Wheat Genetic Improvement Network

John Innes Centre

Tools, resources, genotyping and phenotyping

Clare Lister and Simon Griffiths

20/04/2017

Department for Environment Food & Rural Affairs

Wheat Genetic Improvement Network

WGIN3 Projects: Griffiths' Lab

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1. Dissecting UK drought tolerance in Paragon x Garcia
2. Quantifying agronomic impact of WGIN target genes using the Paragon NIL library
3. Informing multiple marker assisted selection for yield stability using Paragon library
4. A chromosome segment substitution library for Avalon x Cadenza
5. Understanding genotype x environment interaction in Avalon x Cadenza
6. Foundations for a new generation segregating populations for studying yield stability in the UK
7. Applying WGIN data to breeding by design for UK yield stability
8. Curation and distribution of WGIN germplasm

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1. Dissecting UK drought tolerance in Paragon x Garcia

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- Analysis of senescence from 2015-2016 trial outstanding

- **Simon Orfo**rd had taken UAV images at regular intervals

- **Chris Applegate** from **Ji Zhou**'s group (**EI**) analysed the images
- Modified an existing metric for 'Excess Green minus Excess Red (ExG – ExR)' from Mayer and Neto (2008)*
- Generated quantitative data from the UAV images of all the plots from 18 time points (28/04 to 05/08)

- Used data to QTL map traits involved in colour change – assumed to be due to senescence

*"Verification of color vegetation indices for automated crop imaging applications" Computers and Electronics in Agriculture, Volume 63, Issue 2, October 2008, Pages 282–293

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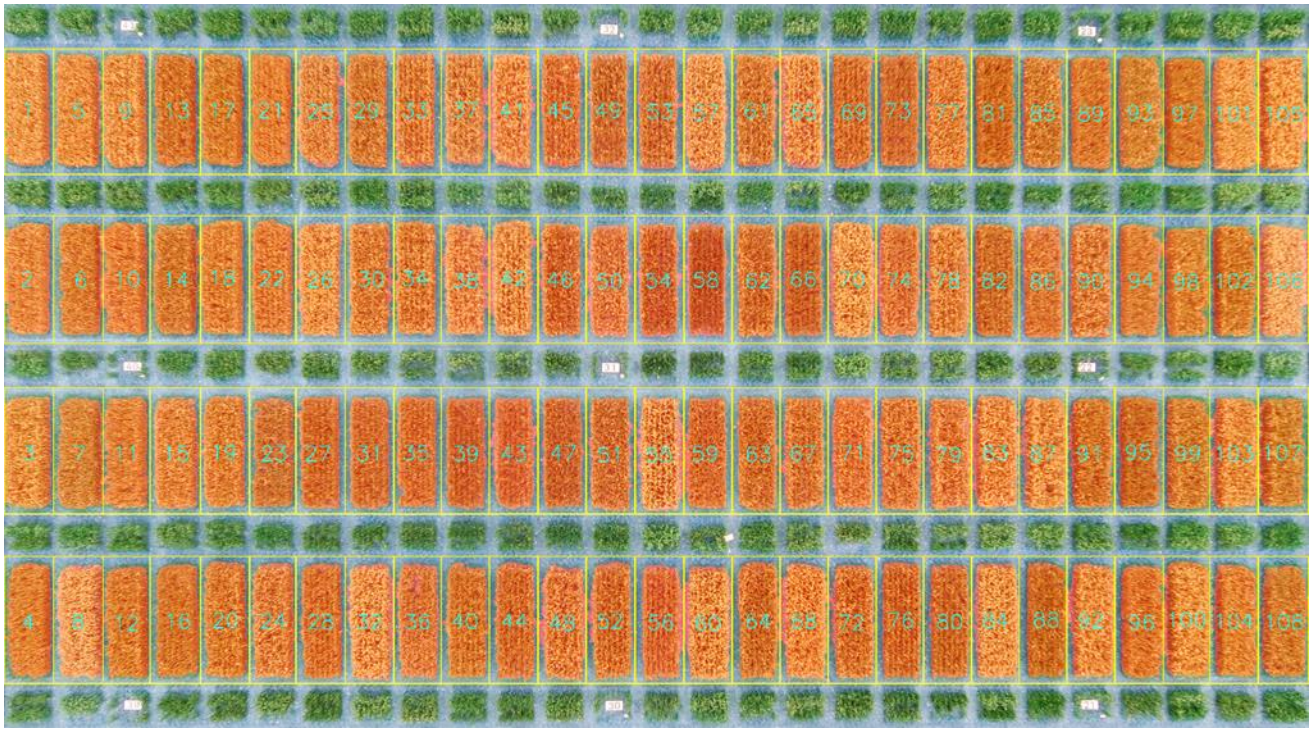
1. Dissecting UK drought tolerance in Paragon x Garcia



- Segmentation of plots
- Colour assignment of plots

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1. Dissecting UK drought tolerance in Paragon x Garcia

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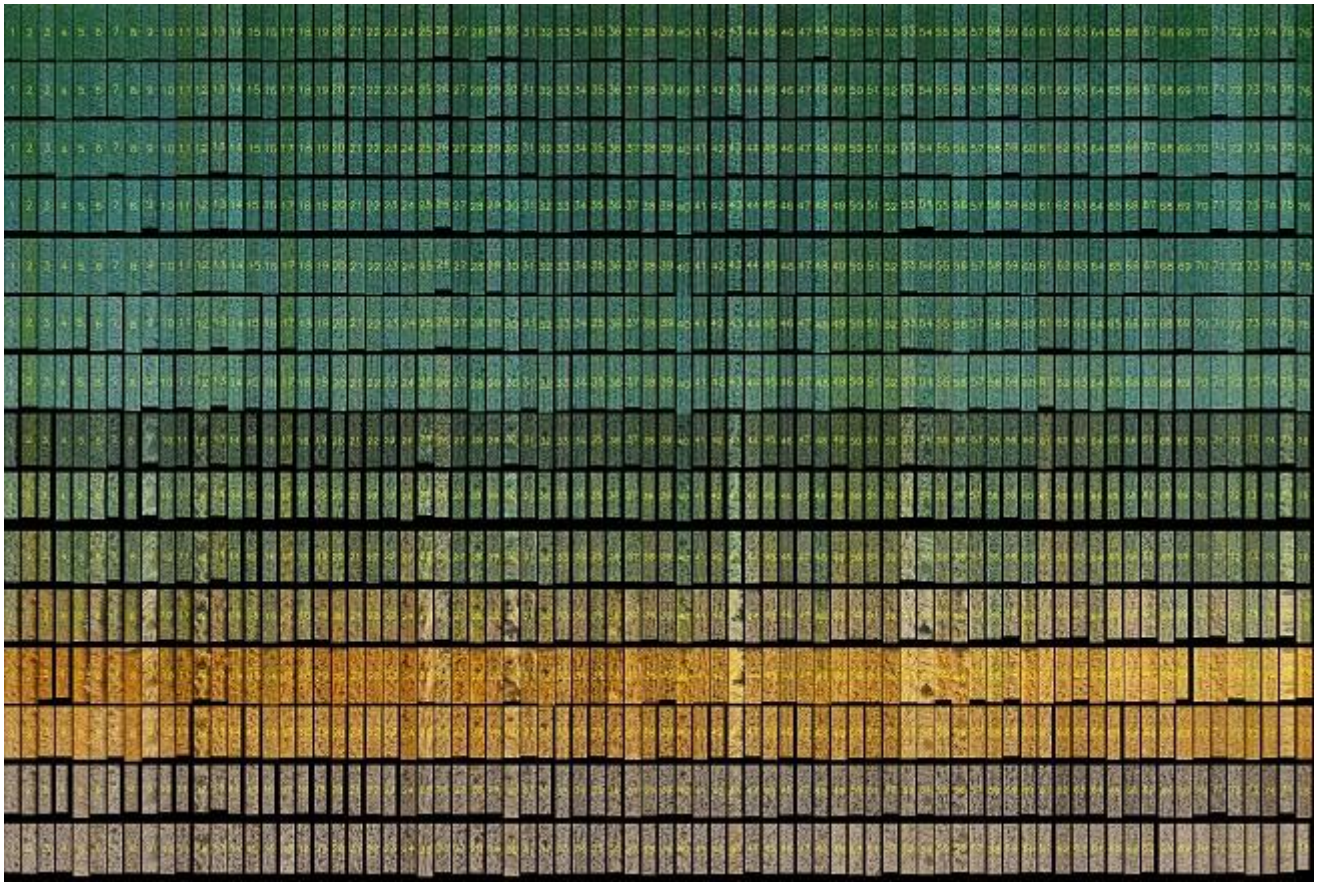

- Example with plots from 15 time points

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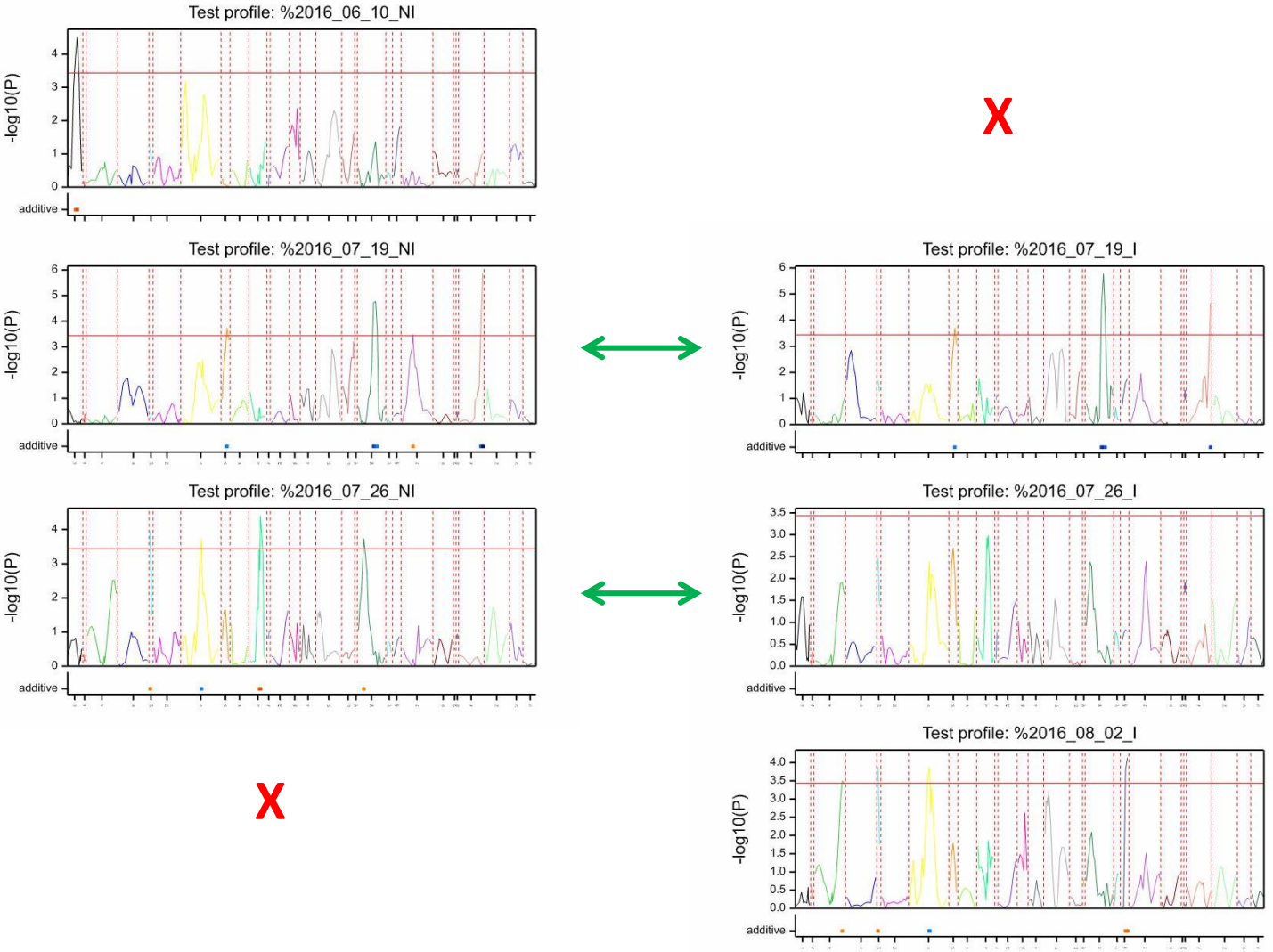
1. Dissecting UK drought tolerance in Paragon x Garcia

Position of QTLs

	NOT IRRIGATED	IRRIGATED
10/06/2016	1A1	
22/06/2016	1A1, 2A2	1A1, 2A2
01/07/2016	1A1, 2A2, 2B	1A1, 2A2, 6A
07/07/2016	2A2, 2B	2B
13/07/2016	2B	2B, 5B2
19/07/2016	2D, 5B2, 6A, 7A1	2D, 5B2, 7A1
22/07/2016	2D	
26/07/2016	2A1, 2B, 3B, 5B2	
02/08/2016		1B, 2A1, 2B, 5D2
05/08/2016		5D2

- Data from last 10 time points
- Shows delayed senescence response in the irrigated plots

1. Dissecting UK drought tolerance in Paragon x Garcia



- Results suggest plot-colour scoring method very effective
- No gene candidates proposed as yet…

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1. Dissecting UK drought tolerance in Paragon x Garcia

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- Drought Trial repeated 2016-2017
- Riverside Field, Church Farm, Bawburgh - field with lighter, sandier soil and gentler slope
- Monitoring soil water content with Delta-T probes
- Will monitor regularly with UAV (and Rothamsted drone!)
- Possibility of spring sowing? X

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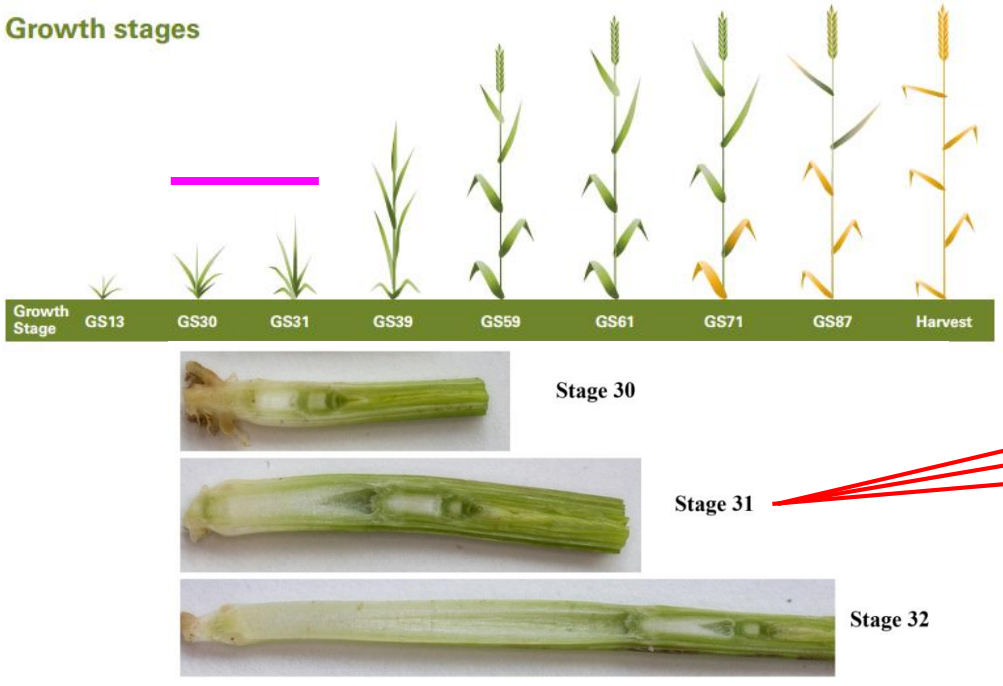
1. Dissecting UK drought tolerance in Paragon x Garcia

- Wheat yields in UK often limited by water deficit during early stages of development around stage 31 and the start of elongation
- Stage 31 is usually reached during April when rainfall can be especially low.



Grain number is determined

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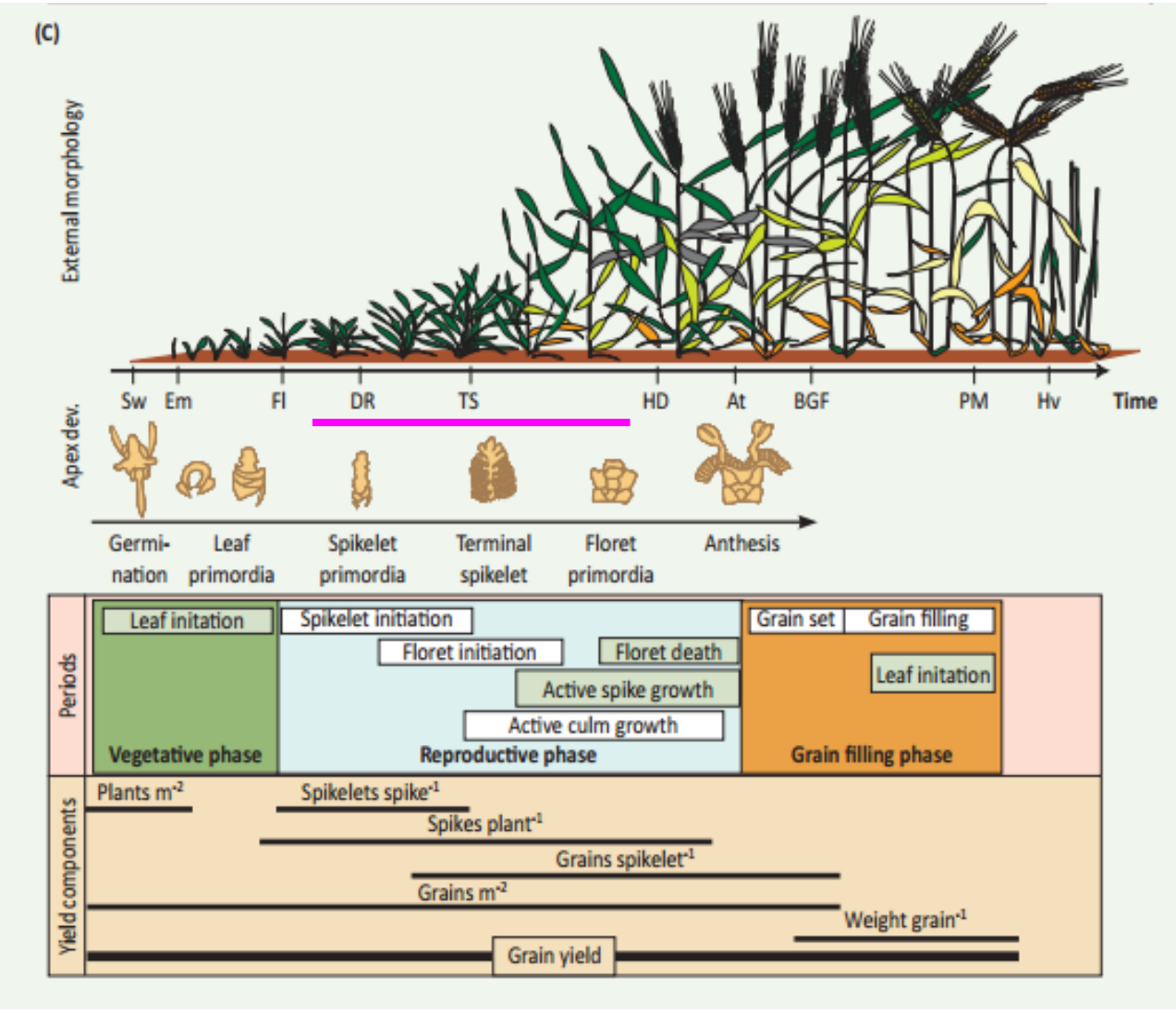
1. Dissecting UK drought tolerance in Paragon x Garcia



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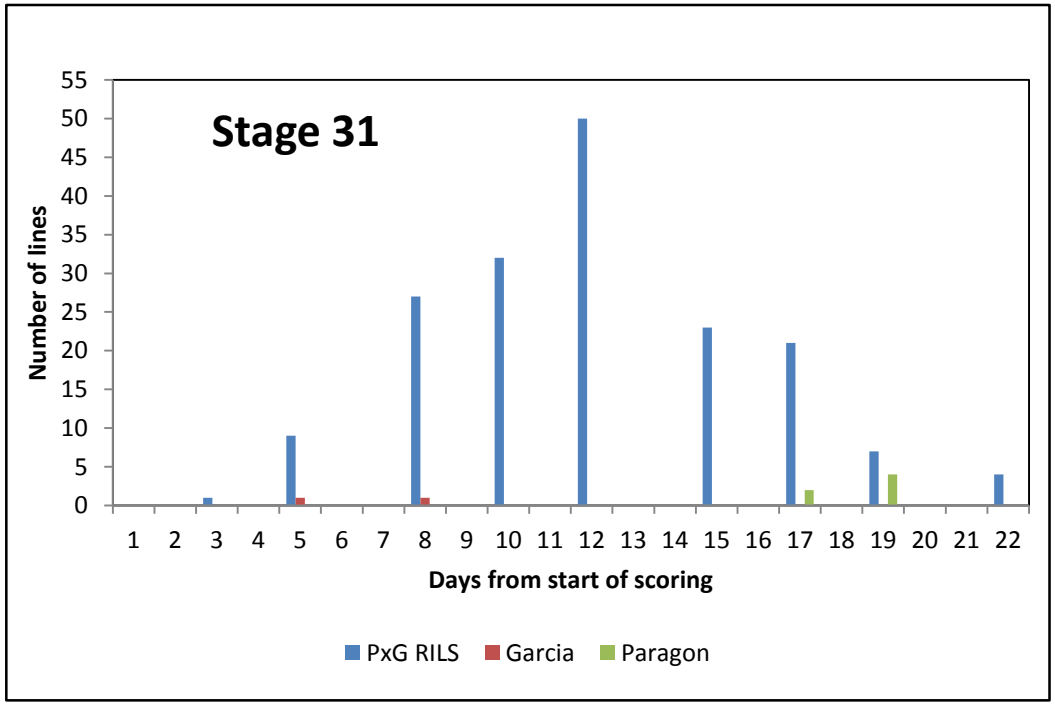
CIMMYT

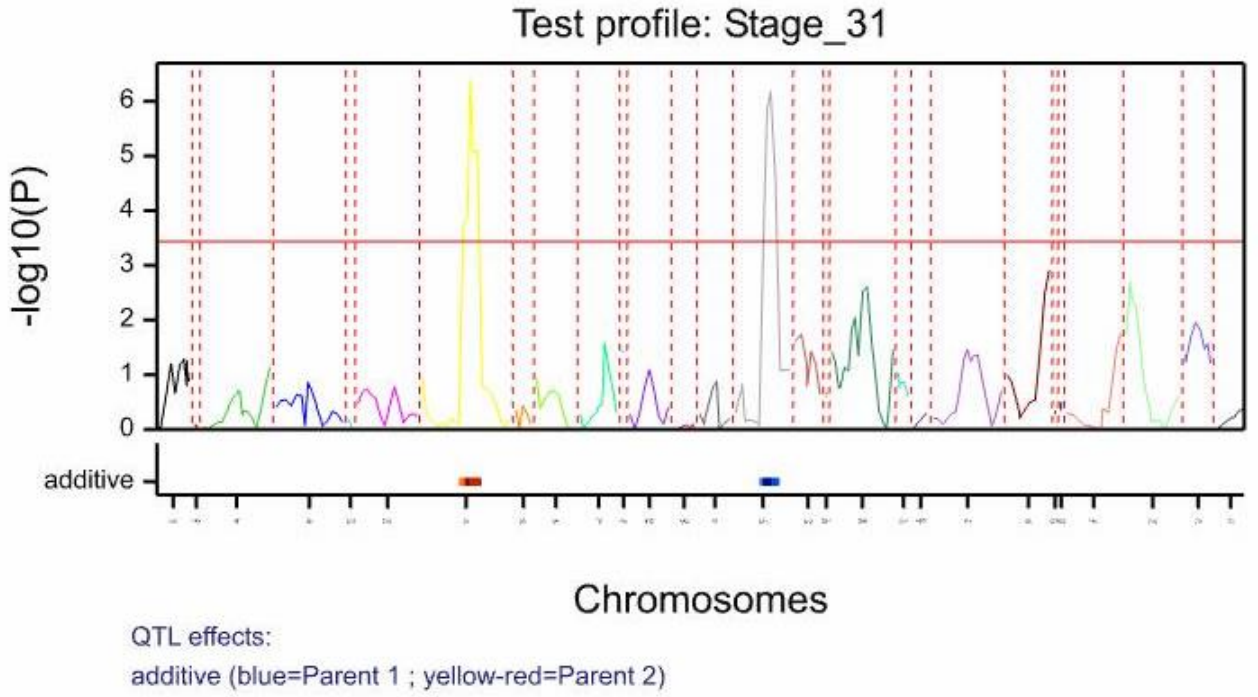
1. Dissecting UK drought tolerance in Paragon x Garcia

- Scored one rep of the trial for Stage 31
- Sectioning and examination of 3-5 stems to give consensus
- Used data for QTL mapping



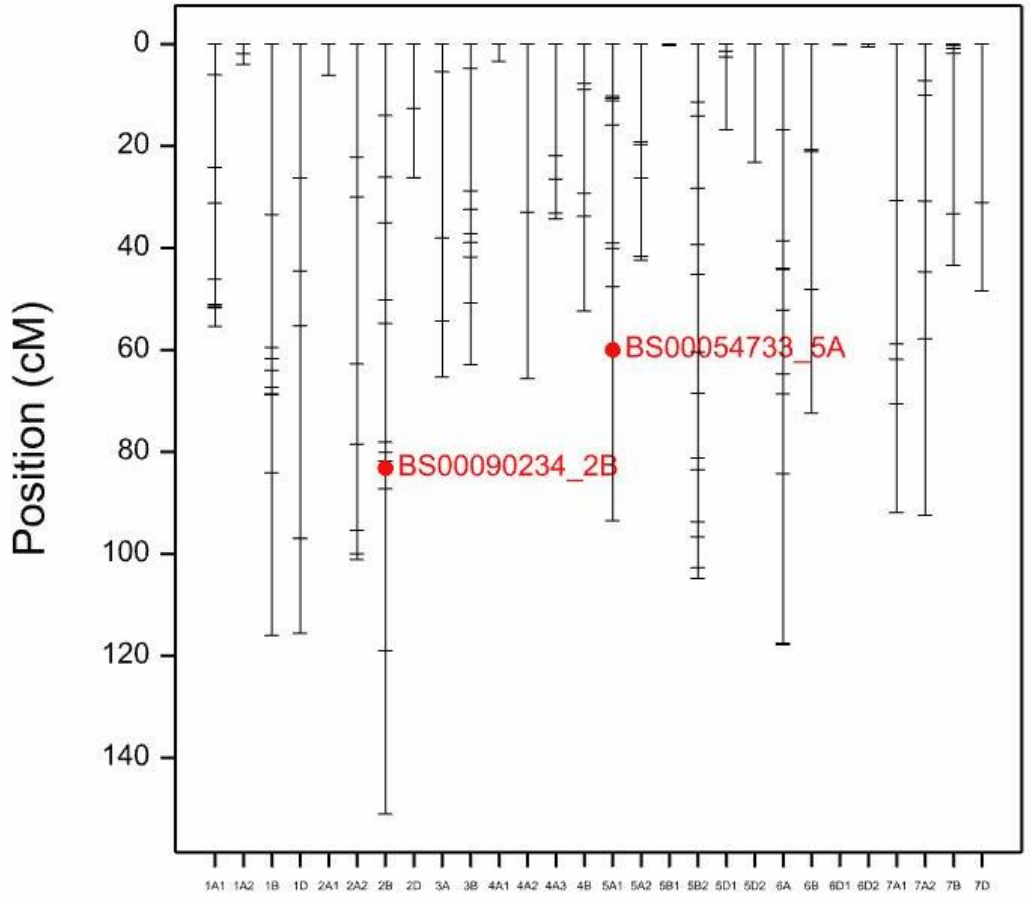
Scoring started 27/03/17

1. Dissecting UK drought tolerance in Paragon x Garcia



Locus name	%Expl. Var.	Add. eff.	High value allele	s.e.
BS00090234_2B	12.140	1.343	Garcia	0.265
BS00054733_5A	12.258	1.349	Paragon	0.264

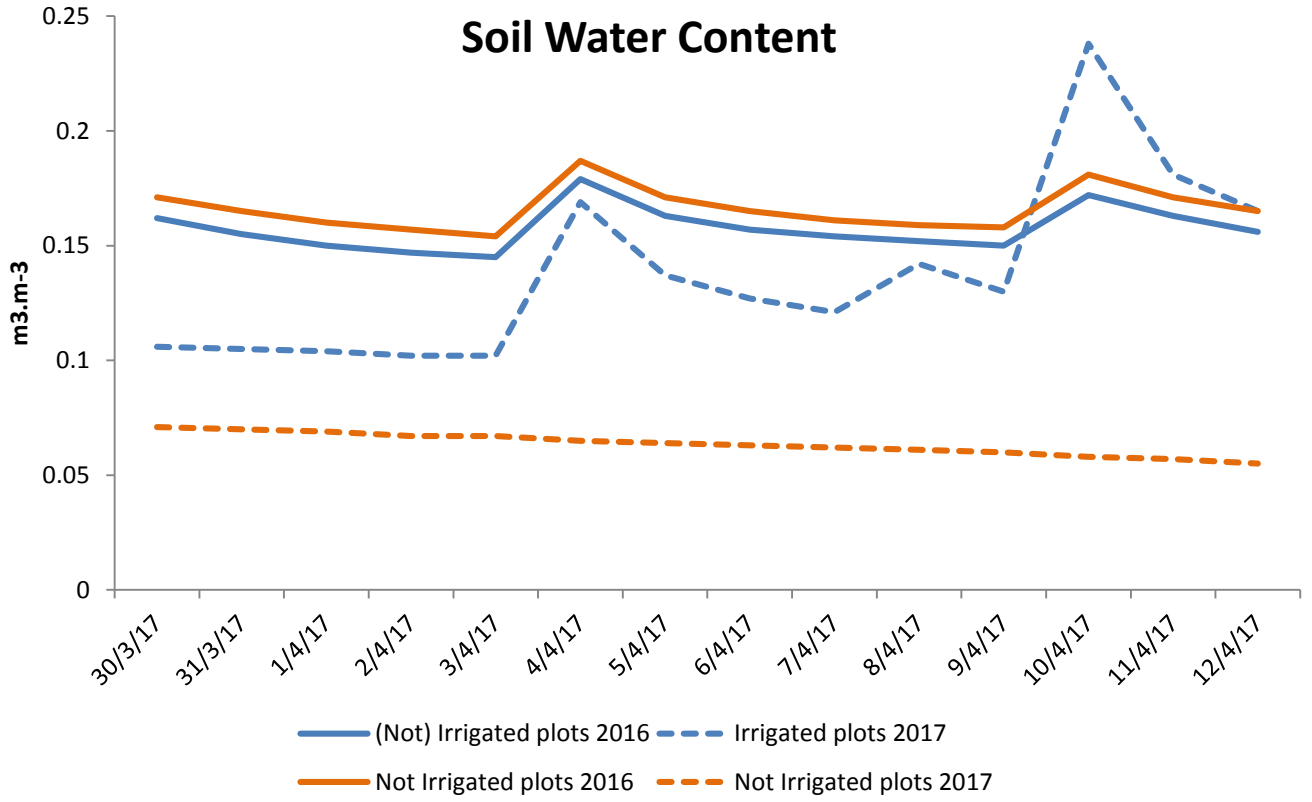
1. Dissecting UK drought tolerance in Paragon x Garcia



QTL at BS00054733-5A likely to be PhyC

QTL at BS00090234-2B is not likely to be PpdB1

1. Dissecting UK drought tolerance in Paragon x Garcia



ML3 probe from Delta-T at 20 cm – roots not yet reached 20 cm

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1. Dissecting UK drought tolerance in Paragon x Garcia

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Soil water matric potential

- Soil matric potential is the negative pressure (or suction) required to extract water from between the matrix of soil particles
- It is an important indication of plant water stress.
- Measured in kilopascal (kPa)
- Using EQ3 probe from Delta-T

- At potential of −33 kPa (−10 kPa for **sand**), soil is at **field capacity**
- Field capacity is viewed as the optimal condition for plant growth and microbial activity.

- Maximum value should be 0 but probe less accurate in this range
- Soil matric potential accurate to:
  - ± 10 kPa from 0 to -100kPa
  - ± 10% of reading from -100kPa to - 1000kPa

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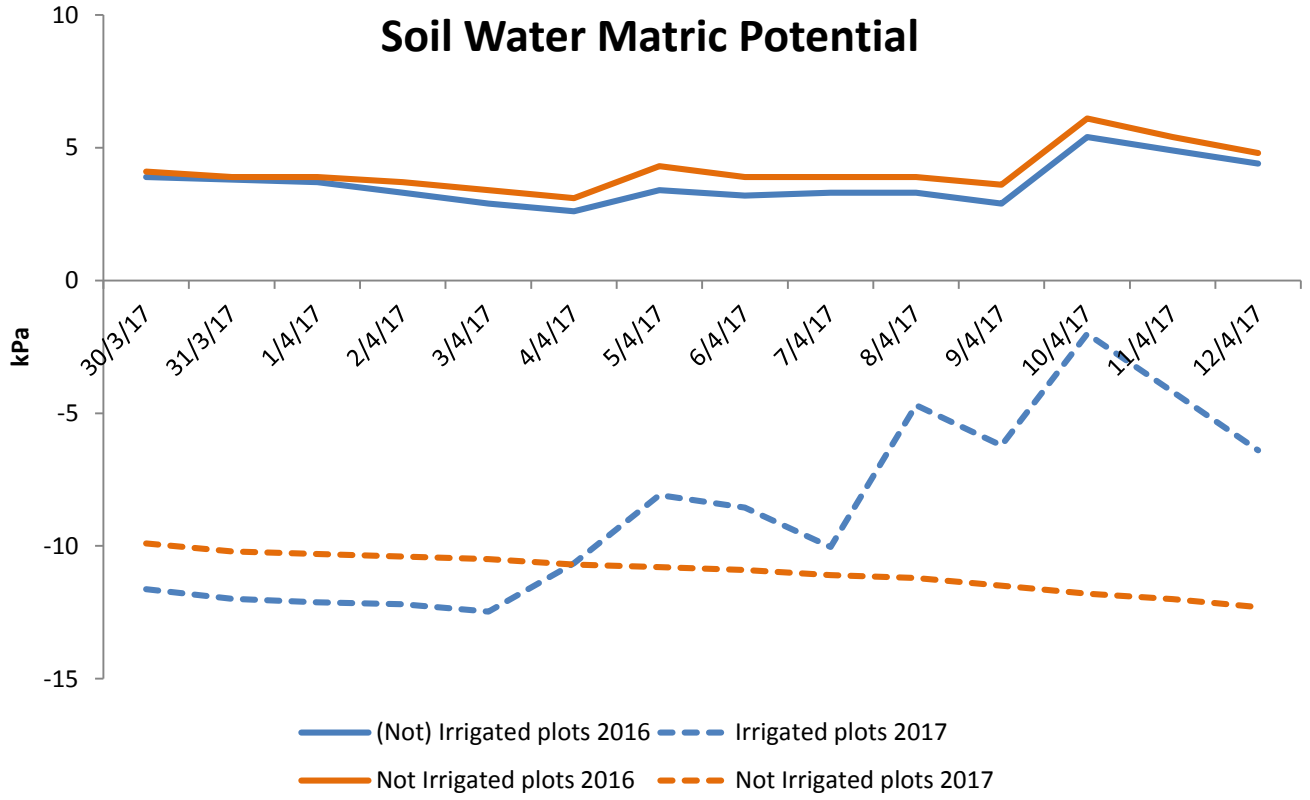
1. Dissecting UK drought tolerance in Paragon x Garcia



- Probe at 50 cm

KDSmart Field Scoring App

- Part of the “KDDart Knowledge Discovery System” from Diversity Array Technology
- Used at and recommended by CIMMYT

KD Smart

KDSmart is an application designed to operate on a variety of Android handheld devices for the collection of data in the field. Containing data selectively exported from KDDart, KDSmart captures and stores Trial data in the field for subsequent uploading to KDDart.

As needs dictate KDSmart can operate in 'standalone' mode without the KDDart infrastructure. This utilises trials defined in CSV files for import and export. So even without KDDart, KDSmart is still a useful tool to capture field data.

The illustration on the right shows the scoring window where most activity occurs. The user can select the traits to display for scoring at any time, along with a range of options to suit the user or task at hand.

Click here to enlarge

- Download free from Google Playstore onto an Android device
- There are several demo trials to practice with.

www.diversityarrays.com/kddart

www.kddart.org/help/kdsmart/

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KDSmart Field Scoring App

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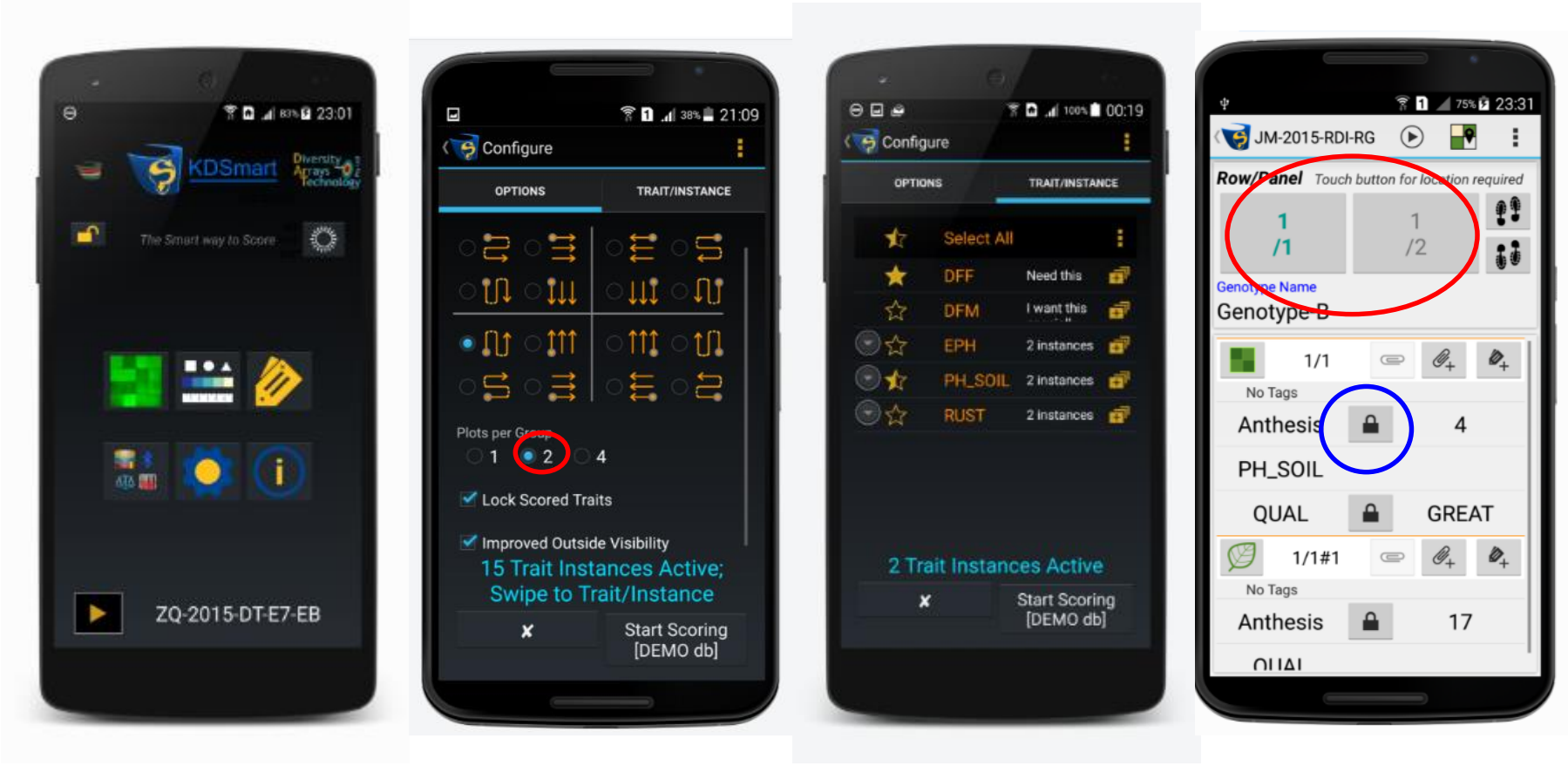

Home page
Settings, Trials, Traits..

Configuring to Score

Portrait Screen
Light Background

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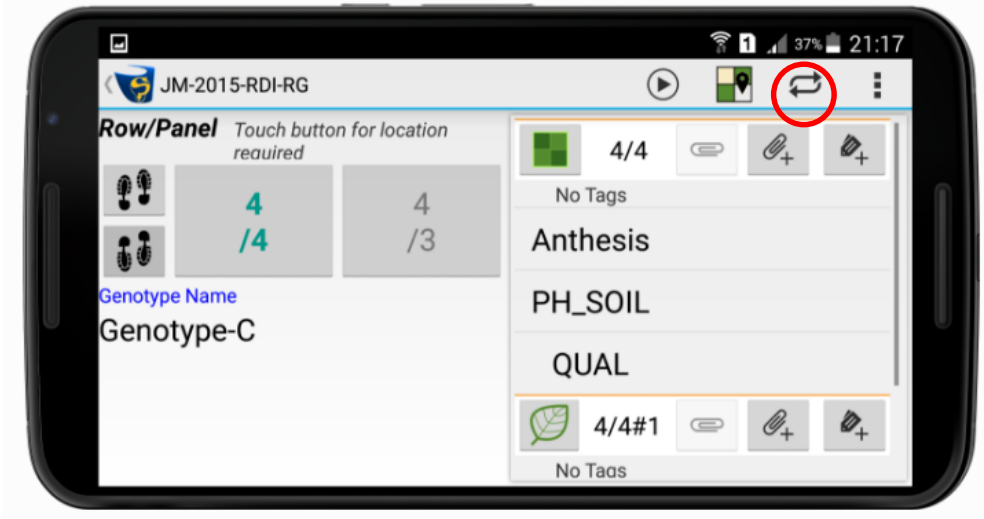
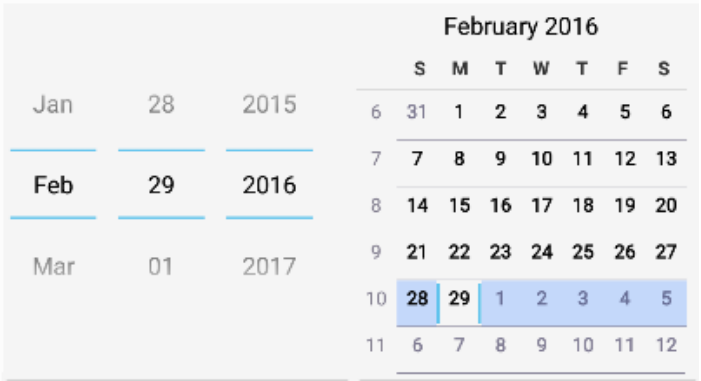
KDSmart Field Scoring App

Landscape Screen



Field View



Tap date required

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KDSmart Field Scoring App

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Input file

Trial Name	Trial Planting Date	* Plot Id	** Plot Column (X)	** Plot Row (Y)	Rep	Entry_No	Genotype	Note	Stage_31	Booting	Date_flowering	Height_cm	Lodging	Senescence	Yield_kg	TGWT	Specific_weight
PxG_DT_2017	24/10/2016	10	1	10	3	114	RIL251										
PxG_DT_2017	24/10/2016	11	1	11	3	52	RIL120										
PxG_DT_2017	24/10/2016	12	1	12	3	16	RIL32										
PxG_DT_2017	24/10/2016	13	1	13	3	60	RIL147										
PxG_DT_2017	24/10/2016	14	1	14	3	35	RIL75										
PxG_DT_2017	24/10/2016	15	1	15	3	176	RIL355										
PxG_DT_2017	24/10/2016	16	1	16	3	82	RIL185										
PxG_DT_2017	24/10/2016	17	1	17	3	94	RIL216										
PxG_DT_2017	24/10/2016	18	2	1	1	94	RIL216										

Output file

TrialName	PlantingDate	PlotId	PlotColumn	PlotRow	Entry_No	Genotype	Rep	Booting	Date_flowering	Height_cm	Lodging	Senescence	Specific_weight	Stage_31	Date:Stage_31	TGWT	Yield_kg
PxG_DT_2017	24/10/2016	10	1	10	114	RIL251	3							03/04/2017	12/04/2017 10:00		
PxG_DT_2017	24/10/2016	11	1	11	52	RIL120	3							07/04/2017	12/04/2017 10:00		
PxG_DT_2017	24/10/2016	12	1	12	16	RIL32	3							07/04/2017	12/04/2017 09:59		
PxG_DT_2017	24/10/2016	13	1	13	60	RIL147	3							03/04/2017	12/04/2017 09:58		
PxG_DT_2017	24/10/2016	14	1	14	35	RIL75	3							03/04/2017	12/04/2017 09:57		
PxG_DT_2017	24/10/2016	15	1	15	176	RIL355	3							07/04/2017	12/04/2017 09:56		
PxG_DT_2017	24/10/2016	16	1	16	82	RIL185	3										
PxG_DT_2017	24/10/2016	17	1	17	94	RIL216	3							10/04/2017	12/04/2017 10:09		

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Import and export of files between PC and tablet through OneDrive

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WGIN3 Projects: Avalon and Cadenza

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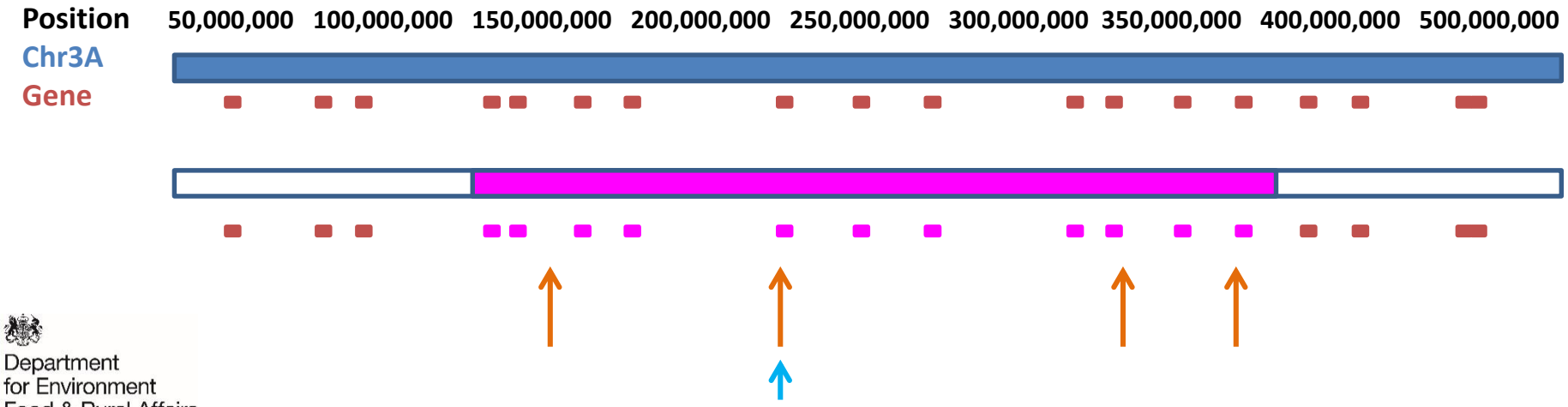
4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza

- The BC3 NILs carry selected genetic foreground in the QTL regions (height, heading, and yield)
- In addition each line carries ~12.5% random chromosomal background.
- Plan to tile the whole genome with chromosome segments to make recombinant substitution lines for genome.

4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza

- Publication and availability of genomic sequence will allow more sophisticated presentation of these data in future
- Possible to present these in an *interactive* format
- Include as part of a searchable genome browser.
- Indication extent of substituted segment.
- Show position of Axiom ↑ and Bristol ↑ markers



4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza

- Genotyping carried out on 94 NILs (+ Av/Cad) using Breeders 35K array
- Estimate of % coverage of background (+ foreground) for each chromosome

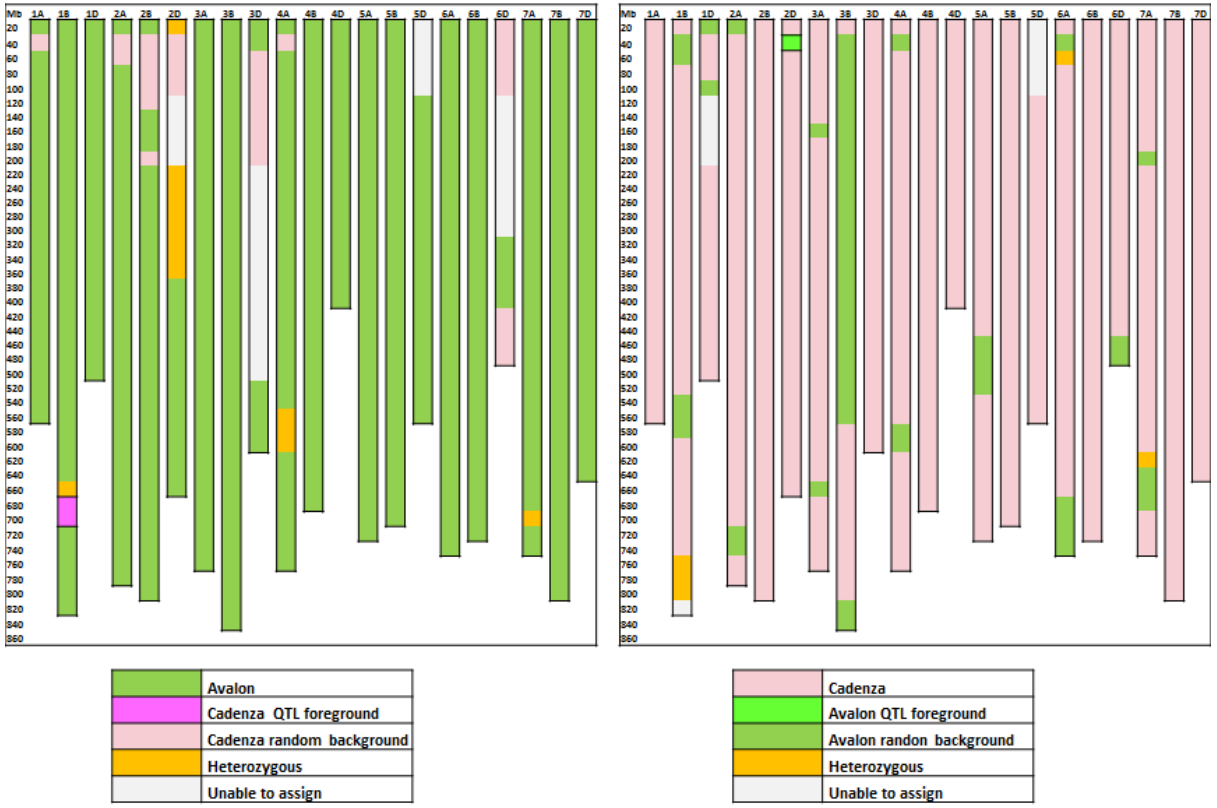
- **Have used several methods to generate map (i.e. based on frame-map, Axiom info and pseudomolecules…)**

- NILs backcrossed to the recurrent parent to generate lines where QTL region and random segments have been separated

	Avalon	Cadenza
	43 lines	46 lines
1A	~80%	~60%
1B	~95%	~90%
1D	~30%	~70%
2A	~80%	~95%
2B	~60%	~90%
2D	~95%	~70%
3A	~95%	~95%
3B	~70%	~95%
3D	~80%	~60%
4A	~80%	~75%
4B	~80%	~85%
4D	~80%	~95%
5A	~90%	~75%
5B	~80%	~90%
5D	~95%	~80%
6A	~95%	~85%
6B	~95%	~95%
6D	~95%	~95%
7A	~60%	~70%
7A or 7D	~40%	~90%
7B	~60%	~90%
7D	~95%	~30%

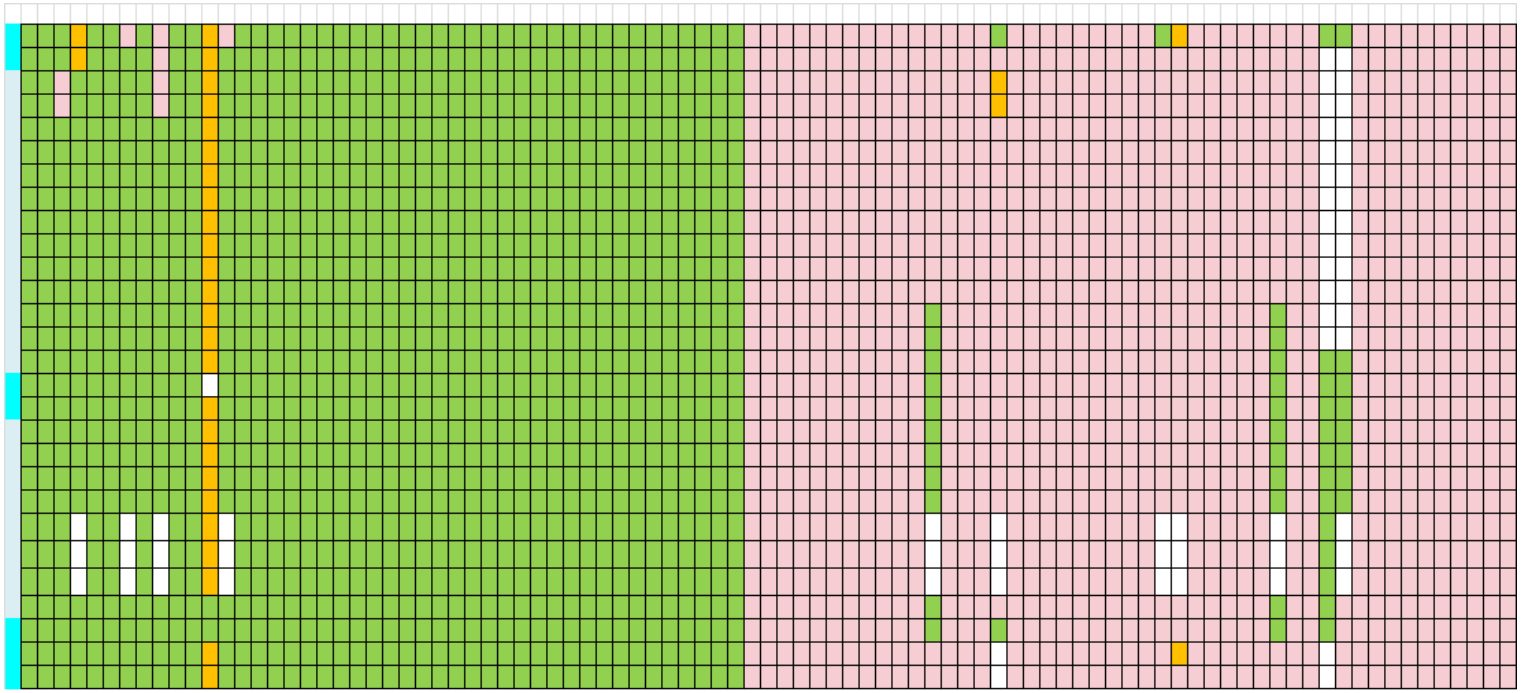
INCLUDES FOREGROUND

4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza



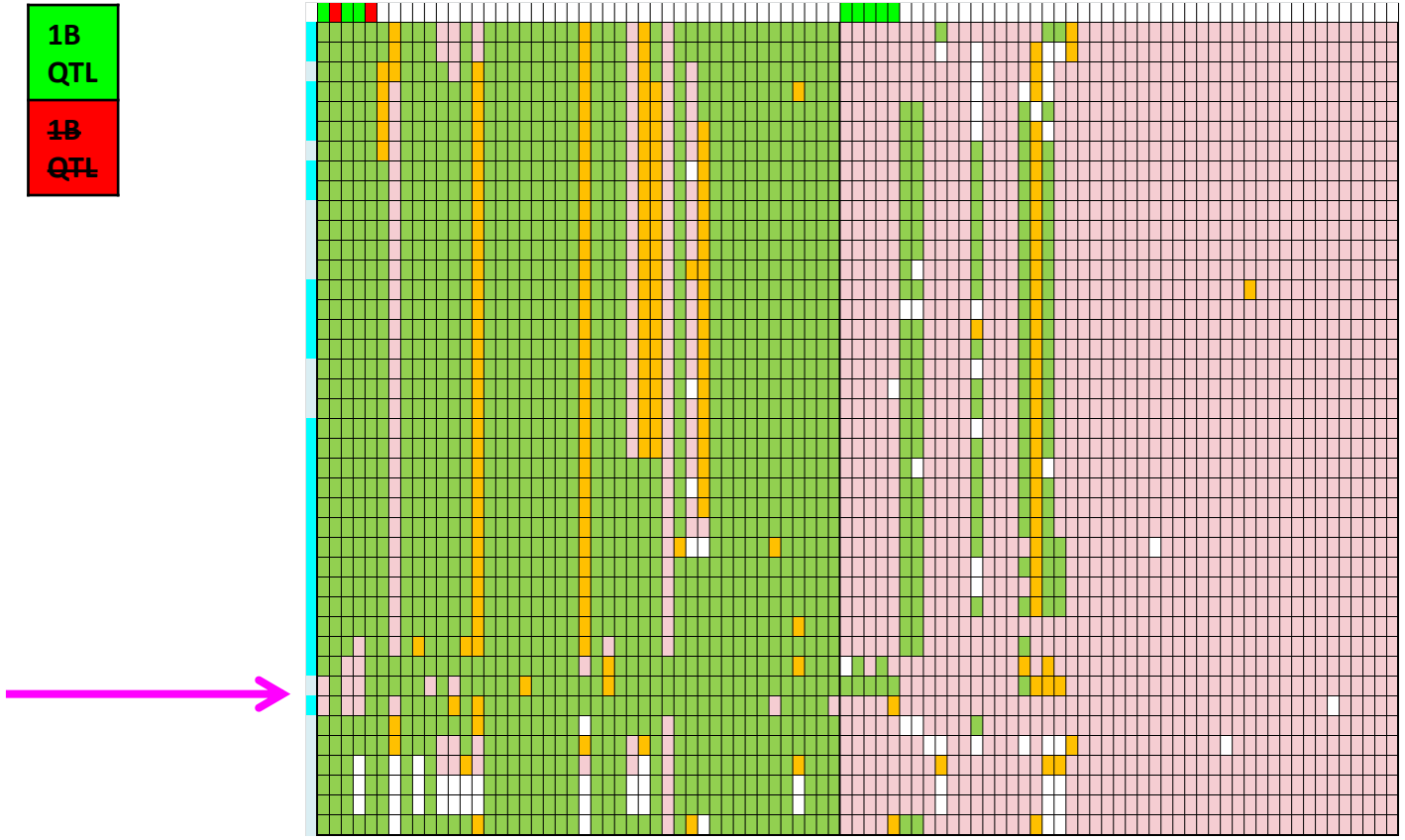
- **'Graphical genotypes' of an Avalon NIL for 1B ear emergence (left) and a Cadenza NIL for 2D height (right).**
- **For each chromosome a representative genotype is shown for each 20 Mb region across the length of the chromosome, based on the WGAv0.4 sequence assembly of Chinese Spring.**

4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza



- ‘Graphical genotypes’ of Chr1A from all the 44 and 47 NILs from with Avalon or Cadenza backgrounds, respectively.
- A representative genotype is shown for each 20 Mb region across the length of the chromosome, based on the NRGene sequence.

4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza



- 'Graphical genotypes' of Chr1B
- The first five NILs in each background were selected for the 1B heading QTL
- Two NILs in the Avalon background appear to be incorrectly selected.

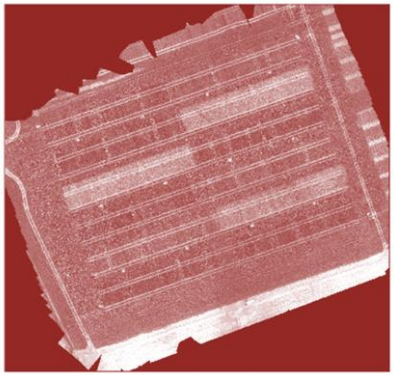
4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza

- Will produce 'Graphical Genotypes' for all 21 chromosomes
- Will select lines to give the optimal tiling path for each chromosome

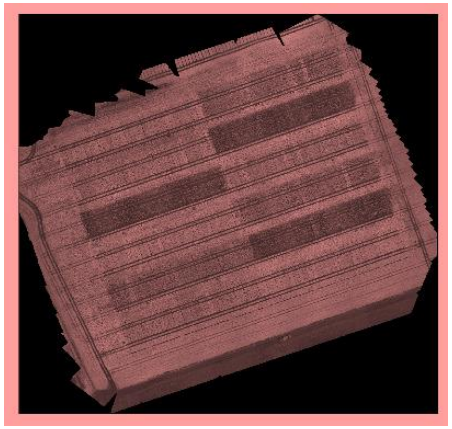
- The F2 progeny of crosses to the recurrent parent of the selected lines will be genotyped with BS markers to determine the presence of the required segment
- Seed of these lines will be bulked and made available to the community

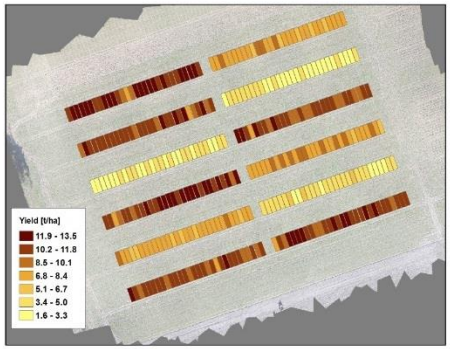
Rothamsted Research
where knowledge grows

Using the WGIN Diversity trial to develop drone applications



Andrew Riche





ROTHAMSTED RESEARCH

Disease detection from drone images

ROTHAMSTED RESEARCH

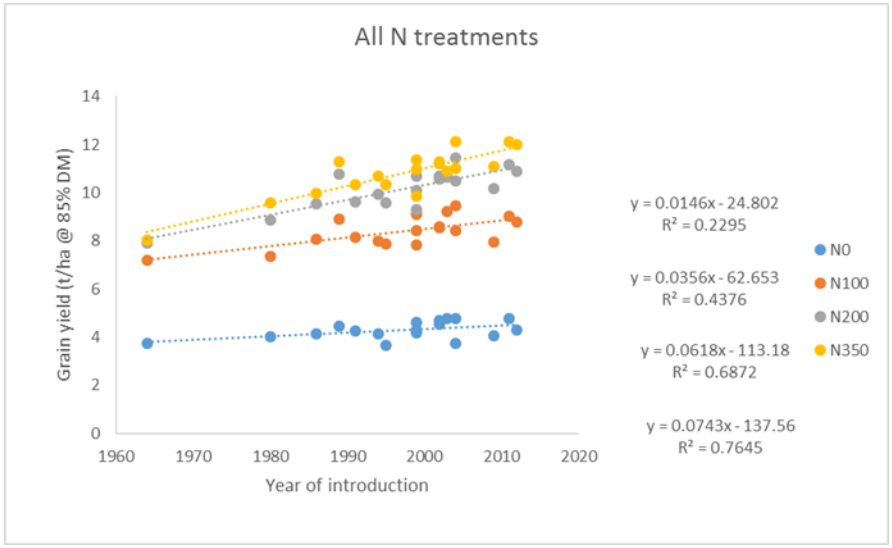
- Unsprayed area of wheat
- Collecting images at different altitudes
- At low altitude rotor wash affects the plants

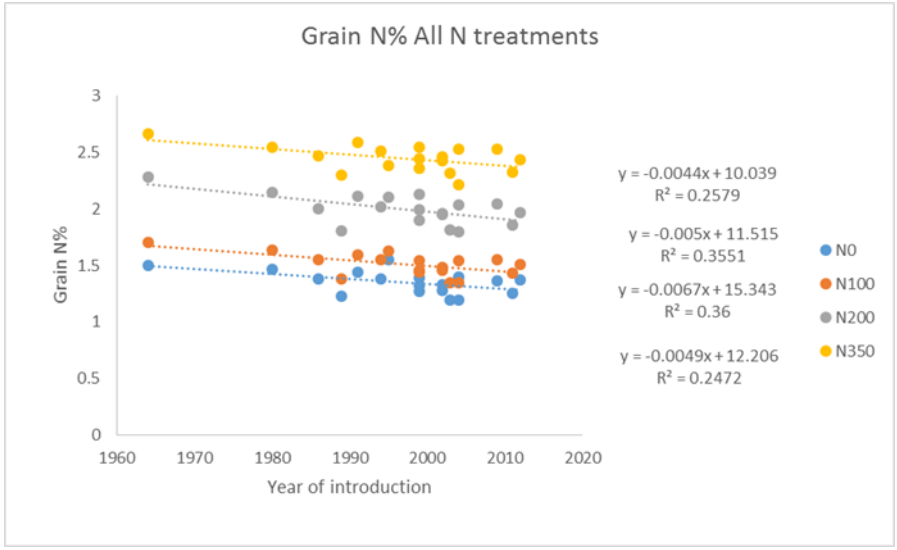
BBSRC bioscience for the future

2017 Diversity trial

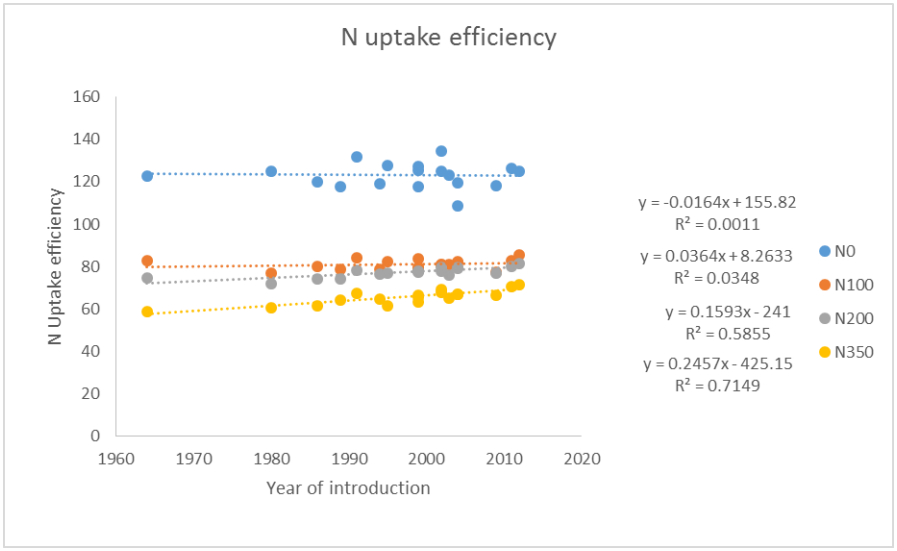
2017	
Avalon	
Cadenza	
Claire	
Cocoon	
Conqueror	
Cordiale	
Crusoe	
Evolution	
Gallant	
Graham	Stigg
Hereford	
Hereward	
Hylux	
Hystar	
Istabraq	
KWS Lili	
Leeds	
Malacca	
Maris Widgeon	
Mercia	
Paragon	
RAGT Illustrious	
Reflection	
Riband	
Robigus	
Siskin	Evoke
Skyfall	
Soissons	
Solstice	
Xi19	

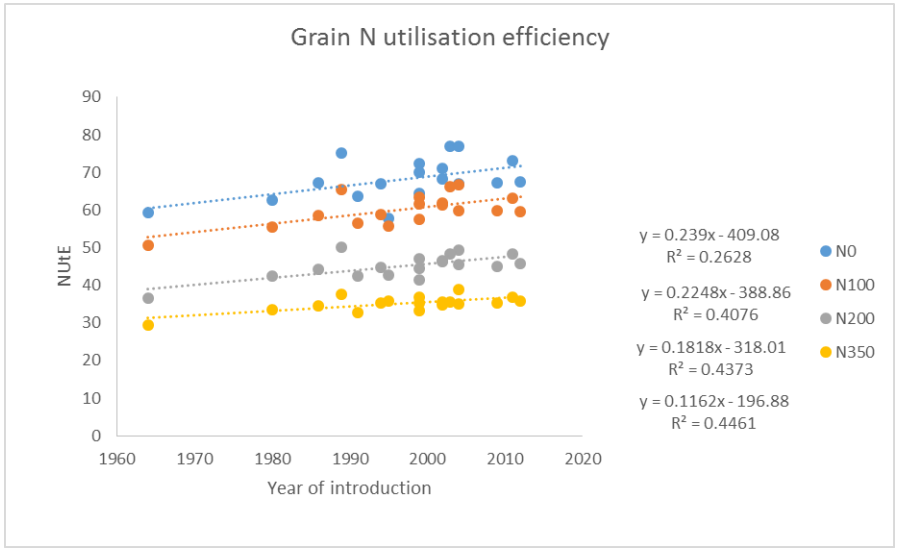
Diversity trial yields and grain nitrogen

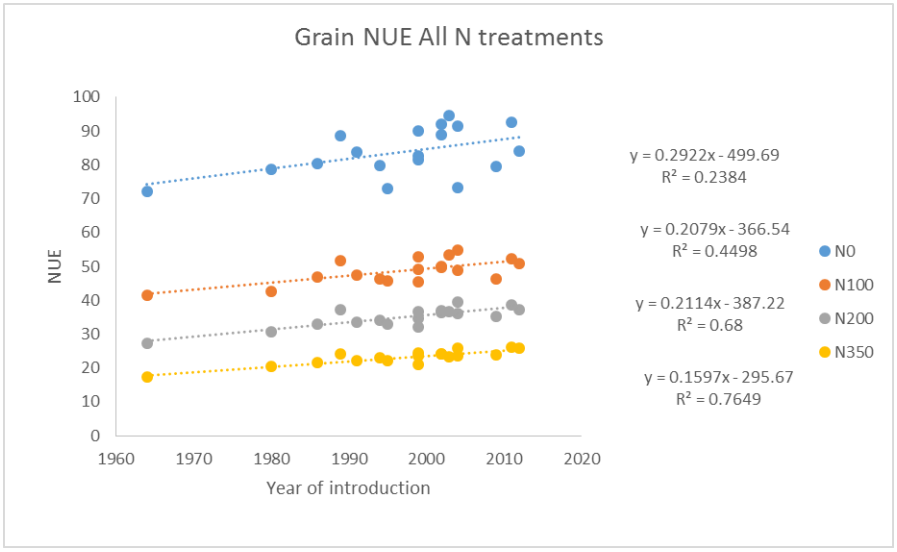




N use efficiency







NUpE = kg taken up per 100kg available (soil + fertilizer)

NUtE = kg of grain per kg N taken up

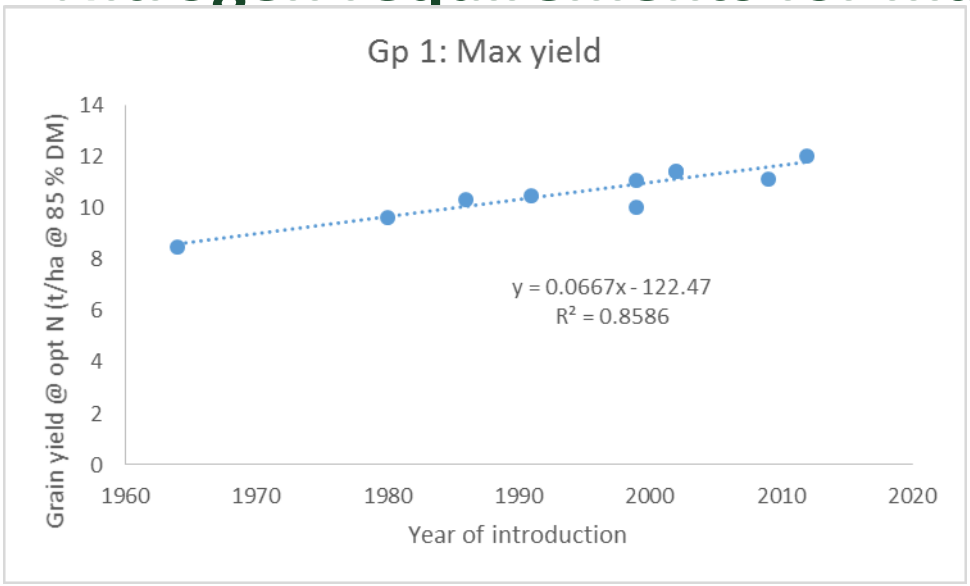
NUE = kg of grain per kg N available

i.e. @ 200kg N, 2 kg per decade, 10kg more grain per kg of N

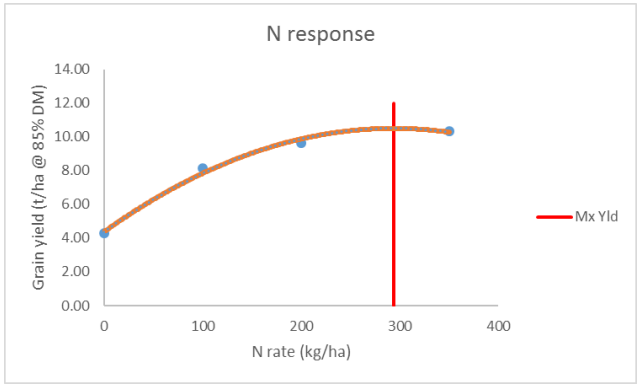
BBSRC bioscience for the future

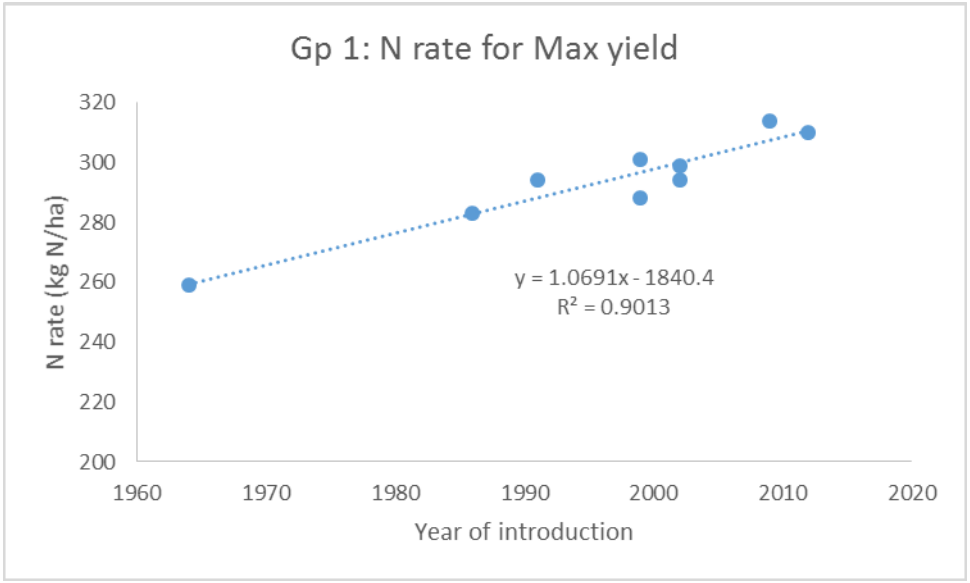
ROTHAMSTED RESEARCH

Nitrogen requirements for maximum yield



3.5 t/ha yield increase over 50 yrs





50 kg N/ha increase in N rate for max yield over 50 yrs

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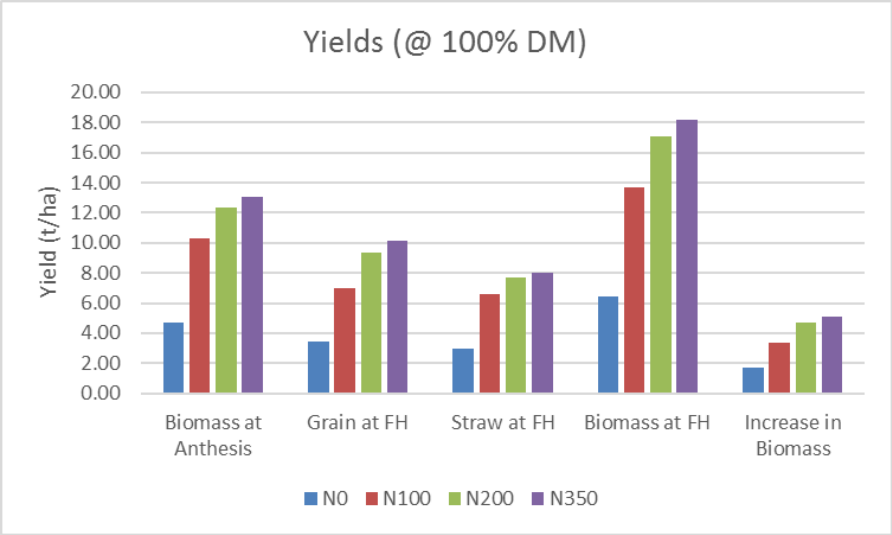
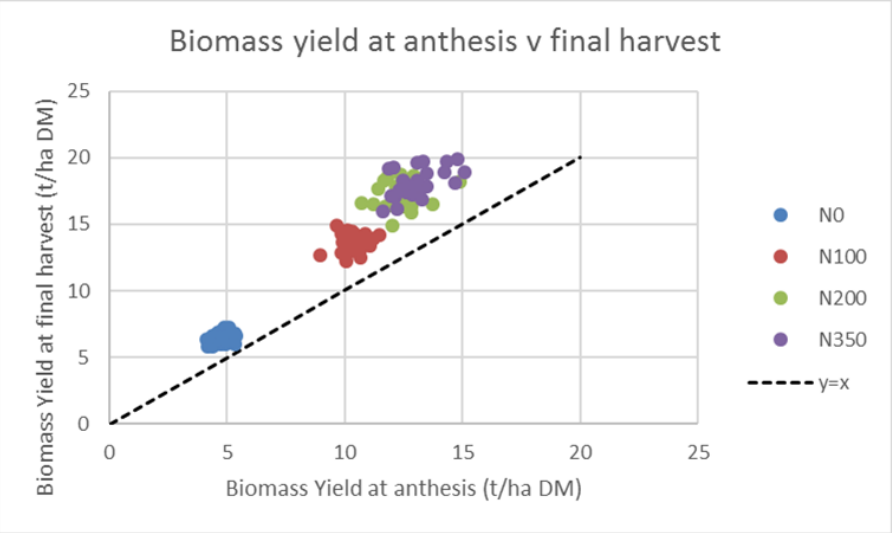
ROTHAMSTED RESEARCH

2015-2016 Diversity trial anthesis sampling

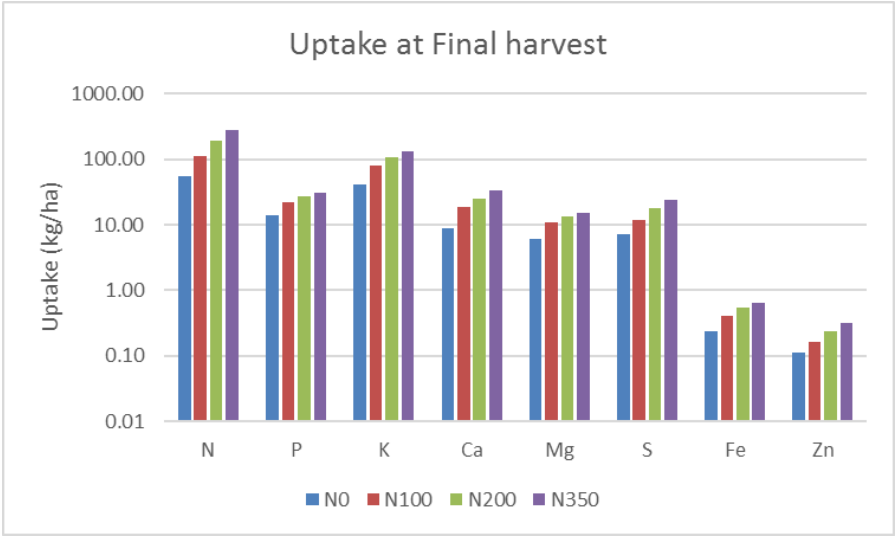




2015-2016 Diversity trial mineral analysis

Key elements:

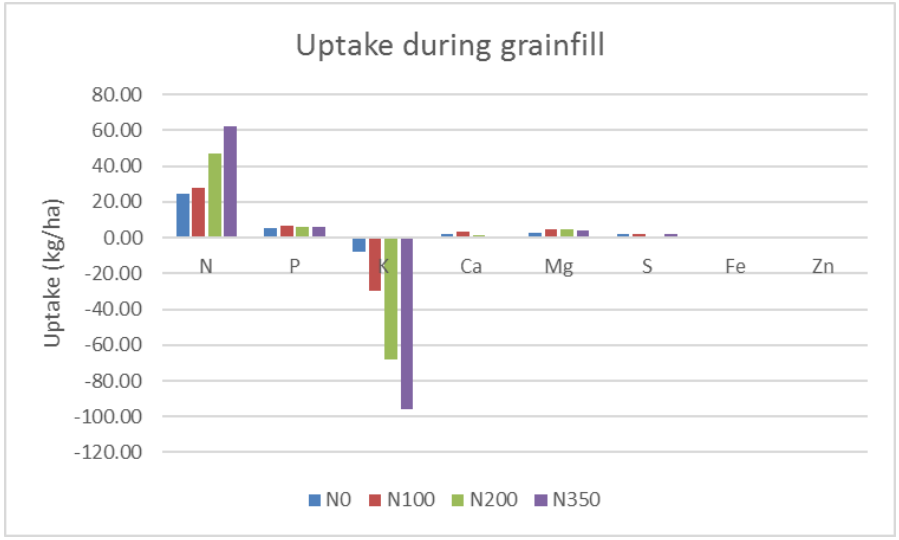
- Nitrogen
- Calcium
- Magnesium
- Sulfur
- Zinc
- Potassium
- Phosphorus
- Iron

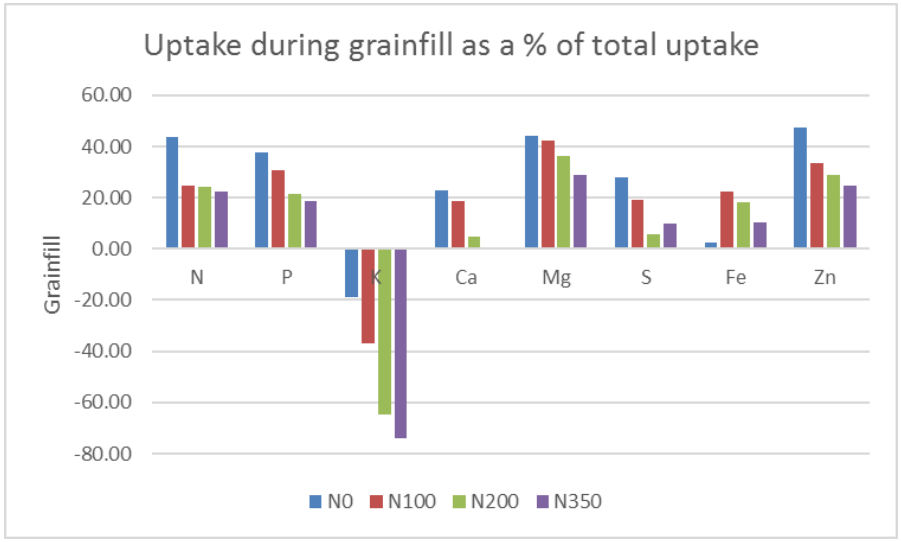


Also:

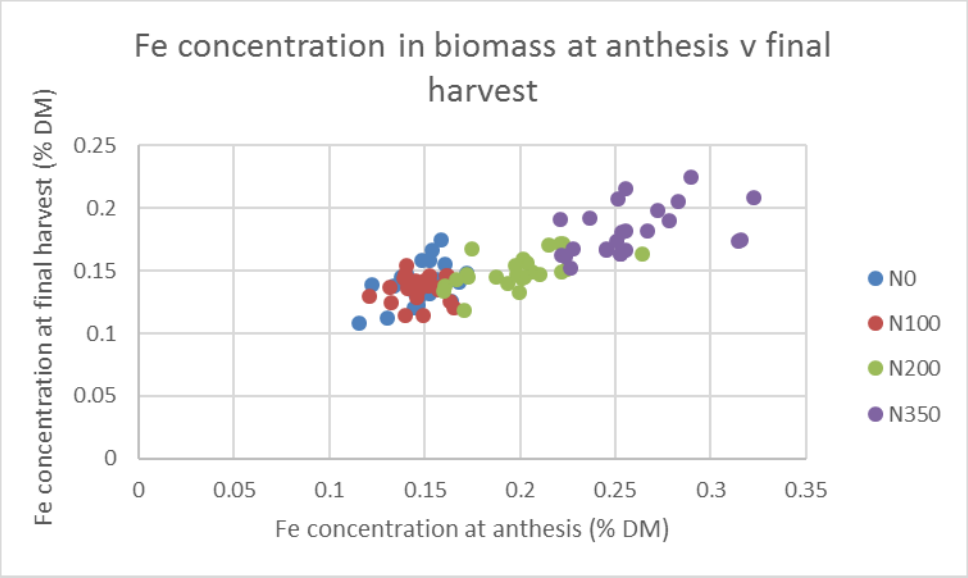
- Al, As, Cd, Co, Cr, Cu, Mn, Mo, Na, Ni, Pb, Se, Ti

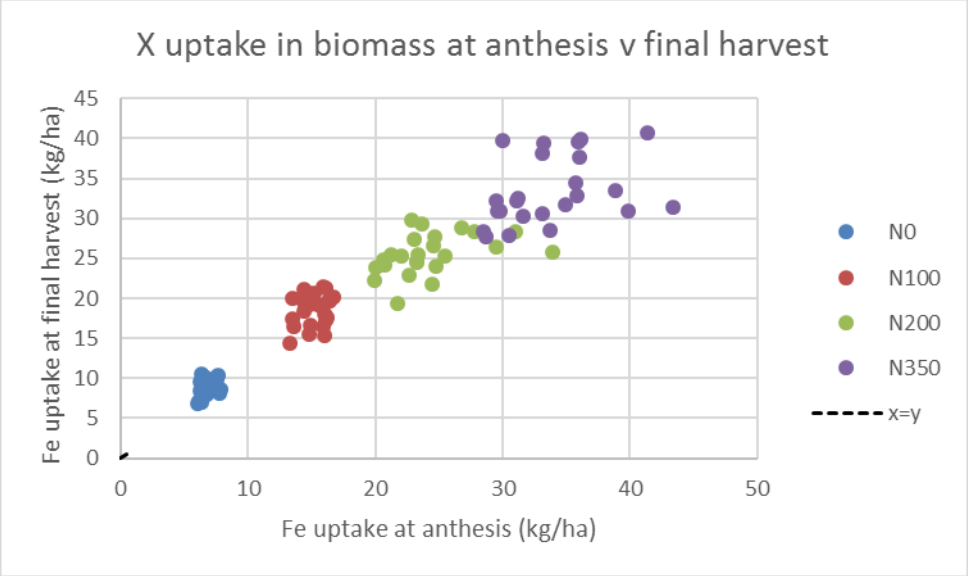
2015-2016 Diversity trial mineral analysis





2017 Diversity trial – Iron uptake and concentration





Acknowledgements

Malcolm Hawkesford
Adam Michalski
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Stephen Goward
Chris Mackay
Nick Chichester-Miles

Rothamsted Research
where knowledge grows

WGIN3 Management Meeting
20th April 2017

Screening germplasm for resilience to aphids (WP2.3)

Lesley Smart

Department for Environment Food & Rural Affairs

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ROTHAMSTED RESEARCH

Screening germplasm for resilience to aphids (WP2.3)

Information to establish the likely genetic basis of resistance to cereal aphids

ROTHAMSTED RESEARCH

- Crosses of *T. monococcum* lines made by Mike Hammond-Kosack: MDR037 (susceptible) x MDR045, MDR049 and MDR657 (all showing evidence of partial resistance)

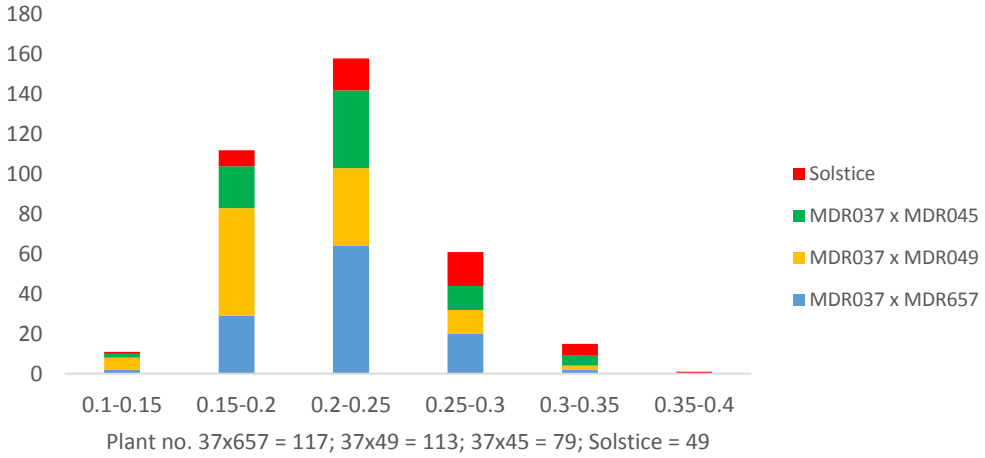
- F1, F2 and F3 generations of these crosses have now been tested in the phenotyping screen against both aphid species. F3s of each cross tested included plants with the best and the worst effective partial resistance to the aphid species.

- Tested plants now being taken to F4.

Screening germplasm for resilience to aphids (WP2.3)

Response to F2 generation of *T. monococcum* crosses

Rhopalosiphum padi on *T. monococcum* crosses F2s
Number nymphs/weight range after 6 days (mg)

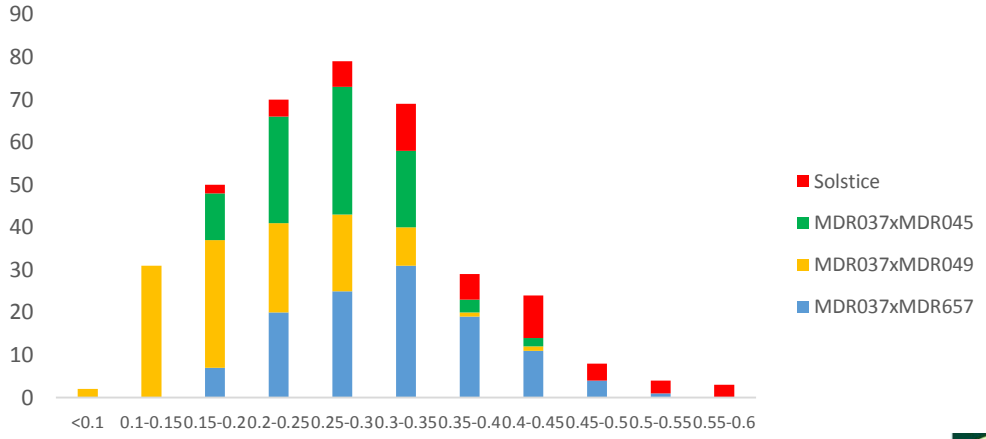


Plant no. 37x657 = 117; 37x49 = 113; 37x45 = 79; Solstice = 49

MDR037 (susceptible) x MDR045, MDR049 and MDR657 (all showing partial resistance)

Partial resistance (reduced weight gain) showing in F2 generation of MDR037 x MDR049, particularly for *S. avenae* the grain aphid.

Sitobion avenae on *T. monococcum* crosses F2s
Number nymphs/weight range at 7 days (mg)



Plant no. 37x657 = 118; 37x49 = 113; 37x45 = 89; Solstice = 49

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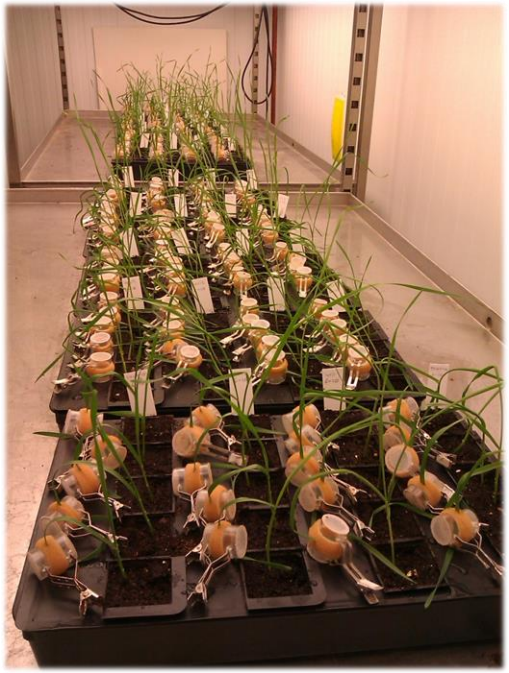
ROTHAMSTED RESEARCH

Screening germplasm for resilience to aphids (WP2.3)

Response to F3 generations of *T. monococcum* crosses



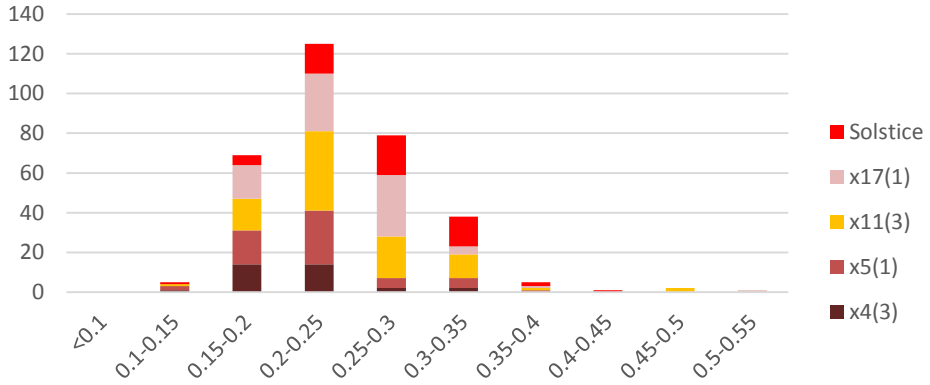
15 seeds (where available) of each selected F3 line sown and seedlings tested against target aphid species in phenotyping screen, compared to Solstice standard.

Number of surviving nymphs recorded and then weighed in their batches to get an average nymph weight. Weights then allocated to weight ranges for comparison.

Screening germplasm for resilience to aphids (WP2.3)

Response to F3 generation of *T. monococcum* MDR037 x MDR049 crossing events

R. padi on *T. monococcum* crosses of MDR37 x 49 at F3
number of nymphs per weight range at 6 days (mg)



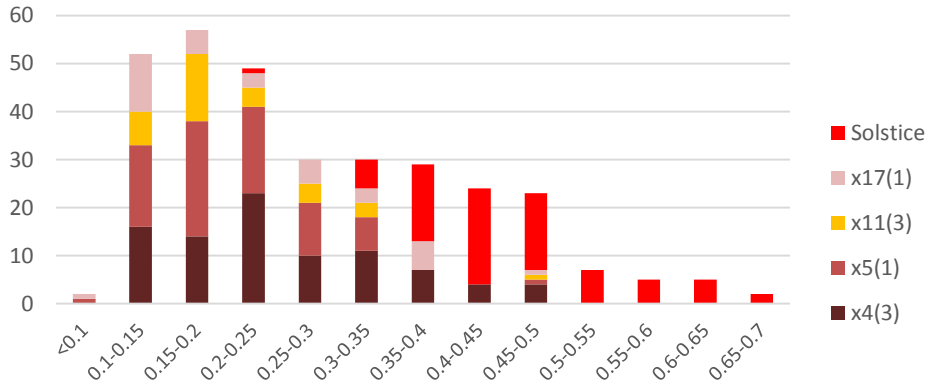
Plant no. x4 33, x5 57, x11 93, x17 83 & Solstice 59

Weight gain by both aphid species on F3 plants selected from the different MDR037 x MDR049 crossing events

R. padi is selected from a narrower weight range or has more plasticity in response?

S. avenae is a better biological indicator in the phenotyping screen?

S. avenae on *T. monococcum* crosses of MDR37 x 49 at F3
number nymphs per weight range at 7 days (mg)



Plant no. x4 89, x5 79, x11 33, x17 36 & Solstice 60

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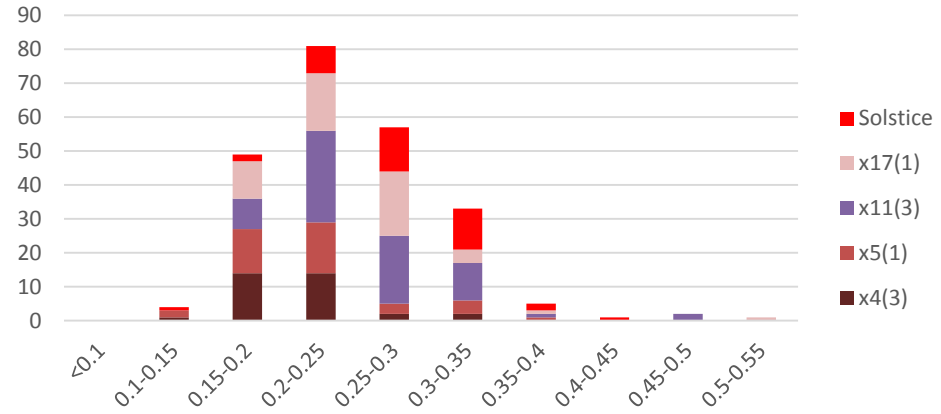
ROTHAMSTED RESEARCH

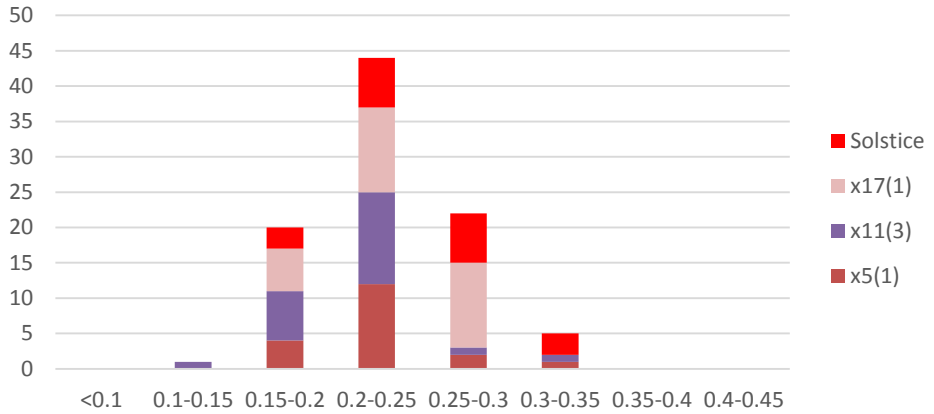
Screening germplasm for resilience to aphids (WP2.3)

Response to F3 generation of *T. monococcum* MDR037 x MDR049 crossing events

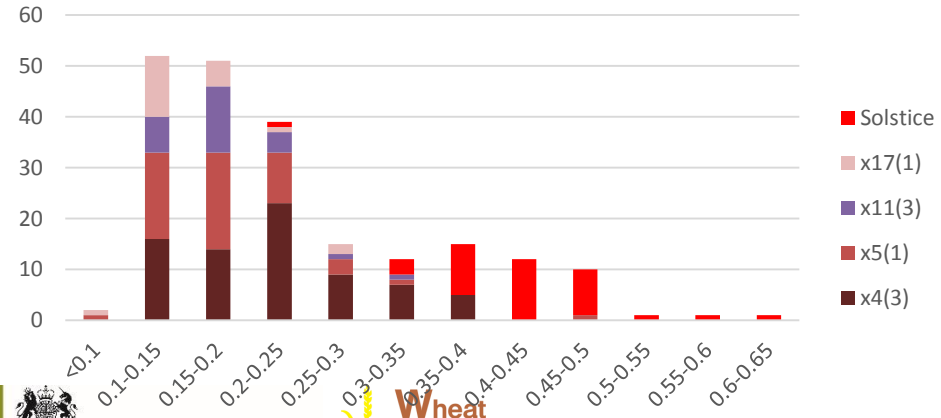
R. padi on *T. monococcum* crosses of MDR37 x 49 on F3s from F2 plants with the best partial resistance; number nymphs per weight range at 6 days (mg)



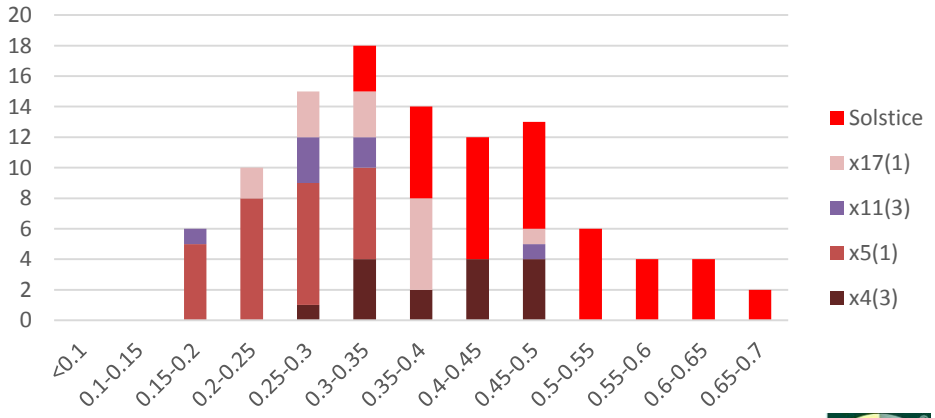
R. padi on *T. monococcum* crosses of MDR37 x 49 on F3s from F2 plants with the worst partial resistance; number nymphs per weight range at 6 days (mg)



S. avenae on *T. monococcum* crosses of MDR37 x 49 on F3s from F2 plants with the best partial resistance; number nymphs per weight range at 7 days (mg)



S. avenae on *T. monococcum* crosses of MDR37 x 49 on F3s from F2 plants with the worst partial resistance; number nymphs per weight range at 7 days (mg)



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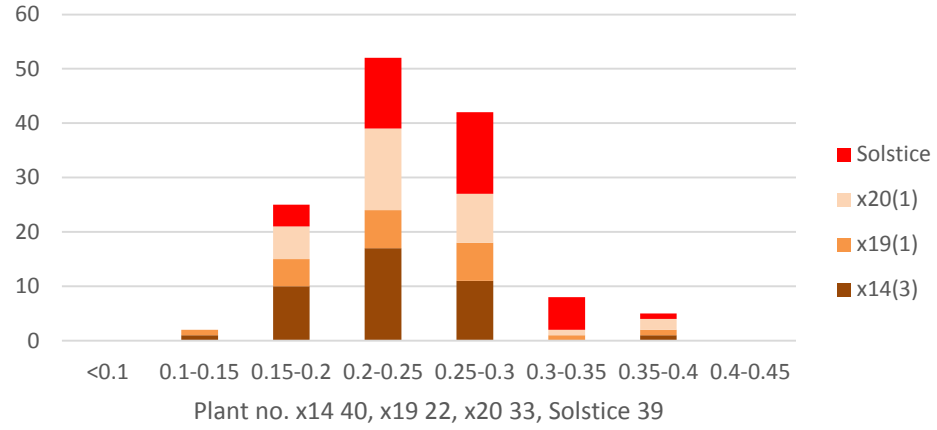
ROTHAMSTED RESEARCH

Screening germplasm for resilience to aphids (WP2.3)

Response to F3 generation of *T. monococcum* MDR037 x MDR045 crossing events

R. padi on *T. monococcum* crosses of MDR37 x 45 at F3
number of nymphs per weight range at 6 days (mg)

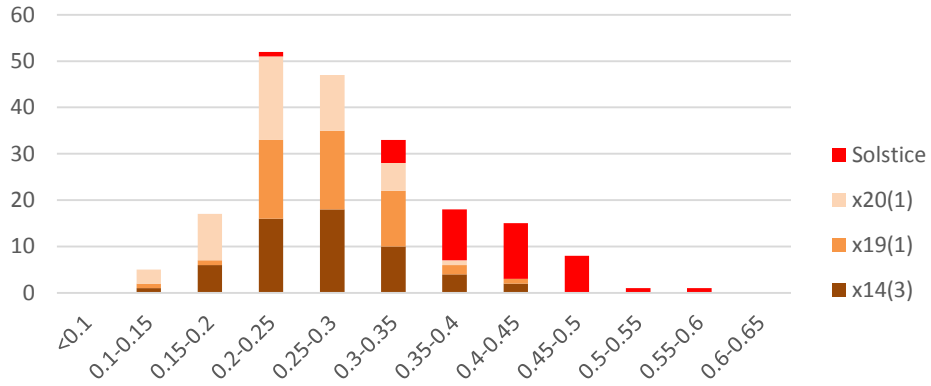


Plant no. x14 40, x19 22, x20 33, Solstice 39

Weight gain by both aphid species on F3 plants selected from the different MDR037 x MDR045 crossing events

Response to different crossing events is similar

S. avenae on *T. monococcum* crosses of MDR37 x 45 at F3
number nymphs per weight range at 7 days (mg)



plant no. x14 57, x19 51, x20 50, Solstice 39

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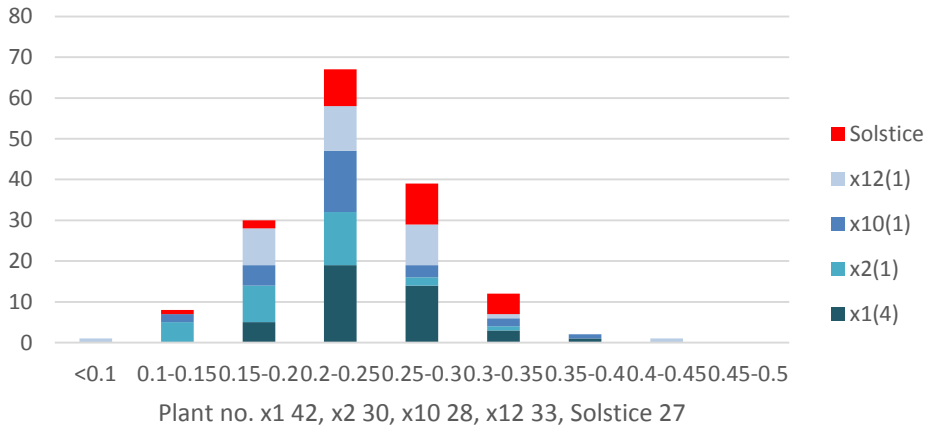
ROTHAMSTED RESEARCH

Screening germplasm for resilience to aphids (WP2.3)

Response to F3 generation of *T. monococcum* MDR037 x MDR657 crossing events

R. padi on *T. monococcum* crosses of MDR37 x 657 at F3 number of nymphs per weight range at 6 days (mg)

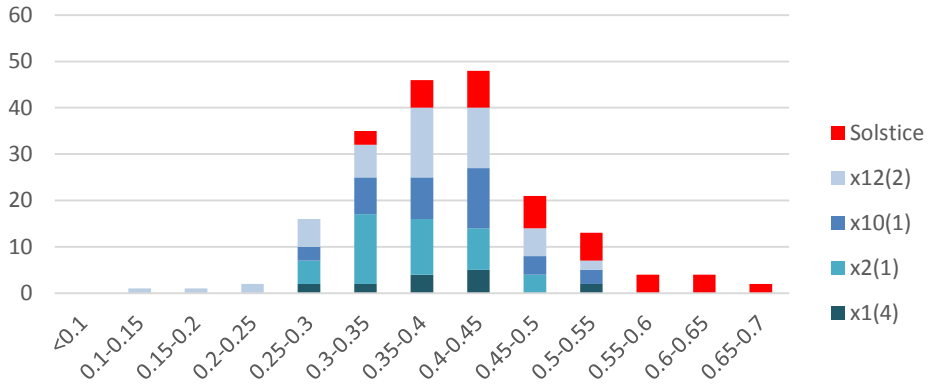


Plant no. x1 42, x2 30, x10 28, x12 33, Solstice 27

Weight gain by both aphid species on F3 plants selected from the different MDR037 x MDR657 crossing events

Response to different crossing events is similar except for x12(2)

S. avenae on *T. monococcum* crosses of MDR37 x 657 at F3 number nymphs per weight range at 7 days (mg)



plant no. x1 15, x2 45, x10 40, x12 53, Solstice 40

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ROTHAMSTED RESEARCH

Summary WGIN3 (WP2.3)

ROTHAMSTED RESEARCH

- F3 generations of *T. monococcum* MDR037 x MDR049, MDR045 and MDR657 crosses, with a range of aphid response at F2 and sufficient seed, have been tested in the phenotyping screen against both aphid species.
- All surviving plants have been vernalised and are being taken to F4
- Plants will be selected from the most viable crossing events for each of the crosses for each aphid, tested and taken to F5.
- DNA samples from F2s still to be tested

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where knowledge grows

WGIN 3
Resistance to take-all and foliar diseases

Vanessa McMillan

Wheat Genetic Improvement Network

Department for Environment Food & Rural Affairs

WGIN MM 20th April 2017

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ROTHAMSTED RESEARCH

Resistance to multiple foliar diseases

ROTHAMSTED RESEARCH

Watkins 2008 Field Trial

10 Watkins accessions with a high degree of resistance to all 4 foliar pathogens

Also a high take-all disease year with root infection early in the season

Was the foliar disease resistance an induced plant response?

			2008 Disease assessments			
Accesssion	Growth habit	Country of Origin	Yellow rust	Brown rust	Septoria	Mildew
18	Spring	India	0	0	T	T
137	Spring	Australia	T	T	0	T
203	Winter	India	0	0	0	T
231	Spring	Hungary	0	0	T	0
262	Spring	Canary Islands	0	0	0	0
399	Spring	China	T	0	T	0
495	Spring	Morocco	0	0	T	0
610	Spring	Yugoslavia	0	0	T	T
733	Spring	Iran	T	T	T	T
786	Spring	USSR	0	T	T	0

0 – no disease , T = trace

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WGIN 3 Watkins foliar disease experiments

ROTHAMSTED RESEARCH

- 10 Watkins lines + controls sown in both **1st wheat (no take-all)** and **3rd wheat (high take-all)** field trials in autumn 2014, 2015 and 2016

- No fungicides applied to allow natural disease to develop

- Score for foliar diseases + take-all

Watkins foliar disease field trial 2015

ROTHAMSTED RESEARCH

26th June 2015 1st wheat Long Hoos 4

Yellow rust dominant disease that developed across 2015 field trials

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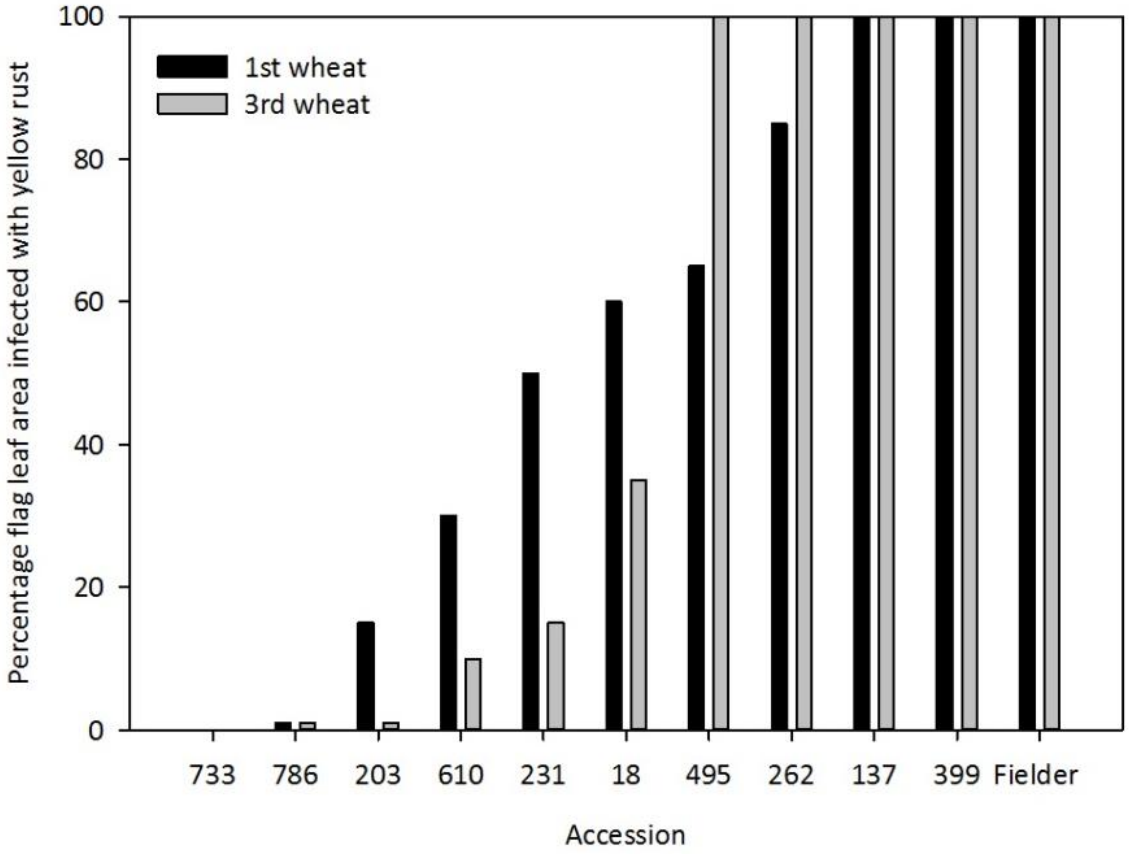
Evidence of resistance to yellow rust

ROTHAMSTED RESEARCH



- Did Watkins lines escape disease in 2008 or change in YR races?
- Evidence of induced response due to take-all?

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Evidence of resistance to yellow rust

ROTHAMSTED RESEARCH

Watkins 203

Low levels of yellow rust sporulation

Watkins 733

No sporulation

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Watkins foliar disease trial 2016

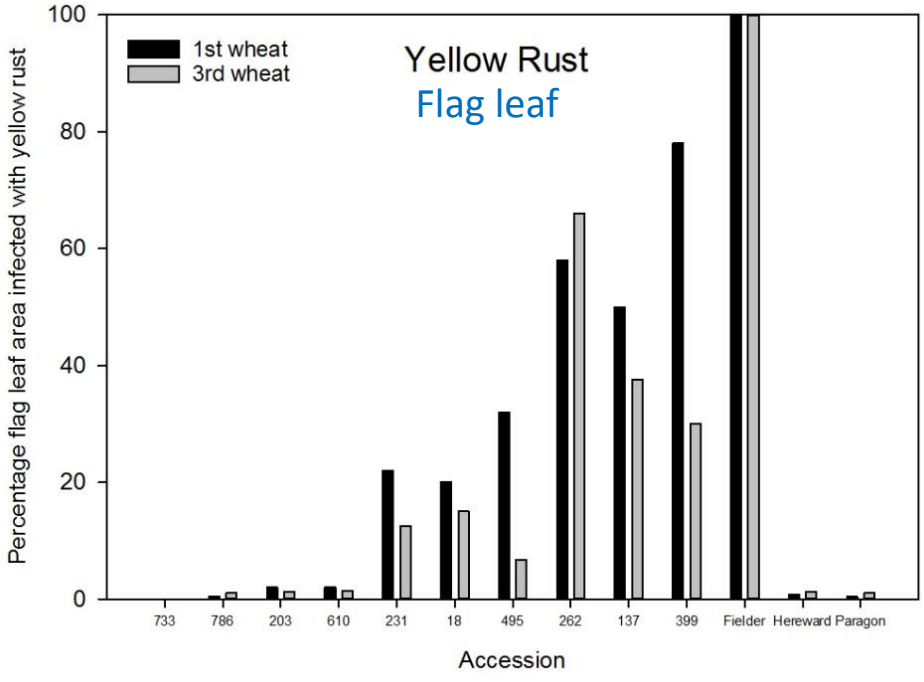
ROTHAMSTED RESEARCH

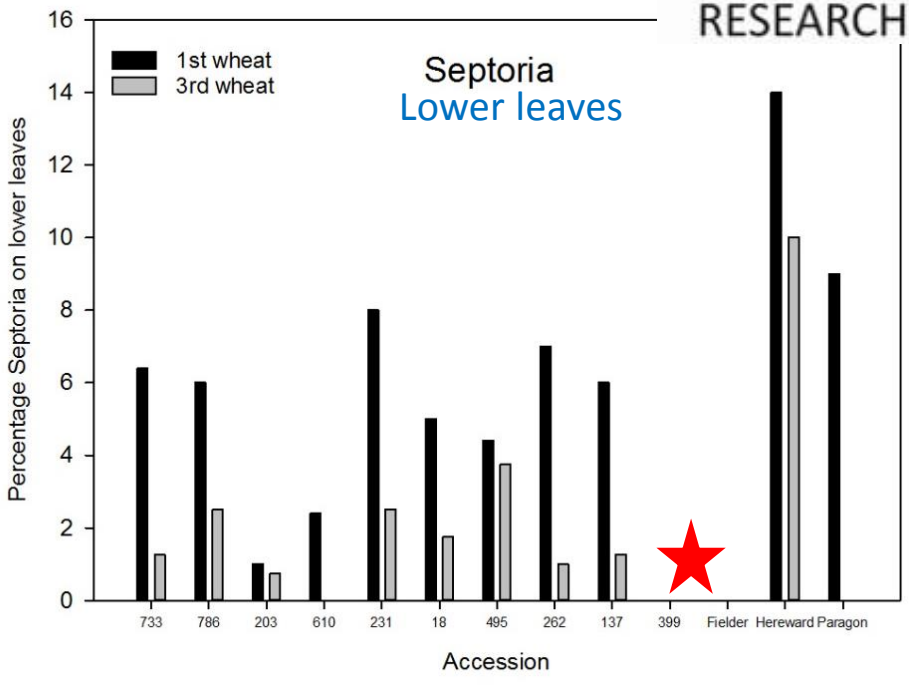
- Repeat field trial with 5 replicates of each genotype sown in autumn 2015 in Long Hoos 5 (1st wheat) and Long Hoos 6/7 (3rd wheat)

- Yellow rust, septoria and brown rust developed

6th June 2016 – Yellow rust and Septoria

ROTHAMSTED RESEARCH





- Yellow Rust shows similar pattern to 2015

★ Low levels of Septoria on all genotypes except 399 and Fielder where high levels of yellow rust are found, therefore impossible to assess Septoria infections

- All genotypes at GS 57-61, except 610 at GS 47

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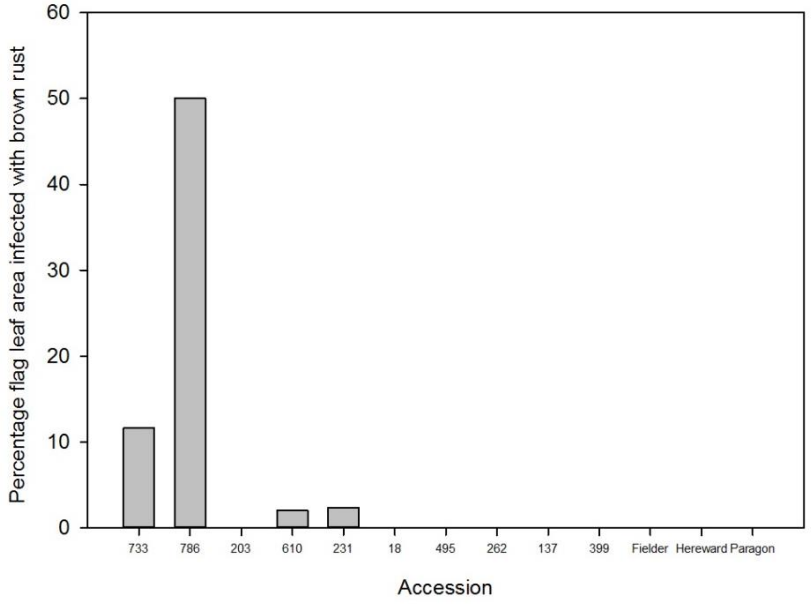
22nd June 2016 – Brown rust developed across the 1st wheat trial site

ROTHAMSTED RESEARCH



Watkins 786

Watkins 231

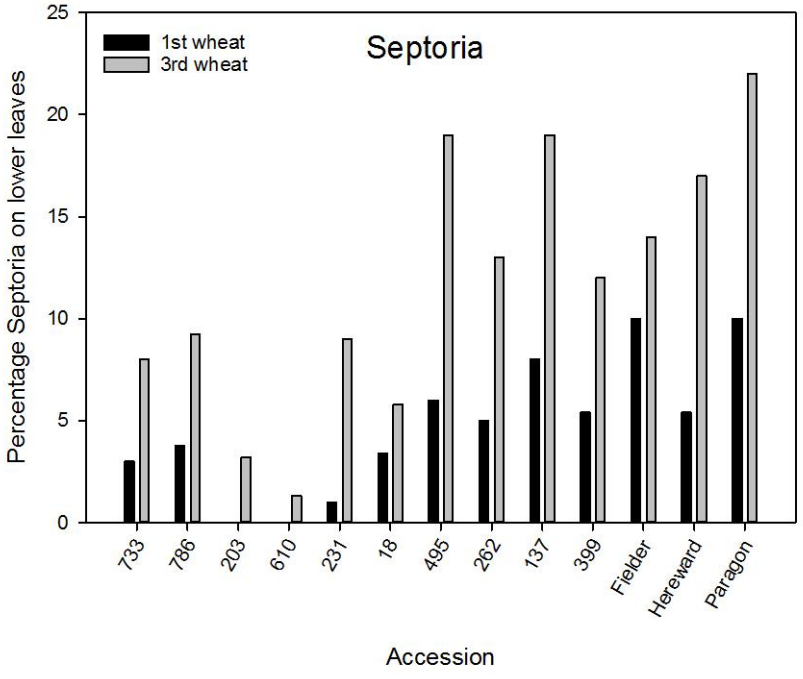
- Watkins 733 and 786 were most resistant to yellow rust but are very susceptible to brown rust – do not possess multi disease resistance

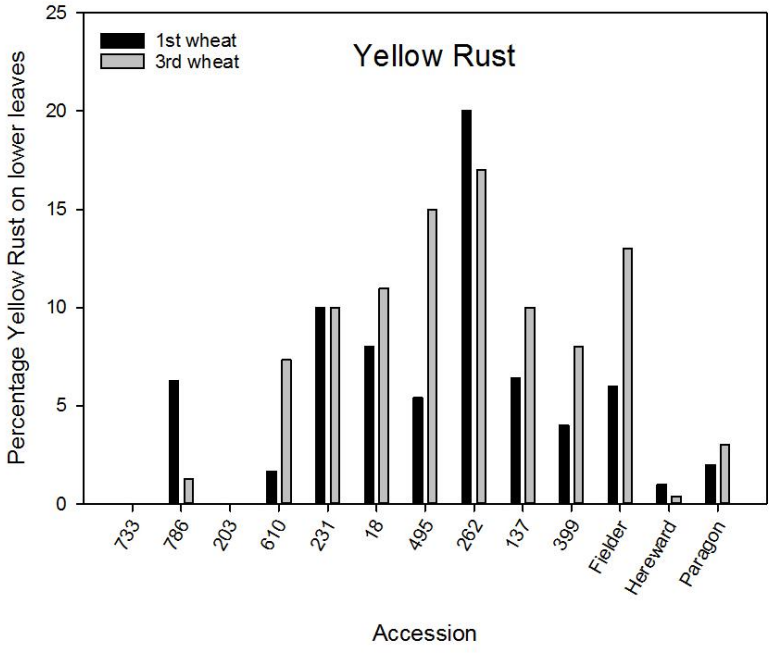
Watkins foliar disease trial 2017

- Repeat field trial with 3-5 replicates of each genotype sown in autumn 2016 in Long Hoos 4 (1st wheat) and Claycroft (3rd wheat)

- Disease assessments carried out 18th April 2017

18th April 2017 – Septoria and Yellow Rust





- Disease assessments on lower leaves
- All genotypes at tillering or beginning of stem elongation
- Higher disease pressure on 3rd wheat site

- Watkins 203 and 610 most promising for showing high levels of resistance against multiple foliar diseases - yellow rust, brown rust and septoria

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Watkins mapping population development

ROTHAMSTED RESEARCH

Summer 2015 Field crossing with cv. Fielder

Accession Number	Growth habit	Country of Origin	Ears crossed	F_1 grains
203	Winter	India	8	31
231	Spring	Hungary	8	54
610	Spring	Yugoslavia	6	33
733	Spring	Iran	6	49
786	Spring	USSR	N/A	N/A

Summer 2016

- F_1 grain sown in glasshouse to generate F2 and for backcrossing to cv. Fielder
- Watkins 786 x Fielder crossing carried out in glasshouse at later date
- F_1 grain included in a spring field trial 2016 to study inheritance

★ Watkins 786 originally excluded from crossing because had high levels of yellow rust during tillering – possibly APR?

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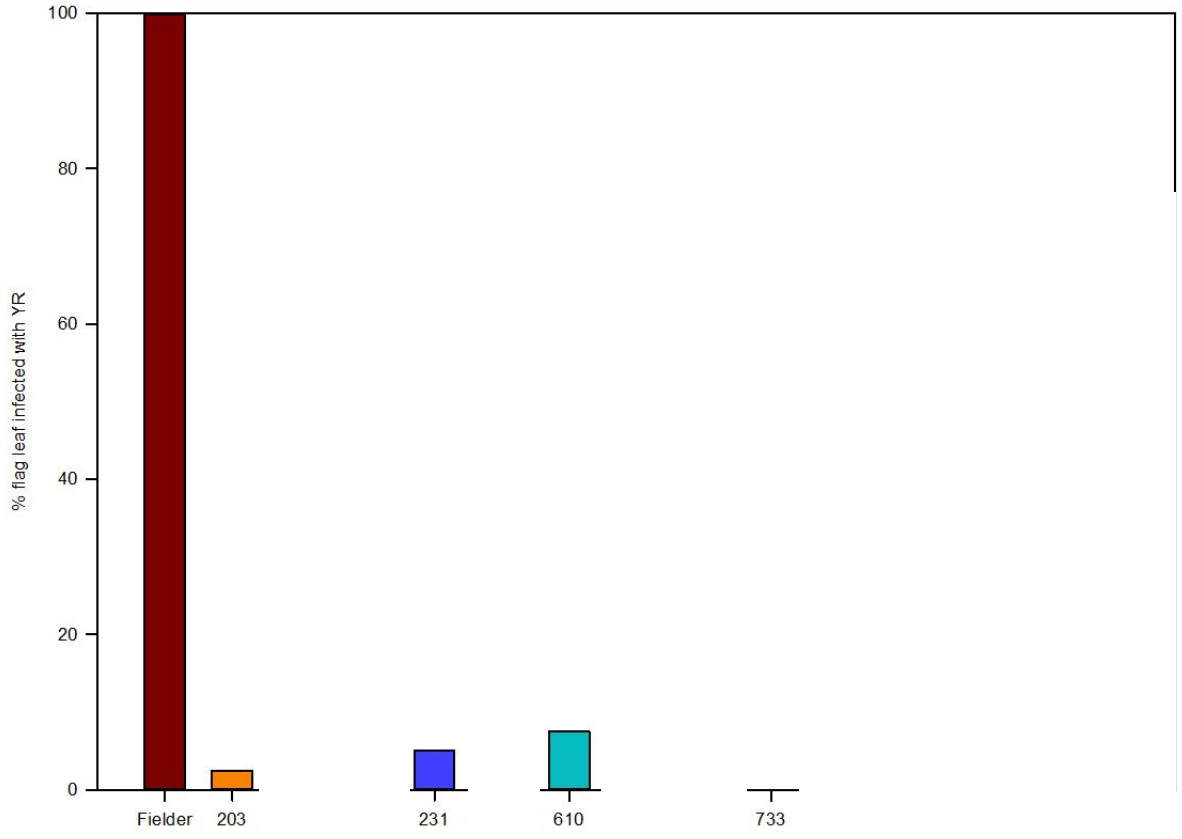
F_1 plants – spring field trial

- Six F_1 grain from each of the 4 crosses sown
- Two replicate plots of parent genotypes (40 seeds per plot)

- Yellow Rust assessments on 30th June 2016



ROTHAMSTED RESEARCH

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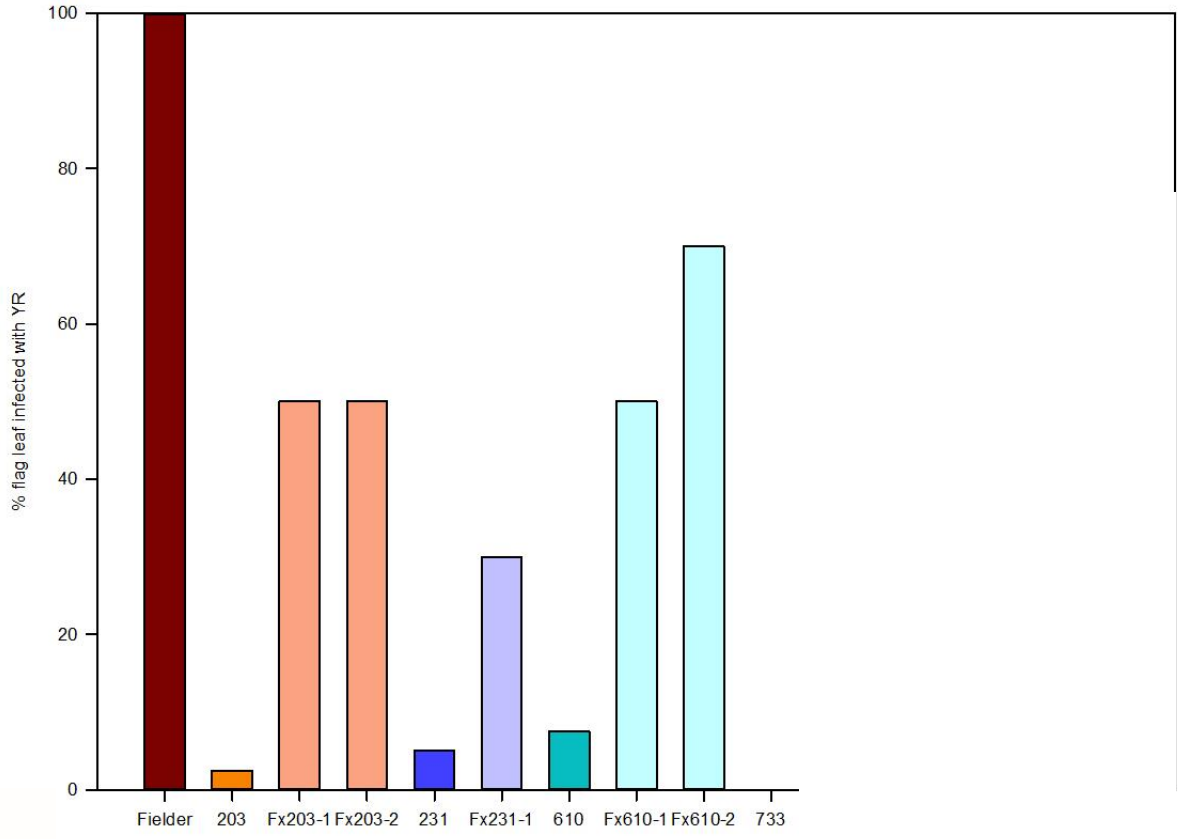

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F_1 plants – spring field trial

ROTHAMSTED RESEARCH

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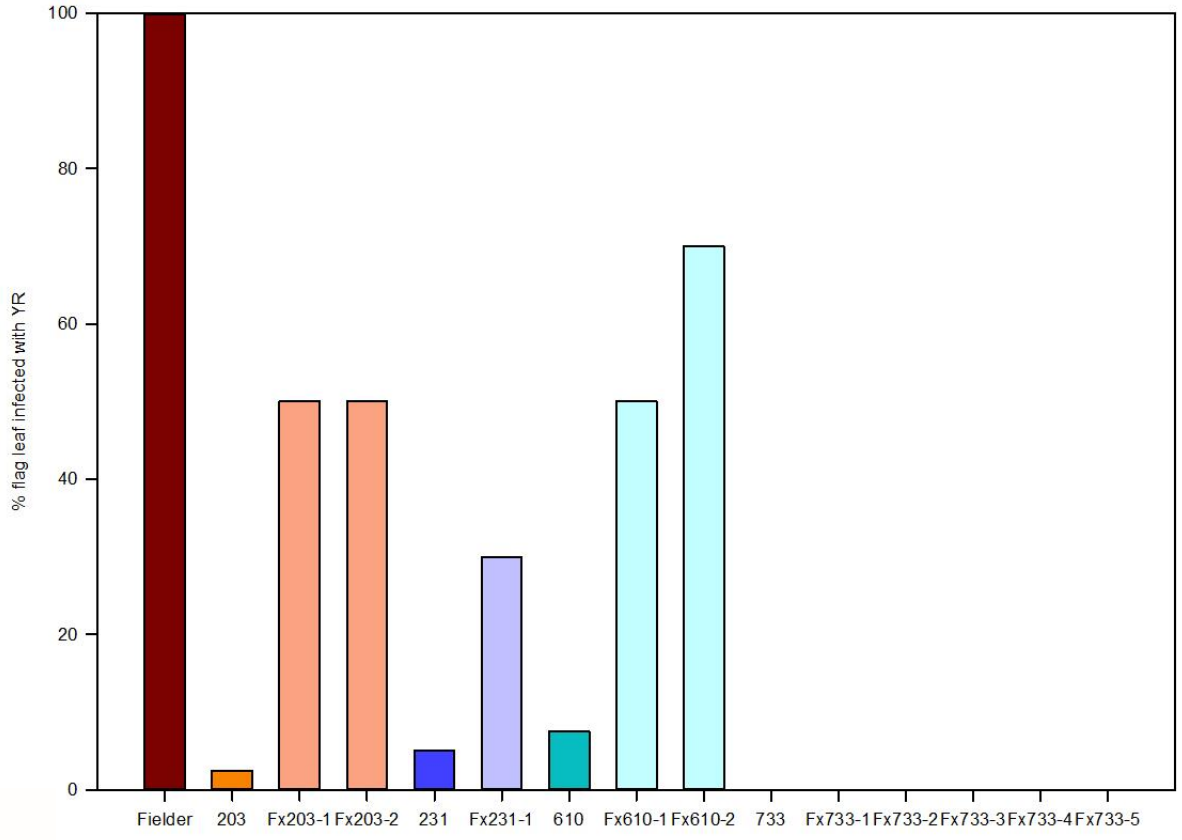

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2017 F_2 field trial

ROTHAMSTED RESEARCH

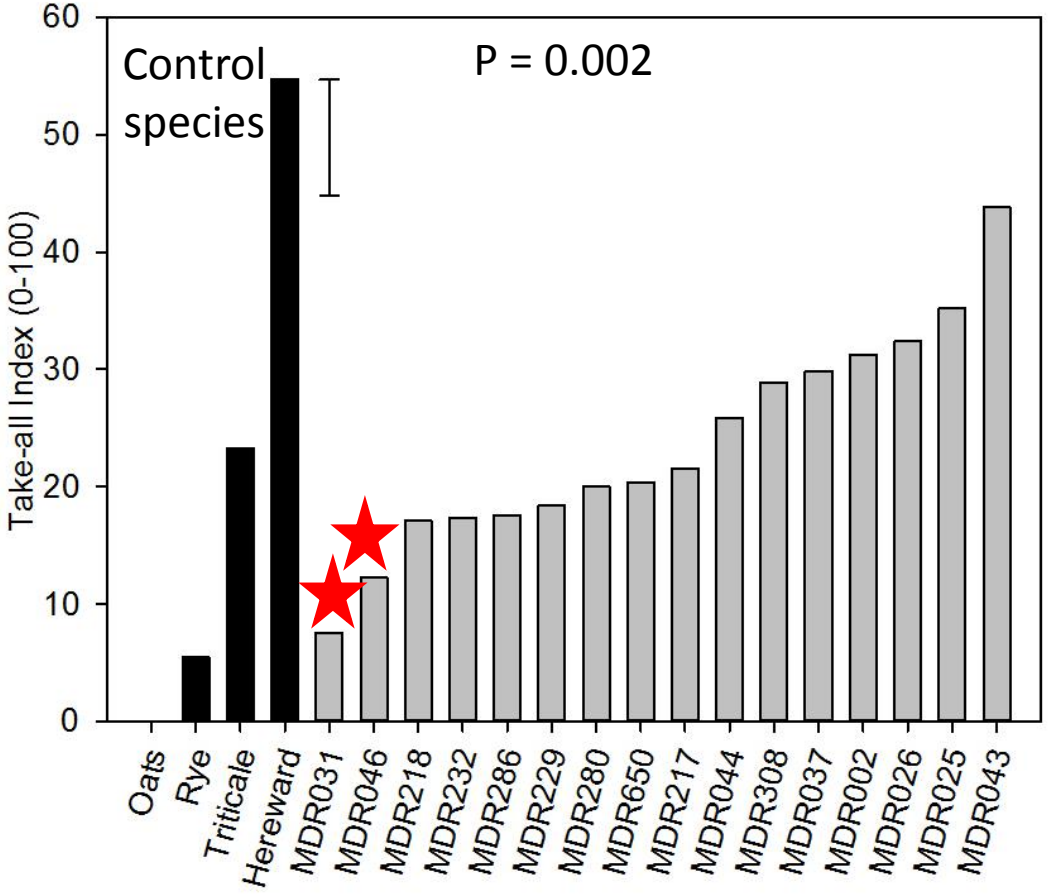
F_2 field trial

- Two F_2 populations from each of the four crosses sown (FxW203, FxW231, FxW610 and FxW733) + parents
- 10 F_1 plants sown from FxW786 cross
- Plot size = 4 rows x 1 m length, 80 seeds sown for each population
- Drilled 14th October 2016 in Sawyers 2
- April 2017 – little foliar disease developing across trial site

Can root resistance to take-all be improved by using an ancient wheat?

ROTHAMSTED RESEARCH

- 3rd wheat field trials 2006-2011 (WGIN 1 and 2)
- **34 *T. monococcum* genotypes (AA diploid genome)** tested over 5 years
- Originally chosen to cover range of countries of origin, subspecies, growth habit



McMillan et al. (2014) BMC Plant Biology 14: 212

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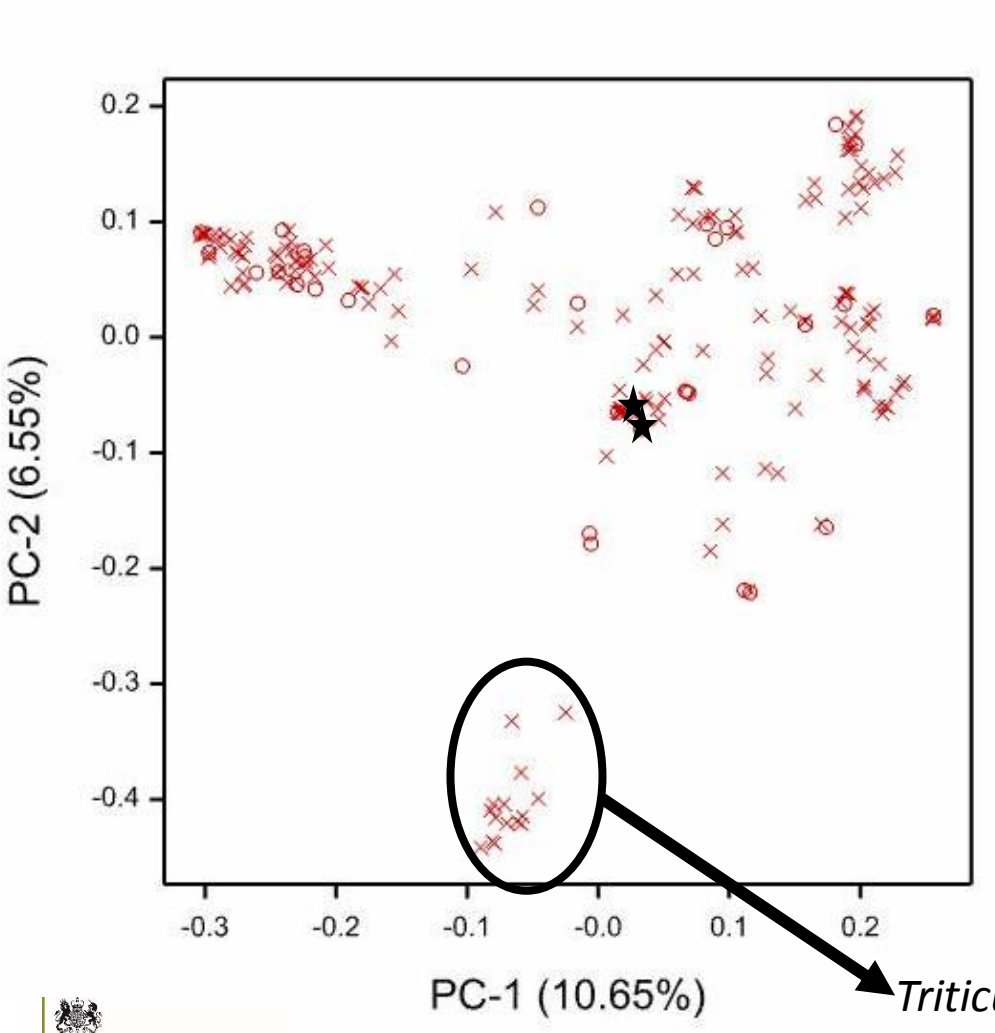
Take-all phenotyping strategy

ROTHAMSTED RESEARCH



★ MDR031 and MDR046

Phenotyping strategy worked well – we have covered a range of genetically dissimilar genotypes from within larger collection

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Triticum monococcum mapping population development

ROTHAMSTED RESEARCH

F6 mapping populations:

MDR037 (S) x MDR046 (R) – 79 lines (take-all resistance, 3 field seasons 2014-2016)

MDR031 (R) x MDR043 (S) (take-all resistance – currently being phenotyped, drilled in 3rd wheat field trial autumn 2016)

MDR037 x MDR229 – 85 lines (root penetration, laboratory screen)

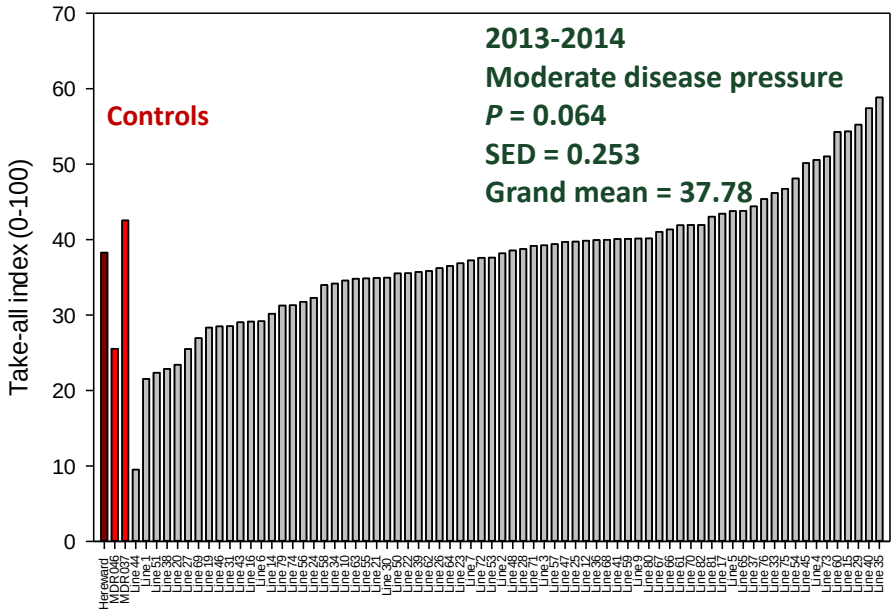
Take-all root resistance
MDR037 (S) X MDR046 (R)

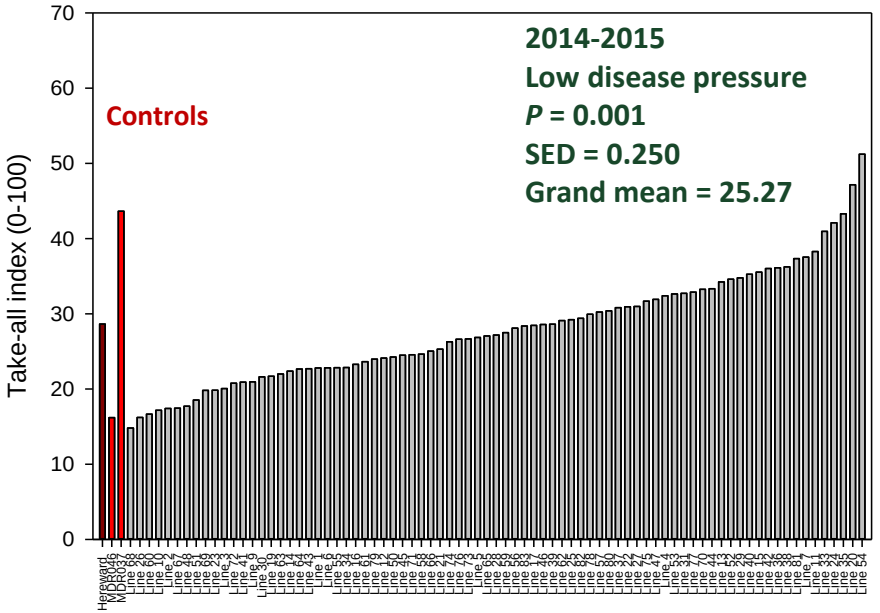
ROTHAMSTED RESEARCH

3rd wheat field trials 2014, 2015 and 2016

- Randomised block design (2-5 replicates/genotype)
- Plant samples taken at GS 75 for take-all assessments

Severe winter flooding 2013-2014





PhD student Sarah-Jane Osborne

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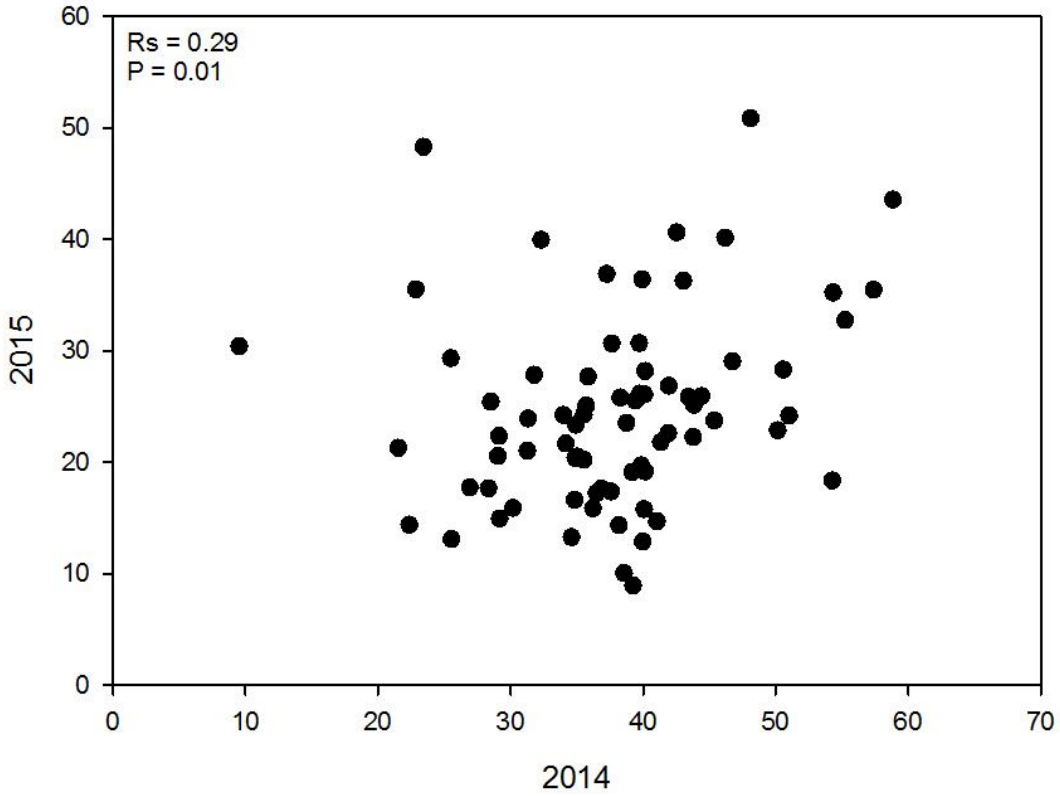
Take-all root resistance
MDR037 (S) X MDR046 (R)

ROTHAMSTED RESEARCH



Weak but significant correlation between the two field trials

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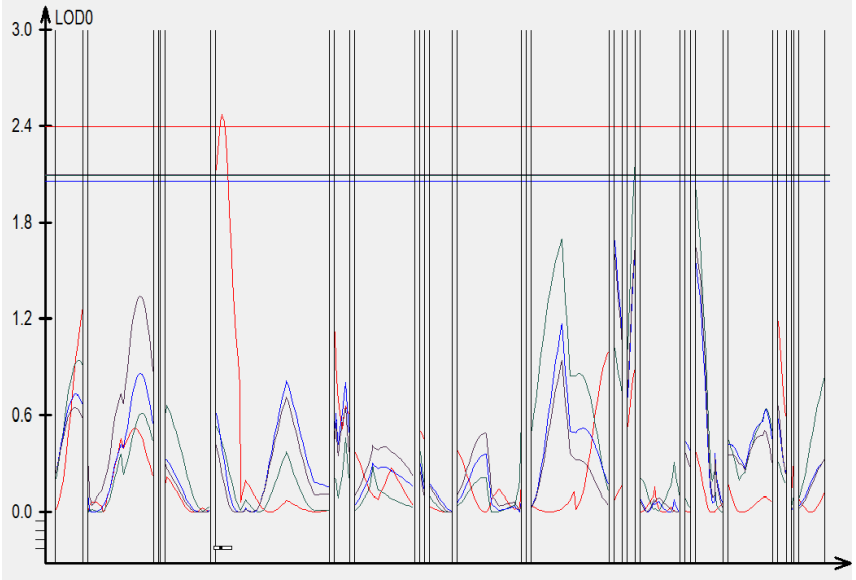
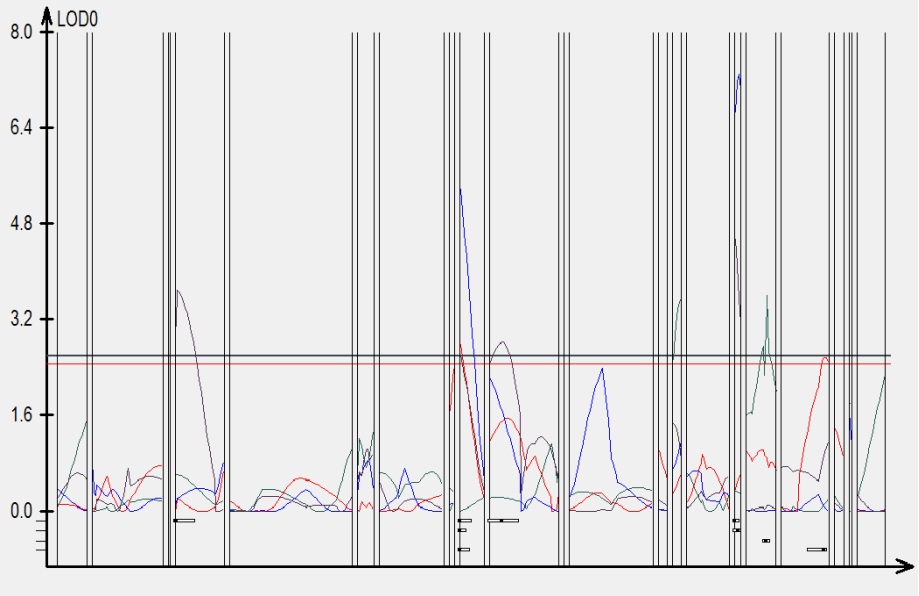
Take-all root resistance
MDR037 (S) X MDR046 (R)

ROTHAMSTED RESEARCH

2014

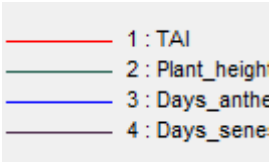


2015



79 lines, 132 markers

Take-all QTLs identified on different linkage groups between the two years



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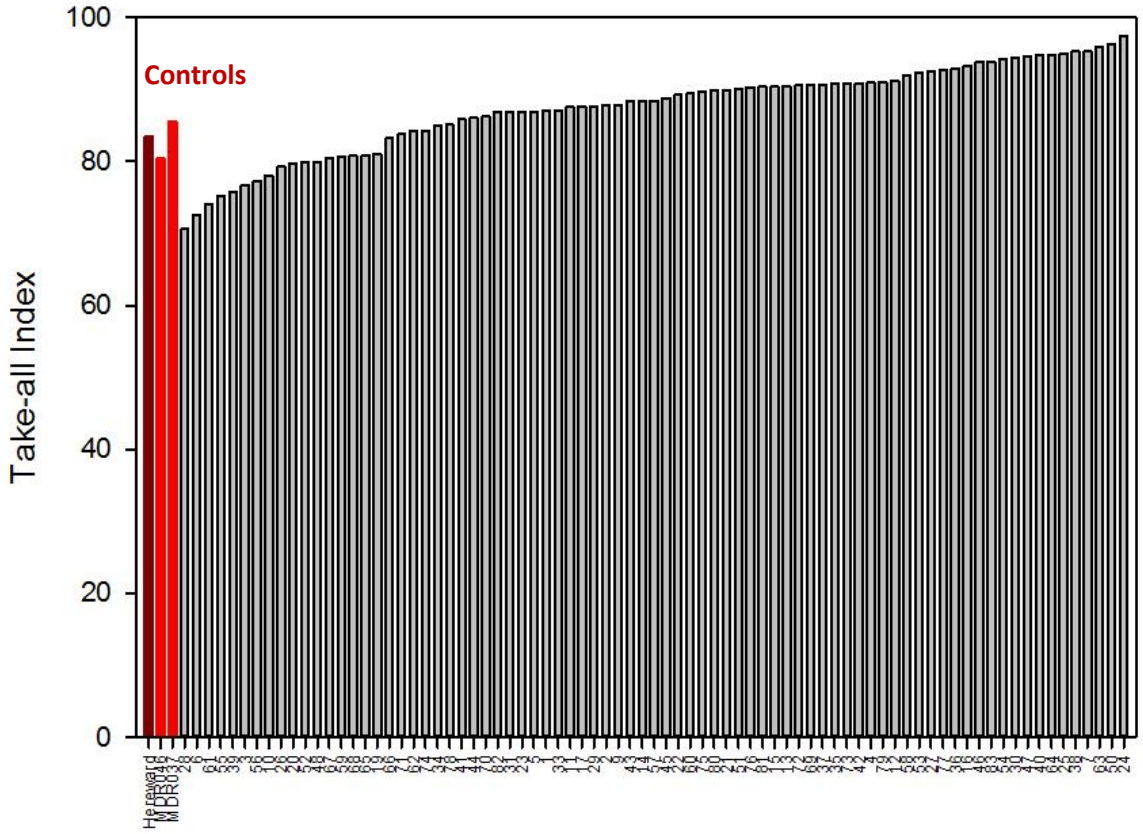
Take-all root resistance
MDR037 (S) X MDR046 (R)

ROTHAMSTED RESEARCH

2015-2016

2016/R/WW/1612
3rd wheat
Long Hoos 6/7

Very high disease pressure
Grand mean = 87
***P* <.001**



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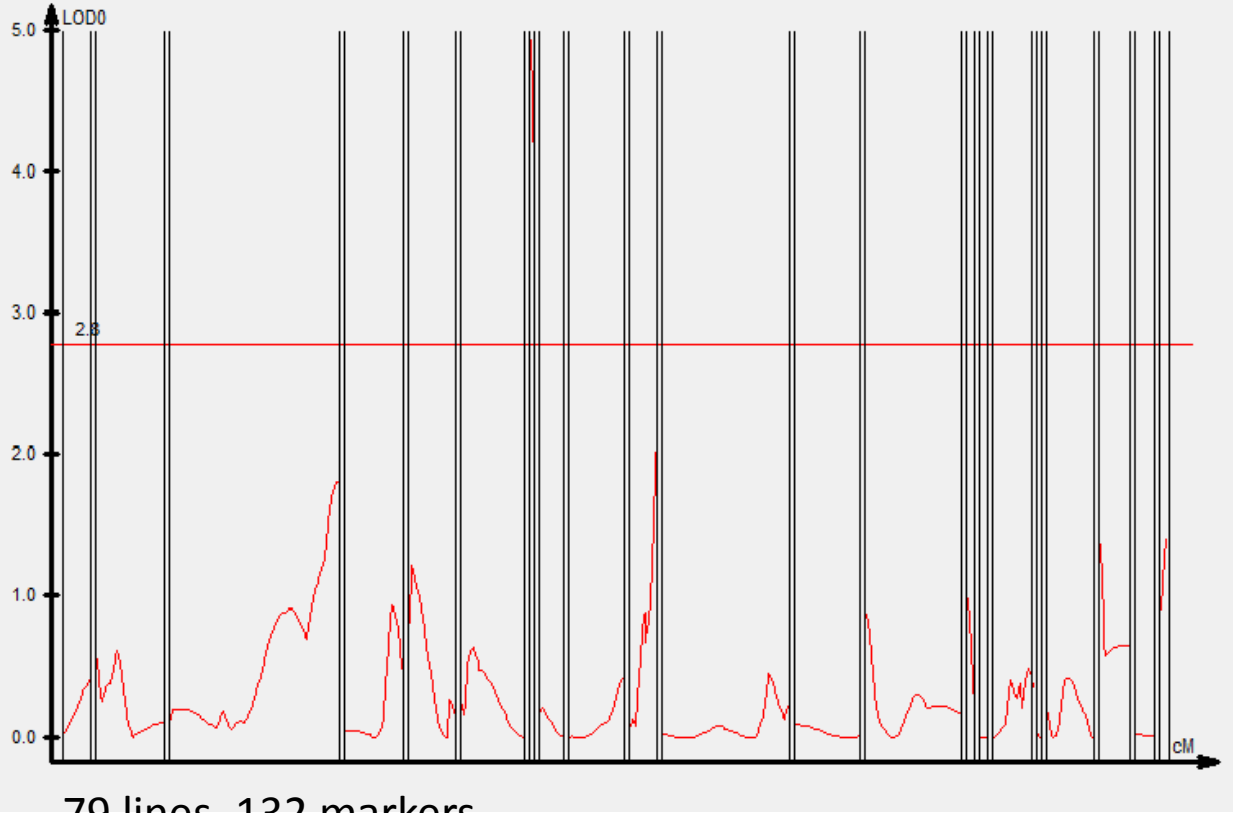
Take-all root resistance
MDR037 (S) X MDR046 (R)

ROTHAMSTED RESEARCH

2016



79 lines, 132 markers

No take-all QTLs identified

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Triticum monococcum take-all resistance

ROTHAMSTED RESEARCH

MDR037 (take-all susceptible) x MDR046 (take-all resistant)

- Preliminary analyses reveal different QTLs between first two field seasons – perhaps exacerbated by flooding of 2013-2014 field trial
- Under very high disease pressure no QTLs detected in 2016
- SSR genotyping to be carried out to improve linkage maps

MDR031 (take-all resistant) x MDR043 (take-all susceptible)

- F_6 take-all phenotyping trial drilled autumn 2016, population still to be genotyped

Many thanks to

ROTHAMSTED RESEARCH

Kim Hammond-Kosack

PhD students
Sarah-Jane Osborne
Joseph Moughan

Undergraduate summer students
Erin Baggs
Eleanor Leane
Tessa Reid
Laurie Neal
Alex Chambers-Ostler
Leanne Freeman

Gail Canning - seed preparation
Mike-Hammond-Kosack - crossing

Rodger White - statistics

RRes farm and glasshouse staff

Wheat Genetic Improvement Network

Department for Environment Food & Rural Affairs

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Tm introgression into durum and hexaploid wheat

ROTHAMSTED RESEARCH

T. monococcum source genotypes

MDR 308 (DV92) - ***TmStb1*** **locus mediated resistance to *Zymoseptoria tritici***

MDR 031 - **Seedling and adult plant root resistance to the take-all fungus (*Gae***

MDR 049 - **Seedling and adult plant resistance to two aphid species**

- o Bird cherry-oat aphid *R*
- o Grain aphid *Sitobion av*

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Towards introgressing *TmStb1* into bread wheat

ROTHAMSTED RESEARCH

Current strategy (so far not very successful**)**

cross *T. monococcum* (*Tm*) to *T. aestivum* cv. Paragon *ph-1*
embryo rescue in F_1
backcross the hybrid to *T. aestivum* cv. Paragon

Trying two alternative strategies

Strategy #1

colchicin treat *Tm* to produce autotetraploid
cross *Tm* autotetraploid directly to wild-type hexaploid and durum wheat

Strategy #2

use tetraploid durum wheat as a bridging species
cross *Tm* with durum wheat
backcross this hybrid to hexaploid wheat

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