	1A	SSR	1A	12.00	12.00
gwm33a	1B	SSR	1B	0.00	0.00
wPt2230	1BS	DArT	1B	1.00	1.00
TaglgapG	1BS	Gene	1B	2.00	2.00
gwm264	5A	SSR	1B	3.00	3.00



Navigation

- Home
- Browse Accession Data
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- Trial Data
- Phenotype Data

Categorical Data Export

From these pages you are able to view phenotypic data that is held by Germinate...

[Go to the Chart Utility](#)

Experiment Name	Description	Date
JIC NUE 2008 Savannah X Rialto DH phenotypes	JIC SaXRi DH phenotypes from field trial in Bawburgh, 2008, at two nitrogen levels (low n and nor n). (Population also wrongly called RiXSa)	2007-10-16
JIC 2007 Avalon X Cadenza DH phenotypes	JIC AvXCa DH phenotypes from field trials in Bawburgh for WGIN project, 2007	2006-10-01

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John Innes Centre

Navigation

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Categorical Data Export

From these pages you are able to view phenotypic data that is held by Germinate.

[Go to the Chart Utility](#)

Dataset Description	Dataset Date	Version	Experiment Name
spikelet number per ear;2007			JIC 2007 Avalon X Cadenza DH phenotypes
ear length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
straw biomass;2007			JIC 2007 Avalon X Cadenza DH phenotypes
ear biomass;2007			JIC 2007 Avalon X Cadenza DH phenotypes
peduncle length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
internode1 length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
internode2 length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
internode3 length;2007			JIC 2007 Avalon X Cadenza DH phenotypes
1000-dehulled grain weight;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes
grain surface area;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes
grain width;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes
grain length;2007	2009-03-18		JIC 2007 Avalon X Cadenza DH phenotypes

Ok we are looking at dataset **1000-dehulled grain weight;2007**

This dataset has the following phenotypes defined against it.

Name	Short Name	Description	Export
1000-dehulled grain weight	TGRWT	The weight, measured in grams, of 1000 well-developed whole grains (without hull).	<input type="checkbox"/>

Submit

[Back](#)

WGIN at JIC



Catherine
Baker



Liz
Sayers



Richard
Goram

Luzie
Wingen

Simon
Orford



Michelle
Leverington

John
Snape

Lesley
Fish

Debora
Gasperini

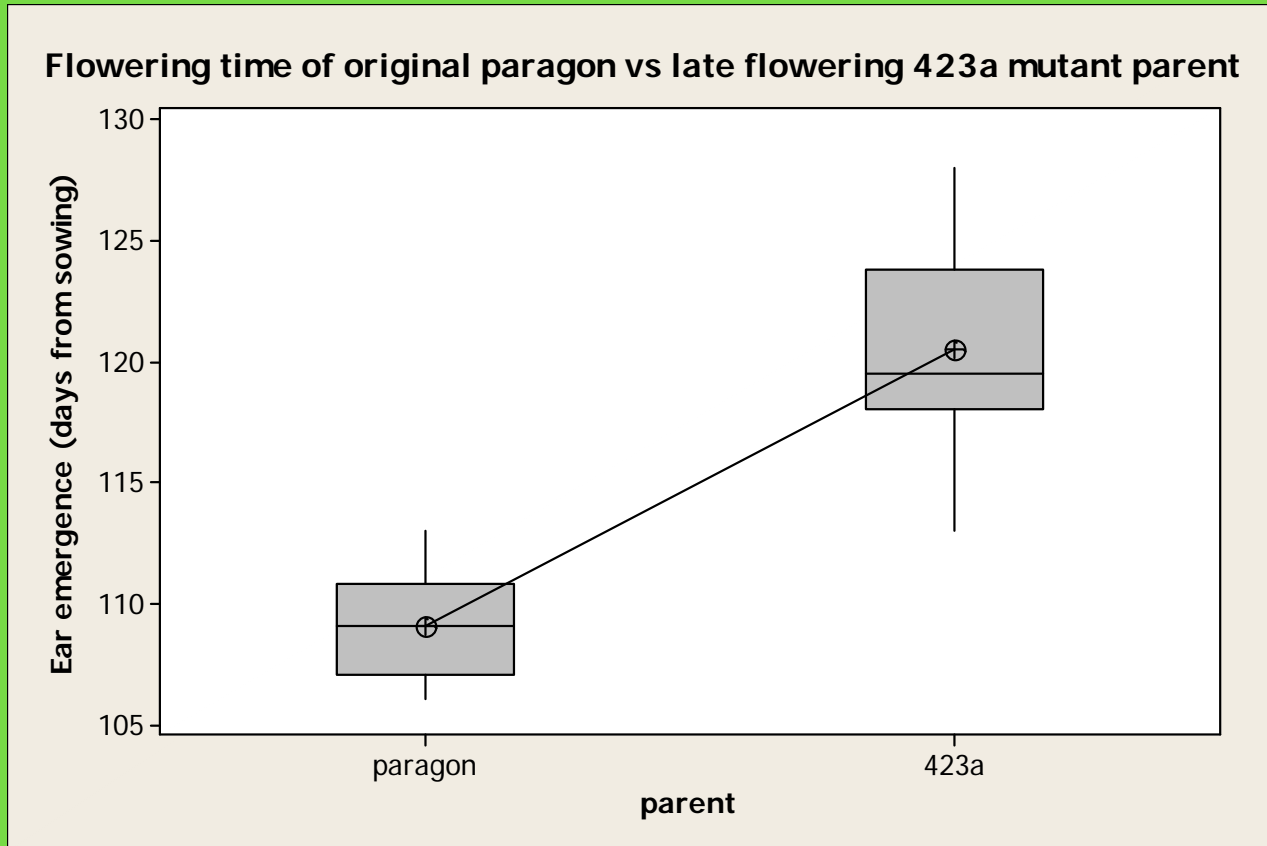
"And he gave it for his opinion, that whosoever could make **two ears of corn** or two blades of grass to grow upon a spot of ground where only one grew before, would deserve better of mankind, and do more essential service to his country, than the whole race of politicians put together."

— [Jonathan Swift](#) ([Gulliver's Travels](#))



Gamma M2 mutants: CS left
Paragon right
Frequent flag leaf rolling

Phenotypes confirmed





Insect resistance in wheat: Cereal aphids (RRes)

Ruth Gordon-Weeks and Lesley Smart

Objective 1. To explore whether the differential response of hexaploid wheats to two different cereal aphid species has a genetic basis.

Milestone 1. Determine the differential susceptibility to two cereal aphid species of targeted lines from the Spark x Rialto mapping population.

Spark x Rialto Mapping population extreme responses

Diuraphis noxia

Genotype	no. of aphids per plant
SR 120	23.33
SR 111	22.6
SR 98	16.29
SR 7	2.00
SR 67	2.00
SR 122	2.00
SR 10	1.86
SR 39	1.22
Spark	4.44
Rialto	2.71

Schizaphis graminum

Genotype	no. of aphids per plant	
SR 21	24.33	most
SR 8	23.50	preferred
SR 92	20.86	
SR 6	18.00	
SR96	18.00	
SR 110	2.83	
SR 95	2.50	
SR 4	2.25	
SR 39	2.00	least
SR 144	1.88	preferred
Spark	16.88	
Rialto	5.43	



Diuraphis noxia
Russian Wheat aphid



Schizaphis graminum
Greenbug

Family

Aphididae

Sub-family

Aphidinae

Tribe

Macrosiphini

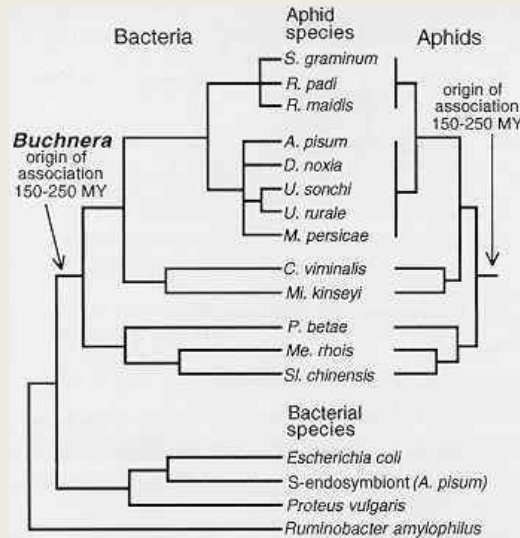
Aphidini



Sitobion avenae
Grain aphid



Rhopalosiphum padi
Bird-cherry oat aphid

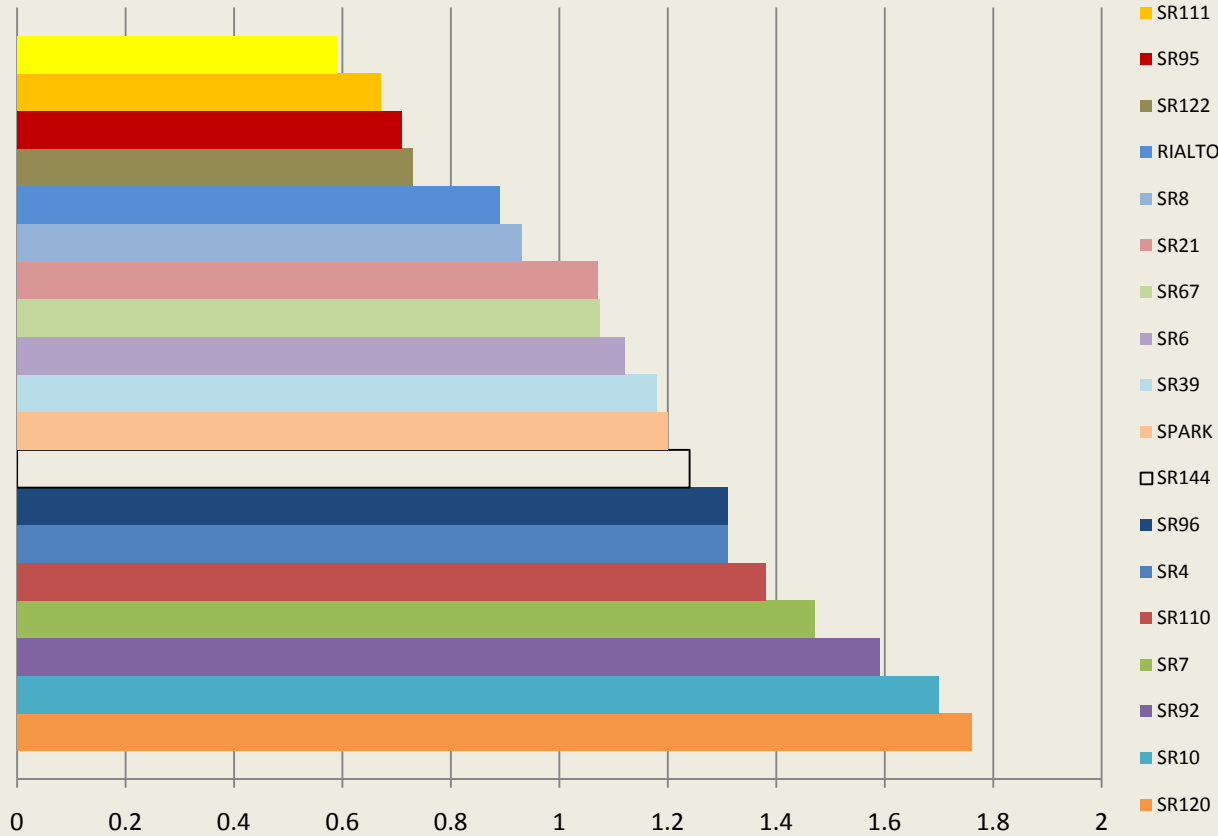




17 Genotypes plus the parental lines tested in choice tests, with cv. Solstice as the standard variety, against *Sitobion avenae* and *Rhopalosiphum padi*.

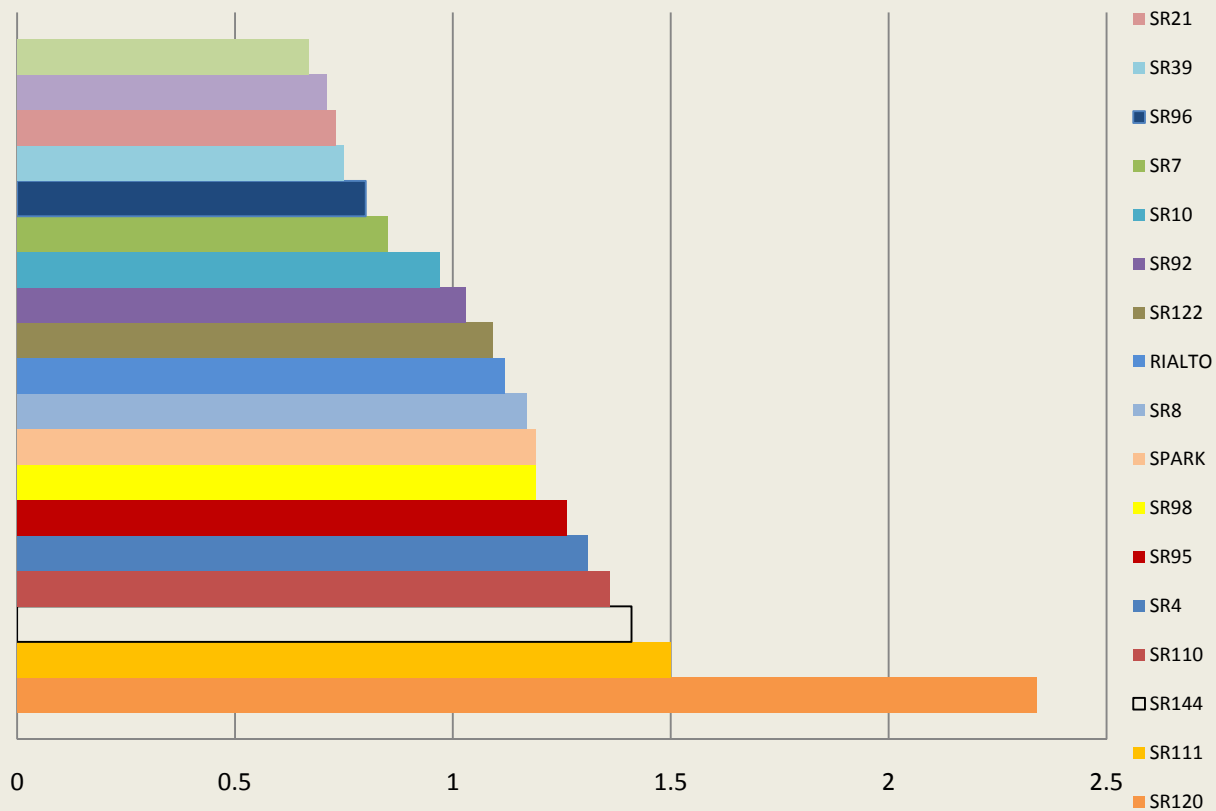
Preference Index *Sitobion avenae*

Sitobion avenae choice tests with Spark x Rialto mapping lines. Nymphs produced at 24h as a proportion of nymphs produced on Solstice = 1

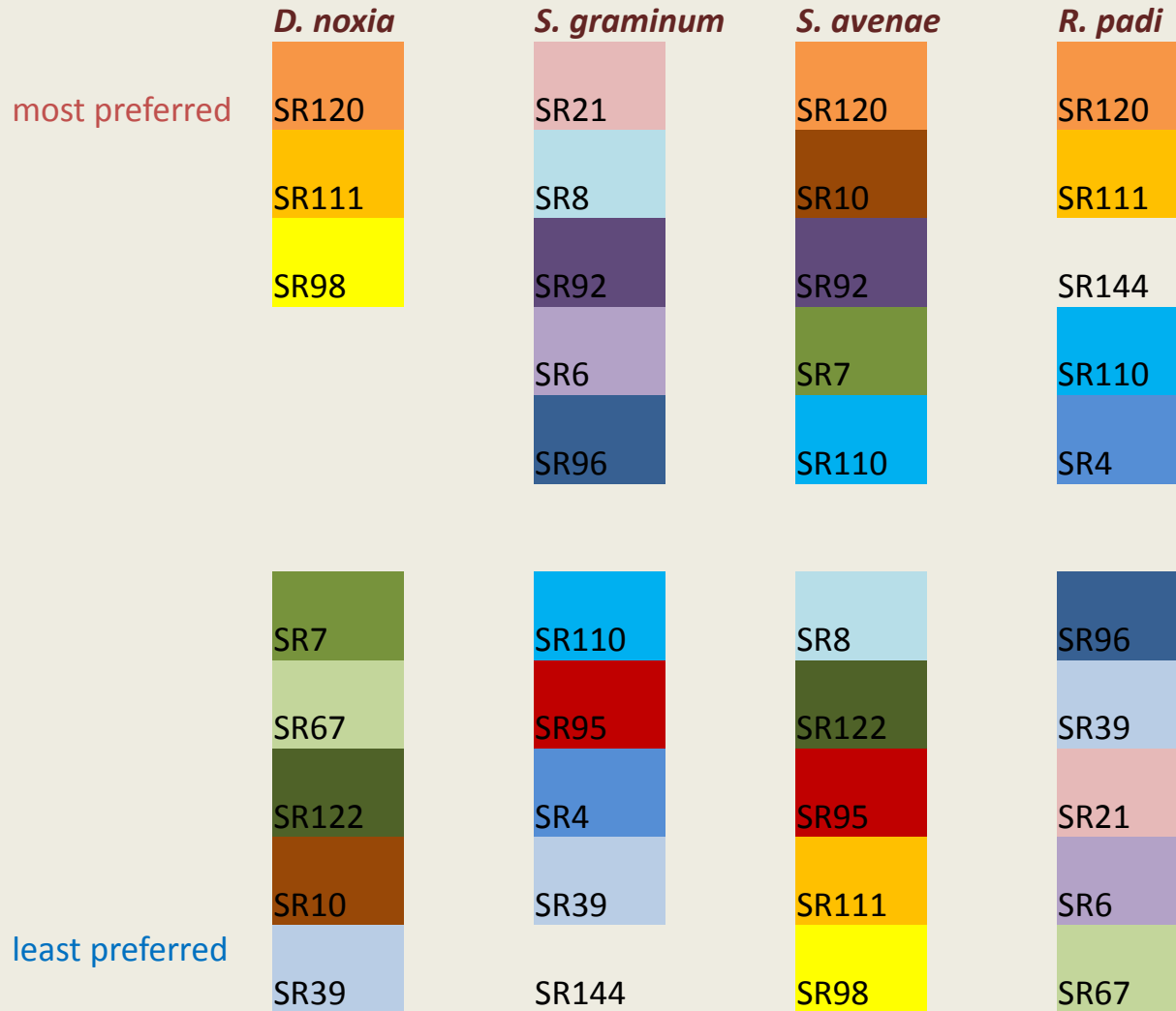


Preference Index *Rhopalosiphum padi*

Rhopalosiphum padi choice tests with Spark x Rialto mapping lines. Nymphs produced at 24h as a proportion of nymphs produced on Solstice = 1

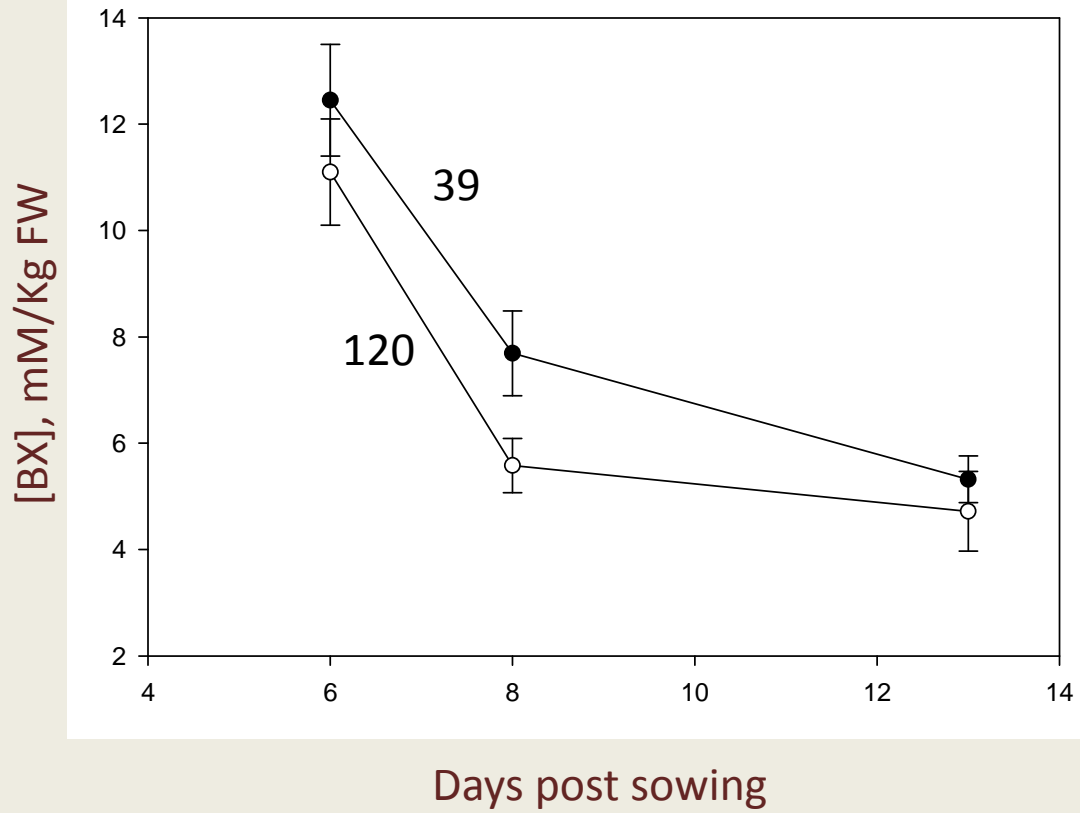


Spark x Rialto antixenosis responses



Of the two parental lines, Spark is preferred to Rialto by all aphid species tested

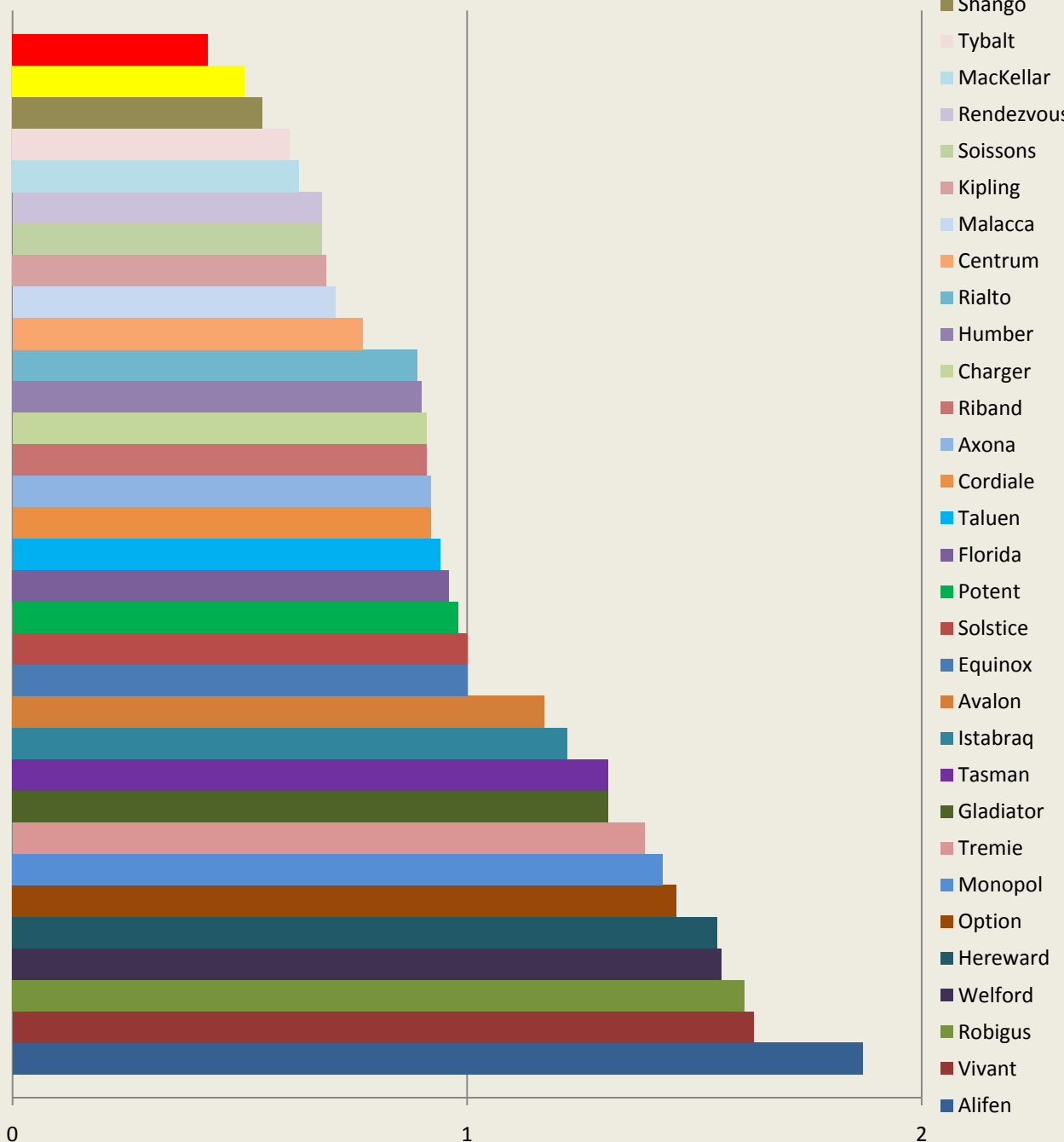
Benzoxazinone concentration in leaf tissue



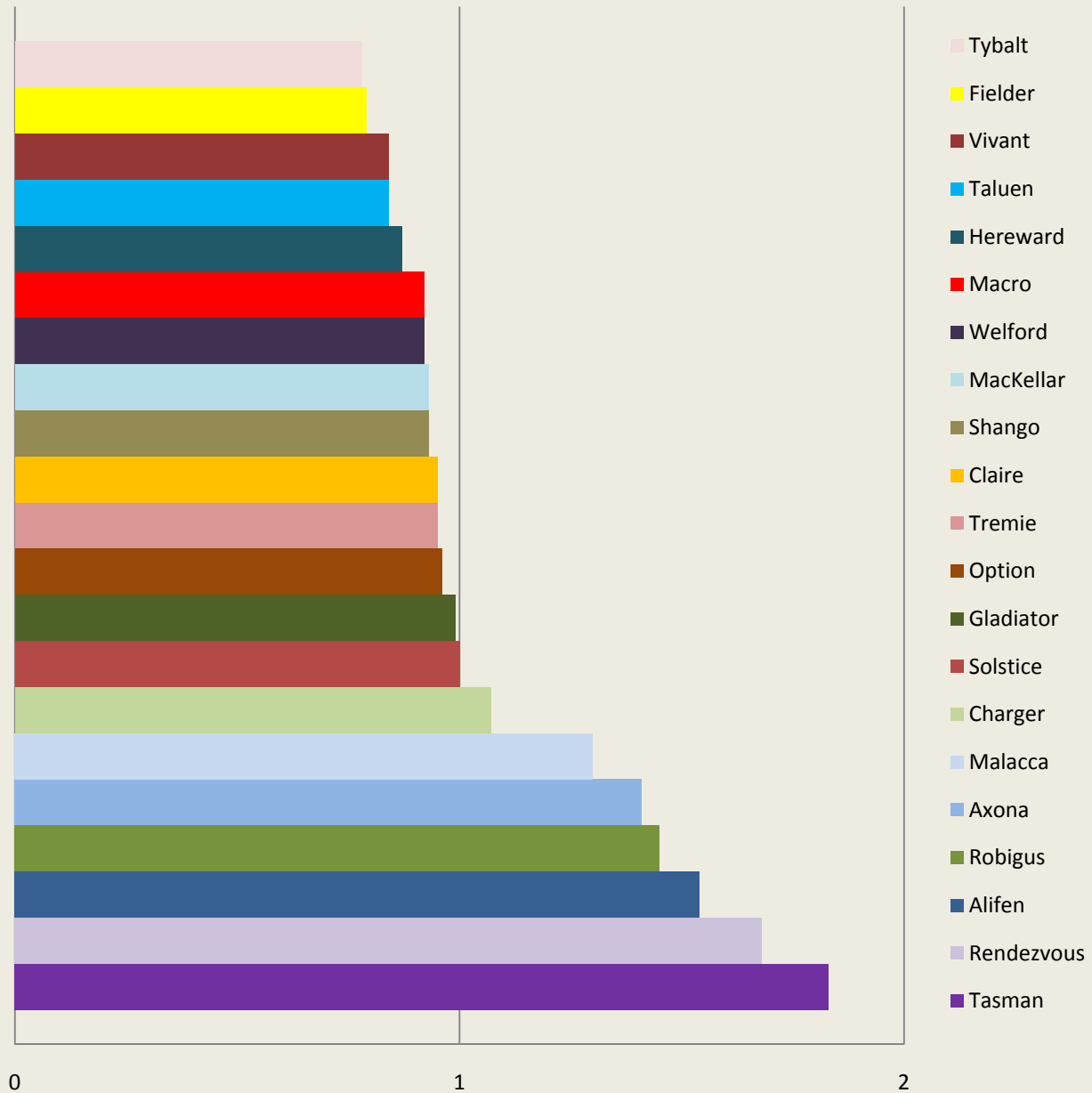
Further Work

- Conduct comparative development tests for both UK cereal aphid species on some of the least and most preferred genotypes
- Investigate levels of *BX* gene upregulation in some of the least and most preferred genotypes after infestation with the UK cereal aphid species
- Determine whether there is any genetic difference between the least and most preferred genotypes

Sitobion avenae choice tests. Nymphs produced at 24h as a proportion of nymphs produced on Solstice which = 1



***Rhopalosiphum padi* choice tests. Nymphs at 24h as a proportion of nymphs on Solstice which = 1**



Objective 8 - NUE and NUE linked QTLs

M J Hawkesford

WGIN management Meeting, 20th
October 2009

Objectives

1. Dissect components of yield and NUE parameters in varieties of interest as identified in the preliminary screening in WGIN 1.
2. Examine physiology/biochemical processes contributing to NUE and quantify expression of key genes in selected varieties.
3. Examine variation in NUE in more 'exotic' germplasm arising from WGIN.
4. Use mapping populations to identify robust key QTLs for NUE.
5. Examine variation in early seedling nitrogen uptake ability.
6. Determine whether functionality can be maintained at reduced grain protein. This will utilise bread making quality QTLs which are independent of protein content (and known storage proteins) as identified in a previous LINK project and derived from the Hereward x Malacca population.

Workplan

- Diversity/N trials 2009-2013 (5years)
 - Core 15
 - Exotics e.g. Watkins
 - Specific A x C lines
 - Other germplasm as deemed appropriate
- Avalon x Cadenza field trials 2009/10/11 (3 years)
 - high/low N (one low, 2 high N)
 - to supplement WGIN1 trials (one high, 2 low)
- Avalon x Cadenza – G/H trial 2012
- Hereward x Malacca NILS
 - fields trials 2012/13
 - 20 lines

Diversity trial

- Germplasm
 - Core set
 - New varieties: Marksman, Gallant, Oakley (Chablis)
 - Inclusion (6 varieties) as part of BBSRC-IPA on quality-yield relationships
 - Inclusion of exotic materials, e.g. A x C, Watkins, suggestions???
- Traits
 - Yield, NUE etc
 - Partitioning information
 - Analysis of post anthesis canopy longevity
 - Analysis of genotypic variation in early N-uptake efficiency

08/09 Diversity Varieties

Wheat varieties for WGIN-NUE
2008/9

Variety	Code	Dressing	Code	Data (04/05/06/07)	Rationale
1. Avalon	Av	recleaned	AV	No/05/06/07	WGIN DH parent; Low NupE & NutE (D)
2. Cadenza	Ca	recleaned	CA	04/05/06/07	WGIN DH parent; Best NupE (W)
3. Claire NEW 2005	Cl	kinto	CL	No/05/06/07	Biggest area on RL; WGIN DH parent; Good second wheat
4. Cordiale NEW 2006	Co	redigo deter	CO	No/no/06/07	Good second wheat
5. Hereward	He	anchor	HE	04/05/06/07	Best protein on RL; benchmark bread variety
6. Hurley NEW 2005	Hu	recleaned	HU	No/05/06/07	Low NupE & NutE (W)
7. Istabraq NEW 2005	Is	kinto lattitude	+IS	No/05/06/07	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat
8. Malacca	Ma	redigo deter	MA	04/05/06/07	Biggest Group 1 area; DH choice; Low NupE, high NutE (W)
9. Marksman	Mk	redigo	MK		new for 2009, PRS request
10. Maris Widgeon	Mw	sibutol	MW	04/05/06/07	Tall (rht), old cultivar
11. Mercia	Me	recleaned	ME	04/no/06/07	Low NupE & NutE (desk); Low Canopy N requirement; In IGF micro-array
12. Monopol	Mo	recleaned	MO	04/05/06/07	Breeder choice; High NupE, worst NutE (W)
13. Paragon	Pa	redigo twin	PA	04/05/06/07	Spring variety; WGIN mutagenesis population; High NupE (W)
14. Riband	Ri	recleaned	RI	04/05/06/07	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W)
15. Robigus NEW 2005	Ro	redigo deter lattitude	+RO	No/05/06/07	Best Group 3 yield; Best NUE, high NupE & NutE (D); Good second wheat
16. Soissons	Ss	redigo	SS	04/05/06/07	WGIN DH parent; Early maturing; High NupE, low NutE (W)
17. Solstice	Sl	beret gold lattitude	+SL	04/05/06/07	Biggest Group 2 area; DH choice; Worst NupE (W)
18. Xi19	Xi	redigo deter	XI	04/05/06/07	Best Group 1 yield; High NUE, NupE, NutE (D); Low NupE (W)
19. AxC line 100	D1	recleaned			new for 2009 - good early export from leaves
20. AxC line 116	D2	recleaned			new for 2009 - poor early export from leaves
21. AxC line 99	D3	recleaned			new for 2009 - high leaf %N at anthesis
22. AxC line 155	D4	recleaned			new for 2009 - low leaf %N at anthesis
23. AxC line 127	D5	recleaned			new for 2009 - high NutE
24. AxC line 82	D6	recleaned			new for 2009 - low NutE

Wheat varieties for WGIN-NUE 2009/10

W=WGIN data, D=desk study

Variety	Code	Dressing	Code	Nabim	Rationale	inclusion in trial requested by	previous years of trials
1. Avalon	Av	recleaned	AV	1	WGIN DH parent; Low NupE & NutE (D)	PB, RG, MJH	No/05/06/07/08/09
2. Cadenza	Ca	recleaned	CA	2	WGIN DH parent; Best NupE (W)	PB, RG, MJH	04/05/06/07/08/09
3. Chablis NEW 09/10	Ch			2	SPRING variety (previous grown in 2004 trial) as very N-responsive variety	MH	only in 04
4. Claire NEW 2005	Cl	kinto	CL	3	Biggest area on RL; WGIN DH parent; Good second wheat	PB,PS	No/05/06/07/08/09
5. Cordiale NEW 2006	Co	redigo deter	CO	2	Good second wheat. BBSRC Quality project	RG	No/no/06/07/08/09
6. Gallant NEW 09/10				1	new claimed high yield and high protein type	MH	
7. Hereward	He	anchor	HE	1	Best protein on RL; benchmark bread variety. BBSRC Quality project	PB,PS	04/05/06/07//08/09
8. Istabraq NEW 2005	Is	kinto + lattitude	IS	4	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat. BBSRC Quality project. WUE trial	PB,PS	No/05/06/07/08/09
9. Malacca	Ma	redigo deter	MA	1	Biggest Group 1 area; DH choice; Low NupE, high NutE (W). BBSRC Quality project	PS	04/05/06/07/08/09
10. Marksman	Mk	redigo	MK	2	new for 2009, PRS request for BBSRC Quality project	PB, AM	only 09
11. Maris Widgeon	Mw	sibutol	MW	1	Tall (rht), old cultivar	PB, AM	04/05/06/07/08/09
12. Mercia	Me	recleaned	ME	1	Low NupE & NutE (desk); Low Canopy N requirement; In IGF micro-array. WUE trial. RHT series	WUE	04/no/06/07/08/09
13. Oakley NEW 09/10	Oa			4 (hard)	Hard milling type. Highest yielding wheat on RL.	MH	
14. Paragon	Pa	redigo twin	PA	1	Spring variety; WGIN mutagenesis population; High NupE (W)	PB	04/05/06/07/08/09
15. Riband	Ri	recleaned	RI	3	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W)	RG	04/05/06/07/08/09
16. Robigus NEW 2005	Ro	redigo deter + lattitude	RO	3	Best Group 3 yield; Best NUE, high NupE & NutE (D); Good second wheat. WUE trial	PB, AM	No/05/06/07/08/09
17. Soissons	Ss	redigo	SS	2	WGIN DH parent; Early maturing; High NupE, low NutE (W)	PB,RG, AM	04/05/06/07/08/09
18. Solstice	Sl	beret gold + lasttitude	SL	2	Biggest Group 2 area; DH choice; Worst NupE (W)	RG	04/05/06/07/08/09
19. Xi19	Xi	redigo deter	XI	1	Best Group 1 yield; High NUE, NupE, NutE (D); Low NupE (W). BBSRC Quality project. WUE trial	PB,PS	04/05/06/07/08/09
20. AxC line 100	D1	recleaned			new in 2009 - high NUTe		09/
21. AxC line 116	D2	recleaned			new in 2009 - low NUTe	MJH	09/
22. AxC line 181	D3	recleaned			new in 2010 - rapid canopy senescence	MJH	10/
23. AxC line 112	D4	recleaned			new in 2010 - slow canopy senescence	MJH	10/
24. AxC line 127	D5	recleaned			new in 2009 - good early export from leaves		
						MJH	09/10/
25. AxC line 82	D6	recleaned			new in 2009 - slow early export from leaves		
						MJH	09/10/

2008/09 Diversity Trial



BBC filming, 3rd August, 2009



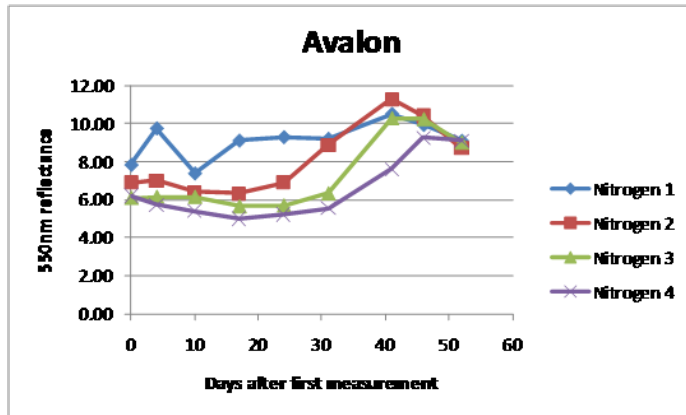
A x C traits - Rothamsted

- Flowering time and height
- Yield (grain and straw) and tgw
- Nitrogen (grain and straw)
- Computed NUtE, N uptake (final)
- Early N uptake

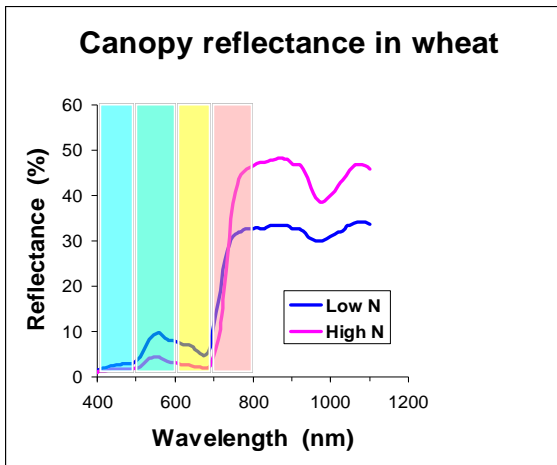
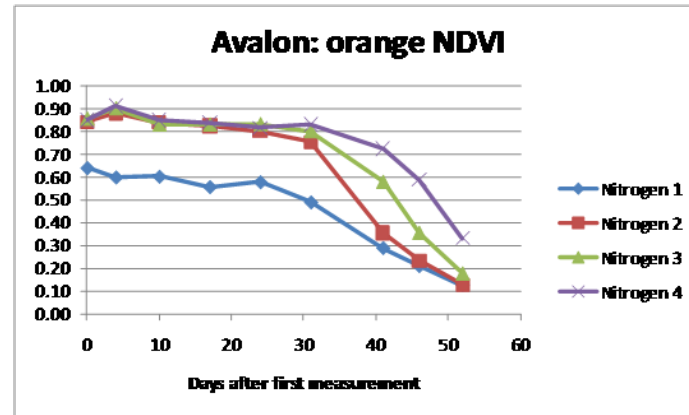
- Leaf N and SPAD (anthesis and 21 dpa)
- Leaf size (leaf 2)
- Canopy longevity, reflectance, rate of senescence
- Gene expression

Canopy screening

Reflectance (550nm)



$oNVDI = (750 - 680) / (750 + 680)$



Drought tolerance

WGIN-2 SG meeting

Sutton Bonington 20 October 2009



The University of
Nottingham

WGIN 2 (Activity 9, Drought tolerance)

- 1. To identify the physiological traits explaining improved water-use efficiency and drought tolerance in elite winter wheat varieties.**
- 2. To identify robust QTLs for water-use efficiency and drought-tolerance traits using one existing DH population in an elite background.**
- 3. To develop one new DH population in an elite modern background segregating for drought-tolerance traits.**
- 4. To identify novel genes and alleles controlling water-use efficiency and drought tolerance using the AE Watkins and Gediflux collections.**
- 5. To collate a diverse germplasm collection (cultivars, advanced lines) from worldwide drought-tolerance wheat breeding programmes as a resource for future association genetics studies.**

WGIN 2 (Activity 9, Drought tolerance)

	Project Month	Milestone
30/11//2011	36	Act 9 Obj1: Complete phenotyping and data analysis for drought tolerance traits in elite winter wheat varieties in 2009/10 &10/11.
30/11/2012	48	Act 9 Obj2: QTL analysis to identify genome locations associated with WUE and drought tolerance traits completed.
31/03/2012	40	Act 9 Obj3. Complete development of one new DH population in an elite modern background segregating for drought-tolerance traits.
28/02/2013	51	Act 9 Obj4: Association genetics analysis of drought tolerance traits using AE Watkins & Gediflux collections completed.
28/02/2013	51	Act 9 Obj5: Collation of diverse germplasm collection (cultivars, advanced lines) from worldwide drought-tolerance wheat breeding programmes completed.

WUE trial 2009-10

Split plot design (3 reps): plot size 1.6 x 12 m

Main plot: Fully irrigated (trickle irrigation)
Unirrigated

Split plot (variety):

1. Var 1 (LINK, Tol)
 2. Var 2 (LINK, Tol)
 3. Var 3 (LINK, Tol)
 4. Var 4 (LINK, Intol)
 5. Var 5 LINK, Intol)
 6. Var 6 (LINK, Intol)
 7. Cadenza ~ parent EMS pop *
 8. Beaver ~ low WUE
 9. Gallant - crossover variety high GPC and yield *
 10. Hereward - standard variety in several NUE projects *
 11. Istabraq - included as a main variety in the 'Green Grain' project *
 12. Oakley - high YP (good for examining trade off between YP and WUE) *
 13. Xi19 - some reports that has high WUE *
 14. Rialto ~ parent DH pop
 15. Savannah ~ parent DH pop
 16. Soissons ~ high WUE
- * Common with NUE trial



ANALYTICAL REPORT

Report Number	78459-09	L935	JOHN ALCOCK	Client	SB53704729
Date Received	12-MAY-2009		DIV. OF AGRIC & ENVIRON		
Date Reported	01-JUN-2009		UNIV OF NOTTINGHAM		
Project	SOIL MINERAL NITROGEN		SUTTON BONINGTON CAMPUS		
Reference	SB53704729		LOUGHBOROUGH		
Order Number			LEICS LE12 5RD		

Laboratory Reference		MINN50605	MINN50607	MINN50608	MINN50609					
Sample Reference		FIELD 2 0-30	FIELD 2 50-90	FIELD 4 0-30	FIELD 4 60-90					
Determinand	Unit	SOIL	SOIL	SOIL	SOIL					
Dry Matter	% w/w	87.7	88.8	87.7	87.7					
Nitrate Nitrogen	mg/kg	55.92	7.21	62.09	7.04					
Ammonium Nitrogen	mg/kg	86.61	1.68	53.34	2.29					
Available Nitrogen 30cm profile	kgN/ha	490.1	35.5	461.7	37.3					
Sand 2.00-0.063mm	% w/w	65	80	82	66					
Silt 0.063-0.002mm	% w/w	23	11	27	15					
Clay <0.002mm	% w/w	12	9	11	19					
WHC at 0.33 Bar	% w/w	13.7	9.4	15.6	14.8					
WHC at 15 Bar	% w/w	6.4	3.5	6.9	7.3					
Textural Class		Sandy Loam	Loamy Sand	Sandy Loam	Sandy Clay Loam					

Notes

Analysis Notes The sample submitted was of adequate size to complete all analysis requested.
 The results as reported relate only to the item(s) submitted for testing.
 The results are presented on a dry matter basis unless otherwise stipulated, with correction for stone content.
 If stones content not stipulated on sample submission form then 0% Stones assumed.
 If the depth was not 30cm, this must be taken into account when calculating nitrogen recommendations.

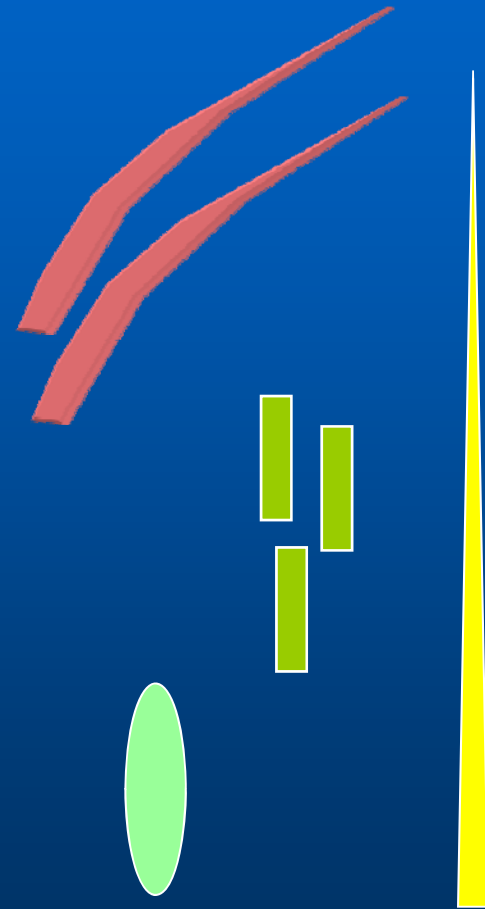
Sample Storage The sample will be kept as the dry ground sample for at least 1 month.

Document Control This test report shall not be reproduced, except in full, without the written approval of the laboratory.

Reported by *Andrew Chase*
 Natural Resource Management Ltd.
 Coopers Bridge, Braziers Lane, Bracknell, Berkshire, RG42 6NS
 Tel: 01344 886338
 Fax: 01344 890972
 email: enquiries@nrm.uk.com

Measurements

- **Combine grain yield, yield components**
- **DM and partitioning at GS31, GS61, harvest**
- **% stem WSC at GS61+10d**
- **Leaf senescence kinetics for flag-leaf, L2 and L3.**
- **TE by ^{13}C Δ grain samples**
- **Stomatal conductance/photosynthetic rate using Licor (subset only)**
- **Water use ~ gravimetric analysis of soil cores (subset only)**



Evaluation of novel genetic resources

- NIAB backcrossing CIMMYT synthetic wheats (shown in Mexico to have improved drought tolerance) in Xi19 background.
- 29 BC1F3 families grown in small plots (4 x 1 m) and the recurrent parent (Xi19) on the drought-prone light sand at Bunny Park Farm.

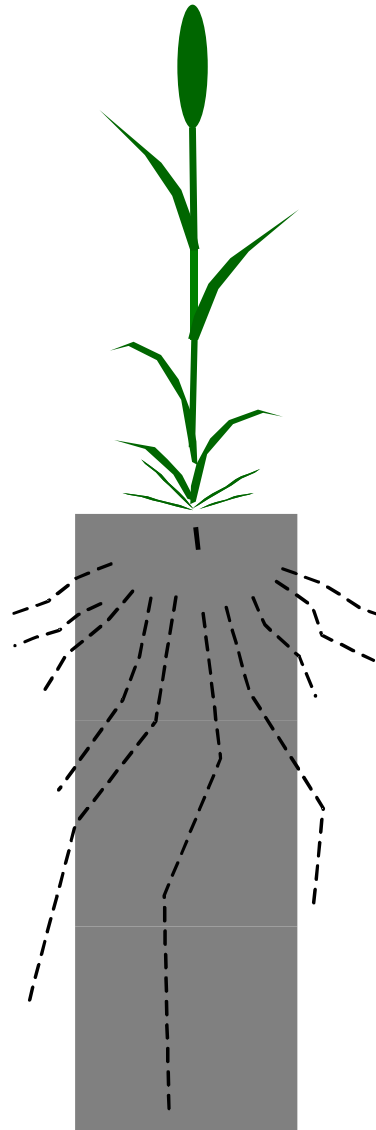
Ideotype for high sustainable yield under drought

OPTIMIZE WUE

- High ^{13}C Δ
- Pn capacity
- Specific leaf N

MAXIMIZE HARVEST INDEX

- Stem CHO reserves
- Stay green



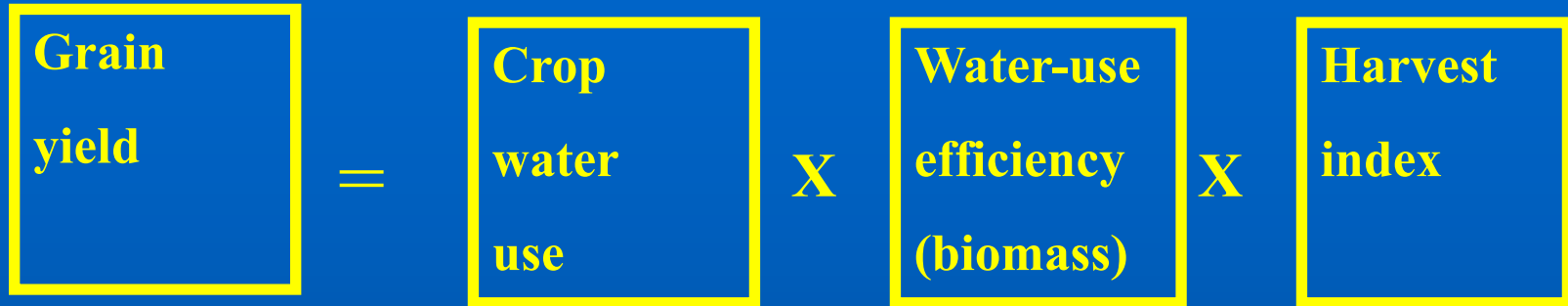
MAXIMIZE WATER CAPTURE

- RLD at depth
- β (distribute roots deeper)
- Specific root length

EARLINESS

- Extend stem elongation phase
- Early onset GS31

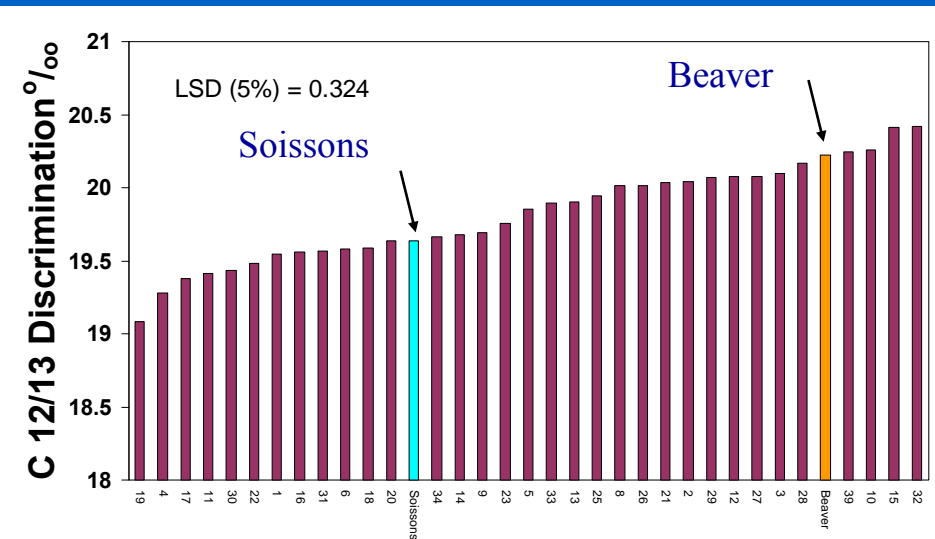
Drought Resistance: Target traits



Target traits →

- Stay-green
 - Root density
 - Transpiration efficiency (^{13}C Δ)
 - Awns
 - Flowering
 - Stem CHO reserves
-

Transpiration efficiency: ^{13}C Isotope Discrimination (grain): Beaver x Soissons DH population



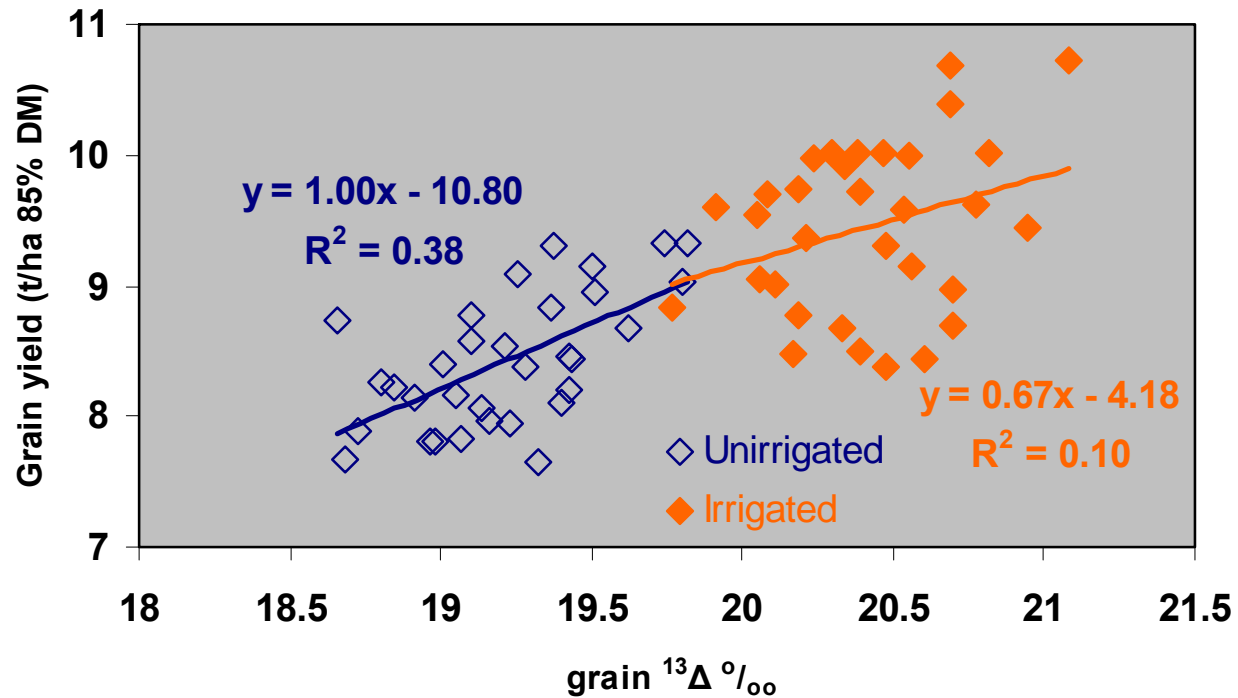
- Beaver x Soissons DHs phenotyped in 2003 and 2005
- Identify lines with contrasting ^{13}C $\Delta \sim$ QTLs
- Investigate role of leaf activity sub-traits

Sutton Bonington 2005

^{13}C Δ grain negatively correlated with TE



Relationship between ^{13}C Δ (grain) and grain yield



Mean GL 2002-3 and SB 2004-5

Resistance to Take-all and Septoria

Richard Gutteridge
Hai-Chun Jing
Kim Hammond-Kosack



WGIN MM@UoN
20th Oct 2009

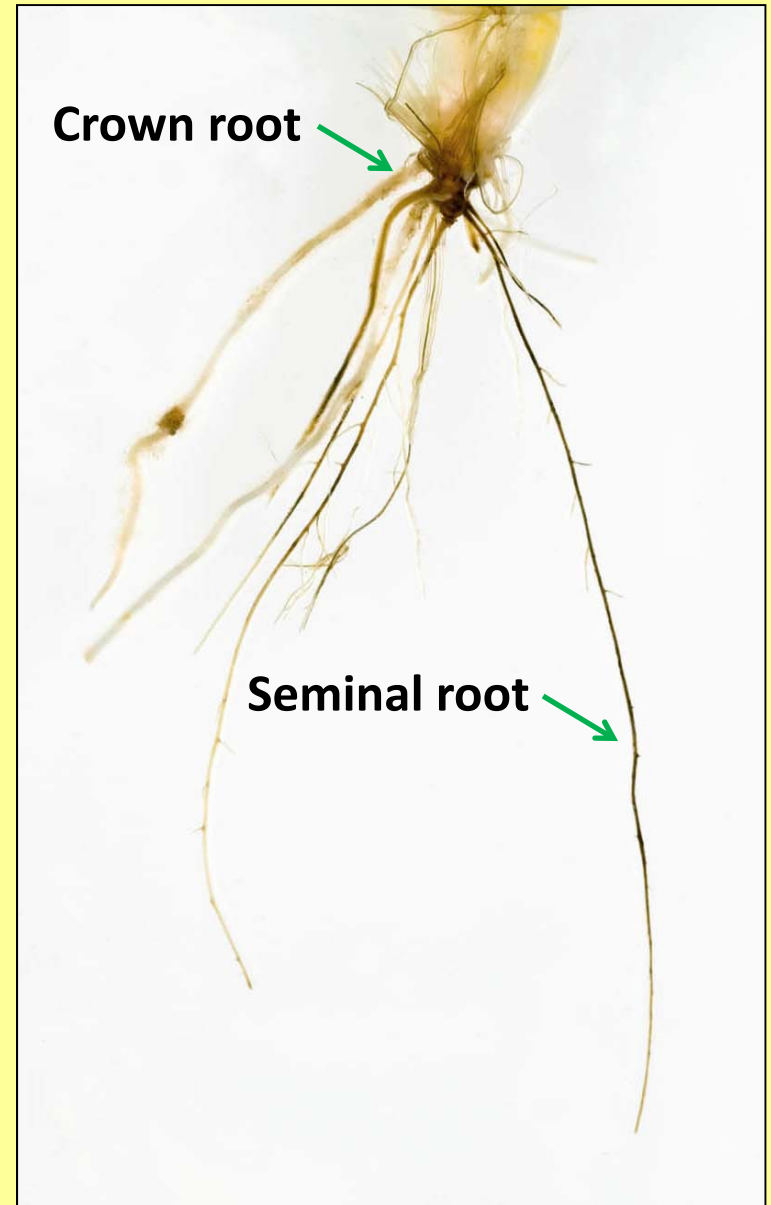
Take-all disease of wheat

- *Gaeumannomyces graminis* var. *tritici* (Ggt)

- ascomycete soil borne fungus

- related to rice blast fungus

- Magnaporthe oryzae* (previously *M. grisea*)



Ggt infected wheat seedling

A *Ggt* infected seminal root

Take-all lesion

Runner hypha





Typical take-all patch showing stunting and premature ripening of the crop

Talk Outline

- **Hexaploid wheat – Watkins / Gediflux collections**
 - field evaluation to identify potentially resistance genotypes
 - results so far / current activities
- **Diploid wheat**
 - phenotyping via pot bioassay and field trials
 - mapping populations
- **Hexaploid wheat – inoculum build-up in 1st wheats**

Watkins Hexaploid wheat collection

Take-all / eyespot assessments

- **2007 – 2008 field season – one plot / genotype – established from 45 seeds**

- **740 lines from the collection**



Watkins collection sown into a 3rd wheat situation

The harvested roots – August 2008



root drying



**Stored at room temp prior
to assessment in a white tray
filled with water**



**severe
infection**



**light
infection**

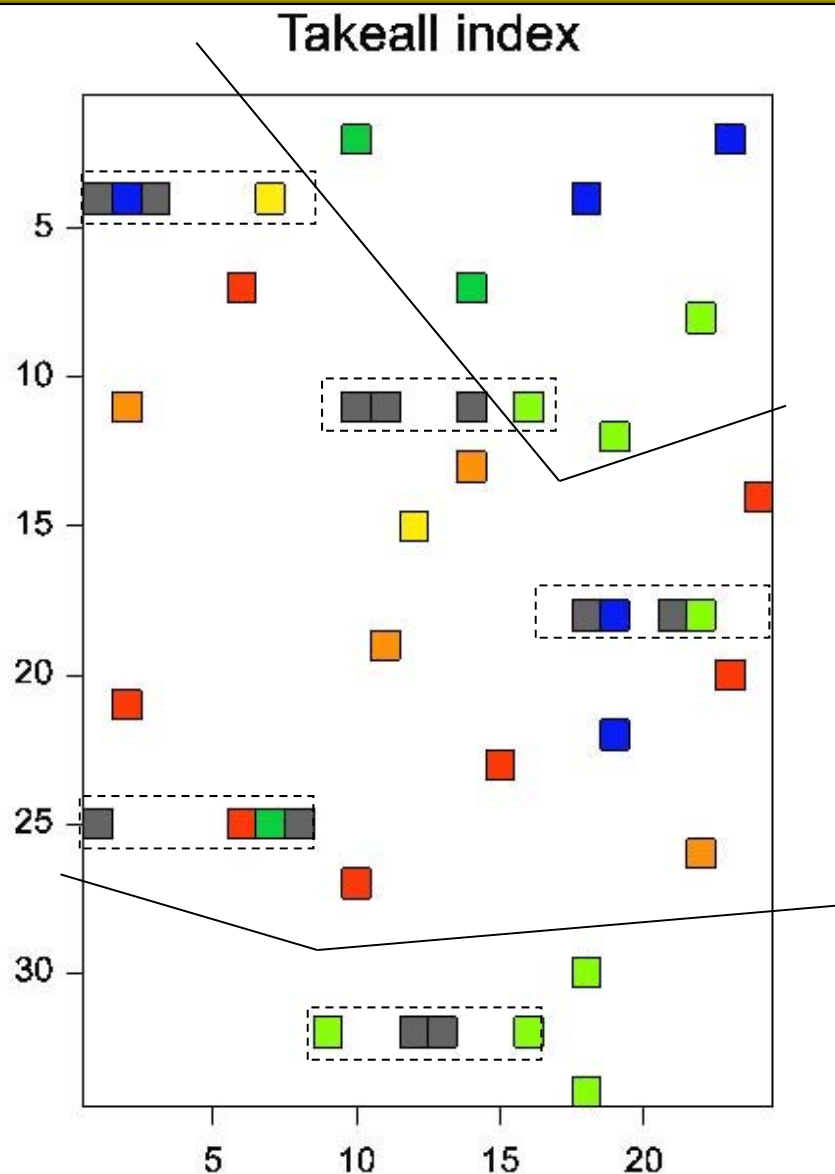
Watkins Experiment 2008 RRes Take-all severity - control plots

5 control blocks

Variety	TAI
Hereward	35.6
Triticale	18.4
Rye	1.7
Oats	0.0

TAI

□	0-5
□	6-15
□	16-25
□	26-35
□	36-45
□	46-55
□	> 55



Alpha design

N = 800 plots

Mean of all plots
Hereward = 43.4

Watkins Hexaploid wheat collection 2008 Take-all / eyespot assessments

- **All assessments completed – 740 lines
12,000 plants**
- **Initial findings suggest that 253 lines
(34%) can be omitted due to
susceptibility to Take-all.**
- **Further lines may also be discarded
once the stats is completed**

Watkins Hexaploid wheat collection 2008 Take-all / eyespot assessments

**All 740 lines also assessed for stem
base diseases**

eyespot

sharp eyespot

brown foot rot (fusarium spp.)

74,000 straws assessed

now in stats

**Note : the 2008-2009 trial was fungicide treated in the
spring 2009 to minimise stem base diseases**

Only this one year of data

Watkins / Gediflux collections assessment 2009 - 2010

Watkins

500 lines carried forward from the 2008 trial but some may be discarded once statistical analysis complete

78 new lines added not previously tested

Gediflux collection – 60 lines in total

All lines: For 2 years

2008 – 2009 - done, roots to be assessed

2009 – 2010 exp planned

A.E.Watkins and Gediflux collection 2008 – 2009 field trial

- **The same single plot – Alpha design**

- **Foliar diseases**

**winter/ spring infection by septoria and mildew
but then did not develop further**

late infection by yellow rust and brown rust

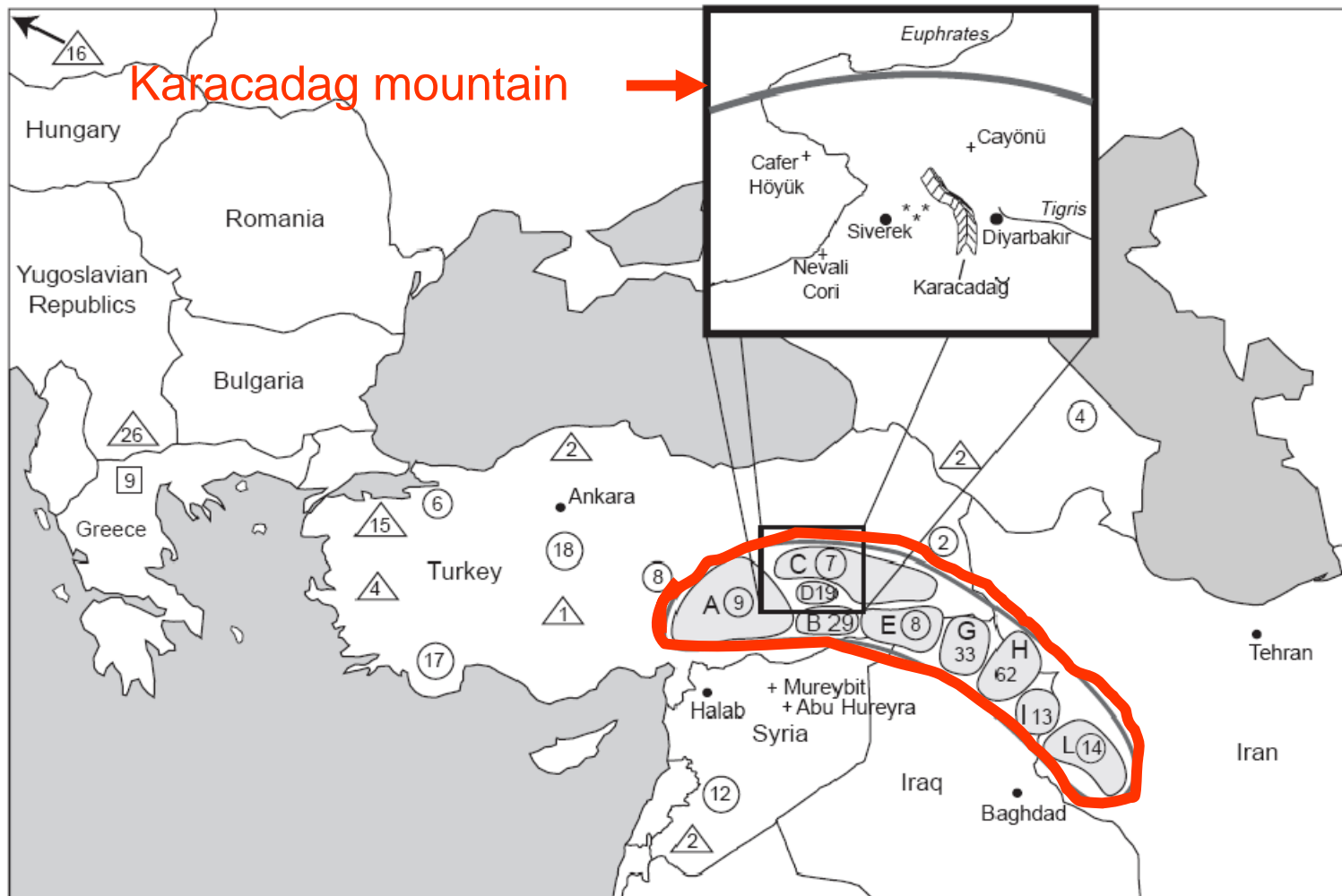
ALL lines affected recorded but not assessed

- overall less FOLIAR disease than in 2007-2008

Talk Outline

- Hexaploid wheat – Watkins / Gediflux collections
 - field evaluation to identify potentially resistance genotypes
 - results so far / current activities
- Diploid wheat
 - phenotyping via pot bioassay and field trials
 - mapping populations
- Hexaploid wheat – inoculum build-up in 1st wheats

T. monococcum domesticated from *T. boeoticum*



Karacadağ mountain →

— Limits of Fertile Crescent

* Sampling of Karacadağ lines

+ Archeological site

○ *T. m. boeoticum*

△ *T. m. monococcum*

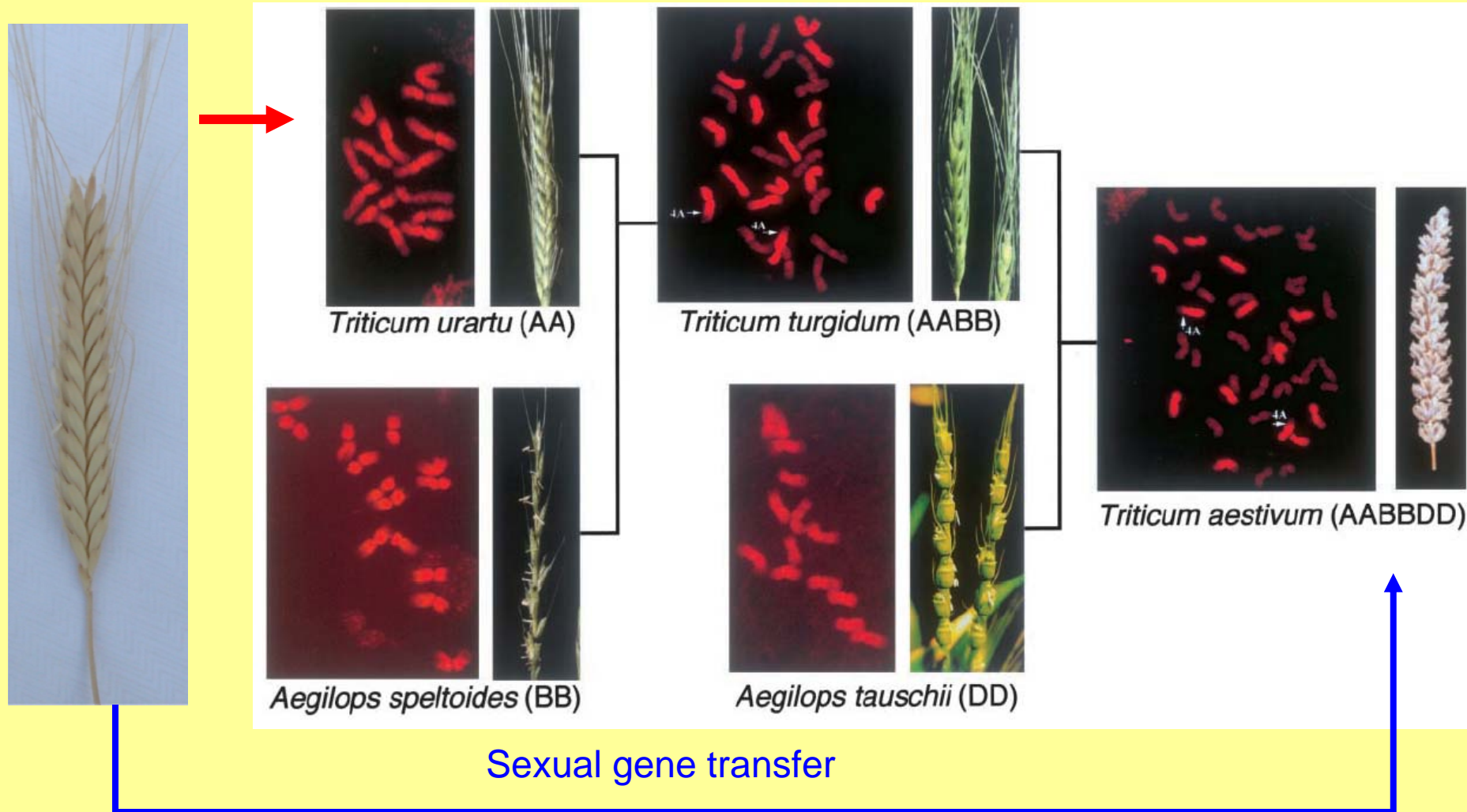
□ *T. m. aegilopoides*

(with number of samples)

A–L: areas of wild *T. m. boeoticum* sampling in the Fertile Crescent

Origin of bread wheat

T. monococcum A^mA^m



***T. monococcum* - pot bioassays and field trials**

Pot bioassays started in 2005

- Naturally infected soil
- Naïve soil + 12 Ggt isolates



Min. 5 reps – total of 50 seeds per genotype

Field trials started in 2006

Some promising results

The Pot Bioassay - Standard two methods

- Collected field soil-crumble to an even texture, with large stones removed, stored in a cold room until required.
- Two experimental set-ups
 1. Fill pot fill with 50cc of moist sand, 300g of naturally infected soil, sown with 10 seeds evenly over the soil surface and covered with horticultural grit.
 2. Artificial inoculum addition - shake 300g of 'naïve' soil with 50g of dilute inoculum in a plastic bag, transfer to bioassay pot. (inoculum = sand/maize meal cultures, 10 different isolates, including both A and B types, mixed together)

Min. 5 reps – total of 50 seeds

Assess - % roots with Take-all

Take-all Assessment of field experiments

Whole plant root systems are assessed in a white dish under water and the proportion of roots affected by the disease are graded as follows:

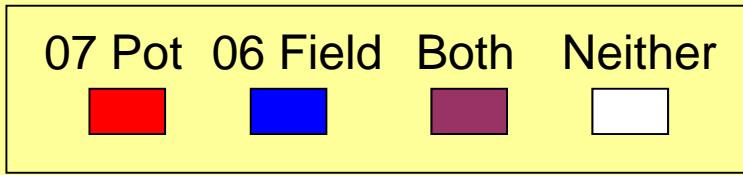
Slight 1: 1 – 12%; **Slight 2:** 13 – 25%; **Moderate 1:** 26 – 50%
Moderate 2: 51 – 75%; **Severe** >75%

Take-all Index (TAI) calculated by:

1 x %plants with slight 1; + 2 x %plants slight 2; + 3 x %plants moderate 1; + 4 x %plants moderate 2; + 5 x % plants severe

Divide by the number of categories (5) ; **Maximum index = 100**

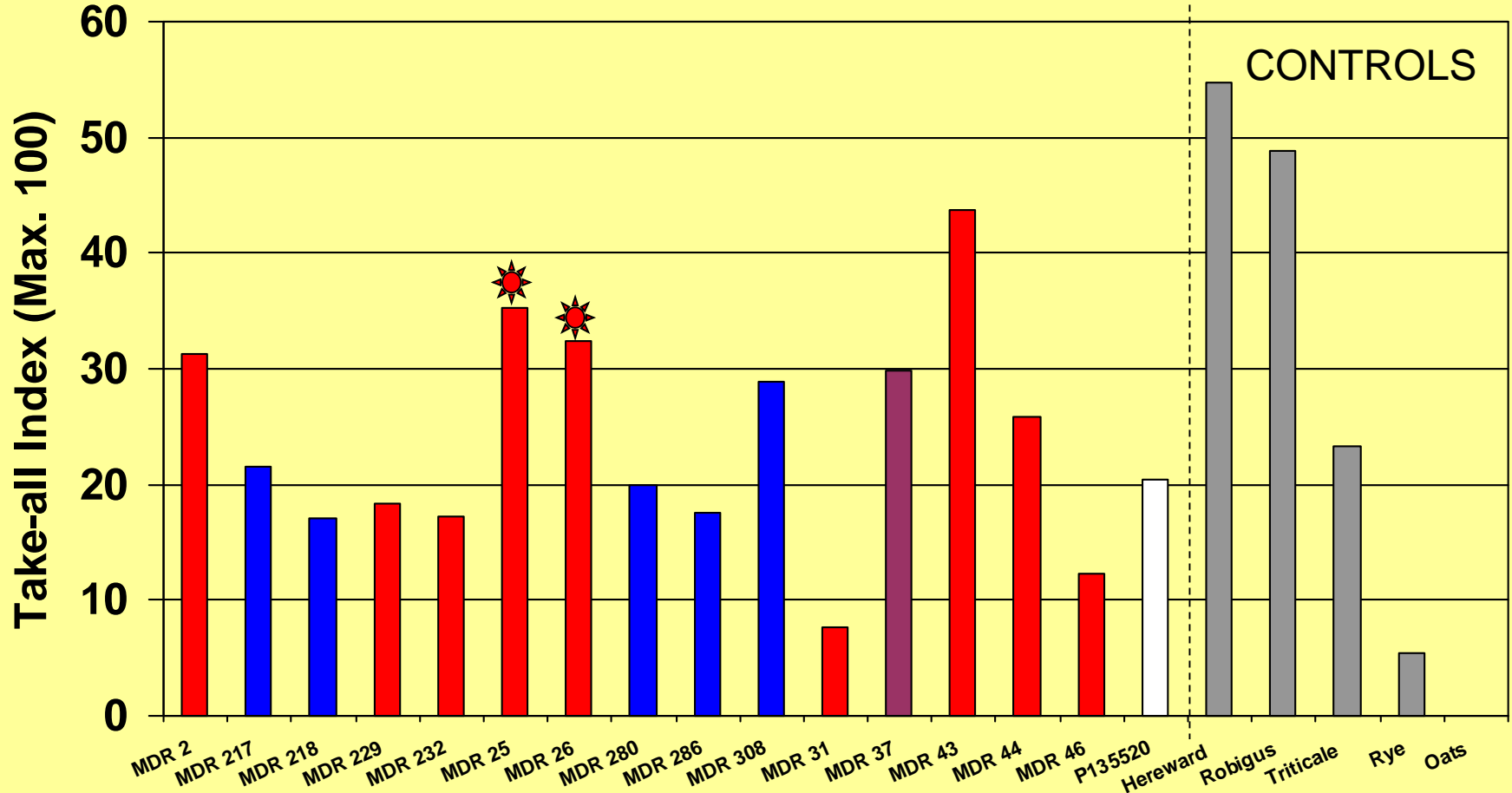
Field experiment 2008



2nd wheat situation

SED = 8.56

FPr < 0.01



5 rep exp but 10 reps MDR 37, MDR 46 and MDR 229

***T. monococcum* lines in the field 2008 - 2009**

Note : Results from the previous field experiment (i.e. those on the previous slide) were not available when deciding which lines to test

Tested 5 *Tm* lines with contrasting Take-all susceptibility

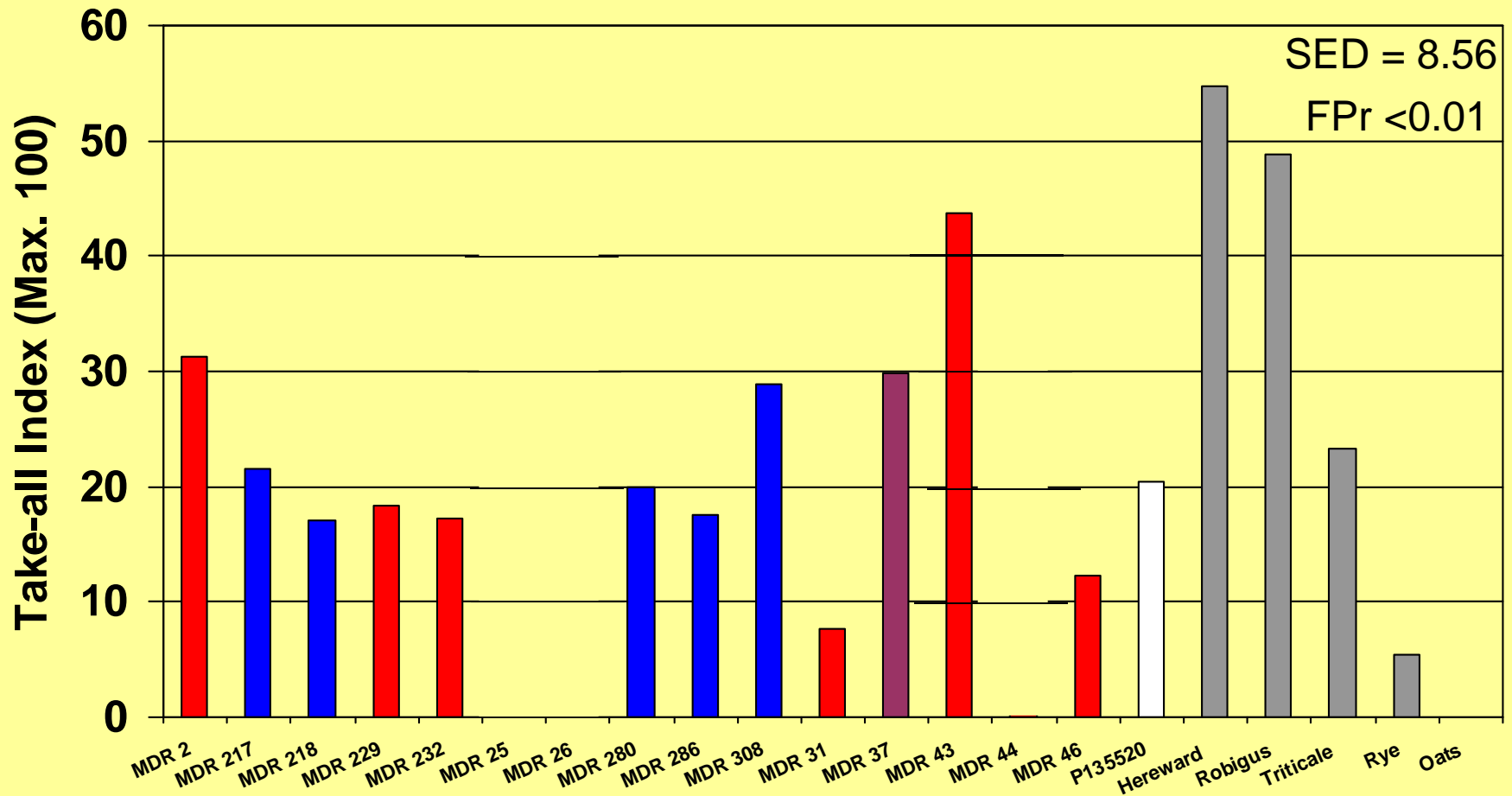
Genotype	TAI (2008 field)
MDR046	12
MDR0229	18
MDR037	30
MDR002	32
MDR308	30

**Plus 5 tetraploids, 10 hexaploids, rye and triticale,
5 replicates of each**

All plots sampled in July. Stored and awaiting assessment

T. monococcum lines in the field 2009 - 2010

Note : This selection is based on the 2008 field data



Triticarte - custom wheat array

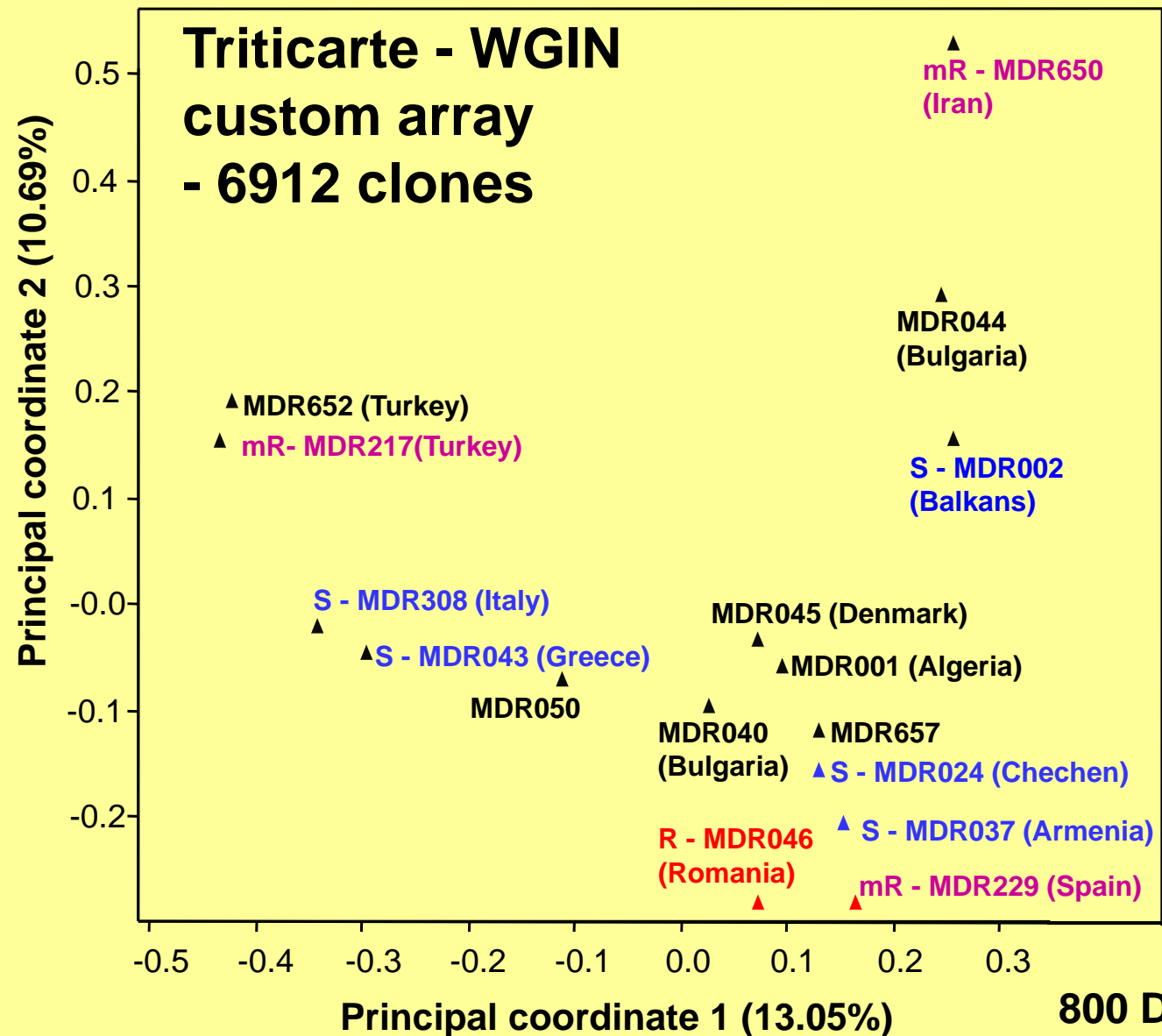
1536 clones derived from the two *T. monococcum* accessions

**2304 clones derived from hexaploid wheats
(including the Triticarte Wheat 2.3 array)**

**1536 clones derived from tetraploid durum wheat
(including the Triticarte Durum 2.0 array)**

1536 clones derived from 15 Iranian accessions of other *Triticum* species with genomes homologous to the A-genome of bread wheat (Ali Mehrabi, unpublished)

DArT marker and PCA analysis of *T. monococcum* accessions



Not yet
in DArT
analysis
MDR218
MDR232
MDR280
MDR286
MDR031

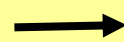
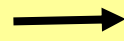
800 DArT markers
297 mapped in *Tm*

Glasshouse crosses completed

2008

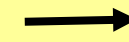
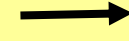
MDR037 x MDR046

MDR037 x MDR229



2009


F₂ seed harvested



~ 85 lines
SSD for
each popⁿ

2009

	Male	MDR043	MDR024	MDR037	MDR308	MDR002	MDR031	MDR046	MDR229	MDR217	MDR650
Female		S	S	S	S	S	R	R	mR	mR	mR
MDR043	S		28	0	15	11	28	6	11	59	18
MDR024	S	10		X	X	X	40	15	2	13	X
MDR037	S	X	X		X	X	28	26	5	31	X
MDR308	S	X	X	X		X	43	23	60	62	48
MDR002	S	X	X	X	X		48	36	31	32	13
MDR031	R	9	28	4	6	13		20	2	38	X
MDR046	R	4	11	2	2	X	10		X	30	X
MDR229	mR	16	50	0	X	X	9	X		X	X
MDR217	mR	14	X	X	X	X	4	X	X		X
MDR650	mR	40	X	X	X	X	X	X	X	X	

 < 10 grain

X = not done

Talk Outline

- Hexaploid wheat – Watkins / Gediflux collections
 - field evaluation to identify potentially resistance genotypes
 - results so far / current activities
- Diploid wheat
 - phenotyping via pot bioassay and field trials
 - mapping populations
- Hexaploid wheat – inoculum build-up in 1st wheats

Take-all and inoculum build up WGIN 1

Background

- The risk of take-all is largely dependent on the amount of inoculum in the soil at the time of sowing
- A soil core bioassay, taken after harvest, is used to measure the take-all infectivity of the soil
- Results from WGIN 1 have suggested that varieties can build up the take-all fungus differentially when grown as a first wheat.



THE SOIL CORE POT BIOASSAY



Soil core bioassay plants



Severe take-all infection



Slight take-all infection

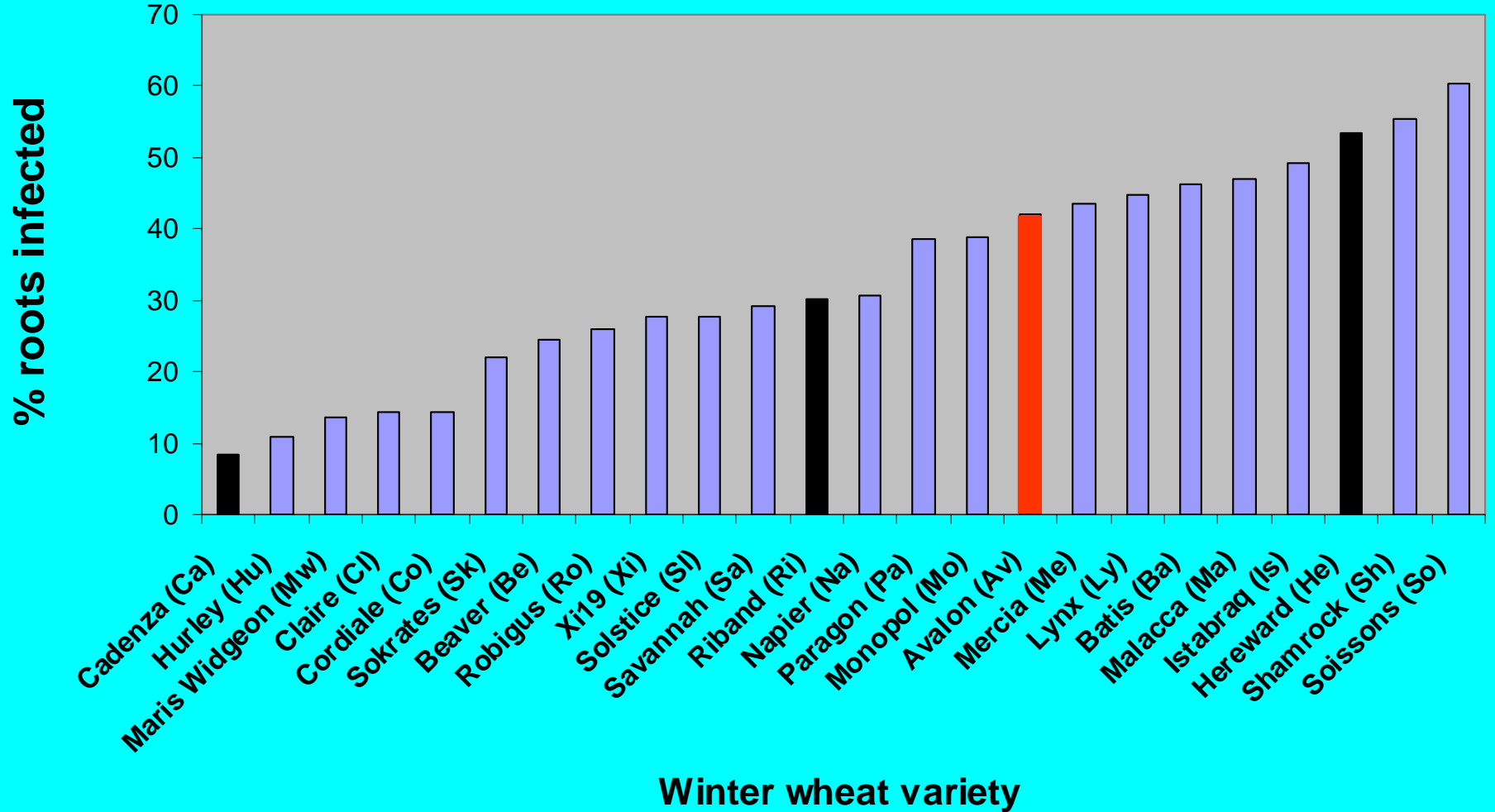
200 kgN plots



www.WGIN.org.uk




WGIN winter wheat bioassay 2008

Take-all infectivity in the soil after different winter wheat varieties



Consistent ranking over 4 years

Take-all inoculum build up ranking by varieties: 1 = Low – 9 = High

Variety	2004	2006	2007	2008	Overall ranking
 Cadenza	1	2	1	1	1.25
Xi19	7	1	2	2	3
 Riband	5	4	4	3	4
Mercia	3	5	3	6	4.25
Monopol	6	7	5	4	5.5
Avalon	nd	6	8	5	6.33
Soissons	8	3	6	9	6.5
Malacca	4	9	7	7	6.75
 Hereward	9	8	9	8	8.5

Objective 10.8 – take-all inoculum build up in 1st wheat situation

Diversity trial 2009 – The experiment included 6 DH lines from A x C (82, 99, 100, 116, 127, 155)

Soil cores taken from all varieties after harvest, one nitrogen rate (N2 ~200kgN/ha, total 360 cores (5 cores per plot), being processed using the pot bioassay.

Diversity trial 2010

Standard varieties –

Hurley and Monopol - omitted

Chablis, Gallant and Oakley - new

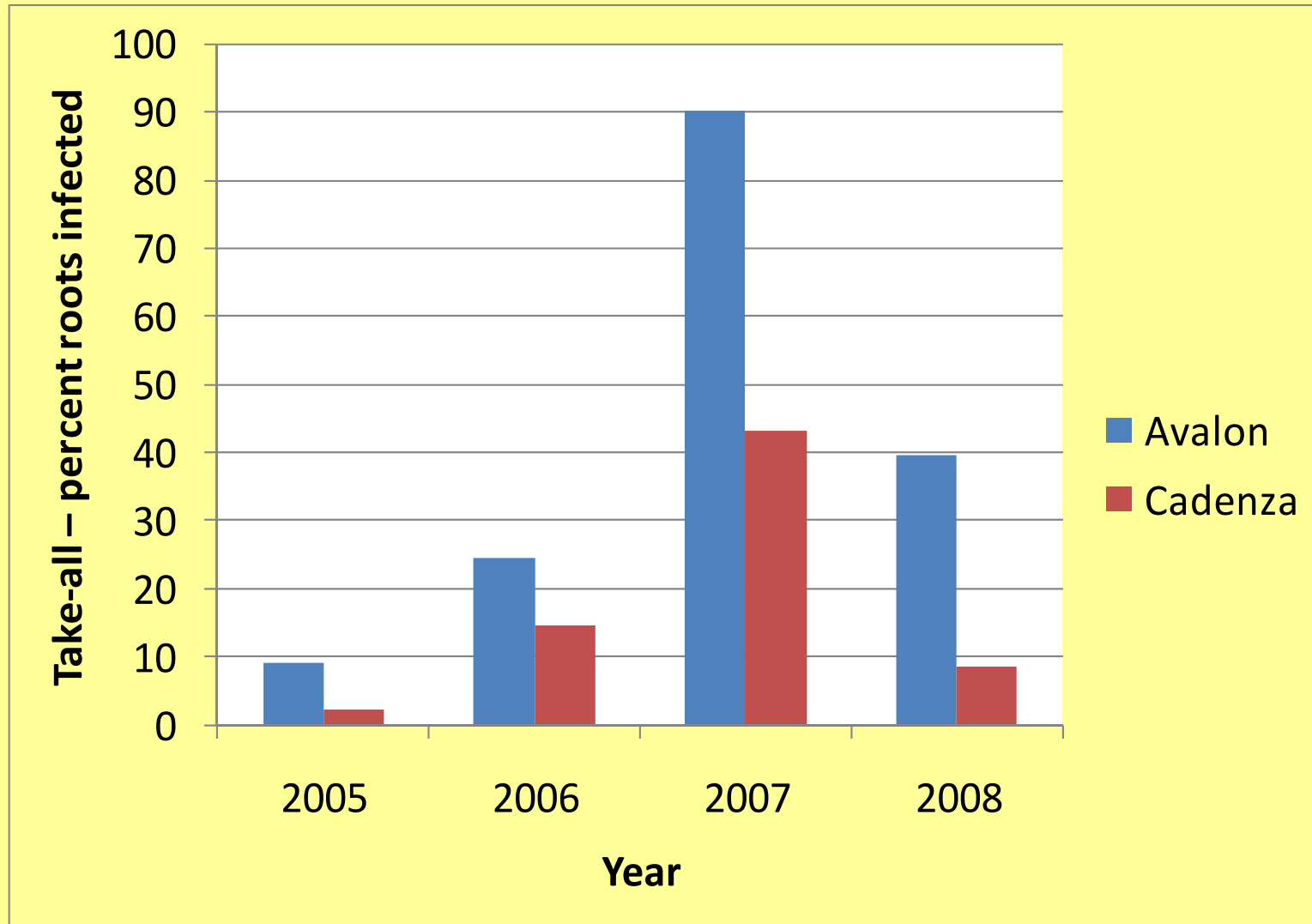
6 DH lines from A x C (82, 100, 116, 112, 127, 181)

Objective 10.9 Avalon x Cadenza

Attempting to define the genetic basis of take-all inoculum build up (TAB)

- A very tough goal

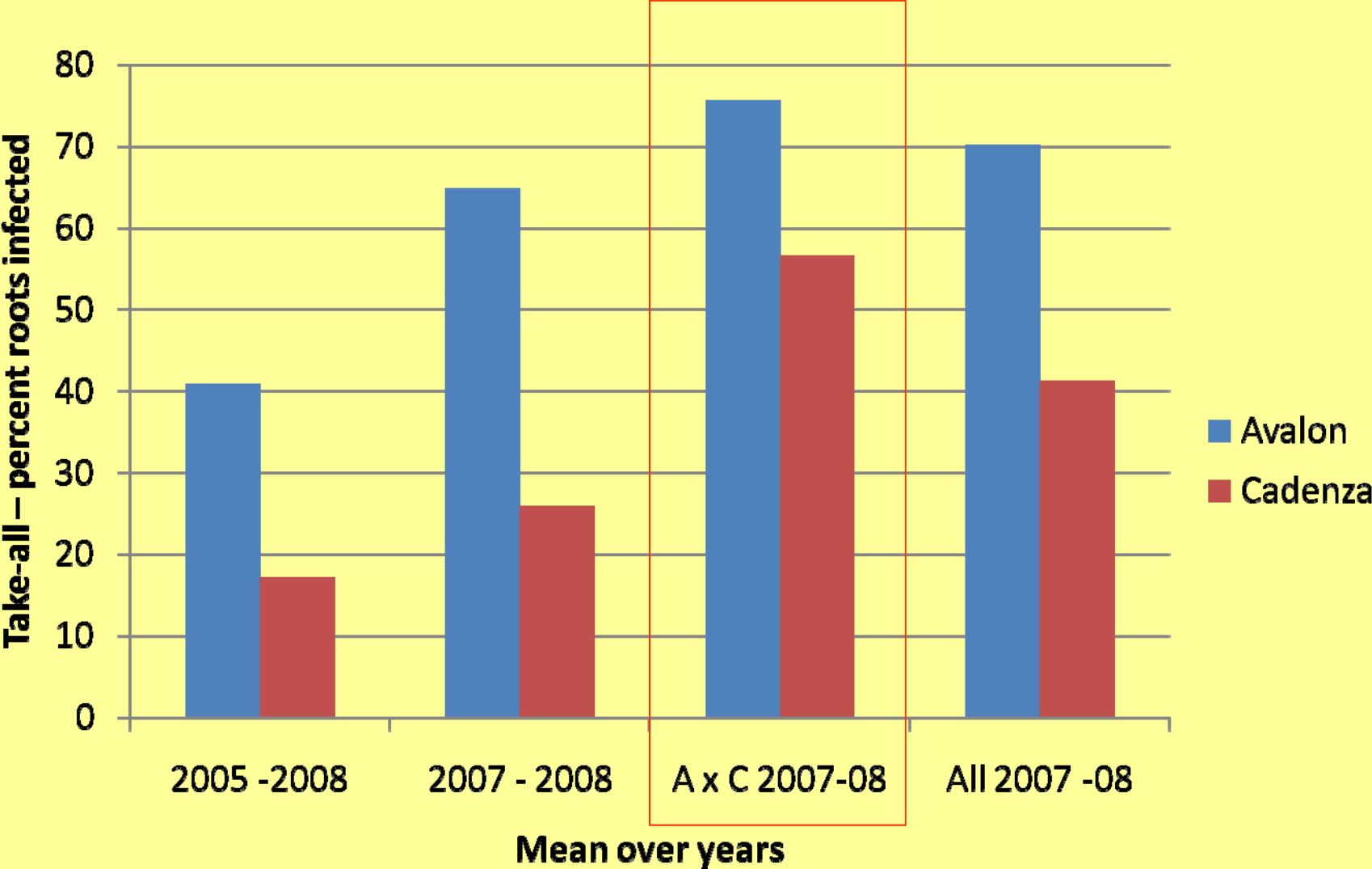
% roots infected with take-all in a soil core bioassay Avalon and Cadenza 2005 - 2008 WGIN Diversity trials



Avalon x Cadenza DH trial

**Just the parental plots soil-core sampled in 2007 and
2008
and the pot bioassays done**

% roots infected with take-all in a soil core bioassay Avalon v Cadenza



Disappointment then a lucky break

Disappointment: Due to the late harvest in 2008 and the present of cereal volunteers the A x C line DH population, this trial was not sampled for the take-all soil infectivity.

The lucky break – 2007-2008 Seed multiplication trial

62 A x C lines in a separate field + parental lines (plot size 20m x 2m) for multiplication in 2008 were ploughed and **then over sown with Oakley**

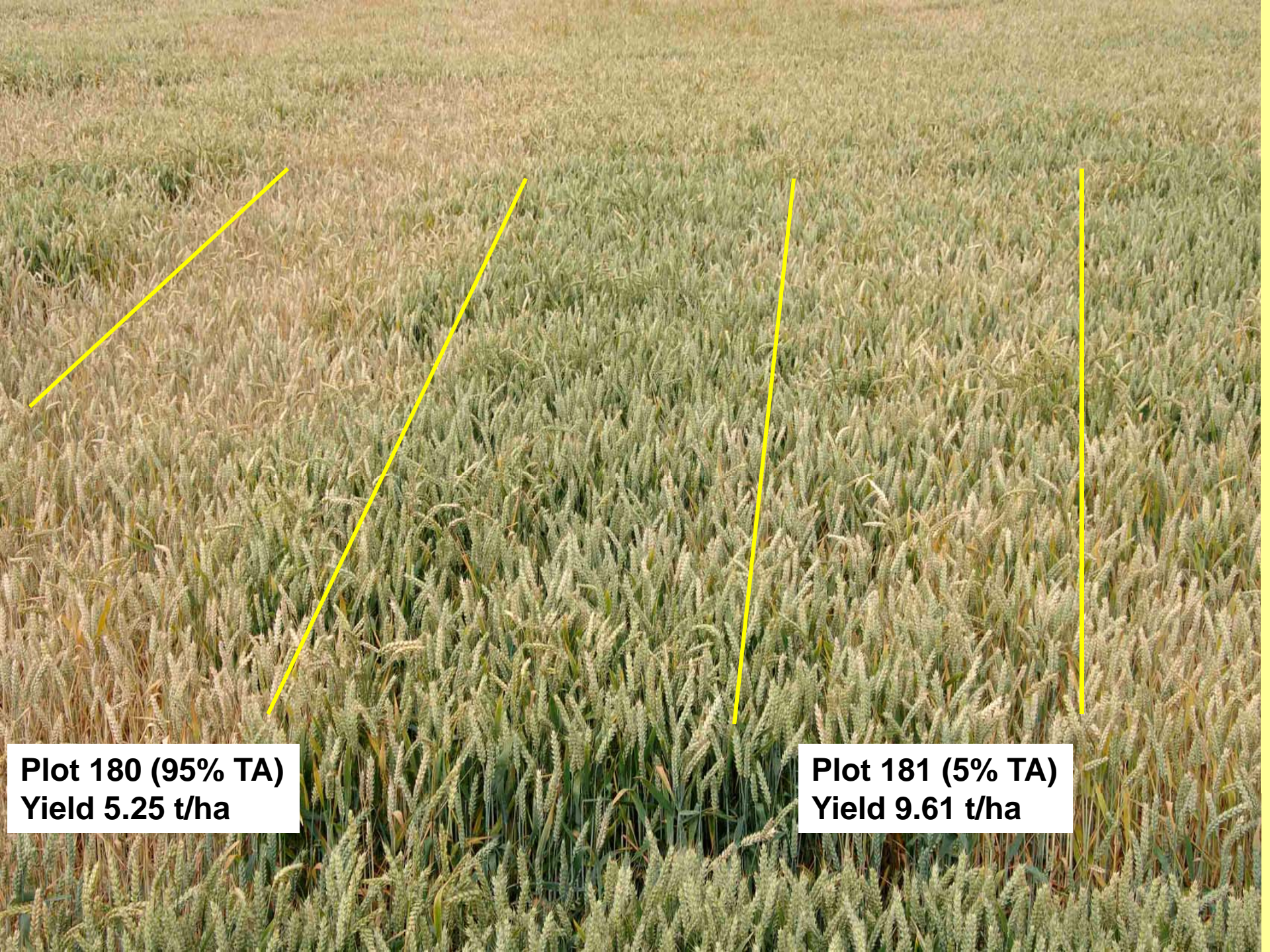
By July 2009 take-all patches were showing in the areas where the 2008 plots had been sown

These areas were scored for take-all patches as a percentage of area affected

Middle 2 m of each plot was harvested and yield measured

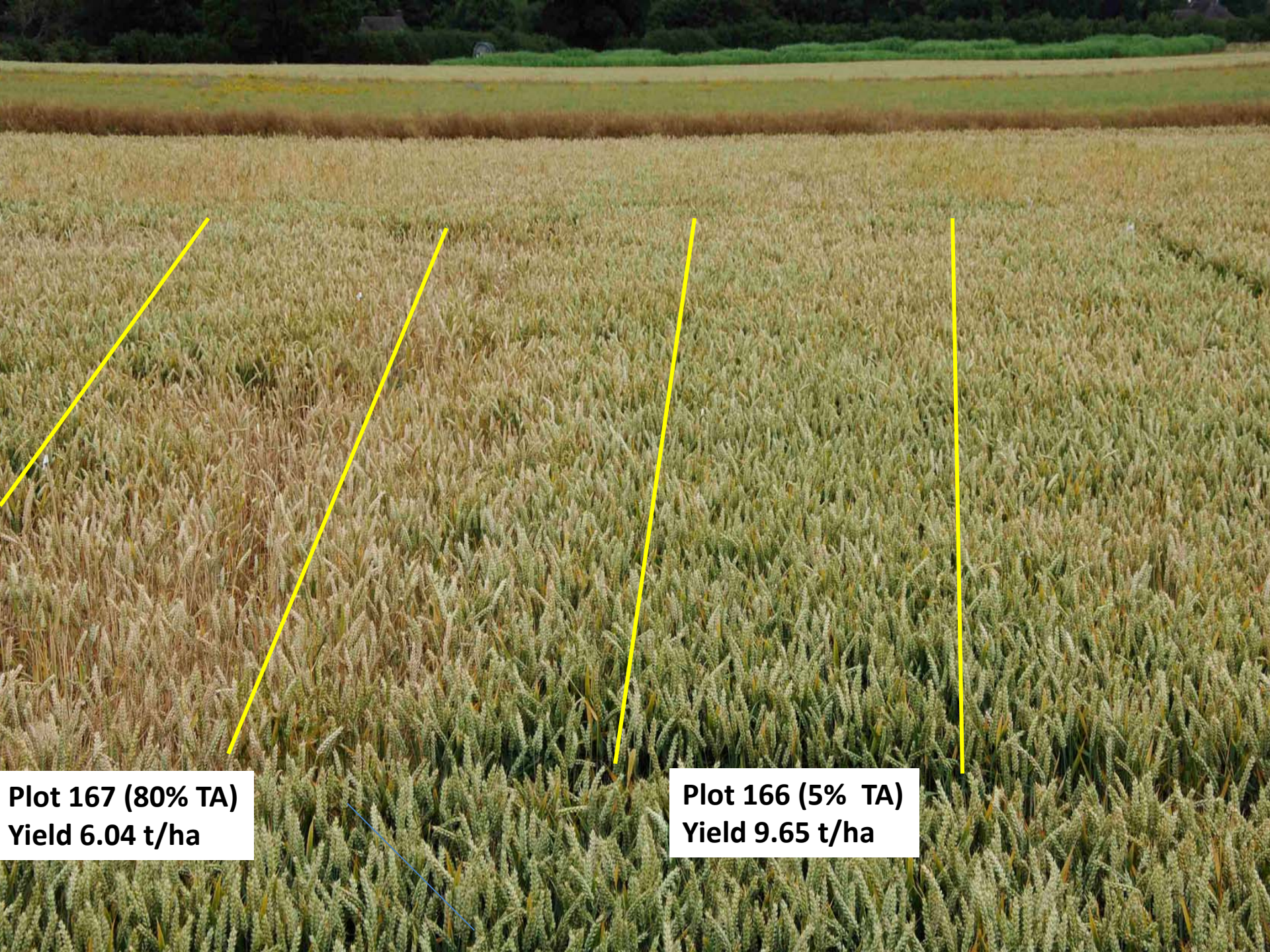


**Square Take-all patches
June 2009**



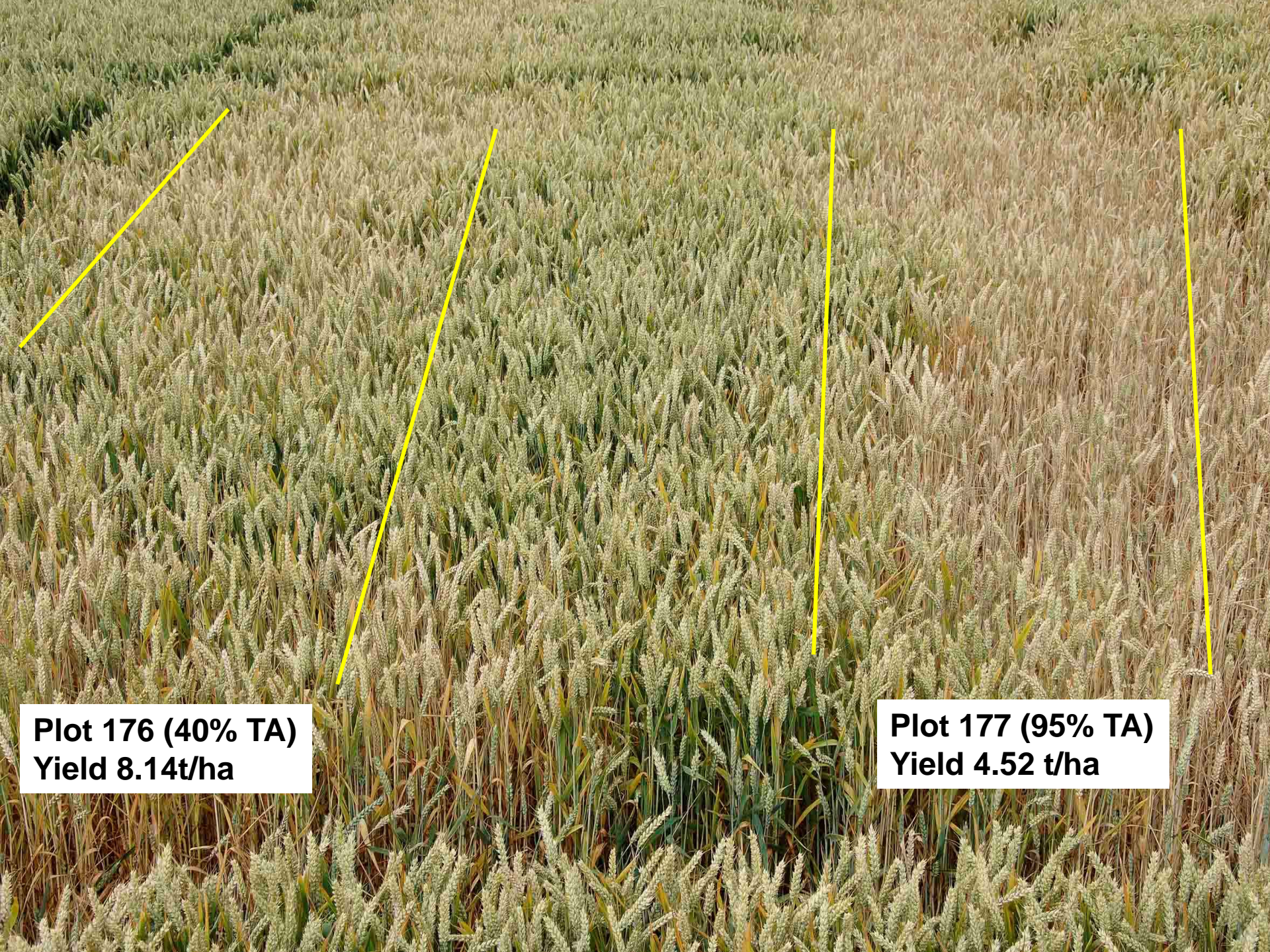
Plot 180 (95% TA)
Yield 5.25 t/ha

Plot 181 (5% TA)
Yield 9.61 t/ha



Plot 167 (80% TA)
Yield 6.04 t/ha

Plot 166 (5% TA)
Yield 9.65 t/ha



Plot 176 (40% TA)
Yield 8.14t/ha

Plot 177 (95% TA)
Yield 4.52 t/ha

Avalon x Cadenza seed multiplication field plots over-sown with Oakley wheat in 2009

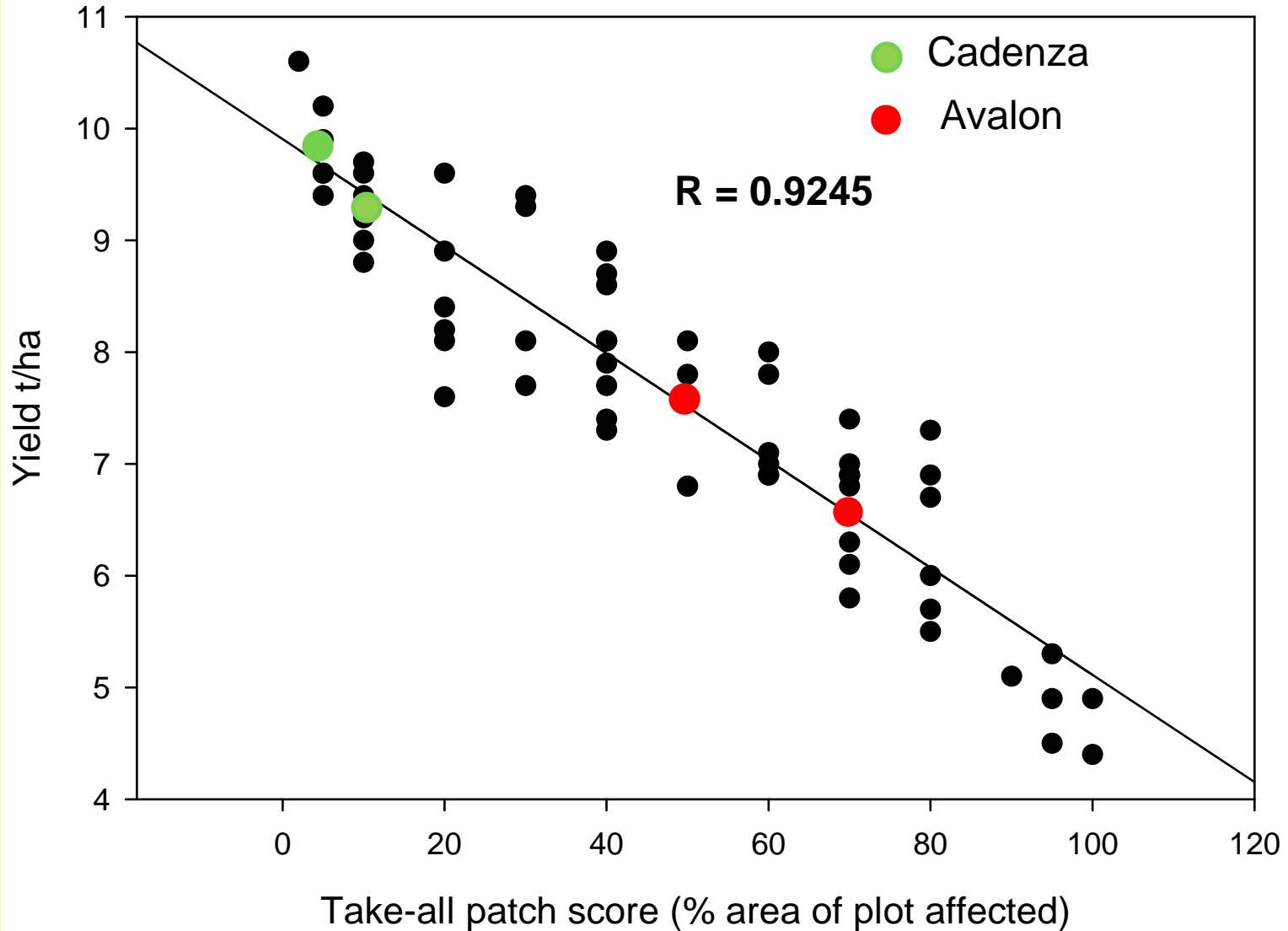


Ahh!!! what is this then?



Hm !!! That is better

Avalon x Cadenza lines in 2008, oversown with wheat cv. Oakley in 2009. Relationship between take-all patch score and yield



Can we genetically analyse and map the trait ?

319 markers on the A x C map
62 DH lines + parentals scored

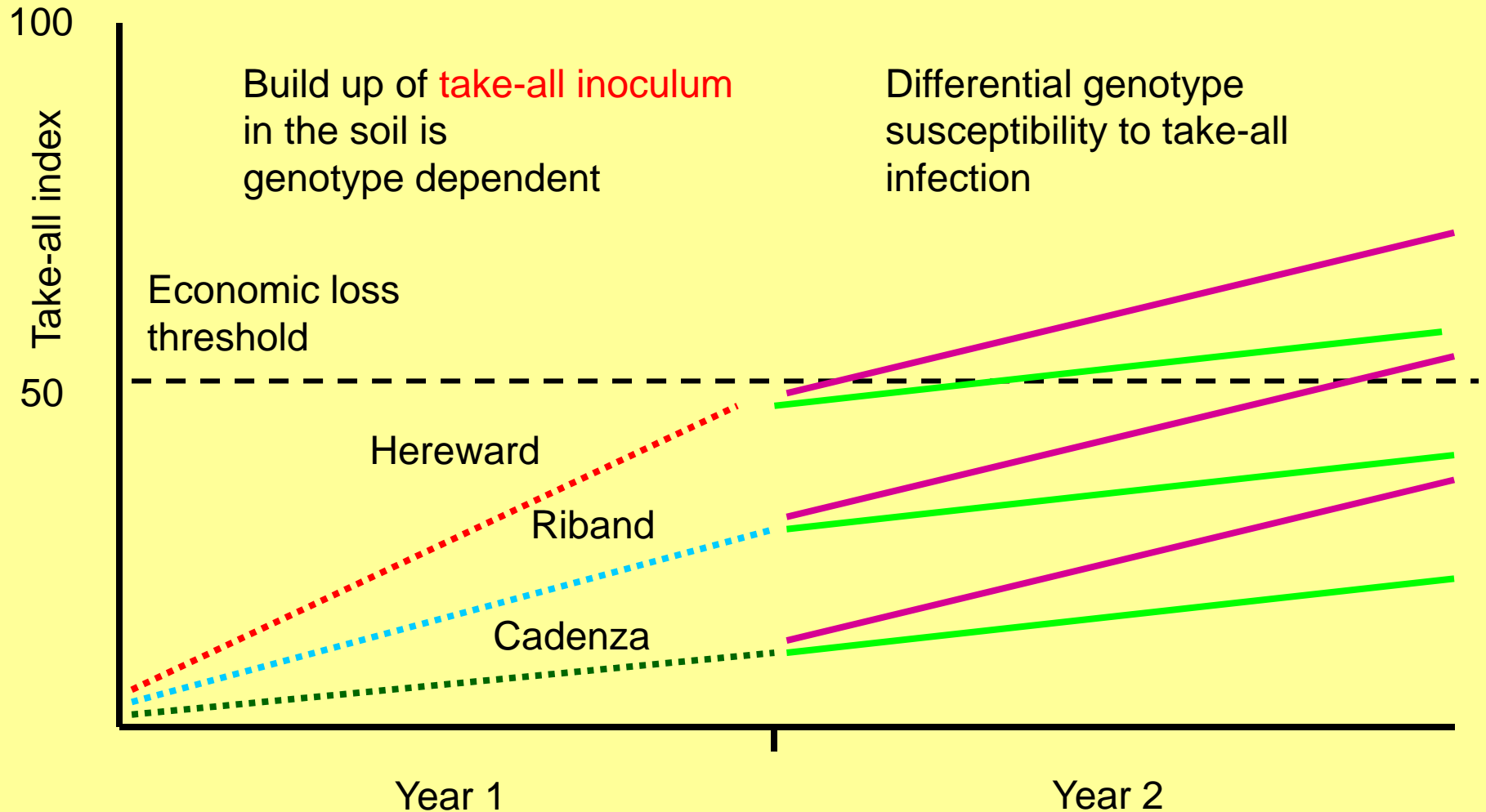
2009 A x C DH trial harvested in August

Soil cores have been taken from A x C field experiment in 2009 from all **203** + parentals lines, total 1272 cores (6 cores / plot from one rep)

Bioassays are in progress

Cultivar rotation trial – R/CS 688

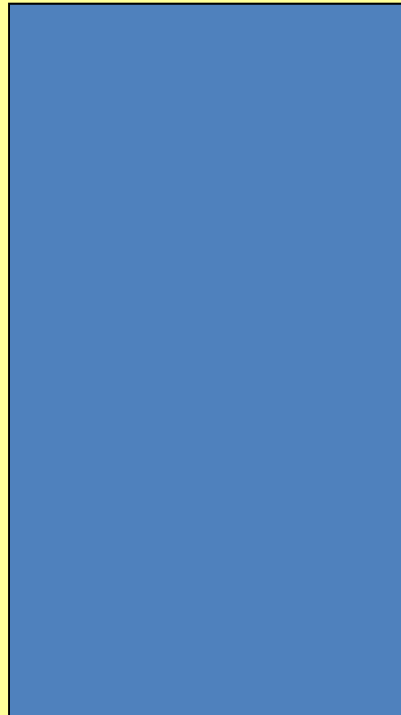
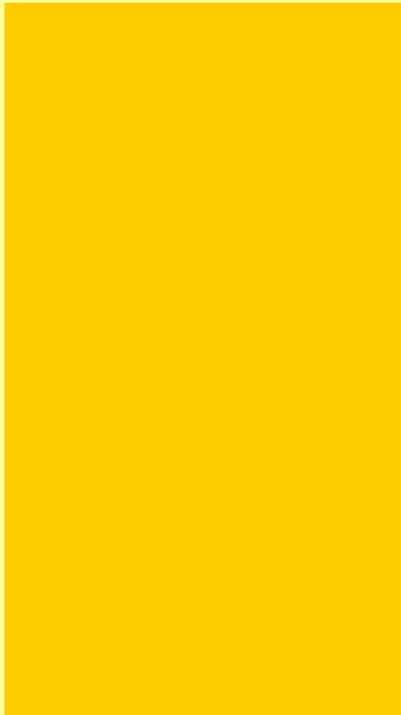
Overall objective: Explore the effect of sowing different sequences of cultivars on take-all disease pressure



Cultivar rotation trial – R/CS 688

Overall objective: Explore the effect of different cultivar sequences on take-all disease pressure

Step 1: Year 1 To create different take-all disease pressures in the field using the varieties **Hereward** (high inoculum build up) and **Cadenza** (low inoculum build up)



**12m x 82m, of each variety
4 replicates of each
done in 2008 – 2009**

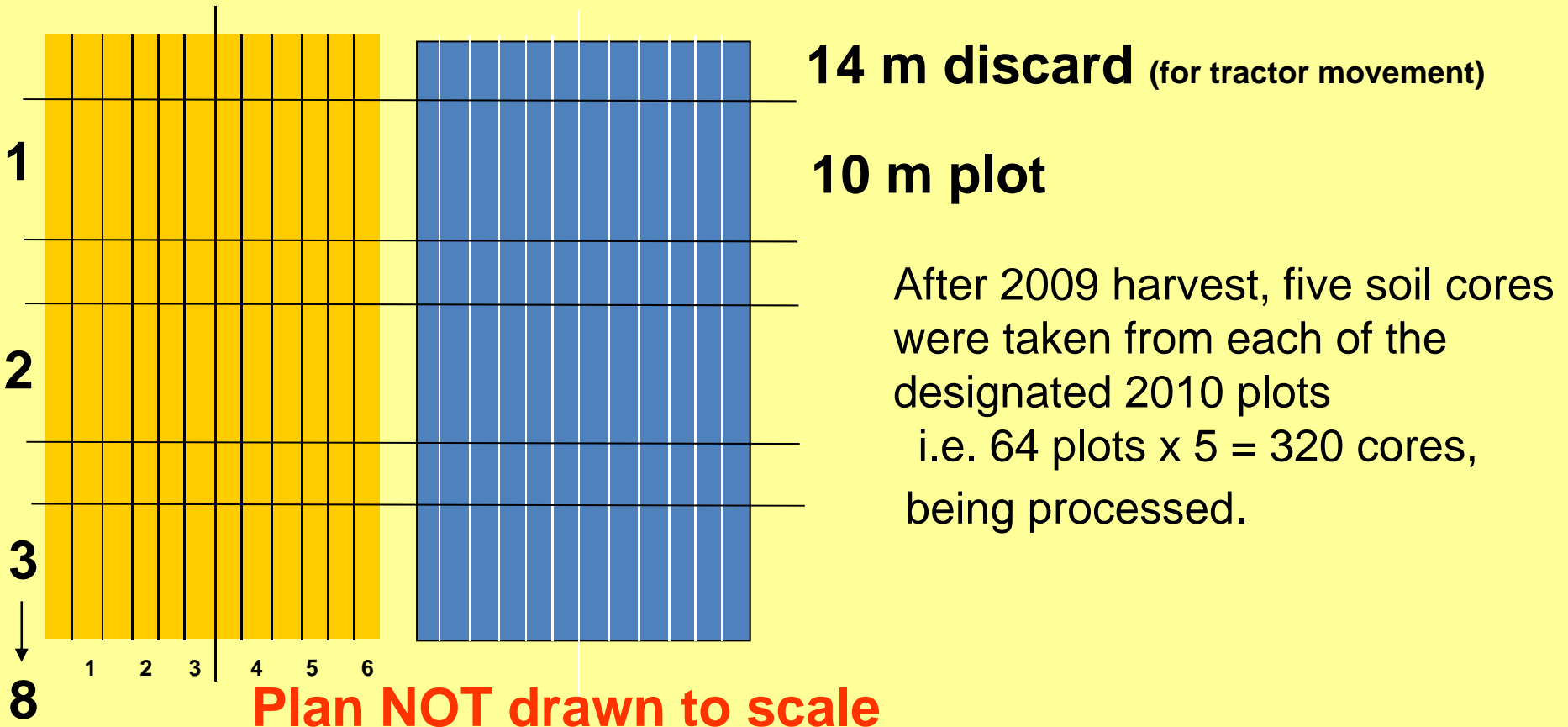
Sown - 10th October 2008

Harvested – 16th August 2009

Cultivar rotation trial – R/CS 688

Overall objective: Explore the effect of different cultivar sequences on take-all disease pressure

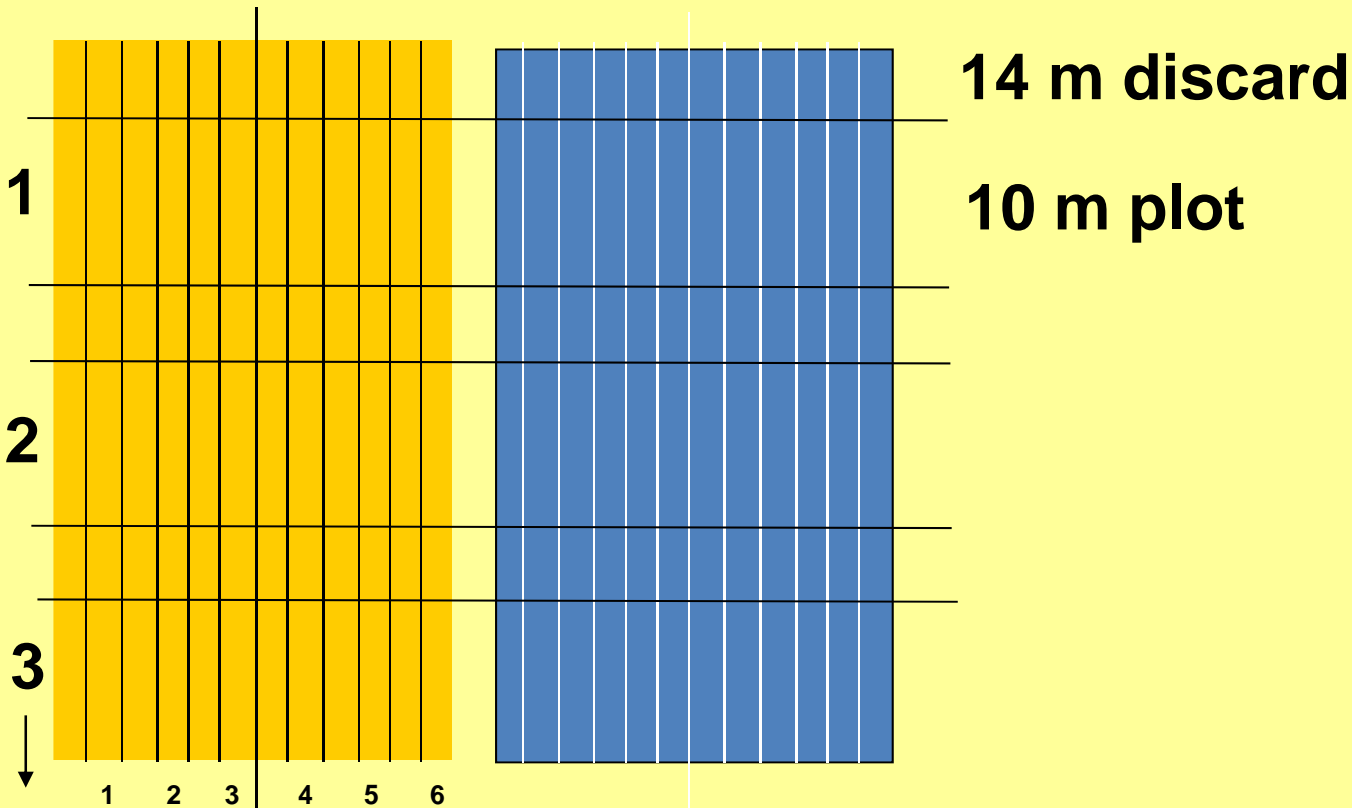
Step 2: Year 2 Each of the 2009 large plots divided into eight 10m x 3m for the 2009 – 2010 field season



Cultivar rotation trial – R/CS 688

Step 2: Year 2 Each of the 2009 large plots divided into eight 10m x 3m for the 2009 – 2010 field season

8 different wheat cultivars representing the NABIM groups 1 – 4 sown



Note : Plan NOT drawn to scale

The eight selected cultivars for the rotation trial

Variety	Group
Hereward	1
Gallant	1
Xi 19	1
Solstice	1
Cordiale	2
Einstein	2
Robigus	3
Duxford	4

HGCA – BBSRC studentship



1st wheat crop-

very little disease

Yield average 12.69t/ha

**1st and 3rd wheat
variety trials; 45 NL
winter wheat varieties.**



**Both variety trials
sown on 09th October
2008 on Rothamsted
Farm.**

**Photographs taken 08th
July 2009.**

3rd wheat crop-

severe disease

Yield average 7.64t/ha

Take-all inoculum build-up under *T. monococcum*

2008-9 Bulking up seed

9 *Tm* lines (MDR 2, 25, 26, 30, 37, 43, 45, 46, 229)
were bulked up in the field

Harvest in August. Awns were removed from individual ears and seed + glumes separated.

Approximately 1.5Kg of seed obtained/line.

2010 Field experiment

The experiment consists of 5 *Tm* lines (MDR 46, 37, 25, 45, 2)
+ Hereward control + Cadenza control x 3 replicates

Overall Take-all summary – root resistant

- **Not known** if root resistance to take-all is controlled by the same mechanism which confers the reduction in take-all inoculum build-up (TAB) in soil
- **Already 250 lines from the Watkins collected discarded - fully Take-all susceptible**
- ***T. monococcum* resistance - as good as Triticale**
 - Current focus**
 - generating mapping populations
 - rapidly advancing them to F₄ by SSD
 - only then screen for resistance in pots

Overall summary – Take-all inoculum build up (TAB) in the soil of a 1st wheat crop

- Ongoing NUE Diversity trial with new genotypes
- Avalon x Cadenza DH population
 - consistent parental differences - years / trials
 - a promising 1st data set on 62 DH lines
 - 212 plot bioassays for 2009 trial in progress (>1200 pots)
- *T. monococcum* – now enough seed to start first TAB trial with 5 MDR lines
 - includes **MDR037, MDR046 mR + 3 S lines**
Hereward (high TAB) and Cadenza (low TAB)

Objective 11

***T. monococcum* – Introgression of the *TmStb1* locus conferring resistance to *Septoria tritici* blotch into hexaploid wheat**

5 years of field assessment of resistance

Hexaploid wheat

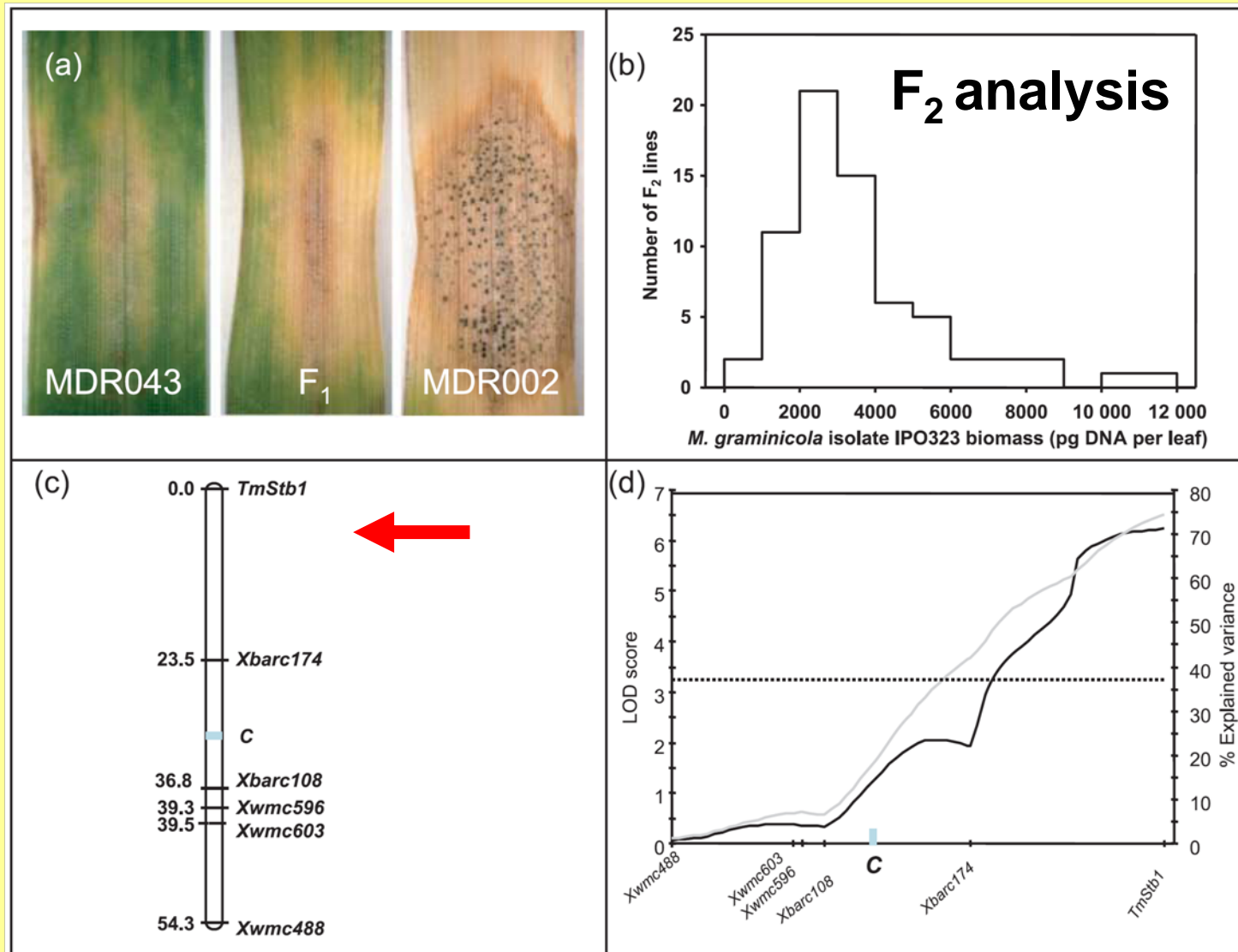


Triticum monococcum
- diploid wheat AA

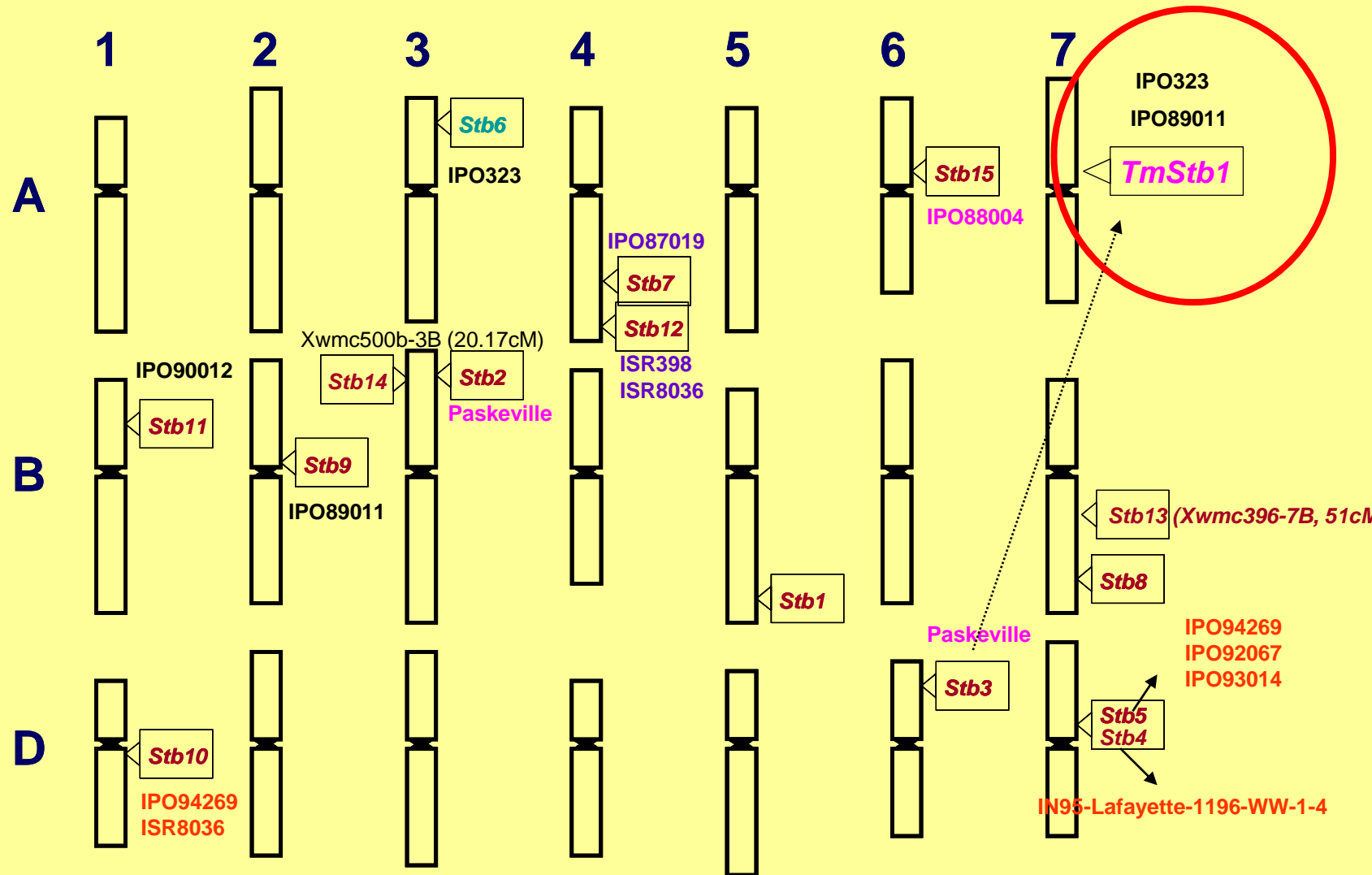


No lesions !!!

Resistance conferred the *TmStb1* locus on 7A^m



Wheat *Stb* genes for resistance to *Septoria tritici* blotch



Introgression of *TmStb1* locus into hexaploid wheat

What has been completed in 2009

Ta x *Tm* crosses

Genotypes tested - Chinese Spring, Cadenza, Riband

14 days post pollination – immature grain recovered
and into embryo rescue

Best F₁ plant recovery rate with Chinese Spring

F₁ plants exhibit Septoria resistance to a normally
virulent fungal isolate on Chinese Spring

Angela Doherty and Mike

Staff change

Hai-Chun Jing – left RRes August 2009

New post

Sorghum – salinity stress

**Head, Centre for Bioenergy Plants Research and Development,
Institute of Botany,**

Chinese Academy of Sciences

20 Nanxincun, Xiangshan,

Beijing 100093, China

Email: hcjing@ibcas.ac.cn

Webpage: www.ibcas.ac.cn

Replacement

Wing-Sham Lee - ‘Sam’

Cambridge – undergraduate and PhD graduate

She starts at RRes 2nd Nov 2009

Introgression of *TmStb1* locus into hexaploid wheat

Plans for 2009 and 2010

Backcross the F₁ plants and F₁ selfed plants exhibit Septoria resistance to Chinese Spring

A. Chromosome counting of all the parental material by root squashes / cytology

B. Use the closest SSR markers to the *TmStb1* locus to check for the presence of *Tm7A* interval

By the A / B strategy we plan to eliminate the plants lacking *Tm7A* interval prior to crossing

Convert the flanking DArT into PCR based markers

Allison van der Meene, Sam, Angela and Mike

Many thanks to.....

Wheat Pathogenomics Team (RRes)

Richard Gutteridge

Sanja Treskic

Vanessa McMillan

James Bruce

Adrian Czaban

Hai-Chun Jing

Watkins Exp.

Simon Orford

Elke Anzinger

Sarah Usher

Steve Freeman

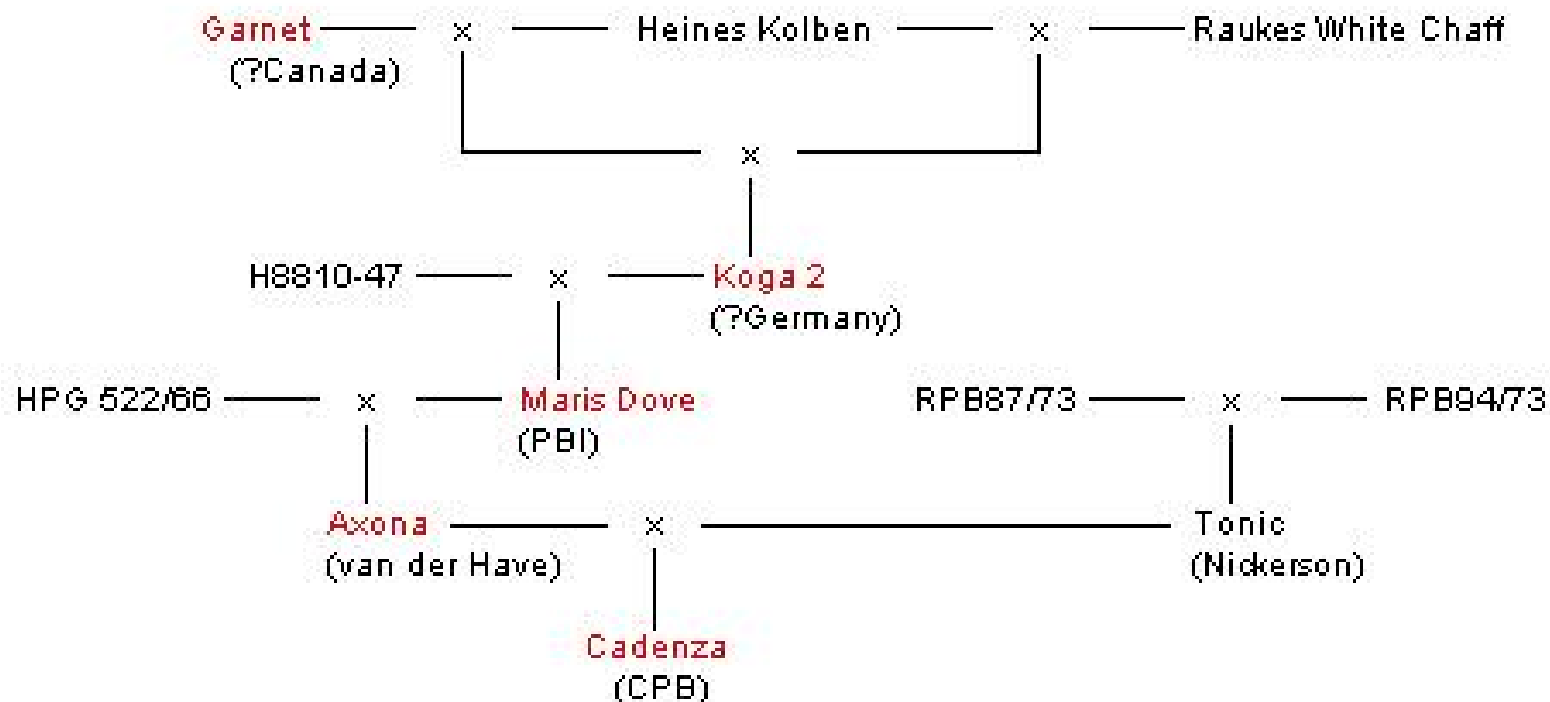
The Triticarte team



**BAB Dept
Statistics**
Sue Welham
Rodger White



Cadenza Pedigree





The Resource Search

A Monogram Facility

with the BBR project

A community resource for wheat functional genomics

PJ Verrier

Biomathematics & Bioinformatics Department

Rothamsted Research

Some history

- **Monogram Cross Institute Programme**
 - The Monogram web site
- **Small Grain Cereals Network**
 - The Monogram Network
- **BBR funded project**
 - A community resource for wheat functional genomics (a 5 year project)

Result of merger

- Monogram network
 - Its own web resources
 - Long term support for web
 - Delivery portal for resources
 - Web pages
 - Working parties
 - Web sites
 - Data resources
 - Merged searches

Monogram CIP - home page - Windows Internet Explorer

http://www.monogram.ac.uk/

File Edit View Favorites Tools Help Google

Monogram CIP - home page

Login (email addr.) password Login Register Get pwd

MONOGRAM

UK focus on grain and grass research

Home Research Activities Monogram CIP The Network Working groups Search News

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Introduction

The UK has a special climate where cool summers, mild winters and ample rainfall provide the environment where small grain cereals and grass may flourish, giving rise to some of the highest yielding and best quality crops in the world.

That world is changing fast. Climatic perturbations which hitherto were known only occasionally are becoming increasingly frequent. Unprecedented high temperatures and rainfalls, unpredictable and unseasonable conditions in which we must now grow our food. In an uncertain political world we no longer wish to rely solely on obtaining vital supplies overseas. Our food needs to be capable of being produced within our shores. We recognise too that our problems are international. The rest of the world is facing difficult challenges; having enough food to feed a growing population needs the careful application of plant science.

And so we must use all the tools at our disposal to adapt our crops, and the plants which give us those crops. The people who are working on the characteristics which make these plants capable of growing in these unpredictable conditions realise that they have a major responsibility to come together and focus their efforts on producing safe, good quality food and feed in an unpredictable world.

Fortunately, the UK has world class research to call on in addressing these issues. The Monogram Network provides a UK focus on grain and grass research and encompasses the Monogram Cross Institute Programme (CIP). We also have strong links to scientists in other countries, working in the same areas of science as ourselves.

This research is specialised and will at times seem impenetrable and complex. Bear with us. Out of it will emerge the future.

This site is primarily for specialists. If you would like more information about plant and crop science for non-specialists go to <http://www.plantsandus.org.uk>.

Acknowledgments

We are grateful to Robert Koebner (JIC) who suggested the name 'Monogram', to Nadia al-Kaff (JIC) who kindly designed the Monogram logo and also to BBSRC who fund the core Monogram activities.

News

Monogram news

19/10/2009 **NEW**
Quantitative Methods in Plant Breeding, March 2010. [more ...](#)

12/10/2009 **NEW**
Monogram Development Officer Position [more ...](#)
23/09/2009

2010 MONOGRAM Network Workshop [more ...](#)
03/09/2009

Eucarpia Cereal Section Flyer [more ...](#)
24/08/2009

Need help from a Mathematician? Bring your problem to the Plant Science Study Group [more ...](#)
14/08/2009

The Bristol Agilent wheat homoeologous array design is now public [more ...](#)
29/07/2009

Important note about extra deletions in some of the Kansas wheat deletion lines [more ...](#)
14/07/2009

1.6 million pounds awarded to develop a physical map of the ryegrass genome [more ...](#)
08/07/2009

EU COST TD0801 - StatSeq workshop: call for abstracts and Monogram open [more ...](#)
30/06/2009

Preliminary announcement: EUCARPIA Cereal Section Meeting [more ...](#)

Local intranet 100%

<http://monogram.ac.uk>

MONOGRAM

UK focus on grain and grass research



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You are here: [News](#) > [Admin](#) >

Monogram Admin Log

102685 hits so far - big hitters like stats checkers and webbots have been filtered out.

View by [Pages](#) [IP](#) [Referer](#) [Username](#)

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- viewed 9867 times
- [papers.php](#) viewed 3563 times
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- [events.php](#) viewed 1013 times
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1.6 million pounds awarded to develop a

The Smart Carbohydrate Centre

Producing and exploiting novel variation for starch properties in wheat and barley



Introduction

Background

The team

The barley collection

Starch characterisation

Gene discovery

Fast-track barley breeding

Our approach in wheat

Contacts and funding



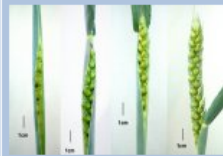
The Smart Carbohydrate Centre provides completely new resources for end-users and breeders of wheat and barley, paving the way for the development of new cultivars with improved or novel food and industrial value, and of new, renewable raw materials for industry.



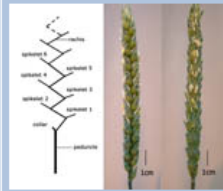
Home	Growth	Grain	Methods	Glossary
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You are here: [Flowering and fertilisation](#) > [Wheat ear pictures](#)

Flowering and fertilisation: Wheat ear pictures



All the events around anthesis must be well co-ordinated for the successful release of pollen and fertilization of the ovule. The ear is quickly raised above the crop canopy by the growth of the last stem internode or peduncle. It remains protected inside the sheath of the flag leaf until the anthers are almost mature.

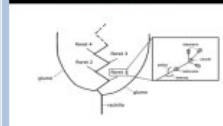


Spikelets are arranged on alternate sides of the rachis. The collar is a rudimentary spikelet which only rarely sets grain. The last-formed spikelets are found on the mainstem than on the primary axis. The rachis is genetically limited; in cv Mercia it is, on average, 22 spikelets long. The conditions will determine how many florets within each spikelet remain viable at anthesis.

The primary axis of the wheat ear, it bears the spikelets.



Each spikelet initiates between eight and twelve florets of which only four or five will be potentially fertile at flowering. The outer glumes are barren, their function is to protect. Similarly the lemma and palea of each floret protect the delicate structures inside.



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Growth

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 - Whole grain photographs
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 - Embryo sac: wall changes
 - Embryo micrographs
- Grain growth 4 to 10 days
 - Whole grain photographs

Monogram Publications

[Add new](#)

Search Publications

You can search the Monogram publications by any of these fields.

Search Author:

AND Search Title:

and Years from

to

Click on reset to see all the publications.

Results of your search

Your search settings are:


With in the title

With in the Author's list

Result: 623 papers

Reference Type: Book or Book Chapter

2009

-  HD Jones and PR Shewry - Editors(2009) "**Transgenic Wheat, Barley and Oats: Production and Characterisation**", *Methods in Biotechnology*, Series Ed. J Walker. Humana Press Totowa NJ (in press)

MONOGRAM
UK focus on grain and grass research



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You are here: [Research Activities](#) > [Conferences](#)

Workshops & Conferences

Conferences [Show past events](#)
[Add a new event](#)

October 4 - EU COST TD0801 -StatSeq workshop
5, 2009

"Statistical challenges on 1000euro genome sequences in plants"
 New sequencing technologies will soon enable us to sequence plant genomes for less than 1000 e.
 This will accelerate plant genomics and biological research.
 The workshop will provide an excellent opportunity to share and discuss statistical challenges, best-practices
 and future directions when dealing with large scale genome sequence data in plants.
 The workshop will be a mixture of invited talks and contributed talks and posters.

-{1}-----
 We now welcome your abstracts!
 The deadline is August 15 2009. Soon after this date we will draft the program and inform the presenters.
 You can upload your abstract on the stateseq website, or by using the following link:
http://www.stateseq.eu/index.php?option=com_jforms&view=form&id=4&Itemid=35

-{2}-----
 Registration open
 The registration fee is 140 euro and covers access, documentation and meals/refreshments of the workshop.

You may use the link below for registration.
http://www.stateseq.eu/index.php?option=com_jforms&view=form&id=1&Itemid=31
 Please note that your registration is only completed after payment of the fee. See the website for details on
 payment.

Looking forward to meet you in Barcelona,
 Sincerely,
 Dr. Marco Bink
 Workshop chair
 Information on EU-COST Action TD0801 is available at www.stateseq.eu

<http://www.stateseq.eu>
 Who's going?

October 25 - 30, 2009 **9th International Plant Molecular Biology Congress**

The conference will highlight a state-of-the-art view of research in plant molecular biology. In addition to
 keynote addresses and invited symposia, individuals are invited to submit abstracts for presentation as talks
 in concurrent sessions, or as posters.
<http://www.ipmb2009.org/index.html>
 Who's going?

St. Louis,
 Missouri, USA

November 25, 2009 **WGIN stakeholder meeting**

Wheat Genetic Improvement Network Research Updates for 2009 and presentations on one specific topic
 from WGIN stakeholders
 Who's going?

Rothamsted
 Research,
 Harpenden, UK

Parallel-Search

Services simultaneous search over multiple resources

Equipment

Germplasm

Databases

Markers

Workflows

Link outs

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- 30/06/2009
Preliminary announcement: EUCARPIA Cereal Section Meeting [more ...](#)

BBR Objectives 2008/9

- *Continue to develop the Monogram web site as the one stop shop for UK wheat activity*
- Bristol – updated resource search to include all genetic resources so far identified
- Rothamsted – updated facilities & tools

MONOGRAM

UK focus on grain and grass research



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You are here: [Search](#) > [Parallel-Search](#)

Parallel Resource Search

enabled by the [BBR project](#): A community resource for wheat functional genomics

This uses your supplied search query string to search in multiple resources available to the Monogram Network (note: still in development).

example: pollen, endosperm, AL825571

Currently the search uses the whole word or phrase only. More advanced searches will come as the system develops.

query :

[Search](#)

Search Results...

News

Monogram news

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Quantitative Methods in Plant Breeding, March 2010. [more ...](#)

12/10/2009 **NEW**

Monogram Development Officer Position [more ...](#)

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03/09/2009

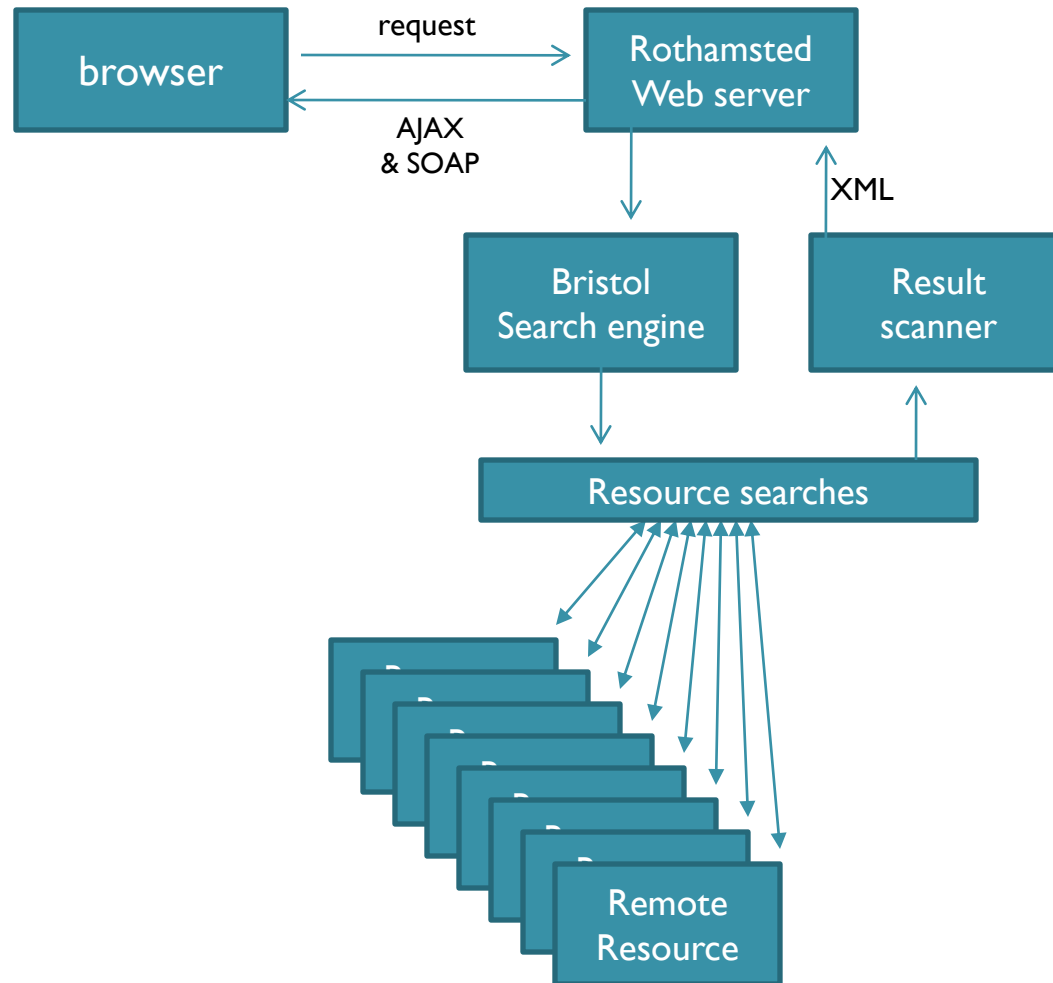
Eucarpia Cereal Section

Flyer [more ...](#)

24/08/2009

Need help from a Mathematician? Bring your

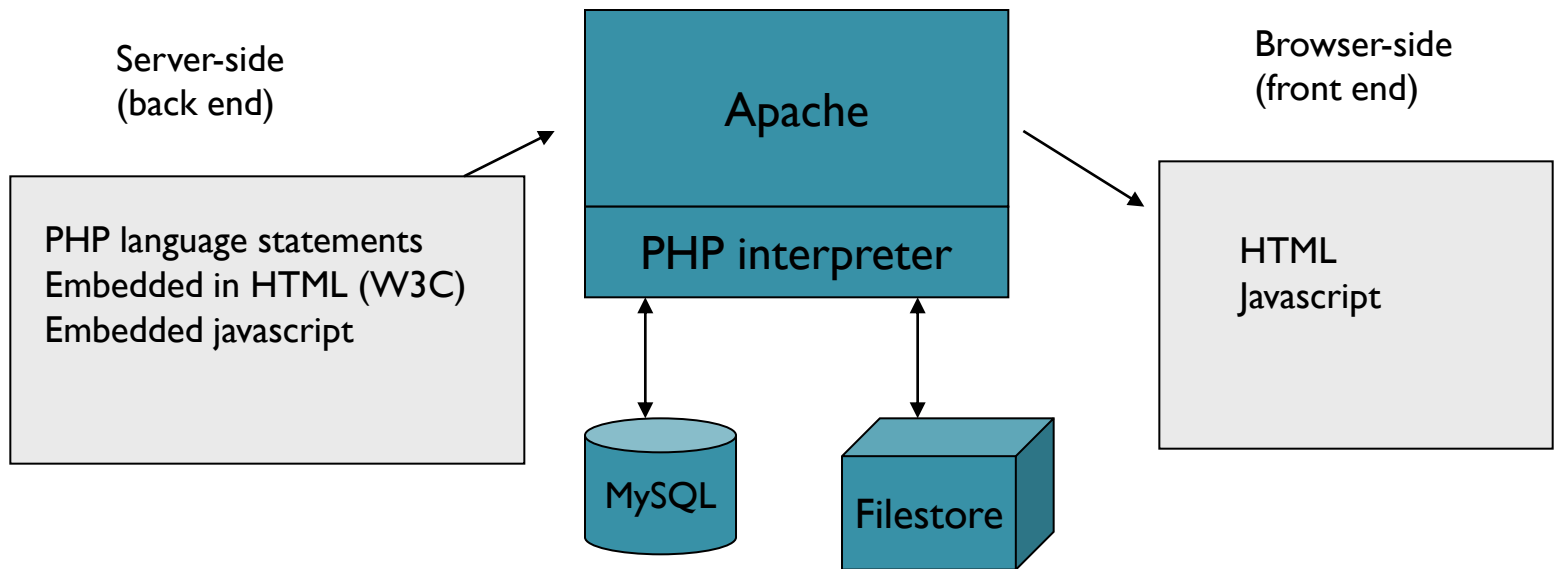
Parallel Search



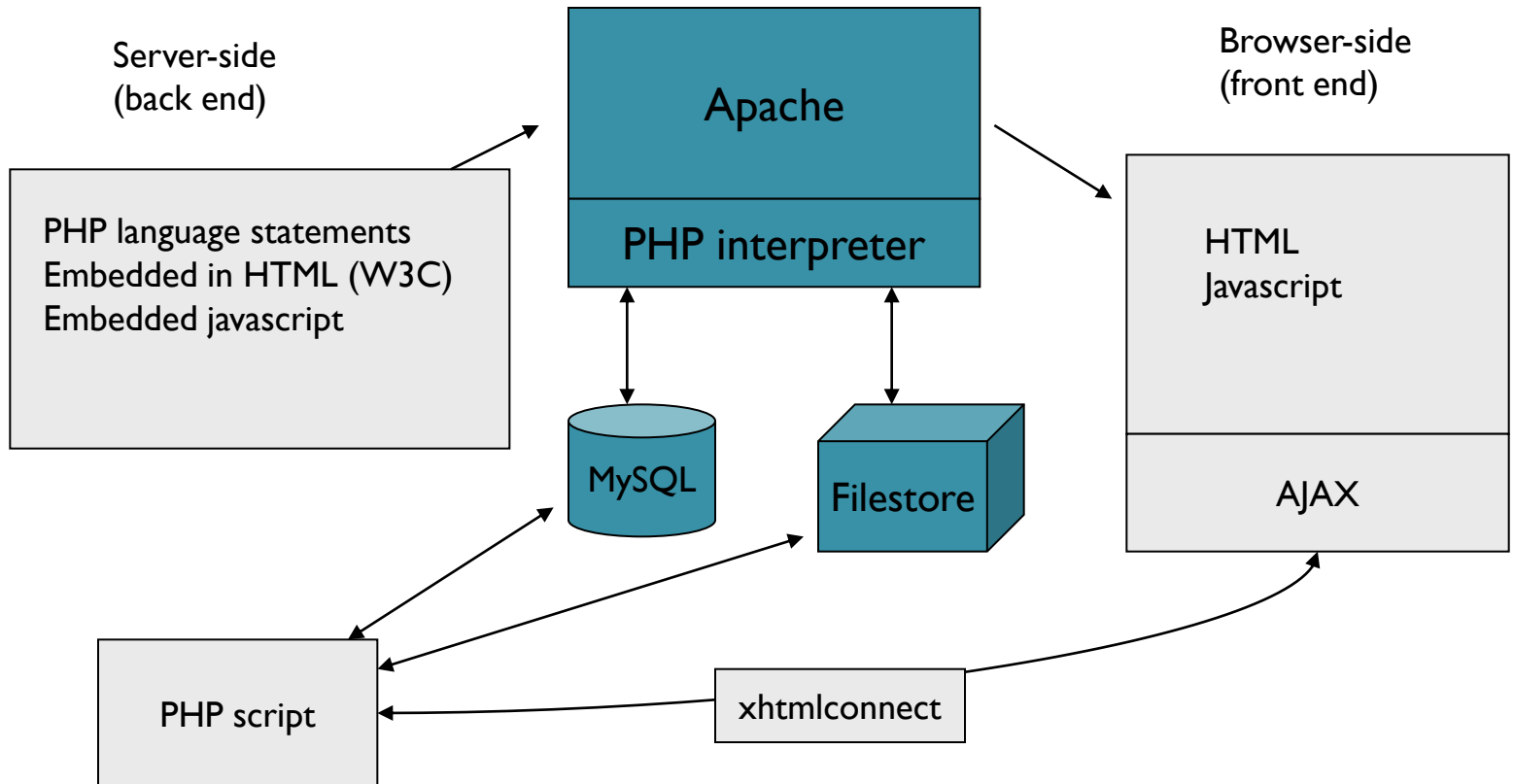
Framework

- Linux based server at Rothamsted
- Apache web server
- MySQL database
- PHP development
- Re-usable scripts
- AJAX techniques for Javascript xhtml transfers
- SOAP based web services for data transfer
- Enable capture of remote site data/pages
- Enable searching of remote site data

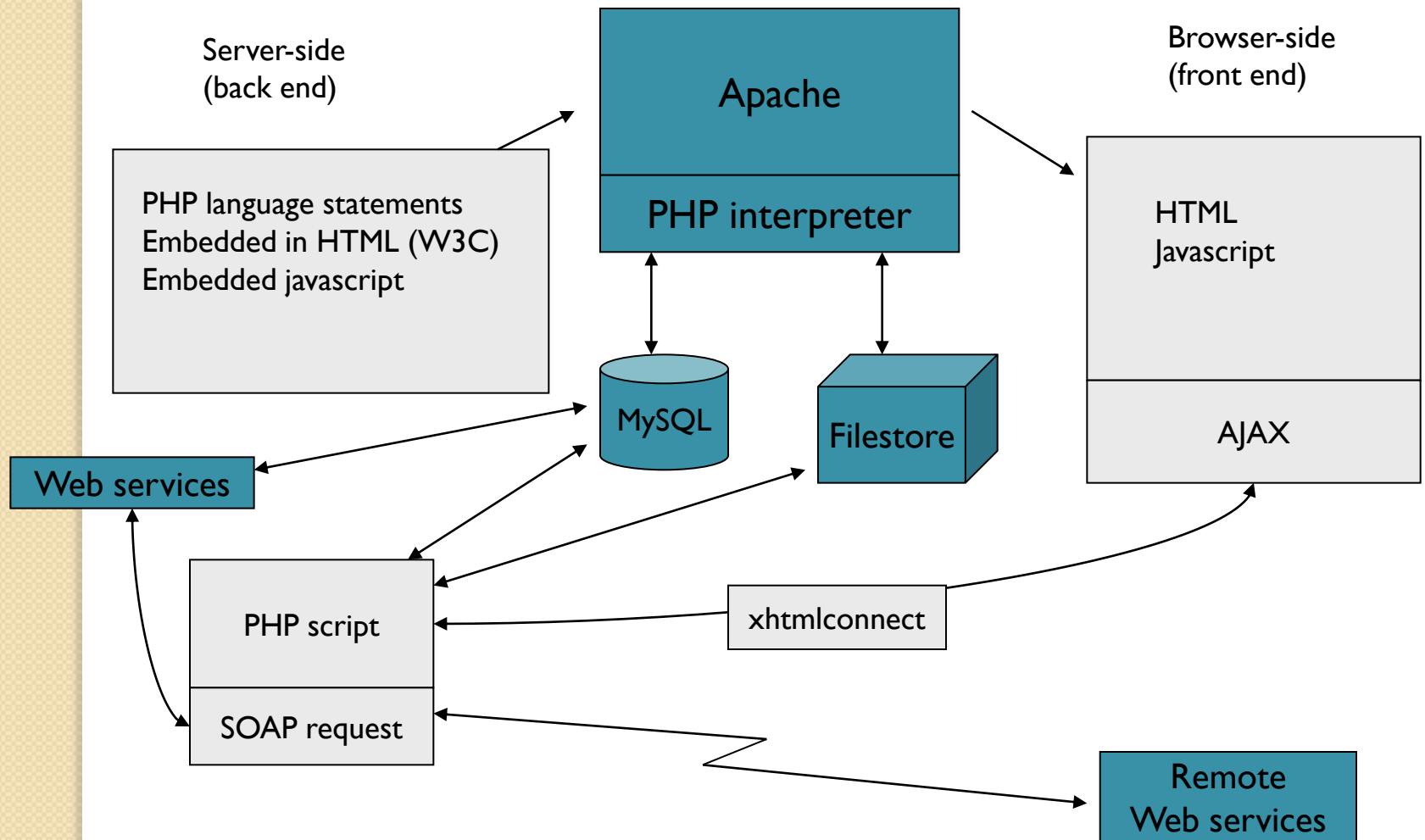
Creating a page



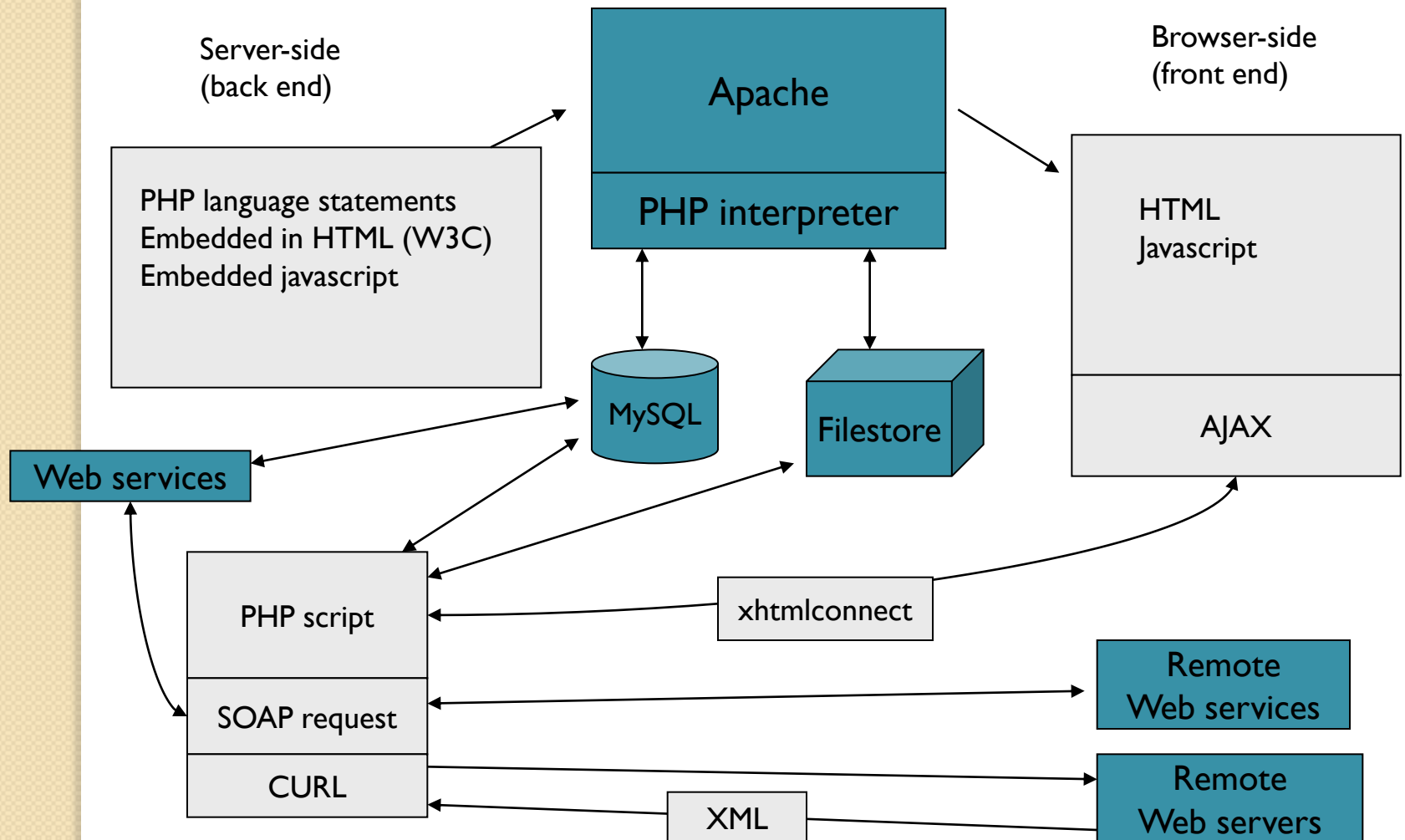
Creating a page



Creating a page



Creating a page



GAIT genotypes (Excel)

WGIN Website

Wheat Genetic Improvement Network

defra
initiated and supported by the Department for Environment, Food and Rural Affairs

Home Research Activities Resources Stakeholders

Research Results

Below are links to WGIN research results. This website is continuously updated to add new research results as soon as they become available.
A detailed account of research findings is also available in the stakeholder newsletters and the WGIN management meeting documents as well as in the Research Activities section.

Research data:
Watkins collection phenotype data from the 2006 JIC field trial
Phenotype data of the EMS mutated Paragon M5 population collected at JIC between March and August 2006
Mapping data for the Avalon x Cadenza DH population
Development and analysis of 146 Conserved Orthologous Sequence (COS) markers in Wheat, Rice and Brachypodium distachyon
Avalon and Cadenza Field Trial 2006

Watkins data

B	C	D	E	F	G	H	J	K	L
COUNTRY of origin	ACCESSION name	06 Rep 2 Heading	06 Rep 3 Heading	06 Rep 4 Heading	06 Rep 5 Heading	Mean Heading	Mean days to Heading	st dev	Heading Uniformity
Morocco		*	*	*	*	*	*	*	*
Crete	Blé mavrathier	*	*	*	*	*	*	*	*
Iran		*	*	*	*	*	*	*	*
Iran	Rustam Exp Farm 99	08-Jun	08-Jun	08-Jun	08-Jun	08-Jun	84	0	yes
Australia		09-Jun	09-Jun	09-Jun	09-Jun	09-Jun	85	0	yes
Australia		16-Jun	*	09-Jun	09-Jun	11-Jun	87.33	4.04	no
Australia		07-Jun	08-Jun	08-Jun	08-Jun	07-Jun	83.75	0.5	yes
Portugal	Trigo Temporal de Coruche	09-Jun	09-Jun	*	10-Jun	09-Jun	85.33	0.58	yes
Portugal	Trigo Precoces	18-Jun	18-Jun	18-Jun	18-Jun	18-Jun	94	0	yes
India	Pusa 80-5	09-Jun	09-Jun	15-Jun	12-Jun	11-Jun	87.25	2.87	no
India	Pusa 111	06-Jun	06-Jun	06-Jun	06-Jun	06-Jun	82	0	yes
India	Pusa 90	13-Jun	16-Jun	16-Jun	13-Jun	14-Jun	90.5	1.73	yes
Bulgaria	Bebrovo	08-Jun	21-Jun	22-Jun	22-Jun	18-Jun	94.25	6.85	no
Yugoslavia		03-Jul	05-Jul	08-Jun	06-Jul	28-Jun	104	13.4	no
Yugoslavia		06-Jul	24-Jun	24-Jun	23-Jun	26-Jun	102.75	6.18	no
Spain	Mocho	22-Jun	22-Jun	23-Jun	22-Jun	22-Jun	98.25	0.5	yes
Spain	Mocho	27-Jun	17-Jun	26-Jun	27-Jun	24-Jun	100.75	5.19	no
India	Gangajali	13-Jun	18-Jun	15-Jun	15-Jun	15-Jun	91.25	2.06	yes
India	Gangajali	15-Jun	15-Jun	15-Jun	15-Jun	15-Jun	91	0	yes
India	Thori	14-Jun	15-Jun	15-Jun	15-Jun	14-Jun	90.75	0.5	yes

Avalon-Cadenza mapping

A	B	C	D	E	F	G	H
Avalon x Cadenza		1	2	3	4	5	
marker name	location	distance cM					
wPt4029	.1AS	0	-	A	A	B	A
wPt9752	.1AS	5.562	-	A	A	A	A
wmc336a	.1AS	23.114	B	A	A	A	A
wPt3904	.1AS	39.672	-	A	A	A	A
barc119	.1AS	44.082	B	A	A	B	A
gwm498	.1ASC	49.606	B	B		B	A
gwm164	.1ALC	50.418	B	B		A	A
wPt6046	.1AL	50.876	B	B		A	A
psp3027	.1ALM	50.856	B	B	A	A	A
Glw-A1	.1ALM	54.511	B	B	-	B	A
wPt9757	.1AL	55.766	B	B	B	B	A
gwm99	.1ALT	72.934	A	B	B	B	A
gwm33	.1BS	0	B	A	A	B	A
wPt2230	.1BS	10.32	B	A	A	A	A
wPt3465	.1BS	10.597	-	A	A	A	A
wPt1580	.1BS	11.011	-	A	A	B	A
wPt2988	.1BS	11.094	-	A	A	B	A
gap(database accession), (c-giadin; gene ta	.1BS	11.115	B	A	A	B	A
gwm264	.1BST	11.659	B	c	A	B	A
wPt5562	.1BS	18.49	B	A	A	A	A
wPt8168	.1BS	34.519	A	B	A	A	A
wPt3451	.1BS	35.246	-	B	A	A	A

BBSRC Small Grain Cereals Collection

BBSRC Small Grain Cereal Collections

JOHN INNES CENTRE

Accession Number: From [] To [] Sort by: Accession Number [] Status: ANY []

Accession Name: minimum of 3 characters []

Genus and Species: Triticum [] aestivum []

Country of Origin: SELECT [] SEARCH CLEAR

All enquiries relating to this data should be addressed to mike.ambrose@bbsrc.ac.uk

Results: 9120

Accession No	Accession Name	Genus	Species	Country	Status
1	Arp 181/121	Triticum	aestivum	GBR	410
2	April Bearded	Triticum	aestivum	GBR	500
3	Glendowe	Triticum	aestivum	GBR	500
4	Maris Butler	Triticum	aestivum	GBR	500
5	Mans Dove	Triticum	aestivum	GBR	500
6	Mans Ensign	Triticum	aestivum	GBR	500
7	TB 56/5/59	Triticum	aestivum	GBR	410

Wheat Pedigree data

BBSRC Wheat Collection Pedigree Report

ACC NAME	PEDIGREE
2 April Bearded	English Land Variety
3 Glendowe	Not recorded
4 Maris Butler	Koga 2*Hybrid 46
5 Arin	H 8810-47*Koga 2
6 Maris Ensign	Breustedts Teutonen*Cappelle Desprez
53 Meteor	April Bearded*Yeoman
55 Clarion	Halle 10*(Carpo*Generoso)
56 Orca	Ministre*Peko
57 Rothwell Sprite	(HD 12*Cappelle Desprez)*Fasan
58 Toro	(Ministre*Peko)*Carpo
59 Arin	Halle 5756*Breustedts 778/40*Weihestephaner GKJ
60 Aronde	(Thatcher*Teutonen)*Koga
61 Carpo	(Lin Calcl*Rimpau Bastard 2)*Jabo
62 Densi	(Marquis*(Peragis*H Kolben))*((Peragis*Marquis)*(Garnet*(Keuzung
56*Ja	
69 ELS	(CA*(Garnet*Zimbera))*Erli
71 Fasan	(Peragis*Garnet)*(Teutonen*H
Kolben*Peragis)*(Ardito*Peragis*H'heim 25	

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Parallel Resource Search

enabled by the [BBR project](#): A community resource for wheat functional genomics

This uses your supplied search query string to search in multiple resources available to the Monogram Network (note: still in development).

example: pollen, endosperm, AL825571

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2009-09-10 10:51:46 database contains **26377** ESTs
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WestDB ID	Top blastx Hit	E-value	NCBI Link	View full blastx output
C04_e310_plate_11	grain softness protein 1 [Triticum aestivum]	3e-75	gb AAG09276.1 AF177218_1	more
E03_e310_plate_11	grain softness protein 1b, 15K - wheat	1e-08	pir S48187	more
E06_e310_plate_3	grain softness protein 1a, 15K (clone TSF69) - wheat	2e-88	pir S48186	more
E07_e310_plate_3	grain softness protein 1a, 15K (clone TSF69) - wheat	1e-88	pir S48186	more
G03_e310_plate_5	grain softness protein 1 [Triticum aestivum]	3e-83	gb AAG09276.1 AF177218_1	more
H01_e310_plate_5	grain softness protein 1 [Triticum aestivum]	2e-88	gb AAG09276.1 AF177218_1	more
H02_e310_plate_5	grain softness protein 1 [Triticum aestivum]	2e-88	gb AAG09276.1 AF177218_1	more
A07_h116_plate_11	grain softness protein 1b, 15K - wheat	3e-72	pir S48187	more
C03_h116_plate_11	grain softness protein 1b, 15K - wheat	3e-46	pir S48187	more
G05_h116_plate_12	grain softness protein 1a, 15K (clone SR3.1) - wheat (fragment)	4e-81	pir S51770	more

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**Search results for:
'(grain or grained or graining or grainer or grains)'**

Match: Format: Sort by:

Refine search:

Documents 1 - 10 of 24 matches. More ★'s indicate a better match.

- ★★★★★ WGIN: Objective 6
- ★★★★★ WGIN: Objective 11
- ★★★ WGIN 2 - home
- ★ WGIN: Project Outline
- ★ WGIN: International Cooperation
- ★ WGIN: Objective 9
- ★ WGIN 2 - home
- ★ WGIN 2 - home
- ★ WGIN 2 - home
- ★ WGIN: Links

Pages:



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Switch to [protein view](#) view contig cluster_137_contig_3 in [fasta format](#)

[emb|CAH10045.1](#) GSP-1 Grain Softness Protein [Triticum aestivum]

Frame: -2 Start: 635 End: 144

Rice bin: 0.0 Wheat nulli bin(s): 5AS 5BS 5DS

Cultivar and tissue source: SNP summary Full sequence

1.....51..

A

varietal?

confident?

Consensus		..M..I..L..H..K..Y..S..F..C..M..C..V..Y..T..L..F.*.V.. ACATGCATAATTAGATGTTTGTAAGAGAAACACATACATACATAAGTAA*GGAA
-----------	--	--

Y1 BQ805765, cv: Butte 86 , tissue: whole grains, dev stage: 3-44 days post anthesis seed,	T
--	---	-------

U2 BE399689, cv: Cheyenne , tissue: endosperm, dev stage: 5-30 days post anthesis,	
--	--	-------

V2 BE399947, cv: Cheyenne , tissue: endosperm, dev stage: 5-30 days post anthesis,	T
--	---	-------

U3 BG604292, cv: Cheyenne , tissue: Endosperm, dev stage: 5 -30 days post anthesis seed,	TTGTAAGAGAAACACATACATACATAAGTAA-GGAA
--	---	--

D1 BJ241590, cv: Chinese Spring , tissue: seed DPA10, dev stage: Feekes' scale 11.2,	C
--	---	-------

E1 BJ232125, cv: Chinese Spring , tissue: seed DPA10, dev stage: Feekes' scale 11.2,	C
--	---	-------

F1 BJ237766, cv: Chinese Spring , tissue: seed DPA10, dev stage: Feekes' scale 11.2,	AGAGAAACACATACATACATAAGTAA-GGAA
--	--	--------------------------------------

G1 BJ234106, cv: Chinese Spring , tissue: seed DPA10, dev stage: Feekes' scale 11.2,	CCATACATACATAAGTAA-GGAA
--	---	-----------------------------

H1 BJ241561, cv: Chinese Spring , tissue: seed DPA10, dev stage: Feekes' scale 11.2,	C
--	---	-------

I1 BJ235554, cv: Chinese Spring , tissue: seed DPA10, dev stage: Feekes' scale 11.2,	C
BJ232169, cv: Chinese Spring , tissue:	

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Germination

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[Grain growth 1 to 4 days](#)

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[Cell layers inside a grain](#)

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[Grain filling 17 to 21 days](#)

[Grain filling 21 to 30 days](#)

[Development of the embryo](#)

[Dry down 30 to 40 days](#)

[How we grew the plants](#)

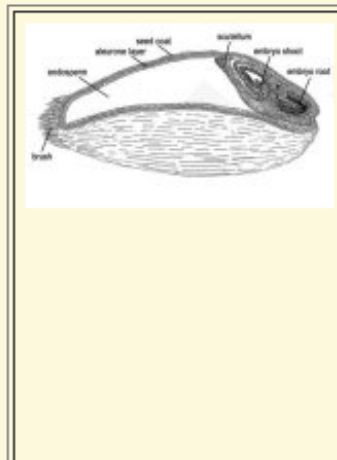
[Photography and microscopy](#)

(**days** = days after flowering)

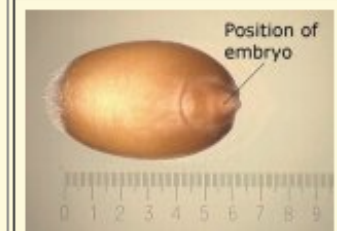
Funded by:



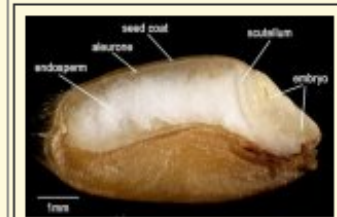
Search Results for **grain**:



Simple diagram of the dry grain showing its principle parts; the endosperm, **aleurone** and seed coat, the **scutellum** and the **embryo** with its primordial shoot and root. During grain milling these tissues are crudely separated: the **endosperm** becomes the white flour, the embryo is the **germ** and the aleurone layer and the **seed coat** are the bran. The seed coat is a complex structure. The Cell Layers inside the Grain are described in detail in a separate section.



Fully imbibed grain just before the **embryo** emerges. After planting the grain quickly takes up water and the chemical processes of germination start.



The imbibed grain, split open along its long axis, shows the **embryo** in close contact, via the scutellum, with the stored reserves of the **endosperm**. The internal processes of germination are well under way. Several hydrolytic enzymes are activated to perform specific tasks. The cell walls of the endosperm are broken down, the starch and storage proteins they contain are degraded and released, and the **aleurone** and embryo are activated ready for growth.



The grain with the **embryo** dissected away from the **endosperm**. The structure between the endosperm and the embryo is the

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All enquires relating to this data should be addressed to mike.ambrose@bbsrc.ac.uk

Results: 6

	Accession No	Accession Name	Genus	Species	Country
	829	Touzelle Barbuza Gros Grains	Triticum	aestivum	FRA
	2865	Newgrain 265	Triticum	aestivum	GBR
	2866	Newgrain 65-112	Triticum	aestivum	GBR
	2867	Newgrain K 7/A5-1	Triticum	aestivum	GBR
	7164	Purple Grain	Triticum	aestivum	*
	7272	Mivhor Multigrain	Triticum	aestivum	ISR



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BBSRC Wheat Collection Pedigree Report

ACC NAME	PEDIGREE
2 April Bearded	English Land Variety
3 Glendowe	Not recorded
4 Maris Butler	Koga 2*Hybrid 46
5 Maris Dove	H 8810-47*Koga 2
6 Maris Ensign	Breustedts Teutonen*Cappelle Desprez
53 Meteor	April Bearded*Yeoman
55 Clarion	Halle 10*(Carpo*Generoso)
56 Orca	Ministre*Peko
57 Rothwell Sprite	(HD 12*Cappelle Desprez)*Fasan
58 Toro	(Ministre*Peko)*Carpo
59 Arin	Halle 5756*Breustedts 778/40*Weihenstephaner GKJ
60 Aronde	(Thatcher*Teutonen)*Koga
61 Carpo	(Lin Calel*Rimpau Bastard 2)*Jabo
62 Densi	(Marquis*(Peragis*H Kolben))*((Peragis*Marquis)*(Garnet*(Keuz
69 ELS	(CA*(Garnet*Zimbera))*Erli
71 Fasan	(Peragis*Garnet)*(Teutonen*H Kolben*Peragis)*(Ardito*Peragis*
72 Grano	Koga*(Koga*Breustedts Teutonen)
78 Heines Kolben	Saumar de Mars Selection
79 Janus	((Von Rumkers Dickkopf*Erli)*(Erli*Hope))*Dickkopf
80 Kloka	Weihenstephaner 43/48 Selection
81 Koga 1	Heines Kolben*Garnet
82 Koga 2	(Heines Kolben*Garnet)*(Heines Kolben*Raeckes White Chaff)
83 Kolibri	(Heine 2174*Peko)*Koga 2
84 Lera	(Marquis*(Peragis*Heines Kolben))*((Peragis*Marquis)*Weihenst
85 Opal	Triesdorfer Ruf*Garnet*Heine Kolben*Koga*Rumkers Erli
86 Peko	Peragis*Heines Kolben
87 Peragis	Blue Dame*Green Dame
89 Teutonen	Heines Kolben*R 1004(=Noe*Squarehead)
90 Trident	(Heine 2174*Peko)*Koga 2
91 Erli	Lichtis Fruh*(Erbachshofer Janetzki*Japhet)
92 Erli	Erli*Heine 2174

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Documents from the website matching the keyword "grain"

www.monogram.ac.uk/announce.php matched grain

www.monogram.ac.uk/links.php matched grain

www.monogram.ac.uk/gbmarkers.php matched grain

www.monogram.ac.uk/germplasm.php matched grain

www.monogram.ac.uk/wg3.php matched grain

www.monogram.ac.uk/universities.php matched grain

www.monogram.ac.uk/institutes.php matched grain

www.monogram.ac.uk/report.php matched grain

www.monogram.ac.uk/newsletter.php matched grain

www.monogram.ac.uk/pastmeetings.php matched grain

www.monogram.ac.uk/meetings.php matched grain

www.monogram.ac.uk/people.php matched grain

www.monogram.ac.uk/indexs.php matched grain

www.monogram.ac.uk/monocip.php matched grain

www.monogram.ac.uk/pastevents.php matched grain

www.monogram.ac.uk/grants.php matched grain

MONOGRAM**UK focus on grain and grass research**

Home

Research Activities

Monogram CIP

The Network

Working groups

Search

News

You are here: [Search](#) > [Parallel-Search](#)**Parallel Resource Search**enabled by the [BBR project](#): [A community resource for wheat functional genomics](#)

This uses your supplied search query string to search in multiple resources available to the Monogram Network (note: still in development).

example: pollen, endosperm, AL825571

Currently the search uses the whole word or phrase only. More advanced searches will come as the system develops.

query : **Matches found with the keyword grain:**

- No hits** to WhETS
- 18 hits** to BLASTX gene annotations at cerealsdb
- 24 hits** to WGIN web site
 - 1 hits** to wheat SNPs
- 84 hits** to images at wheatbp
 - 1 hit** to grain in the wheatbp glossary
- 6 hits** to wheat Germplasm at JIC
- 5 hits** to wheat Pedigree data at JIC
- 20 hits** to the MONOGRAM site
- 3 hits** to WGIN results files
- 1 hits** to the SmartCarb site

Search completed

News**Monogram news**03/09/2009 **NEW**

Eucarpia Cereal Section Flyer [more ...](#)

24/08/2009

Need help from a Mathematician? Bring your problem to the Plant Science Study Group

[more ...](#)

14/08/2009

The Bristol Agilent wheat homoeologous array design is now public [more ...](#)

29/07/2009

Important note about extra deletions in some of the Kansas wheat deletion lines [more ...](#)

14/07/2009

£1.6 million awarded to develop a physical map of the ryegrass genome

[more ...](#)

08/07/2009

EU COST TD0801 -StatSeq workshop: call for abstracts & registration open [more ...](#)

30/06/2009

Preliminary announcement: EUCARPIA Cereal Section Meeting [more ...](#)

03/06/2009


Brachypodium Sequence Released [more ...](#)

27/05/2009

Molecular study of the wheat-ergot interaction funded [more ...](#)

20/05/2009

OECD-GenomeAssociation-O700 Call for abstracts



Documents from the Wheat genetic Improvement ([WGIN](#)) website matching the keyword "grain"

[DiversityTrialGrainYields.xls](#)

[WGINTakeAllReport.pdf](#)

[Traits field trial 2003-5.pdf](#)

[Back to Monogram search page](#)



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query : **Matches found with the keyword grain:****No hits** to WhETS**18 hits** to BLASTX gene annotations at cerealsdb**24 hits** to WGIN web site**1 hits** to wheat SNPs**84 hits** to images at wheatbp**1 hit** to grain in the wheatbp glossary**6 hits** to wheat Germplasm at JIC**5 hits** to wheat Pedigree data at JIC**20 hits** to the MONOGRAM site**3 hits** to WGIN results files**1 hits** to the SmartCarb site

Search completed

News**Monogram news**03/09/2009 **NEW****Eucarpia Cereal Section****Flyer** [more ...](#)

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[more ...](#)

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Preliminary announcement: EUCARPIA Cereal Section

Meeting [more ...](#)

03/06/2009

Brachypodium Sequence Released [more ...](#)

27/05/2009

Molecular study of the wheat-ergot interaction funded [more ...](#)

20/05/2009

OECD-GenomeAssociation-O700 Call for abstracts

The Smart Carbohydrate Centre

Producing and exploiting novel variation for starch properties in wheat and barley



Introduction

Background

The team

The barley collection

Starch characterisation

Gene discovery

Fast-track barley breeding

Our approach in wheat

Contacts and funding

Our approach in wheat

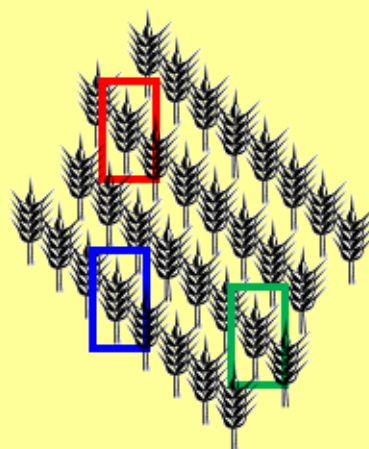
Wheat is a much more important source of starch and flour than barley. It is of very considerable commercial interest to produce wheat varieties with new starches. Unfortunately this is extremely difficult to do because wheat has three sets of each of its chromosomes (called the A, B and D genomes). In other words, wheat is a hexaploid. We cannot apply to wheat the simple genetic approaches we are using in barley (a diploid).

To generate variation in wheat we need to alter expression of target genes in all three genomes. To do this we are, we are using TILLING (Targeting Induced Local Lesions in Genomes) in collaboration with Rothamsted Research. TILLING is a non GM, reverse genetics technique. It enables us to find mutations in wheat in genes we think (based on our work with barley and our knowledge of other cereals) will influence the properties of starch. Once we have found plants with mutations in the target gene in the A or B or D genome, we can cross them together to produce a line in which the starch should have new properties. This line can then be tested by users of wheat such as millers and bakers. Importantly, we also need to backcross the mutant plants to eliminate the thousands of other mutations they carry.

In collaboration with Andy Phillips,



ROTHAMSTED
RESEARCH



Step 1. Utilise an existing population of mutagenised grain

Step 2. Screen the population for plants that contain mutations in the target gene. Plants with mutations in the A, B and D genomes are required



Next Steps

- SNPs from Bristol
- 454 wheat data
- Gbrowse
- Revised Resource centric web

FUTURE: Resource centered

- Consortium → resources
- New Menu:


The screenshot displays the MONOGRAM website navigation menu. The menu is organized into several vertical columns. The 'Resources' column is highlighted in a light brown color, indicating it is the new focus. The 'Working groups' column is also highlighted. The 'Information' column is partially visible on the right. The 'Home' column is on the left. The 'MG Sites' column is in the middle. The 'Resources' column contains the following items: Parallel-Search, Services, Equipment, Germplasm, Databases, Markers, Workflows, and Publications. The 'Working groups' column contains: Germplasm & markers, Structural Genomics, Gene expression, Gene Validation, Bioinformatics, and Meetings. The 'Information' column contains: Web Links, Vacancies, and Conferences. The 'MG Sites' column contains: SmartCarb and WheatBP. The 'Home' column contains: Research Activities and Monogram CIP. The 'Networking' column contains: My Monogram, People, Institutes, Universities, Network Steering, MG Meetings, Conferences, and News. The 'MONOGRAM [dev]' logo is at the top left, followed by the text 'UK focus on grain and grass research'. A search bar with a 'Go!' button is at the top right. A navigation bar at the bottom contains links for Home, Networking, Working groups, Resources, MG Sites, and Information. A logo of a wheat stalk is at the bottom right.

Home	Networking	Working groups	Resources	MG Sites	Information
Research Activities	My Monogram	Germplasm & markers	Parallel-Search	SmartCarb	Web Links
Monogram CIP	People	Structural Genomics	Services	WheatBP	Vacancies
	Institutes	Gene expression	Equipment		Conferences
	Universities	Gene Validation	Germplasm		
	Network Steering	Bioinformatics	Databases		
	MG Meetings	Meetings	Markers		
	Conferences		Workflows		
	News		Publications		

MONOGRAM [dev]
UK focus on grain and grass research

Home Networking Working groups Resources MG Sites Information

Go!



Monogram - Resource searching - Windows Internet Explorer
 http://www.monogram.ac.uk/dev/devMG1/ressrch4.php

File Edit View Favorites Tools Help Google C Go Bookmarks Settings

Monogram - Resource searching

Logged in user <Paul Verrier(System Administrator)>

MONOGRAM [dev/devMG1] UK focus on grain and grass research

Search the site: Go!

home Networking Working groups Resources MG Sites Information

You are here: Search > Parallel-Search >




Parallel Resource Search

enabled by the BBR project: A community resource for wheat functional genomics

This uses your supplied search query string to search in multiple resources available to the Monogram Network (note: still in development).

example: pollen, endosperm, AL825571
 Currently the search uses the whole word or phrase only. More advanced searches will come as the system develops.

query : Search

	cerealsDB: 18 hits				
	<table border="1"> <thead> <tr> <th>Links to results</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>Go to Results</td> <td><i>Investigating gene function in cereals</i></td> </tr> </tbody> </table>	Links to results	Description	Go to Results	<i>Investigating gene function in cereals</i>
Links to results	Description				
Go to Results	<i>Investigating gene function in cereals</i>				
	JIC-Germ: 6 hits				
	<table border="1"> <tbody> <tr> <td>Go to Results</td> <td><i>Wheat Germplasm held at John Innes Center</i></td> </tr> </tbody> </table>	Go to Results	<i>Wheat Germplasm held at John Innes Center</i>		
Go to Results	<i>Wheat Germplasm held at John Innes Center</i>				
	JIC: Wheat pedigree data: 5 hits				
	<table border="1"> <tbody> <tr> <td>Go to Results</td> <td><i>BBSRC Wheat Collection Pedigree Report</i></td> </tr> </tbody> </table>	Go to Results	<i>BBSRC Wheat Collection Pedigree Report</i>		
Go to Results	<i>BBSRC Wheat Collection Pedigree Report</i>				

News

Monogram news

19/10/2009 **NEW**
 Quantitative Methods in Plant Breeding, March 2010. [more ...](#)

12/10/2009 **NEW**
 Monogram Development Officer Position [more ...](#)

23/09/2009
 2010 MONOGRAM Network Workshop [more ...](#)

03/09/2009
 Eucarpia Cereal Section Flyer [more ...](#)

24/08/2009
 Need help from a Mathematician? Bring your problem to the Plant Science Study Group [more ...](#)

14/08/2009
 The Bristol Agilent wheat homoeologous array design is now public [more ...](#)

29/07/2009
 Important note about extra deletions in some of the Kansas wheat deletion lines [more ...](#)

Monogram Vacancies

07/10/2009 **NEW**
 Monogram Development Officer [more ...](#)

14/08/2009
 SCRI - MOLECULAR GENETICIST/INFORMATICIST [more ...](#)

Monogram web updates

14/08/2009

Done Local intranet 100%






Monogram - Resource searching - Windows Internet Explorer

http://www.monogram.ac.uk/dev/devMG1/ressrch4.php


File Edit View Favorites Tools Help Google G Go Bookmarks Settings

Monogram - Resource searching

New Search Feature on Monogram more ...

	Monogram: 20 hits <table border="1"> <thead> <tr> <th>Links to results</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>Go to Results</td> <td><i>This site</i></td> </tr> </tbody> </table>	Links to results	Description	Go to Results	<i>This site</i>
Links to results	Description				
Go to Results	<i>This site</i>				
	Smart Carbohydrate Center: 1 hits Go to Results <p><i>The Smart Carbohydrate Centre provides completely new resources for end-users and breeders of wheat and barley, paving the way for the development of new cultivars with improved or novel food and industrial value, and of new, renewable raw materials for industry.</i></p>				
	SNP search (cerealDB): 1 hits Go to Results <p><i>The most abundant genetic polymorphisms between individuals are Single Nucleotide Polymorphisms and small insertions/deletions, which are both emerging as a new generation of markers, due to their abundance and amenability to fully automated genotyping.</i></p>				
	WGIN: Defra Wheat Genetic Improvement Network : 3 hits Go to Results <p><i>Documents from the Wheat genetic Improvement (WGIN) website matching the keyword</i></p>				
	Wheat: The big picture: 84 hits Go to Results <p><i>The life cycle of WHEAT, from seed germination to harvest ripe with special emphasis on the development of the grain after fertilisation.</i></p>				

Contact Us | BBSRC Monogram Cross Institute Programme | The Monogram Network

 BBSRC

Local intranet 100%

Brassica tools into Wheat tools



home | si

RESEARCH RESOURCES INFORMA

HOME > CropStore > MAP interface

CropStore :: Maps

Species Selection

Select All *B. juncea* *B. nigra* *B. napus* *B. oleracea*

Optional Text Search

Population Name Year(e.g 1996)

Display Reset

Office 2007 users: Please ignore the File Error: data may have been lost message. This only affects the Excel 2007, we are in the process of fixing this. Thank you.

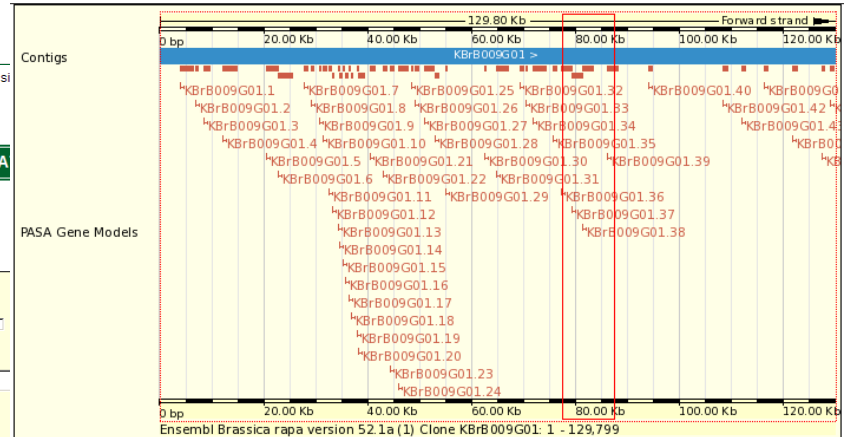
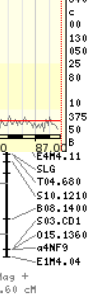
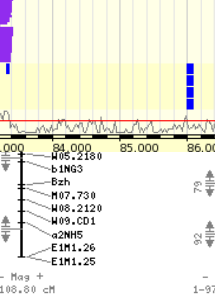
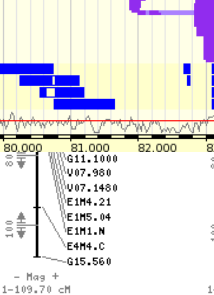
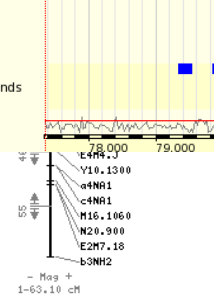
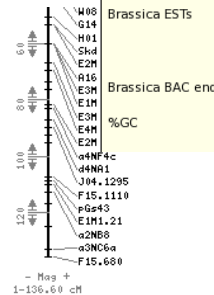
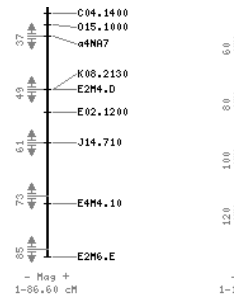
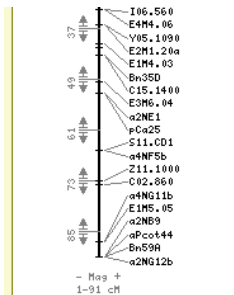
Your selections have found 16 Maps (of 29 in the database)

For comments and data source attributions please download the relevant Excel spreadsheet below

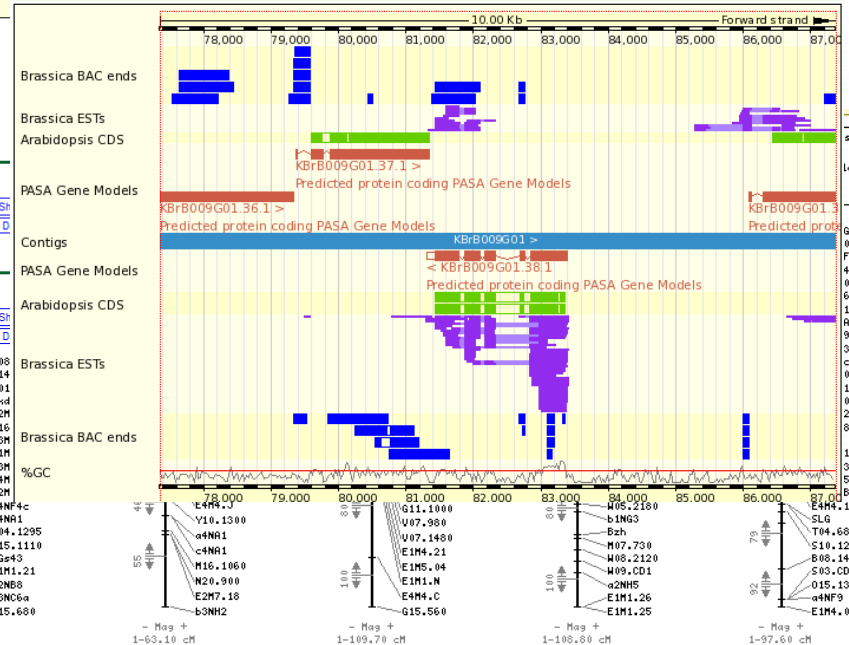
[Download map list only](#)

[Download map list with Linkage Group Details](#)

Species	linkage map	map description	mapping sub population	version	map date
napus	BnaDEIT_01_2001a	B. napus consensus Lombard Delourme (2001a)	BnaDEIT_01	1	2000-10-31
back to top					
Species	linkage map	map description	mapping sub population	version	map date
napus	BnaSDSH_00_2001a	B. napus DSDH Lombard Delourme (2001a)	BnaSDSH_00	1	2000-10-31



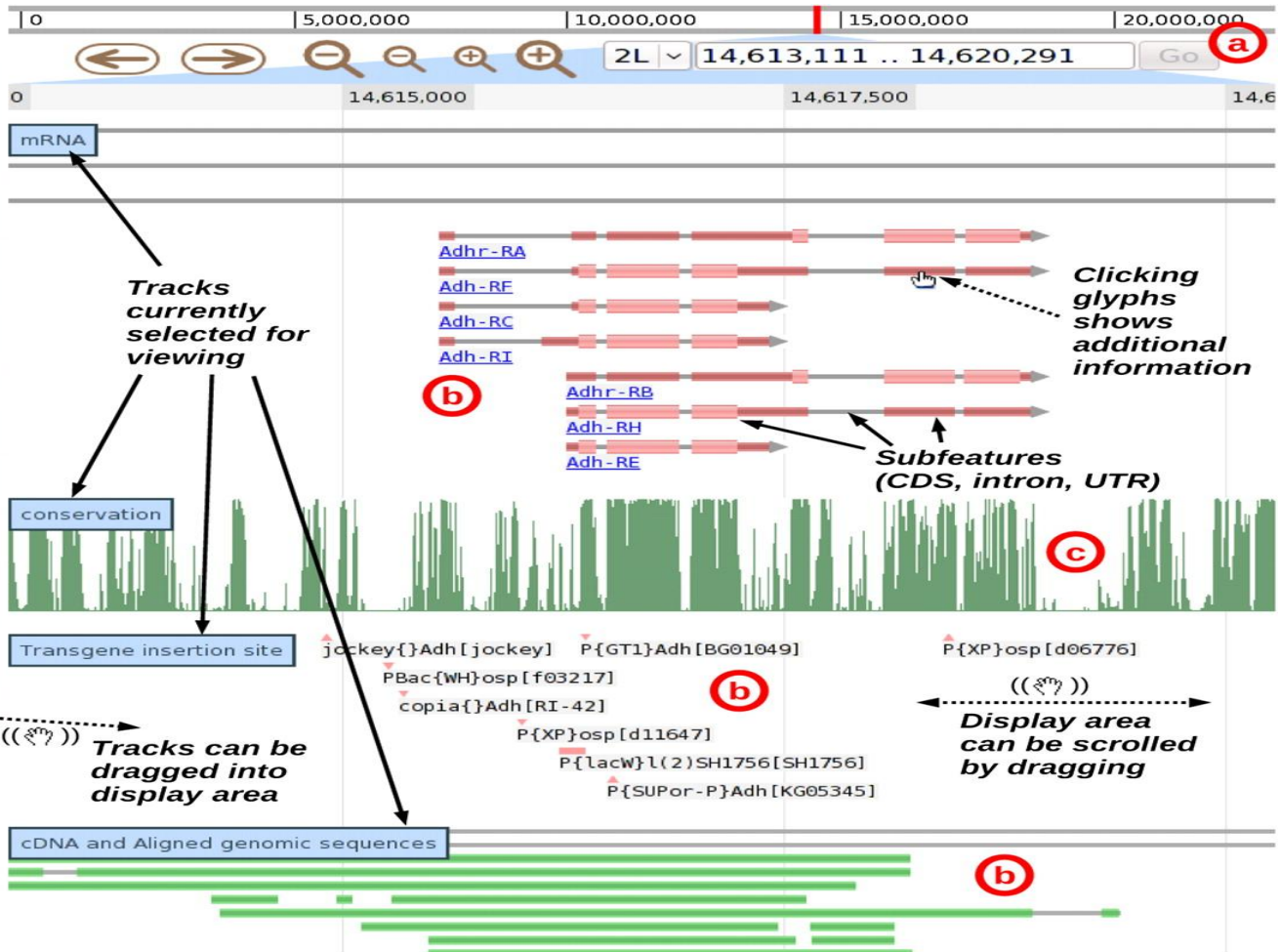
Location: KBrB009G01: 77352 - 87351 Go>



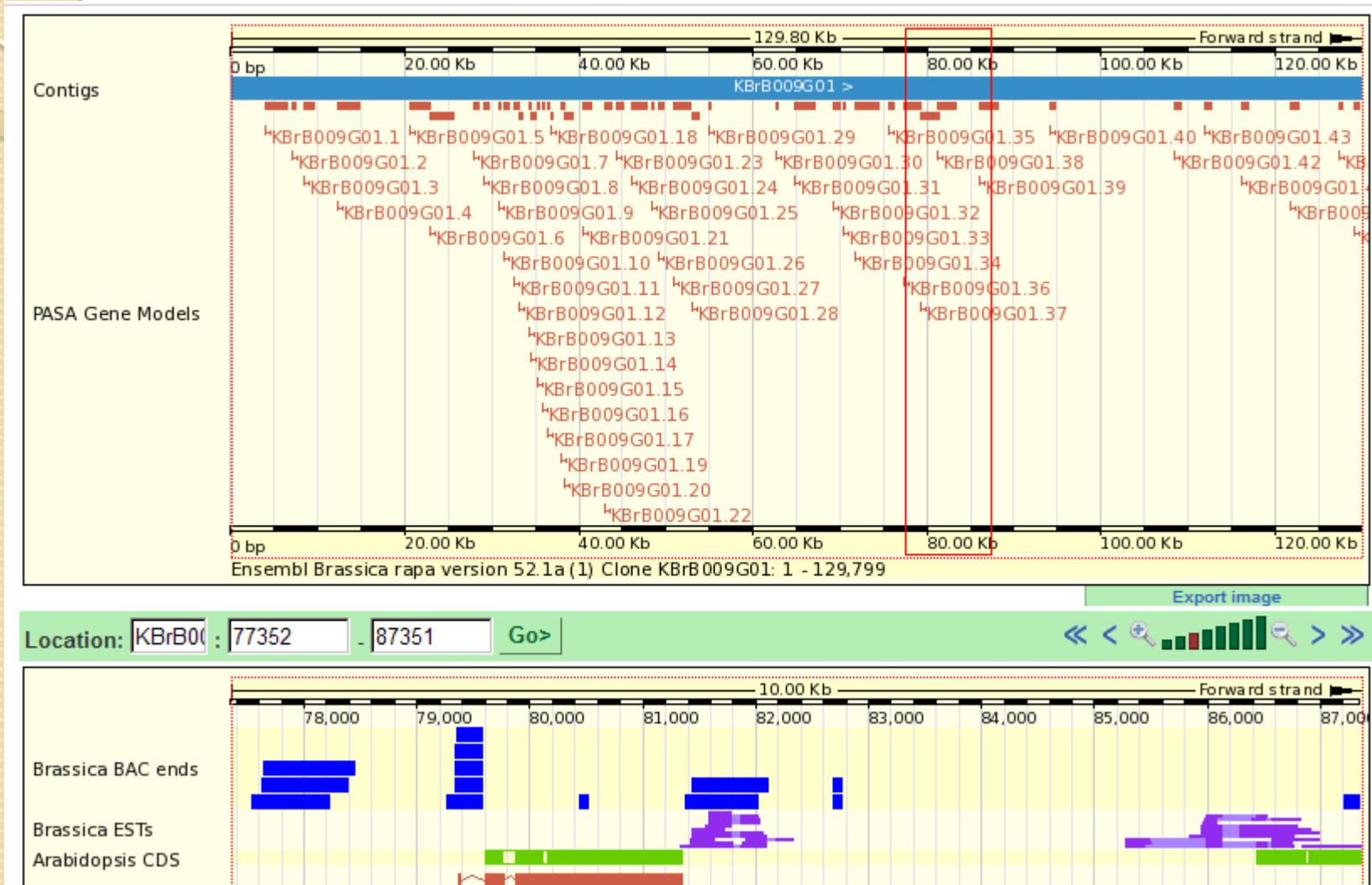
Jbrowse vs GBrowse

Available Tracks:
(Drag → to view)

- Gene Span
- Cytological band
- tRNA
- Natural transposon
- Oligonucleotides
- Tiling BAC
- protein binding site
- enhancer
- rescue fragment
- regulatory region
- Mutation: point mutation
- Mutation: sequence variant
- Mutation: aberration junction
- Non coding RNA



Future: wheat Ensembl?



Aknowledgments

- Bristol
 - Gary Barker (who supplied many of the slides)
 - Keith Edwards
- Rothamsted
 - Nathalie Castells
 - Chris Love
- The Community
 - Adding items to Monogram Web
 - Enabling searches to resources