

# Tools, resources, genotyping and phenotyping

**Clare Lister and Simon Griffiths**  
**1/2/2018**

**Cathy Mumford and the JIC Field Experimentation Team**  
**Simon Orford, Rajani Awal, Axel Lucmort**  
**Alba Farre-Martinez, Ji Zhou**  
**Griffiths Group – past and present**  
**Andrew Riche and RothRes Drone Team**  
**WGIN3 team**

# WGIN3 Projects: Par Library

1. **Dissecting UK drought tolerance in Par x Gar**
2. **Quantifying agronomic impact of WGIN target genes using the Par NIL library**
3. **Informing multiple marker assisted selection for yield stability using Par 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

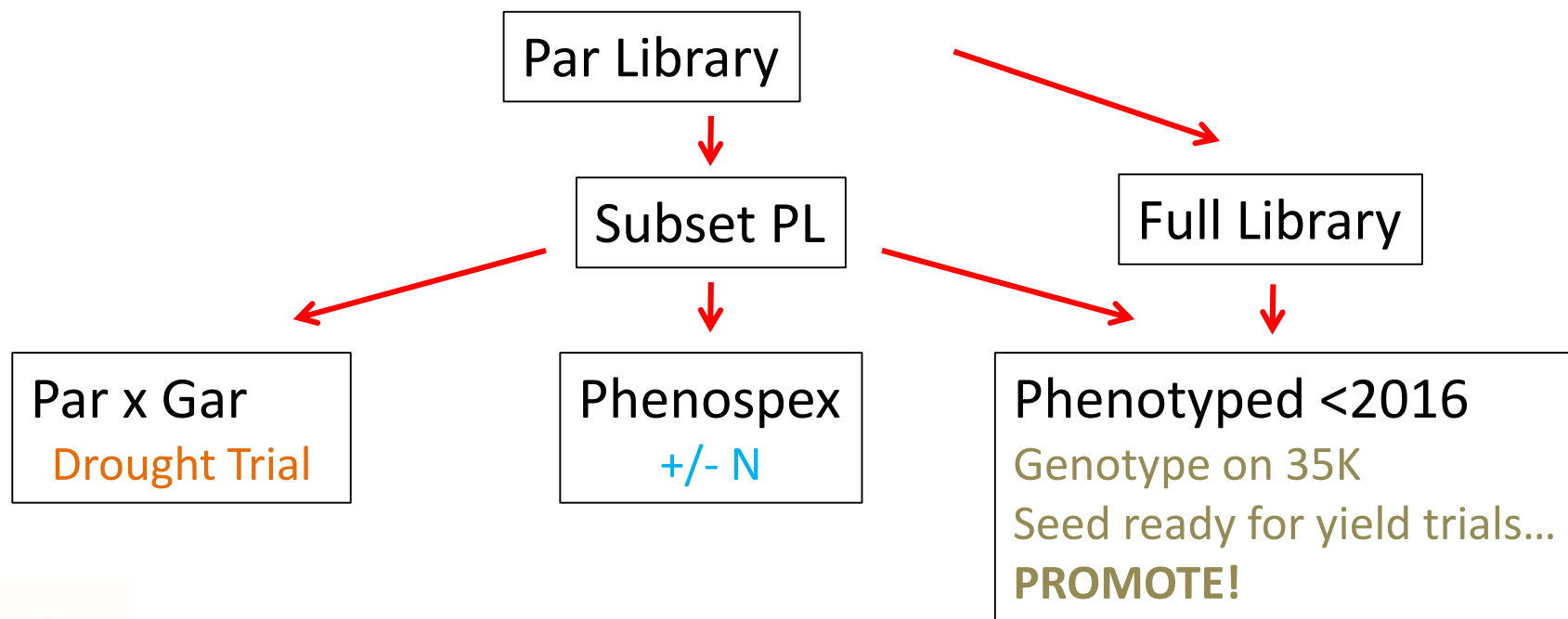


# WGIN3 Projects: Par Library

## NILs in the genetic background of **Paragon**

NILs are available for multiple alleles of:

*Rht-D1*, *Rht-B1*, *Rht8*, *Ppd-B1* *Ppd-D1*, *Lr19*, *1BL.1RS* and *7B* (yield),  
10 Heading Date QTL, *Vrn1*, *Vrn3*, grain size (5A, 7A), and selected  
WGIN mutants, such as EMS.



# 1. Dissecting UK drought tolerance in Par x Gar

- 3 x Drought Trials with 177 PxG lines – autumn drilled
- Church Farm, Bawburgh, Norfolk
  - 2015-2016 – no drought in April
  - 2016-2017 – April drought
  - 2017-2018 - ?
- 2 randomised reps each of Irrigated (IR) and Not Irrigated (NI) plots
- Multiple traits scored, measured or observations made
- Aerial monitoring (JIC and RRes drones)

Date	Measured	Observations
Stage 31	Height	Awns
Booting	Yield	Ear Compactness
Ear Emergence	Specific Weight	Lodging
	TGWT	Tillering
		Waxiness
		Senescence

- QTL mapping carried out where sufficient data

# 1. Dissecting UK drought tolerance in Par x Gar

	2016			2017		
	Linkage group	%Expl. Var	High value allele	Linkage group	%Expl. Var	High value allele
Booting NI	2B	10.0	Gar	2B	9.3	Gar
	2D	21.5	Par	2D	21.2	Par
	4D	6.4	Gar			
				5B	11.0	Par
	7A	17.0	Par	7A	10.8	Par
Booting IR	2B	9.5	Gar	2B	6.2	Gar
	2D	14.9	Par	2D	53.9	Par
	7A	19.7	Par	7A	14.9	Par
DTEM NI	2B	10.3	Gar	2B	6.6	Gar
	2D	22.3	Par	2D	21.3	Par
				5B	12.0	Par
	7A	17.1	Par			
DTEM IR	2B	9.8	Gar	2B	4.7	Gar
				2D	38.4	Par
	7A	15.3	Par	7A	21.1	Par
Height NI	1A	4.4	Gar	1A	4.8	Gar
	3B	3.7	Gar			
	4D	62.3	Par	4D	62.3	Par
Height IR	1A	6.4	Gar	1A	5.1	Gar
	3B	4.0	Gar	3B	3.9	Gar
	4D	59.6	Par	4D	59.3	Par
				7A	5.4	Par



	2016			2017		
	Linkage group	%Expl. Var	High value allele	Linkage group	%Expl. Var	High value allele
Yield NI				2B	17.7	Gar
	7B	16.8	Gar			
Yield IR	NO QTLs DETECTED			1A	11.4	Gar
				2B	17.0	Gar
Specific Weight NI	2B	9.0	Gar	2B	11.3	Gar
	3A	6.1	Par			
	4D	29.2	Par	4D	33.7	Par
	5A	2.5	Gar			
Specific Weight IR				7D	5.2	Gar
				1A	5.0	Gar
				2B	9.4	Gar
	4D	38.1	Par	4D	33.0	Par
	5A	6.8	Par			
TGWT NI	5A	7.0	Gar			
	1A	18.2	Gar	1A	14.6	Gar
	3B	4.5	Gar			
				4D	16.6	Par
	5A	6.3	Gar	5A	5.0	Gar
TGW IR				5B	8.4	Gar
				7A	12.3	Gar
	1A	15.0	Gar			
	4D	5.2	Par	4D	18.7	Par
	5A	6.5	Gar	5A	7.1	Gar
			5B	9.2	Gar	
			7A	8.2	Gar	



2B and 1A - good candidates for increased yield, in both IR and NI

# 1. Dissecting UK drought tolerance in Par x Gar

	2016			2017		
	Linkage group	%Expl. Var	High value allele	Linkage group	%Expl. Var	High value allele
Booting NI	2B	10.0	Gar	2B	9.3	Gar
	2D	21.5	Par	2D	21.2	Par
	4D	6.4	Gar			
				5B	11.0	Par
	7A	17.0	Par	7A	10.8	Par
Booting IR	2B	9.5	Gar	2B	6.2	Gar
	2D	14.9	Par	2D	53.9	Par
	7A	19.7	Par	7A	14.9	Par
DTEM NI	2B	10.3	Gar	2B	6.6	Gar
	2D	22.3	Par	2D	21.3	Par
				5B	12.0	Par
DTEM IR	2B	9.8	Gar	2B	4.7	Gar
				2D	38.4	Par
	7A	15.3	Par	7A	21.1	Par
Height NI	1A	4.4	Gar	1A	4.8	Gar
	3B	3.7	Gar			
	4D	62.3	Par	4D	62.3	Par
Height IR	1A	6.4	Gar	1A	5.1	Gar
	3B	4.0	Gar	3B	3.9	Gar
	4D	59.6	Par	4D	59.3	Par
			7A	5.4	Par	



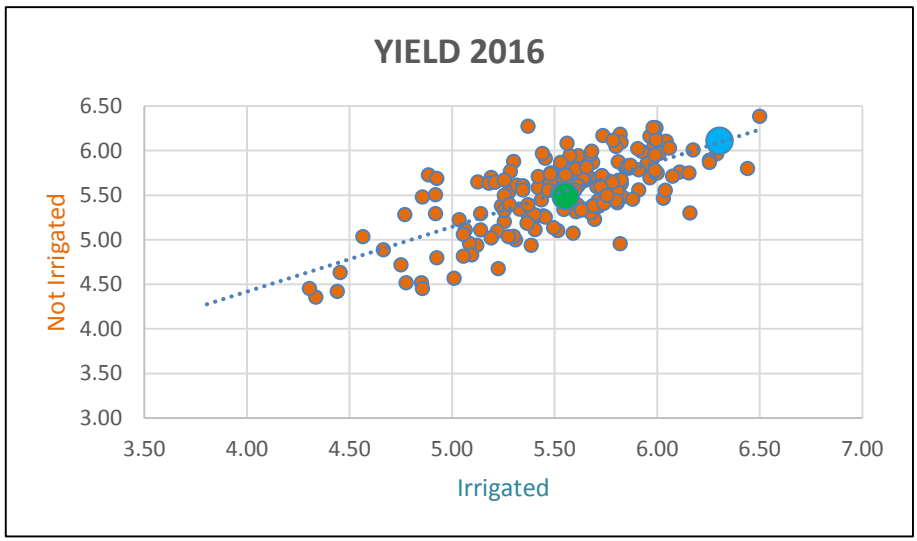
	2016			2017		
	Linkage group	%Expl. Var	High value allele	Linkage group	%Expl. Var	High value allele
Yield NI				2B	17.7	Gar
	7B	16.8	Gar			
Yield IR	NO QTLs DETECTED			1A	11.4	Gar
				2B	17.0	Gar
Specific Weight NI	2B	9.0	Gar	2B	11.3	Gar
	3A	6.1	Par			
	4D	29.2	Par	4D	33.7	Par
	5A	2.5	Gar			
Specific Weight IR				7D	5.2	Gar
				1A	5.0	Gar
				2B	9.4	Gar
	4D	38.1	Par	4D	33.0	Par
	5A	6.8	Par			
TGWT NI	5A	7.0	Gar			
	1A	18.2	Gar	1A	14.6	Gar
	3B	4.5	Gar			
				4D	16.6	Par
	5A	6.3	Gar	5A	5.0	Gar
TGW IR				5B	8.4	Gar
				7A	12.3	Gar
	1A	15.0	Gar			
	4D	5.2	Par	4D	18.7	Par
	5A	6.5	Gar	5A	7.1	Gar
			5B	9.2	Gar	
			7A	8.2	Gar	



2B and 1A - good candidates for increased yield, in both IR and NI

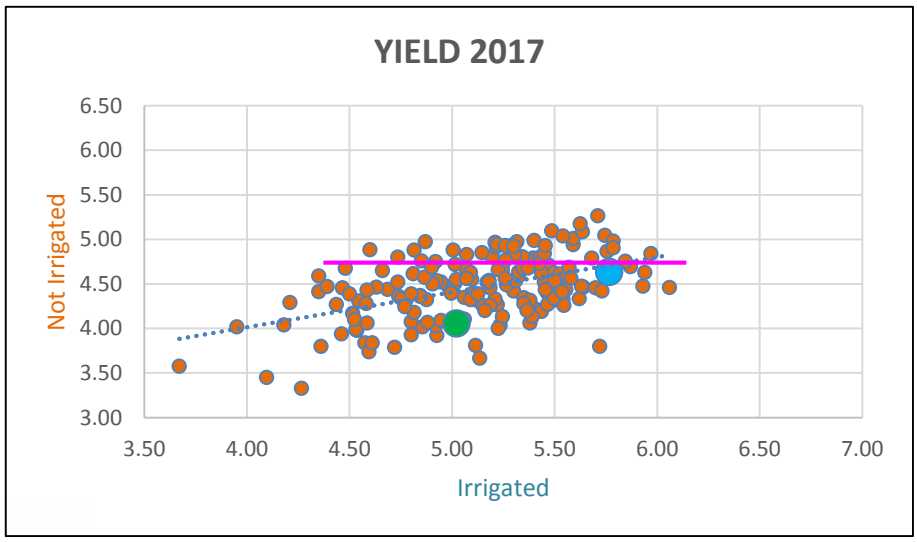
In 2017 1A for TGWT is specific to the NI plots

# 1. Dissecting UK drought tolerance in Par x Gar



Same yield for Par in NI and IR plots  
Slightly higher yield for Gar in IR plots

Gar one of highest yielding lines



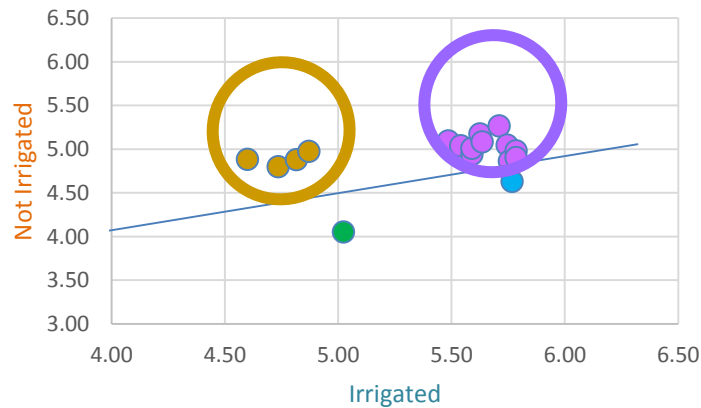
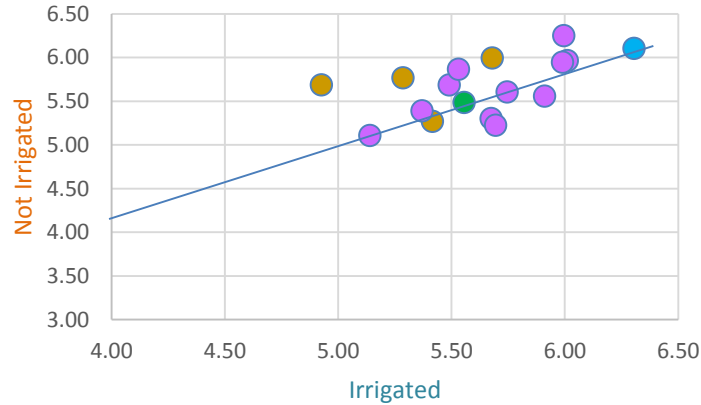
Yields at least 1.5 kg lower than 2016

20% yield reduction for Par and Gar between the IR and NI plots

Many lines performing better than Gar in NI

# 1. Dissecting UK drought tolerance in Par x Gar

Yield



Selected lines which perform better than Gar under drought conditions  
 Lines have highest yield in NI compared to IR  
 Lines have higher yield than Gar in NI



# 1. Dissecting UK drought tolerance in Par x Gar

- **Lines** carry Gar allele (↓) for a TGWT QTL on **4D** (=Rht)
- Has *smaller* grains but can produce *more grains* under drought conditions than other lines?
- **Lines** carry the Gar allele (↑) for a HT, YLD and SW QTL on **1A**
- 14/15 **lines** carry the Gar allele (↑) for YLD QTL on **2B** (not *Ppd*)
- Possible gene candidate for this QTL (from promotome input)
- A gene involved in GA biosynthesis, inactivation and signalling
- The 1A and 2B QTL's will be nominated for **DFW BTK**

## 2. Quantifying agronomic impact of WGIN target genes using the Par NIL library

### HAVE YOU HEARD ABOUT THE PARAGON LIBRARY?

WGIN has been part of an informal consortium developing NILs in the genetic background of the UK spring wheat **Paragon**. The collection, known as the **Paragon Library**, was developed at JIC and consists of around 350 lines.

The project involves crossing different combinations of genes, QTLs and mutations into the common background of Paragon and then studying the phenotypic effects. This uniform genetic background this will provide a unique insight into the potential value of these genetic effects for UK breeding and agriculture. Most of the effects were discovered in work funded by DEFRA, the BBSRC and AHDB and represent hundreds of person-years' of research.

Most of the Paragon Library has already been trialled in 1 m and 6 m plots for the duration of WGIN. Phenotypic data from these trials (phenotypes underlying grain yield and crop adaptation) should become available on the WGIN website from spring 2018.

The Paragon Library will be genotyped on the Axiom 35k Breeders' Array shortly and seed from the genotyped plants will be used to generate the resource for distribution.

NILs are available for multiple alleles of:  
*Rht-D1*, *Rht-B1*, *Rht8*, *Ppd-B1* *Ppd-D1*, *Lr19*, *1BL.1RS* and *7B* (yield), 10 Heading Date QTL, *Vrn1*, *Vrn3*, grain size (5A, 7A), and selected WGIN mutants, such as EMS.

Clare Lister and Simon Griffiths

## 2. Quantifying agronomic impact of WGIN target genes using the Par NIL library

- Par Library (PL) to be genotyped on 35K array
- *Currently* PL library of 354 lines – remainder are controls
- Data to WGIN website

5A and 7A Grain Size
7B Yield
1B1R Yield
Lr19 - Alien Introgression
<i>RhtD1</i>
<i>RhtB1</i>
<i>RhtB1/RhtD1</i> crosses with <i>Rht8</i>
Par EMS mutants, including <i>Staygreen</i>
<i>Ppd</i> copy number
Paragon + <i>Vrn</i>
Heading date loci on 1B, 1D, 3A, 3B, 4A, 6A, 7A, 7B, 7D from different donors

## 2. Quantifying agronomic impact of WGIN target genes using the Par NIL library

### Subset of Par Library

Lr19 Kamb1	Alien introgression
Par Mutant 2316b	Staygreen
Ppd 1x Early	DTEM
Ppd 2x Early	DTEM
Ppd 3x Early	DTEM
Ppd KO 2x	DTEM
Rht 8 Mara	Height
Rht B1 Robigus	Height
Rht D1 Alchemy	Height

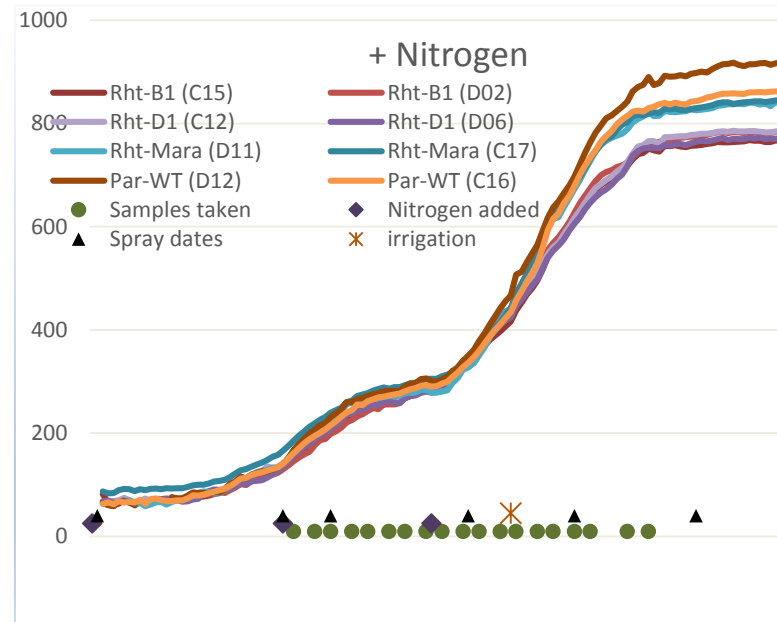
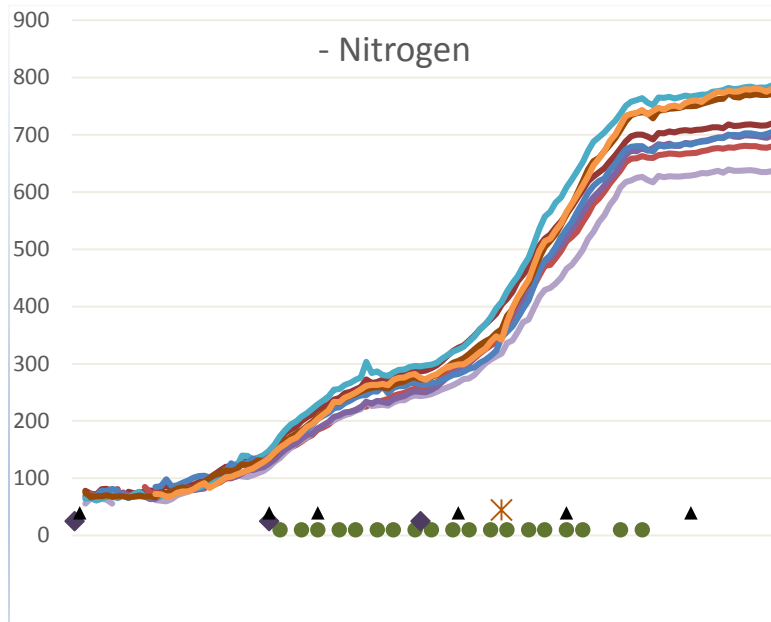
### Drought Trial 2016 Drought Trial 2017



### Phenospex 2016 Phenospex 2017

- Two randomised blocks of 16
- One treatment – all plots + nitrogen (40 kg/h)
- Two subsequent treatments +/- additional nitrogen (250 kg/h)

## 2. Quantifying agronomic impact of WGIN target genes using the Par NIL library



- Collaboration with Ji Zhou and Wilfried Haerty groups (EI) and Richard Morris (JIC)
- Phenospex measurements show time when growth rates of Paragon/Rht8 diverge from RhtB1/RhtD1
- Single plant collected from each plot at each time point
- RNA seq analysis and gene network modelling to be funded by JIC ISF

### 3. Informing multiple marker assisted selection for yield stability using the Par library

Combining gibberellic acid-sensitive and insensitive dwarfing genes in breeding of higher-yielding, sesqui-dwarf wheats

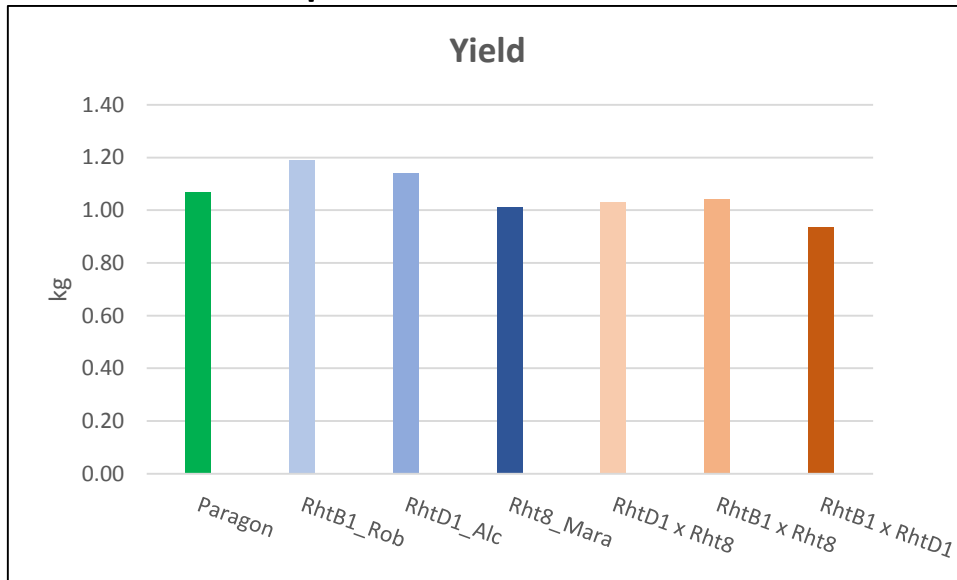
G.J. Rebetzke\*, D.G. Bonnett<sup>1</sup>, M.H. Ellis<sup>1</sup>

- Reductions in plant height are associated with increase harvest index and wheat yields.
- Largest increase due to development of semi-dwarf wheats through introgression of the gibberellic acid (GA)-insensitive, Rht-B1 and Rht-D1 alleles.
- Selection of Rht8C + Rht-B1B or Rht-D1D could facilitate development of high-yielding varieties targeting favourable and unfavourable environments, such as drought and low N



# 3. Informing multiple marker assisted selection for yield stability using the Par library

- Lines generated to test this:
- *RhtB1* x *Rht8*
- *RhtD1* x *Rht8*
- *RhtB1* x *RhtD1*
- 1 m plots 2016-17



*RhtB1+RhtD1*      *Rht8+RhtD1*  
*Rht8+RhtB1*      Par

Three rep Yield Trial  
(6m plots) drilled Oct 2017

# WGIN3 Projects: Avalon and Cadenza

1. Dissecting UK drought tolerance in Par x Gar
2. Quantifying agronomic impact of WGIN target genes using the Par NIL library
3. Informing multiple marker assisted selection for yield stability using Par 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





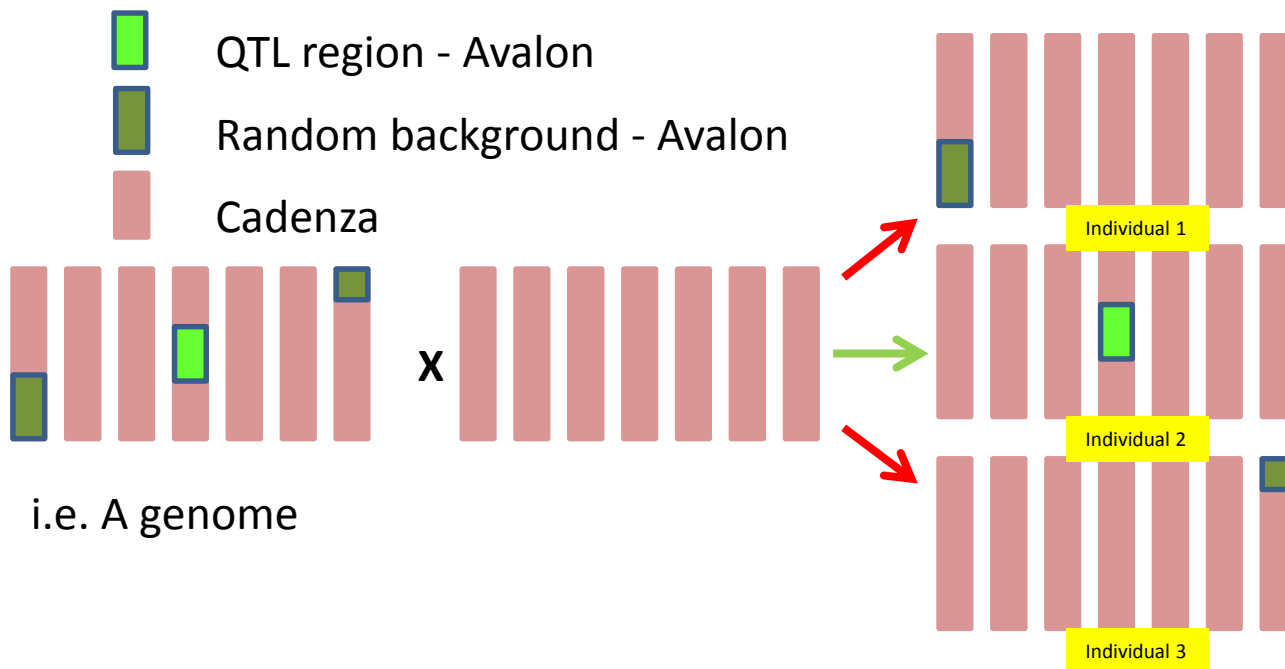
# WGIN3 Projects: Avalon and Cadenza

- WGIN successfully promoted the AxC DH population as UK reference population
  - A x C population most densely mapped in the world
  - Much phenotypic data also available
  - NILs derived from these have validated QTLs
4. A chromosome segment substitution library (CSSL) for Avalon x Cadenza
  5. Understanding genotype x environment interaction in Avalon x Cadenza
  7. Applying WGIN data to breeding by design for UK yield stability



# 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.
- Undertaking tiling the whole genome with chromosome segments to make recombinant substitution lines.



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

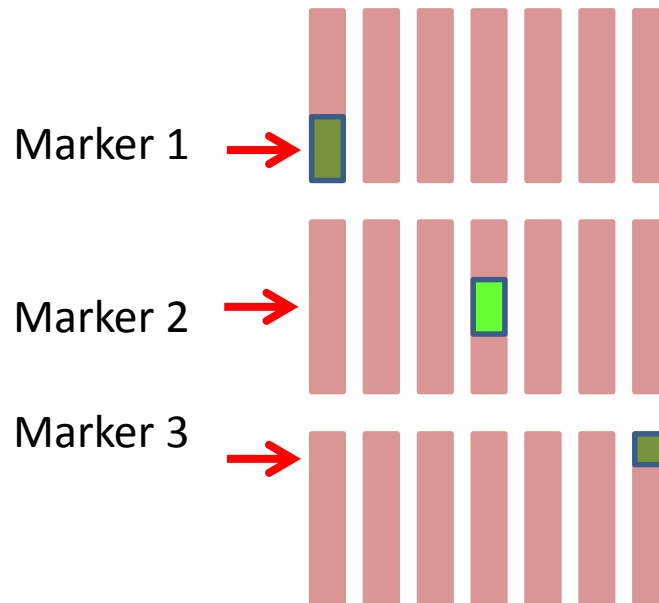
- Have used several methods to generate maps of (i.e. based on frame-map, Axiom info, pseudomolecules and now **NRGene v1.0 sequence**)
- Genotyping carried out on 94 NILs (+ Av/Cad) using Breeders 35K array
- **Estimate** of % coverage of background (+ foreground) for each chromosome based on NRGene v1.0 sequence
- NILs backcrossed to the recurrent parent and selfed to generate lines where QTL region and random segments have been separated

SUBSTITUTION COVERAGE		
	Avalon	Cadenza
	43 lines	46 lines
1A	~10%	>95%
1B	>95%	~90%
1D	~30%	~90%
2A	~20%	~95%
2B	~20%	~90%
2D	~20%	~90%
3A	~95%	~95%
3B	~95%	~95%
3D	~80%	~60%
4A	~80%	~75%
4B	~90%	~95%
4D	?	?
5A	~90%	~95%
5B	~95%	~95%
5D	~75%	~80%
6A	~95%	>95%
6B	~95%	~80%
6D	~95%	~95%
7A	~70%	~85%
7B	~60%	~75%
7D	~95%	~70%
INCLUDES QTL FOREGROUND		



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

- Fifty-seven lines selected – to give maximum coverage with minimum number of lines
- Seedling growing in 96-well trays...
- DNA preps
- Will genotype with markers for introgressed regions.



# 5. Understanding genotype x environment interaction in Avalon x Cadenza

Farré et al. *BMC Plant Biology* (2016) 16:161  
DOI 10.1186/s12870-016-0849-6

BMC Plant Biology

RESEARCH ARTICLE

Open Access



## Application of a library of near isogenic lines to understand context dependent expression of QTL for grain yield and adaptive traits in bread wheat

Alba Farré, Liz Sayers, Michelle Leverington-Waite, Richard Goram, Simon Orford, Luzie Wingen, Cathy Mumford and Simon Griffiths<sup>\*</sup>

### Abstract

**Background:** Previous quantitative trait loci (QTLs) studies using the Avalon x Cadenza doubled haploid (DH) population identified eleven QTLs determining plant height, heading date and grain yield. The objectives of this study were: (i) to provide insight into the effects of these QTLs using reciprocal multiple near isogenic lines (NILs) with each pair of alleles compared in both parental backgrounds (Avalon or Cadenza), (ii) quantifying epistasis by looking at the background effects and (iii) predict favourable allelic combinations to develop superior genotypes adapted to a target environment.

**Results:** To this aim, a library of 553 BC<sub>2</sub> NILs and their recurrent parents were tested over two growing seasons (2012/2013 and 2013/2014). The results obtained in the present study validated the plant height, heading date and grain yield QTLs previously identified. Epistatic interactions were detected for the 6B QTL for plant height and heading date, 3A QTL for heading date and grain yield and 2A QTL for grain yield.

**Conclusion:** The marker assisted backcrossing strategy used provided an efficient method of resolving QTL for key agronomic traits in wheat as Mendelian factors determining possible epistatic interactions. The study shows that these QTLs are amenable to marker assisted selection, fine mapping, future positional cloning, and physiological trait dissection.

**Keywords:** Yield, Wheat, Near isogenic lines, QTL



## 6. Foundations for a new generation segregating populations for studying yield stability in the UK

Female		Male	RL value Diversity target	RL value Diversity target	RL value Diversity target
Grafton	x	Conqueror	lodging	mildew	eyespot
Grafton	x	Revelation	heading	brown rust	fusarium
Beluga	x	Cordiale	protein	hagberg	TGW
Scout	x	Denman	lodging		
Revelation	x	Gallant	heading	fusarium	
KWS Sterling	x	Alchemy	height		
KWS Santiago	x	Scout	yield	eyespot	
KWS Santiago	x	Solstice	yield		
KWS Santiago	x	Gallant	hagberg	market share	
KWS Kielder	x	Scout	yield		
KWS Kielder	x	Einstein	yield		
KWS Gator	x	Gallant			
KWS Gator	x	Revelation	septoria tritici		
KWS Croft	x	Scout	lodging		
Icon	x	Skyfall			
Horatio	x	KWS Gator	GS31		
Grafton	x	Solstice	height	eyespot	
Gallant	x	Invicta	heading	market share	
Gallant	x	KWS Kielder	market share		
Einstein	x	KWS Santiago	yield		
Cougar	x	Claire	yield untr		
Cordiale	x	Revelation	heading	brown rust	
Cordiale	x	Crusoe	GS31	market share	
Cordiale	x	Alchemy	height		
Cordiale	x	Invicta	heading		
Conqueror	x	Scout	lodging	eyespot	
Claire	x	Revelation	yield untr		

Simon Orford

- Populations in pink at F5 (-> F5/F6) aiming for <400 lines each
- Populations in yellow at F4 (-> F5/F6) aiming for <400 lines each
- All other crosses at F2

# 7. Applying WGIN data to breeding by design for UK yield stability

Mol Breeding (2015) 35:70  
DOI 10.1007/s11032-015-0268-7

## Using the UK reference population Avalon × Cadenza as a platform to compare breeding strategies in elite Western European bread wheat

Juan Ma · Luzie U. Wingen · Simon Orford · Paul Fenwick · Jiankang Wang · Simon Griffiths

Received: 9 May 2014 / Accepted: 15 September 2014  
© The Author(s) 2015. This article is published with open access at Springerlink.com

**Abstract** Wheat breeders select for qualitative and quantitative traits, the latter often detected as quantitative trait loci (QTL). It is, however, a long procedure from QTL discovery to the successful introduction of favourable alleles into new elite varieties and finally into farmers' crops. As a proof of principle for this process, QTL for grain yield (GY), yield components, plant height (PH), ear emergence (EM), solid stem (SS) and yellow rust resistance (*Yr*) were identified in segregating UK bread wheat reference population, Avalon × Cadenza. Among the 163 detected QTL were several not reported before: 17 for GY, the major GY QTL on 2D; a major SS QTL on 3B; and *Yr6 on 7B*. Common QTL were identified on ten chromosomes,

most interestingly, grain number (GN) was found to be associated with *Rht-D1b*; and GY and GN with a potential new allele of *Rht8*. The interaction of other QTL with GY and yield components was discussed in the context of designing a UK breeding target genotype. Desirable characteristics would be: similar PH and EM to Avalon; *Rht-D1b* and *Vrn-A1b* alleles; high TGW and GN; long and wide grains; a large root system, resistance to diseases; and maximum GY. The potential of the identified QTL maximising transgressive segregation to produce a high-yielding and resilient genotype was demonstrated by simulation. Moreover, simulating breeding strategies with F<sub>2</sub> enrichment revealed that the F<sub>2</sub>-DH procedure was superior to the RIL and the modified SSD procedure to achieve that genotype. The proposed strategies of parent selection and breeding methodology can be used as guidance for marker-assisted wheat breeding.

**Electronic supplementary material** The online version of this article (doi:10.1007/s11032-015-0268-7) contains supplementary material, which is available to authorized users.



# 7. Applying WGIN data to breeding by design for UK yield stability

- ‘Ideal’ ACDH lines to be crossed were selected by analysis of the QTL data
- These would have three high yielding QTL (GY) alleles
- However most ‘ideal’ lines had unfavourable QTL alleles elsewhere
- Therefore made best selection possible...

Cross	Parent 1	Parent 2	
Cross 1	DH109	DH160	DH109 is high yielding parent. DH160 has complementary alleles at all selected loci for achieving target genotype
Cross 2	DH61	DH182	Neither parents carried all favourable GY alleles, but between the parents all favourable alleles were present.
Cross 3	DH27	DH61	Neither parents carried all favourable GY alleles, but between the parents all favourable alleles were present.

Cross	Parent 1	Parent 2	
Cross 1	DH109	DH160	F2 progeny only from 1 plant*
Cross 2	DH61	DH182	F2 progeny from many plants
Cross 3	DH27	DH61	F2 progeny from many plants

- F2 lines need to be genotyped but lack resources to do this.

\* poor F1 seed set and few F2, reason for this?





# WGIN3 Projects: Additional Populations

- 3N alien introgressions (from *Aegilops uniaristata*) into Chinese Spring (three lines Rec4-1, Rec5-1 and Rec 6-3)
- Shows aluminium tolerance
- Al toxicity primarily affects the division and elongation of the root apex
- 3N line shows prolific root phenotype.
- Crossed to winter elite lines – **Cordiale**, Napier and Robigus



- 3N alien introgressions (from *Aegilops uniaristata*) into Chinese Spring (three lines Rec4-1, Rec5-1 and Rec 6-3)
- Shows aluminium tolerance
- Al toxicity primarily affects the division and elongation of the root apex
- 3N line shows prolific root phenotype.
- Crossed to winter elite lines – Cordiale, Napier and Robigus
- Currently only one combination homozygous
- Drilled 1 m plots autumn 2017
- Suggested this line nominated for DFW BTK

# WGIN3 Projects: Exploring New Technology

## A REALLY USEFUL FIELD SCORING APP!

One of **WGIN**'s remits is to explore and disseminate new technology. **KDSmart** is part of the "KDDart" platform from **DART**. However the app can also be used in standalone mode for the collection of field data and is recommended by CIMMYT

<http://www.cimmyt.org/>

**KDSmart** can be downloaded **free** from **Google Playstore** onto an **Android** device. There are several demo trials to practice with (recommended!).

There is very detailed information available on how to use the app and they are responsive to feedback.

<http://www.kddart.org/kdsmart.html>

<http://www.kddart.org/help/kdsmart/index.html>

We used **KDSmart** for scoring the Paragon x Garcia Drought Trial at JIC this year and were very impressed with it's user-friendliness and performance.

We therefore feel confident in recommending it to farmers, breeders and researchers.

Give it a try, it's **free** after all!

Clare Lister and Simon Griffiths

KDSmart

(KDXplore)

# Wgin Diversity Trial Update



2004



2011



2012



2013



2014



2015



2016



2017

**Andrew Riche**  
February 2018



Department  
for Environment  
Food & Rural Affairs



ROTHAMSTED  
RESEARCH

# Introduction

Wheat Variety + Nitrogen  
interaction experiment

2004 - 2018

N applications:                      0kg /ha

50:50:0                                  100kg/ha

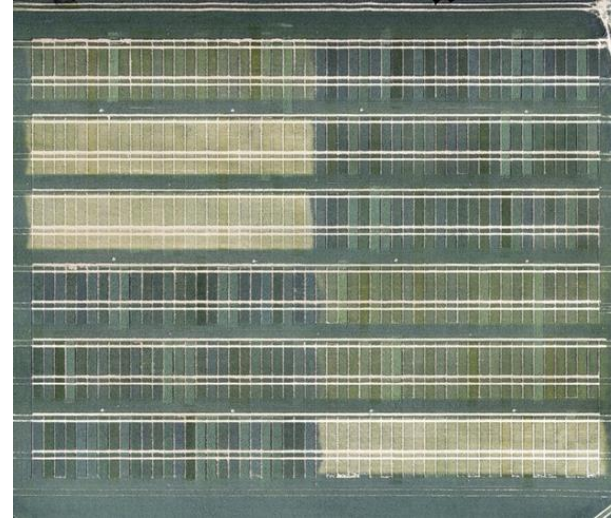
50:100:50                                200kg/ha

50:250:50                                350kg/ha

**2018:**

Added Barrel, Zyat

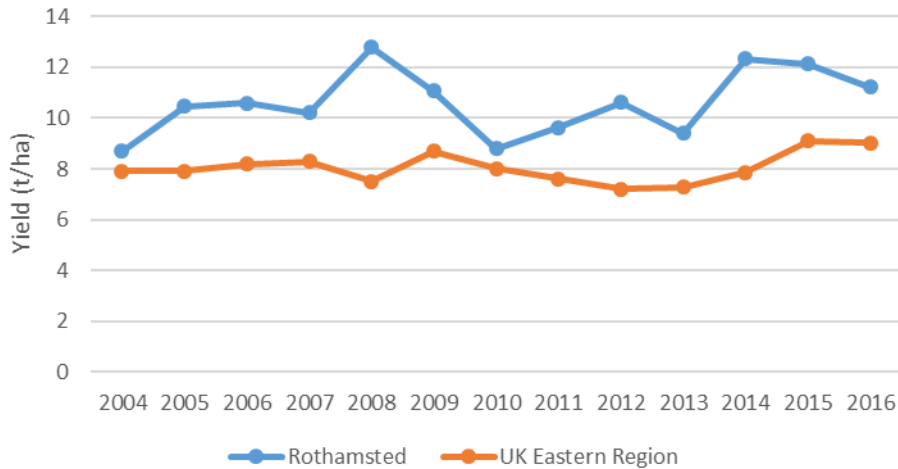
Dropped Cocoon, Gallant



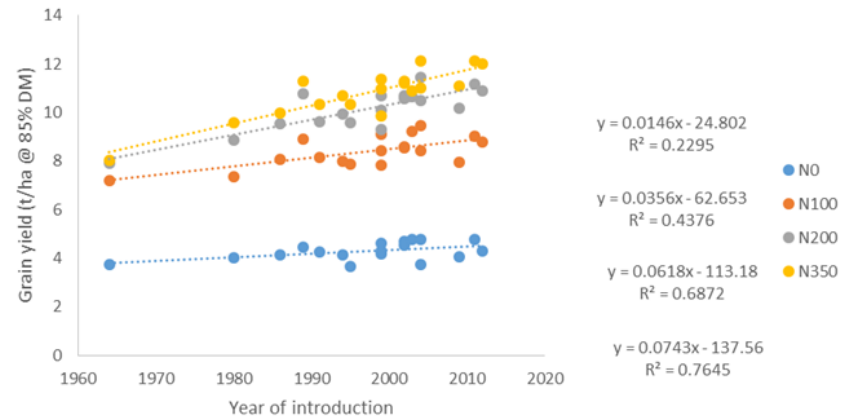
ROTHAMSTED  
RESEARCH

# Diversity Yields

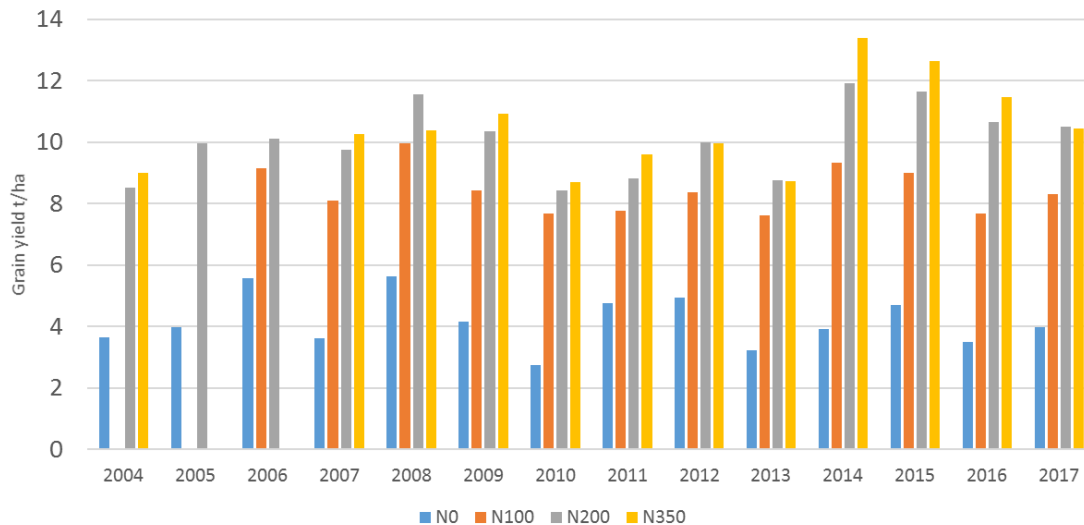
Grain Yield



All N treatments



Diversity Mean grain yields 2004-2017

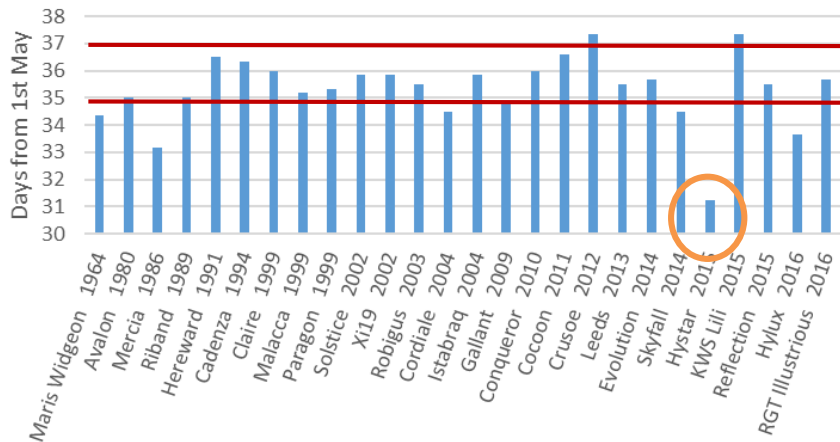


At N200 0.6 t/ha /decade increase



# Phenology (I)

Anthesis (N200)

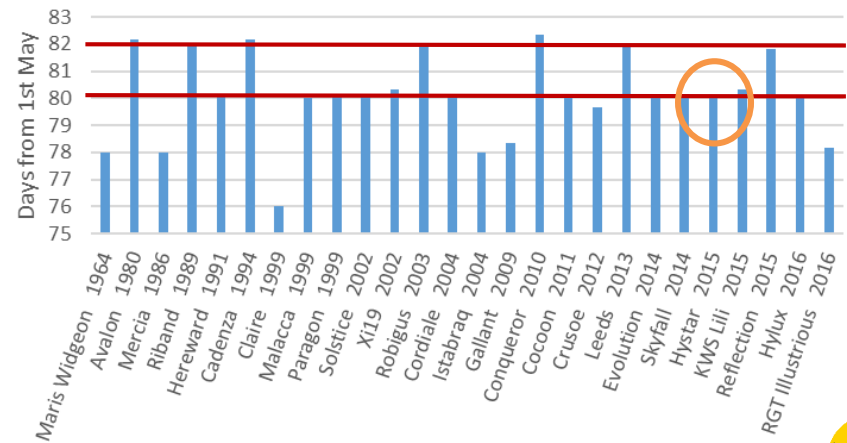


2 years data, 2016 + 2017  
Ordered by year of introduction

Ignoring Hystar, just 4 days difference between earliest and latest, most within 2 days.

Surprised by Hystar!  
Just 6 days difference,  
many within 2 days

Maturity (N200)



# Phenology (II)

	<b>N0</b>	<b>N100</b>	<b>N200</b>	<b>N350</b>
Anthesis (days after May 1 <sup>st</sup> )	36	35	35	35
Maturity (days after May 1 <sup>st</sup> )	82	82	80	82

2 years data, 2016 + 2017

Means of all lines  
- No effect of N

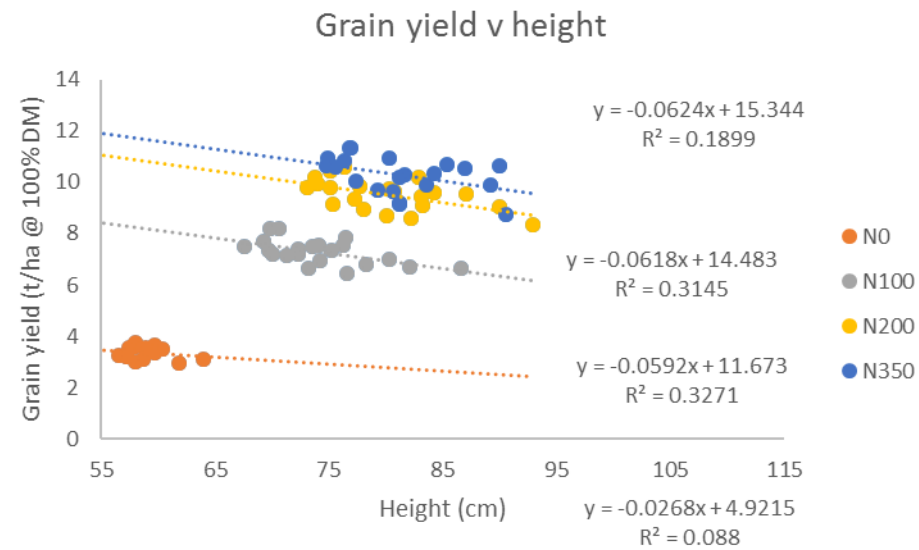
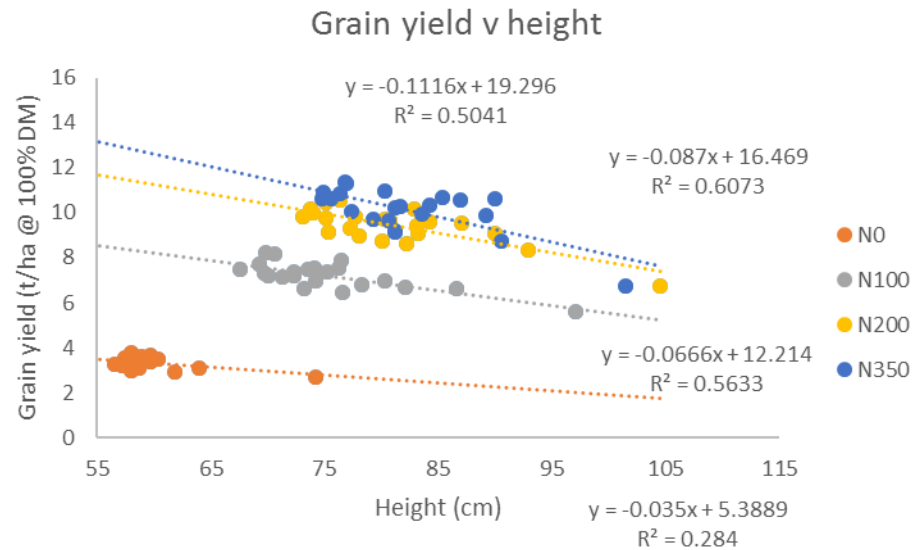


ROTHAMSTED  
RESEARCH



# Height

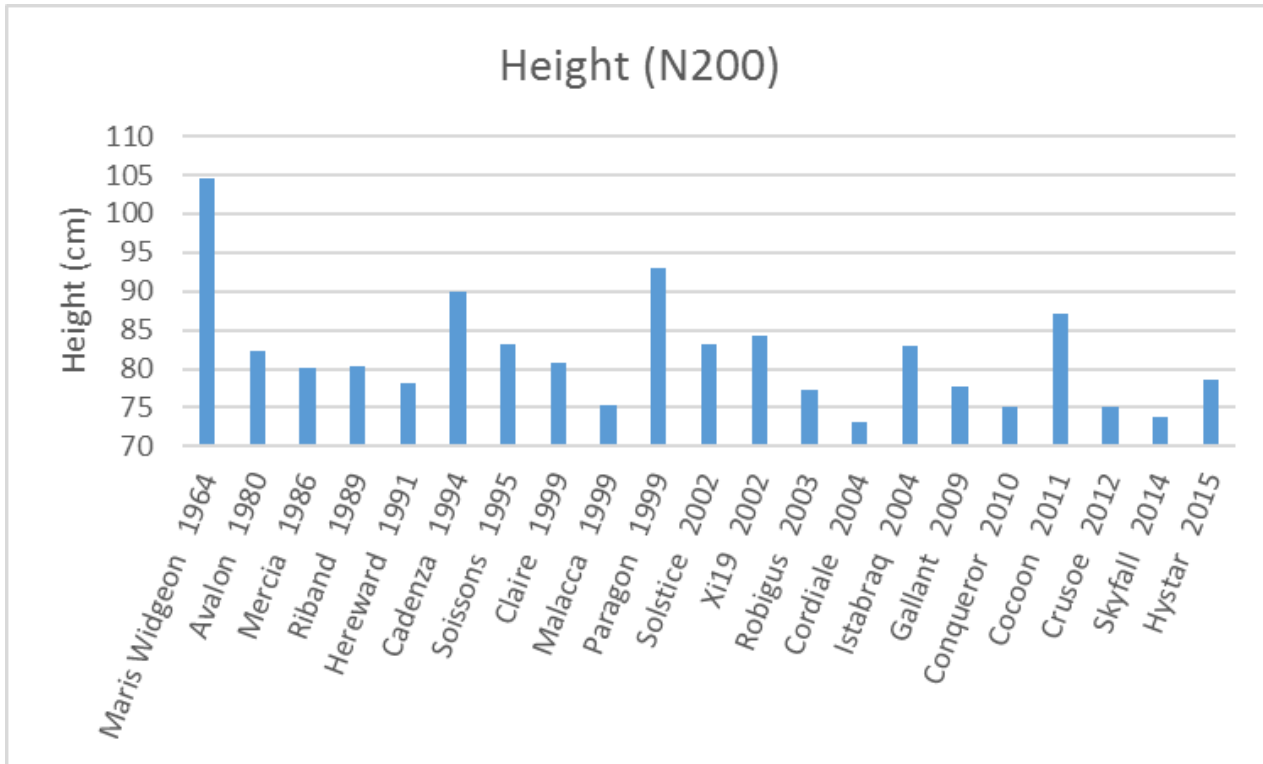
2015-2017



Slight evidence that taller lines yield less  
– biased by Maris Widgeon

Heights do not vary much – 16 within  
10cm





	<b>N0</b>	<b>N100</b>	<b>N200</b>	<b>N350</b>
Mean Height (cm)	58	76	82	82

No increase between N200 & N350

# Components of yield

$$\text{Yield} = \text{TGW} \times \text{Grains/spike} \times \text{spikes/unit area}$$



2014-2017 spikes were counted as part of anthesis sampling,  
2017 TGW data not yet received, so mean of 3 years



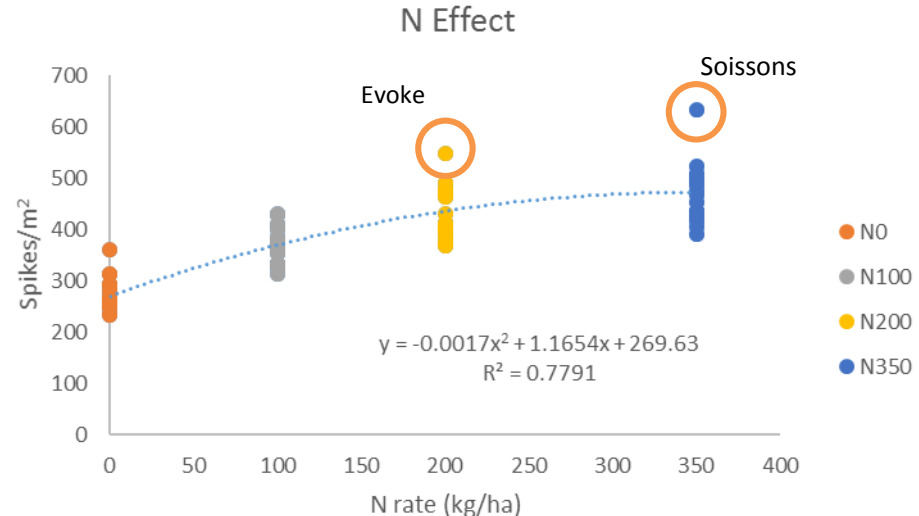
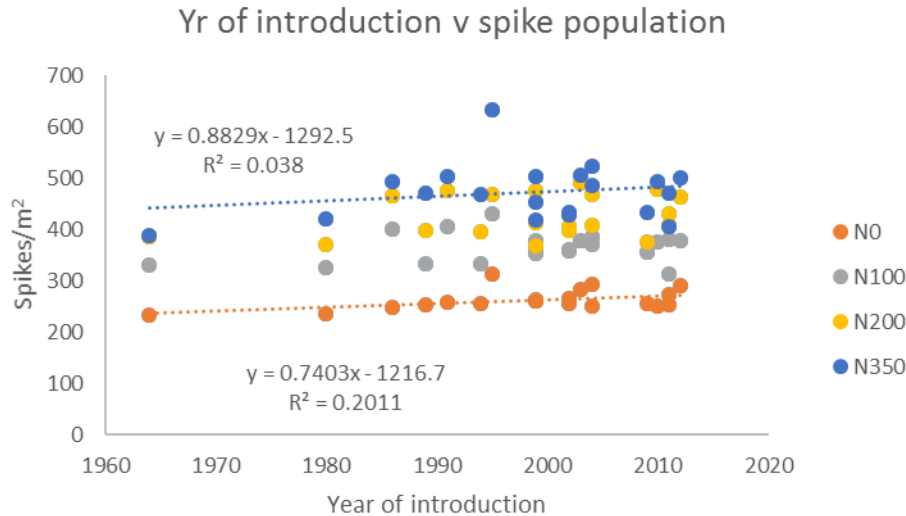
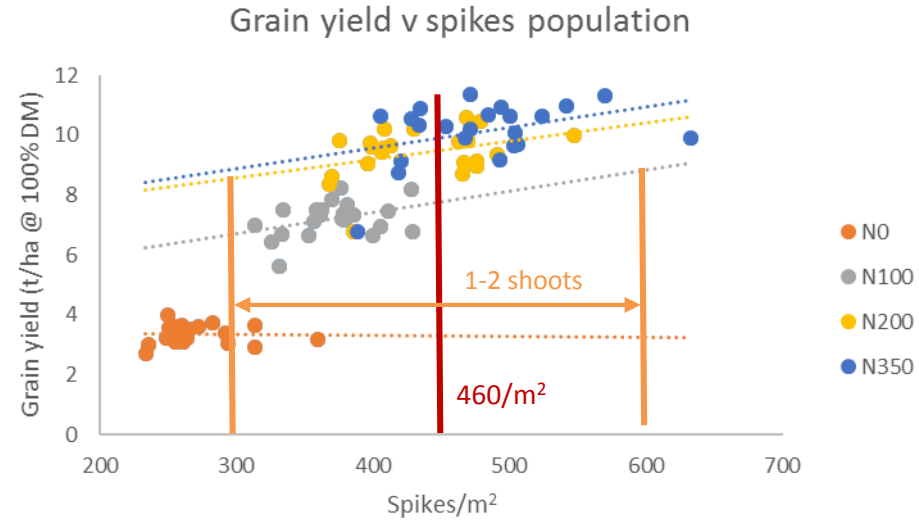
# Components of yield – spikes/unit area

Spikes/unit area = spikes/plant x plants/unit area

Increase in yield with spike population  
Above N0.

N affects spike population/tillering/plant survival

Very small effect of breeding

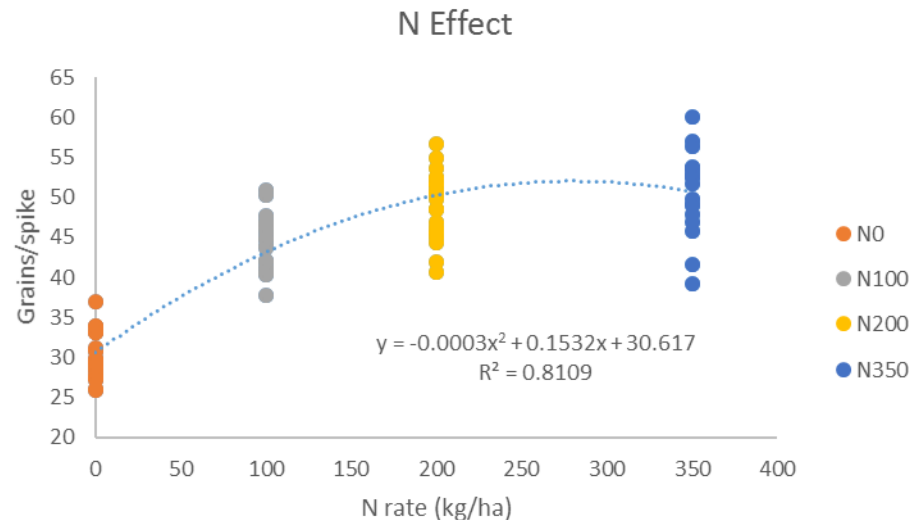
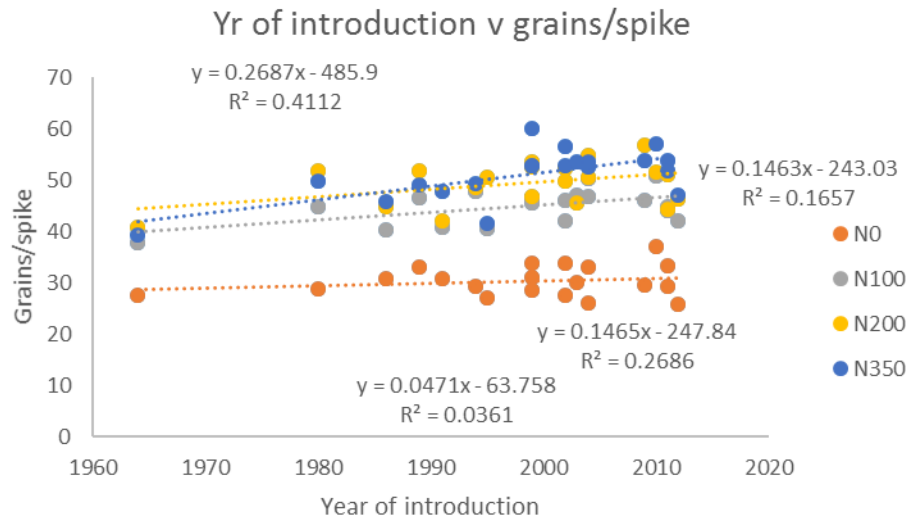
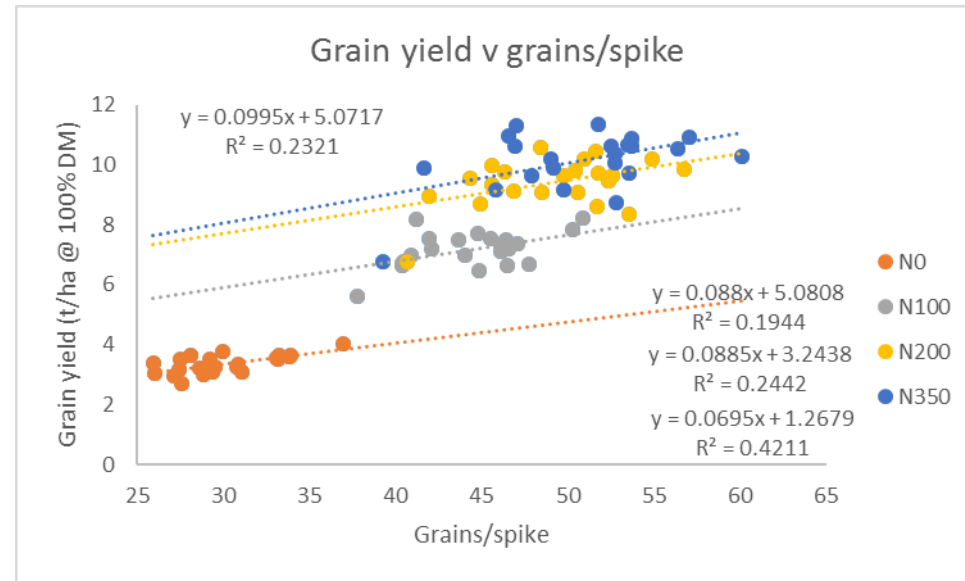


# Components of yield – grains/spike

Yield increases with grains/spike at all N levels

N level affects grains/spike

Grains/spike increasing through breeding – combined with N

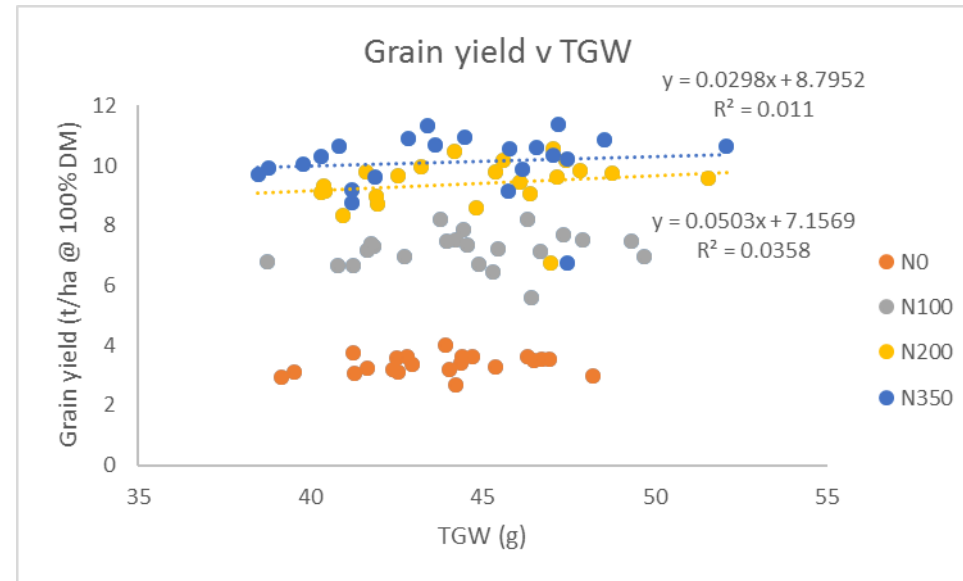


# Components of yield - TGW

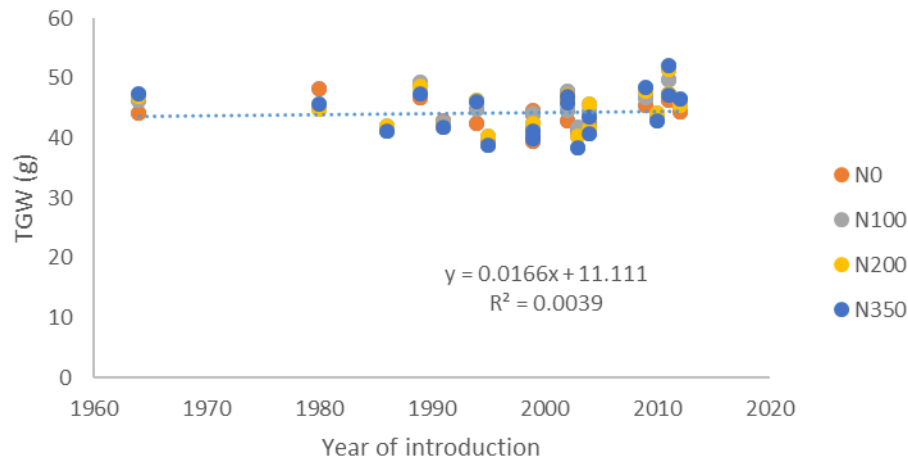
Very slight increase in yield with TGW  
Unlikely to be significant

N has no effect on TGW

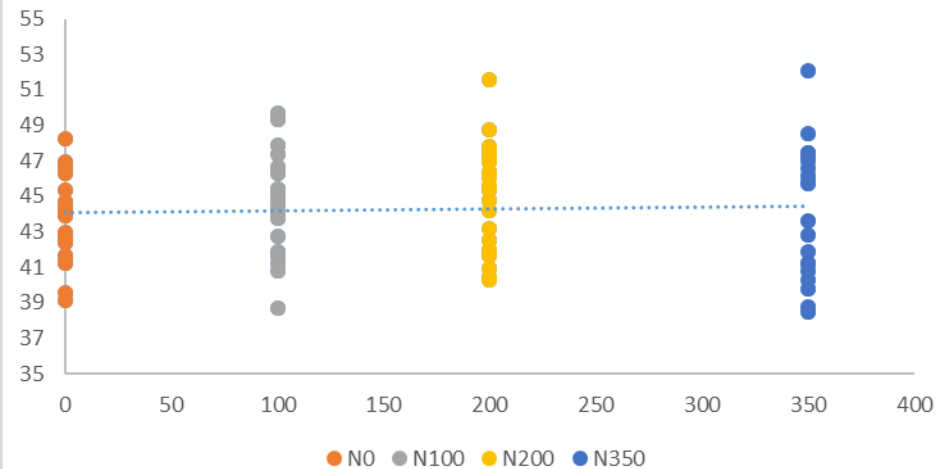
No evidence that breeding has affected TGW



Year of introduction v TGW



N Effect

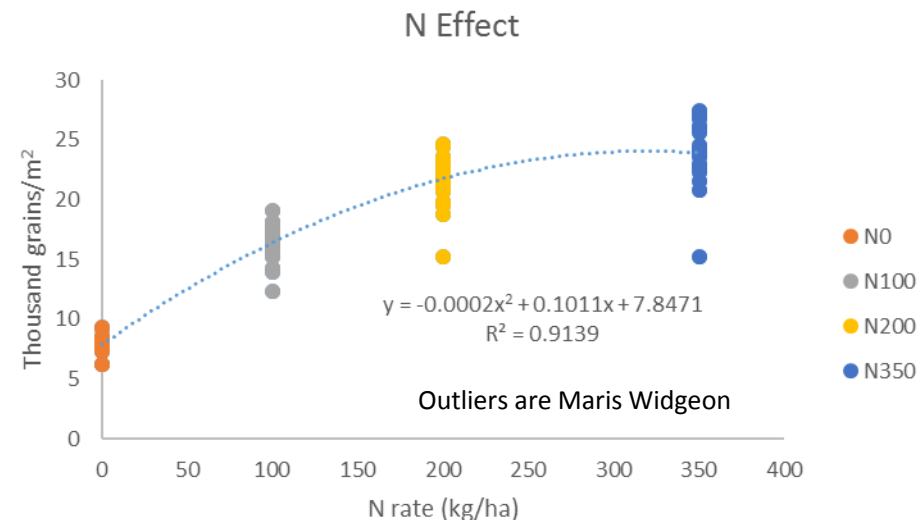
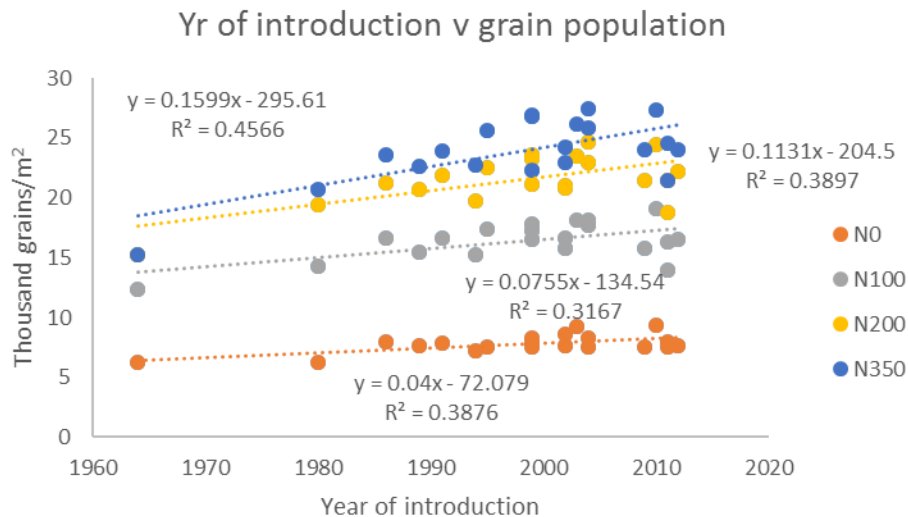
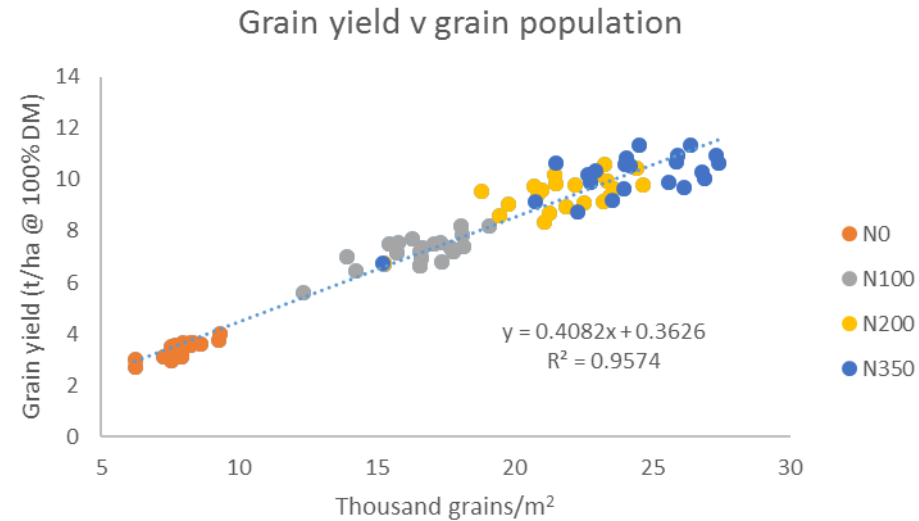


# Components of yield – grains/unit area

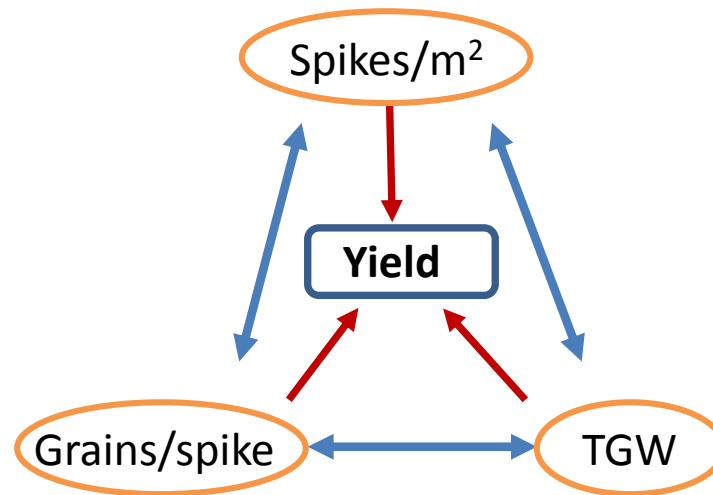
Large increase in yield with grain population

N affects grain population

Very small effect of breeding

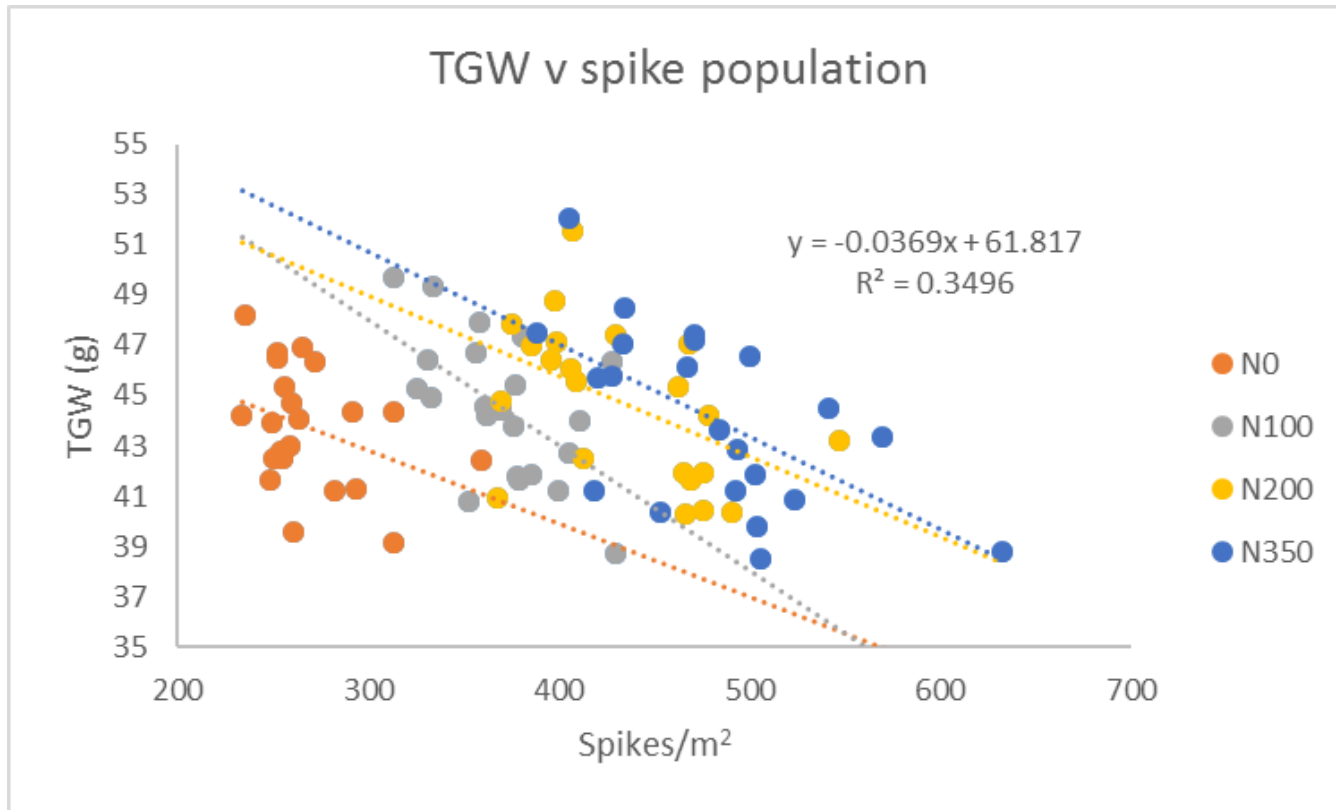


# Wheat yield plasticity





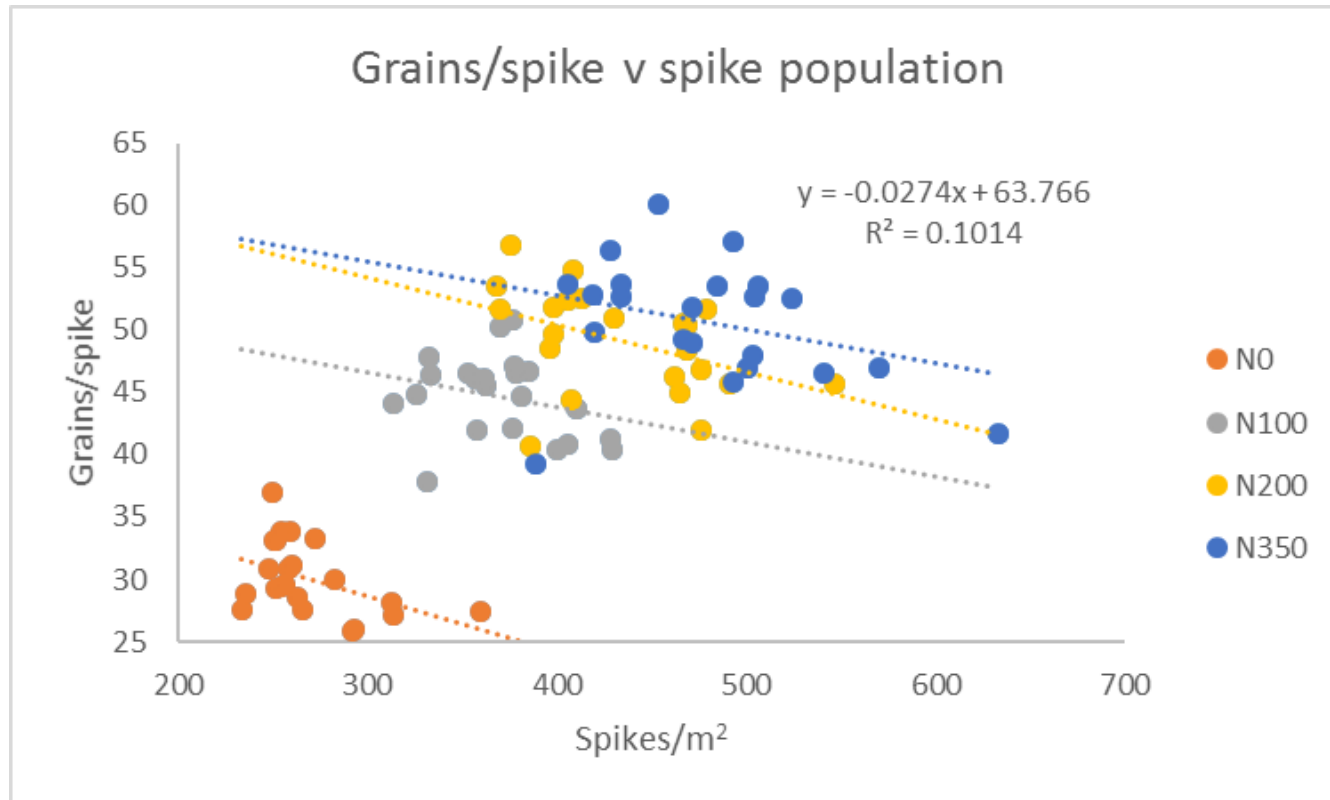
# Wheat yield plasticity



- Increasing spike number tends to decrease TGW



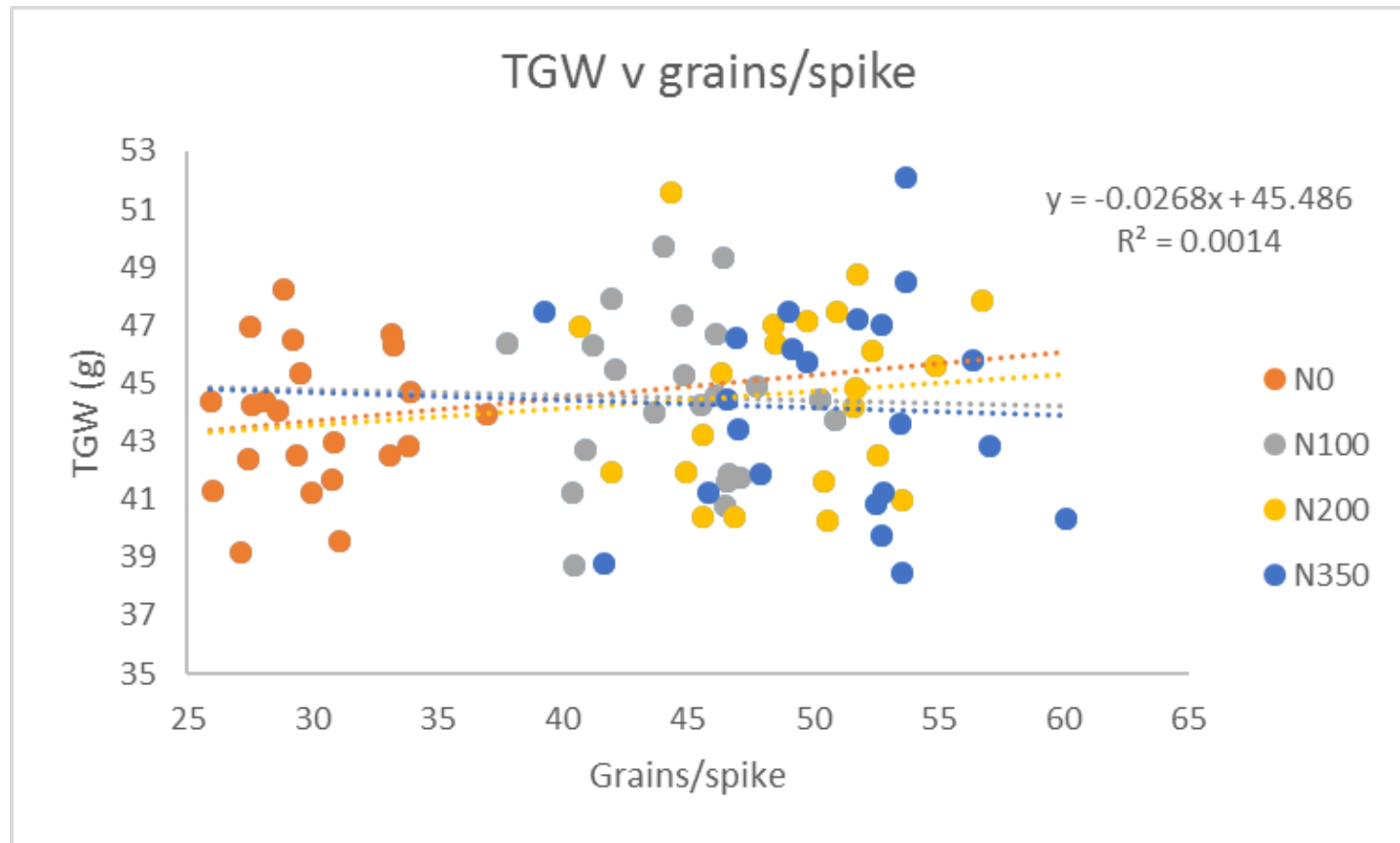
# Wheat yield plasticity



- Increasing spike number tends to decrease grains/spike



# Wheat yield plasticity



- Grains/spike independent of TGW

# Conclusions

1. Little difference between anthesis date and maturity for current varieties.
2. Hybrids tend to be earlier
3. Height: little variation between varieties
4. TGW not affected by breeding or N, may be weakly related to yield
5. Grains/spike related to yield, affected by N and/or breeding
6. Spike population related to yield, affected by N, little effect of breeding
7. Grains/unit area highly correlated with yield – influenced by grains/spike



# Acknowledgments

## **Rothamsted**

Malcolm Hawkesford

March Castle

David Steele

Saroj Parmar

Peter Barraclough



ROTHAMSTED  
RESEARCH



## **Farm Staff**

Stephen Goward

Chris Mackay

Nick Chichester-Miles

Mark Gardener



Department  
for Environment  
Food & Rural Affairs



# Cereal aphids - WGIN update

Gia  
Aradottir



# Introduction



ROTHAMSTED  
RESEARCH



Bird-cherry oat aphid  
(*Rhopalosiphum padi*)



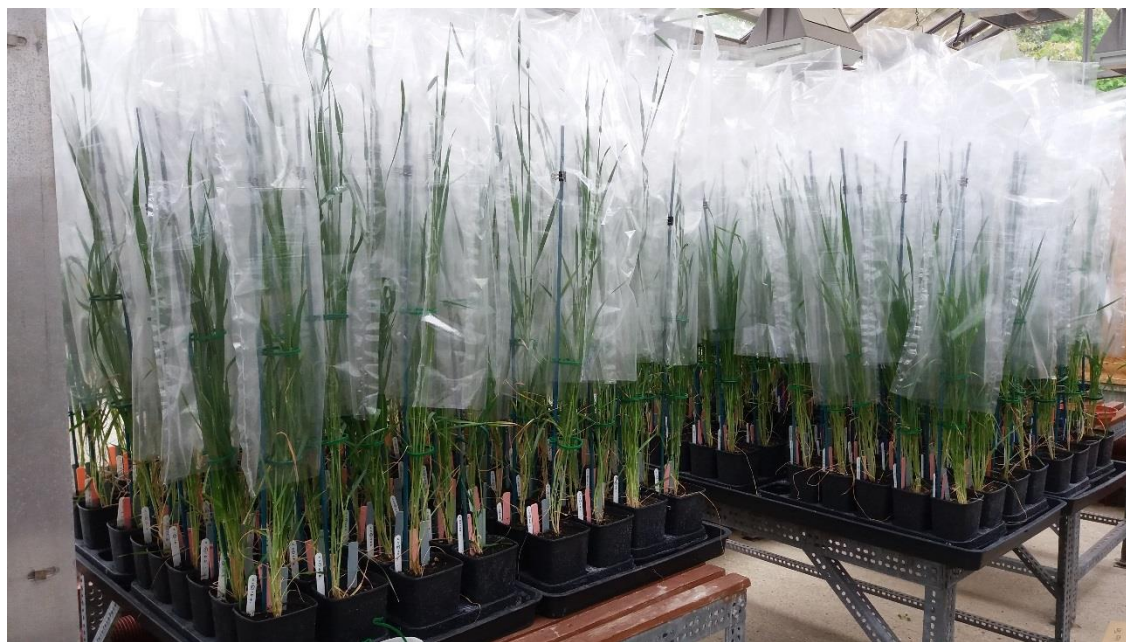
English grain aphid  
(*Sitobion avenae*)



# Mapping populations



ROTHAMSTED  
RESEARCH



## Crosses

MDR037 x MDR045  
MDR037 x MDR049  
MDR037 x MDR657

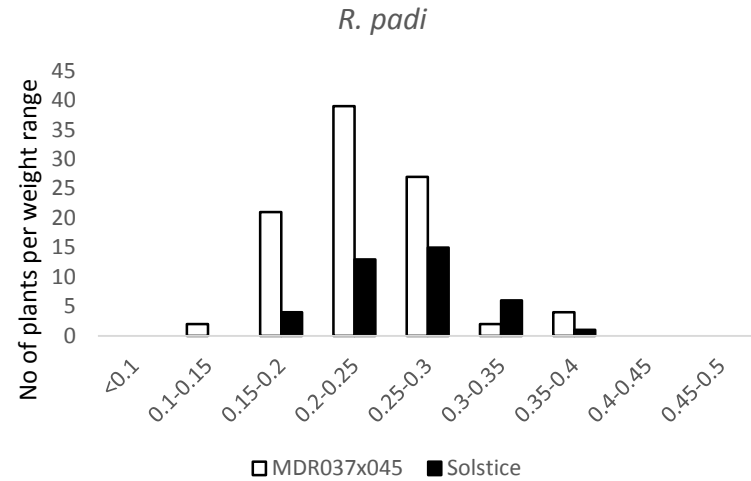
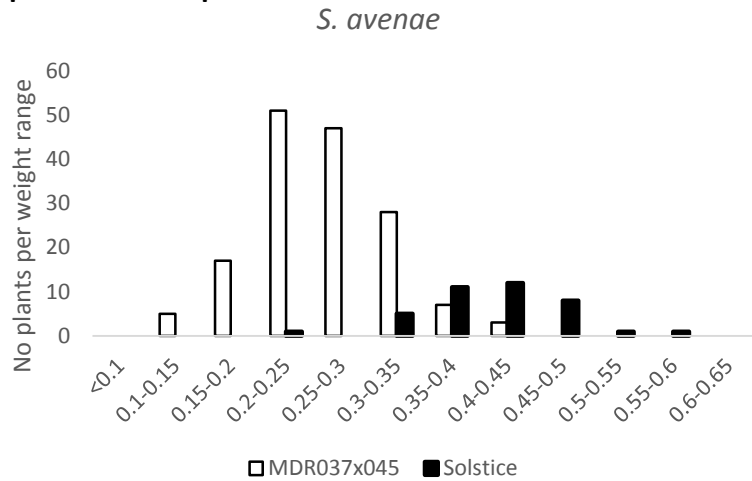
F1, F2 and F3 generations of these crosses have now been tested in the phenotyping screen against both aphid species.



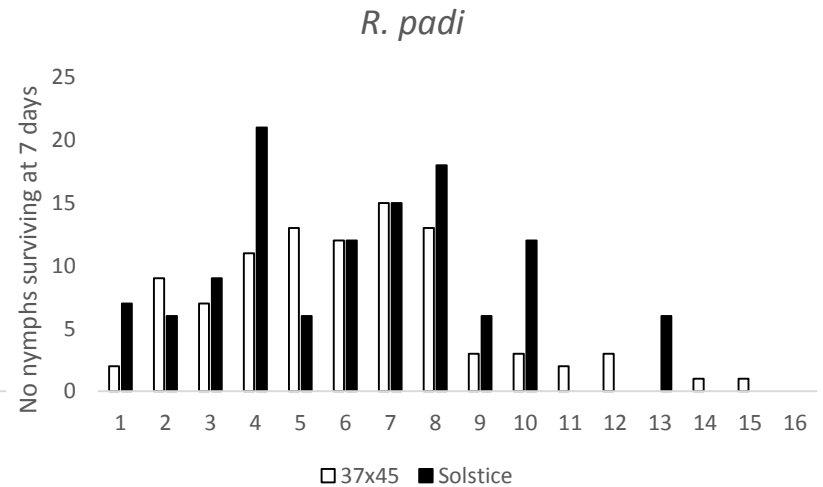
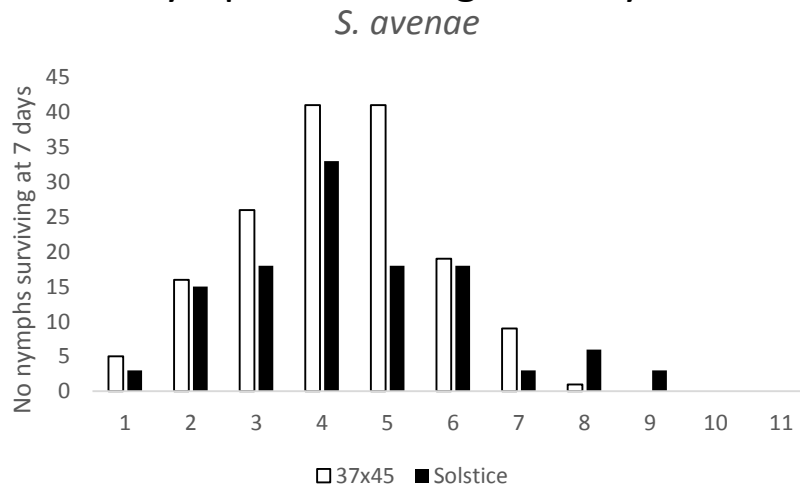


# Cross MDR037 x MDR045 (F3)

## Nymph development

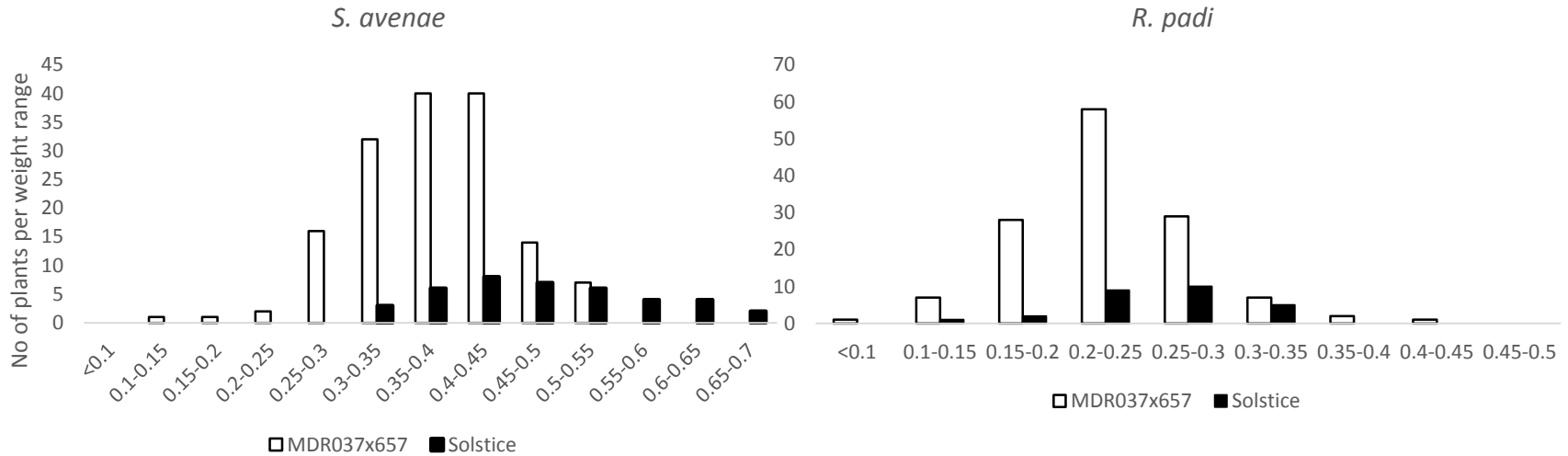


## Number of nymphs surviving at 7 days

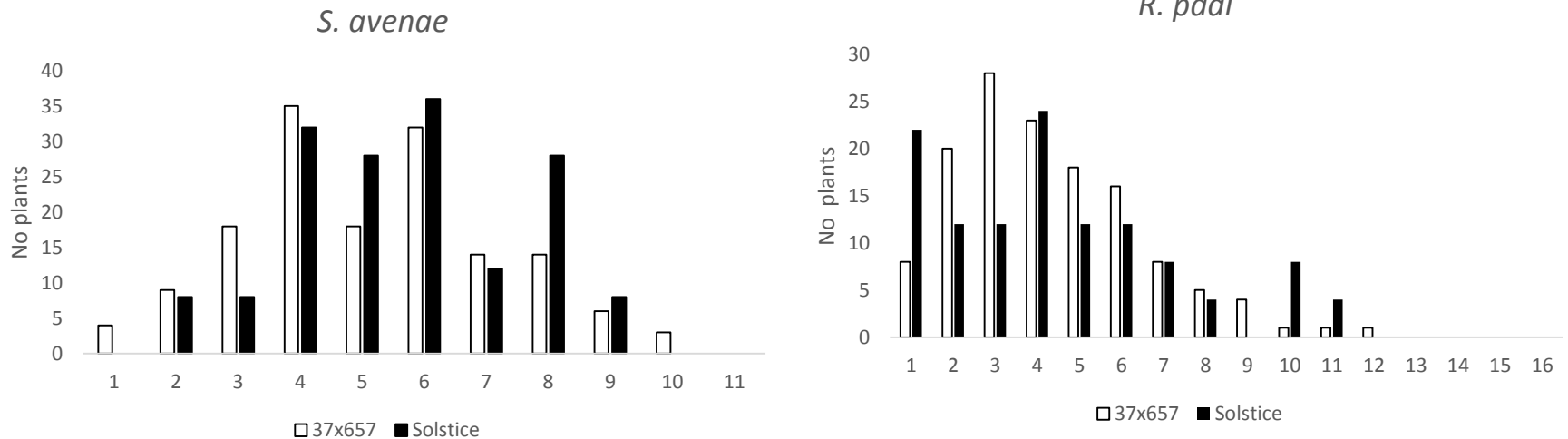


# Cross MDR037 x MDR657 (F3)

## Nymph development



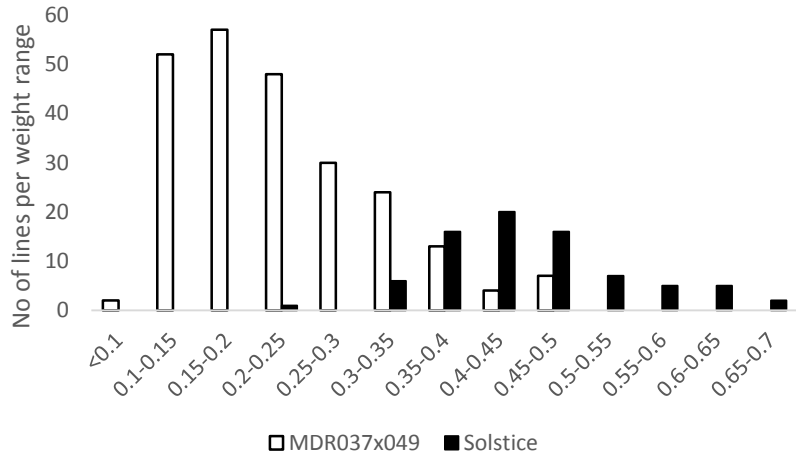
## Number of nymphs surviving at 7 days



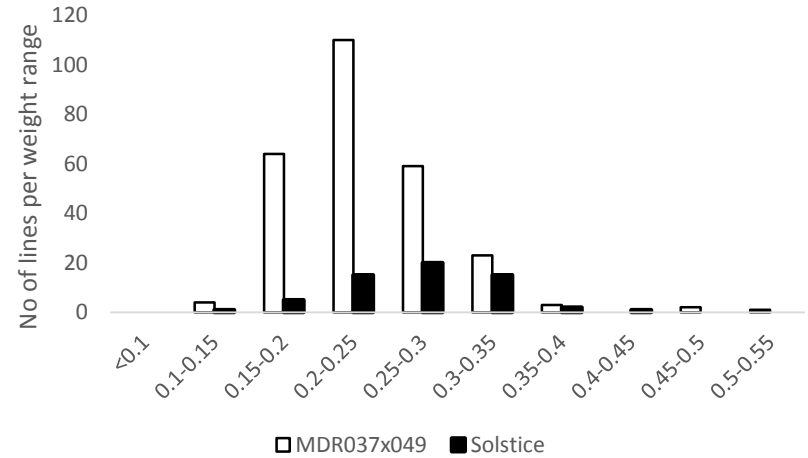
# Cross MDR037 x MDR049 (F3)

## Nymph development

*S. avenae*

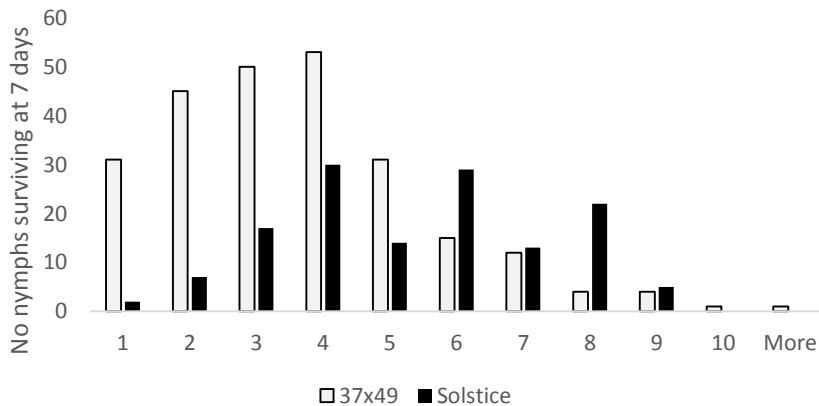


*R. padi*

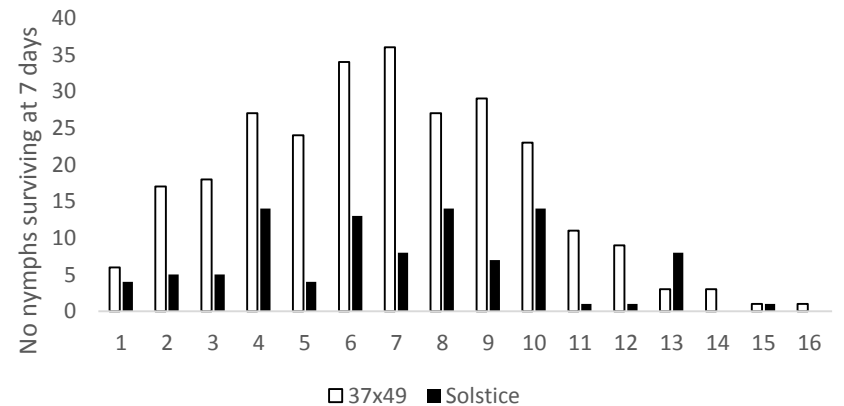


## Number of nymphs surviving at 7 days

*S. avenae*



*R. padi*



# Identification and assessment of aphids and BYDV in wheat



ROTHAMSTED  
RESEARCH

- Development of identification techniques
  - taq-man assay
  - Imaging



# Conclusions



ROTHAMSTED  
RESEARCH

- Some success with mapping populations, especially MDR037x049 cross
- F4 seed being threshed and will be screened (probably under DFW)
- Imaging technique being developed to help future screening of aphid infestation and BYDV



# WGIN 3

## Resistance to foliar diseases

Vanessa McMillan  
Kim Hammond-Kosack



Department  
for Environment  
Food & Rural Affairs

# Watkins foliar disease field trials



ROTHAMSTED  
RESEARCH

1<sup>st</sup> and 3<sup>rd</sup> wheat replicated field trials

Three field seasons

2014-2015

2015-2016

2016-2017



26<sup>th</sup> June 2015

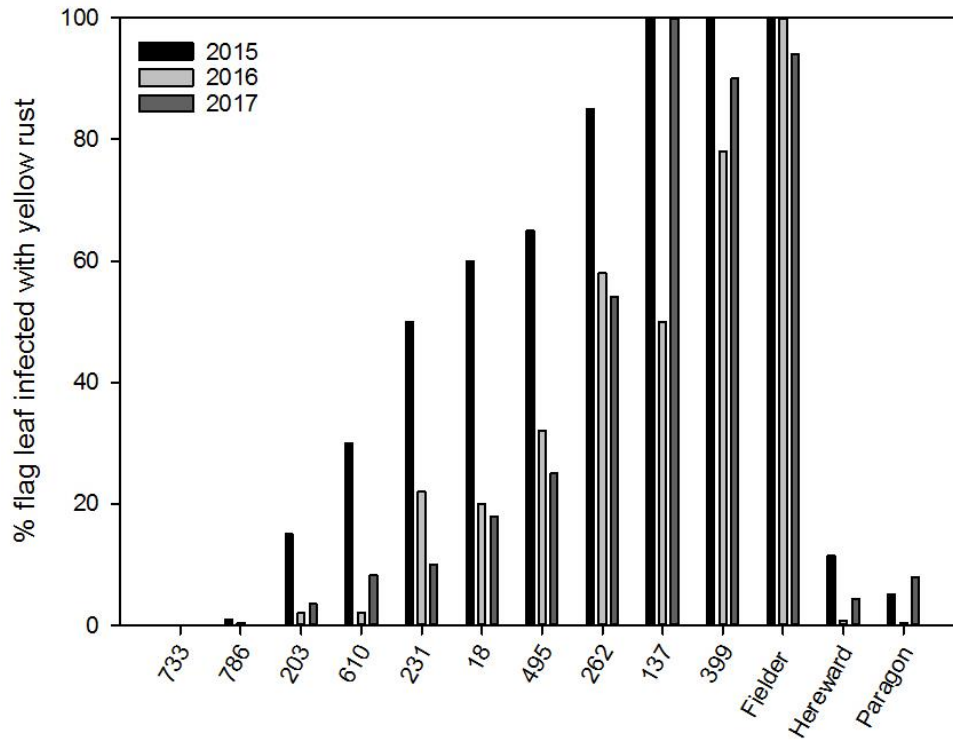
1<sup>st</sup> wheat Long Hoos 4



# Evidence of resistance to yellow rust



ROTHAMSTED  
RESEARCH



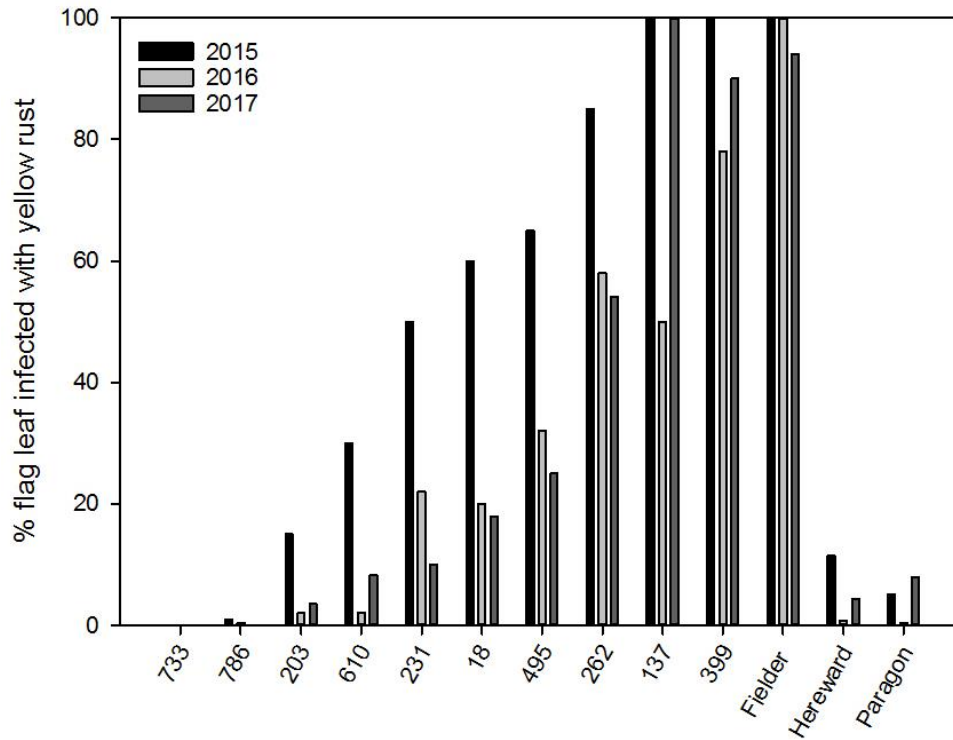
- Hereward and Paragon are good sources of resistance to current YR races
- Watkins 203 and 610 most promising for multi-disease resistance (YR, BR, S and PM)
- Watkins 733 and 786 do not possess multi disease resistance – very susceptible to BR
- Watkins parents currently being screened for some known rust resistance genes by RAGT



# Evidence of resistance to yellow rust



ROTHAMSTED  
RESEARCH



## YR races

Year	Variety
2000	Robigus
2008	Solstice
2011	Sterling
2011	Warrior 1
2012	Warrior 4
2014	Kranich
2015	Invicta

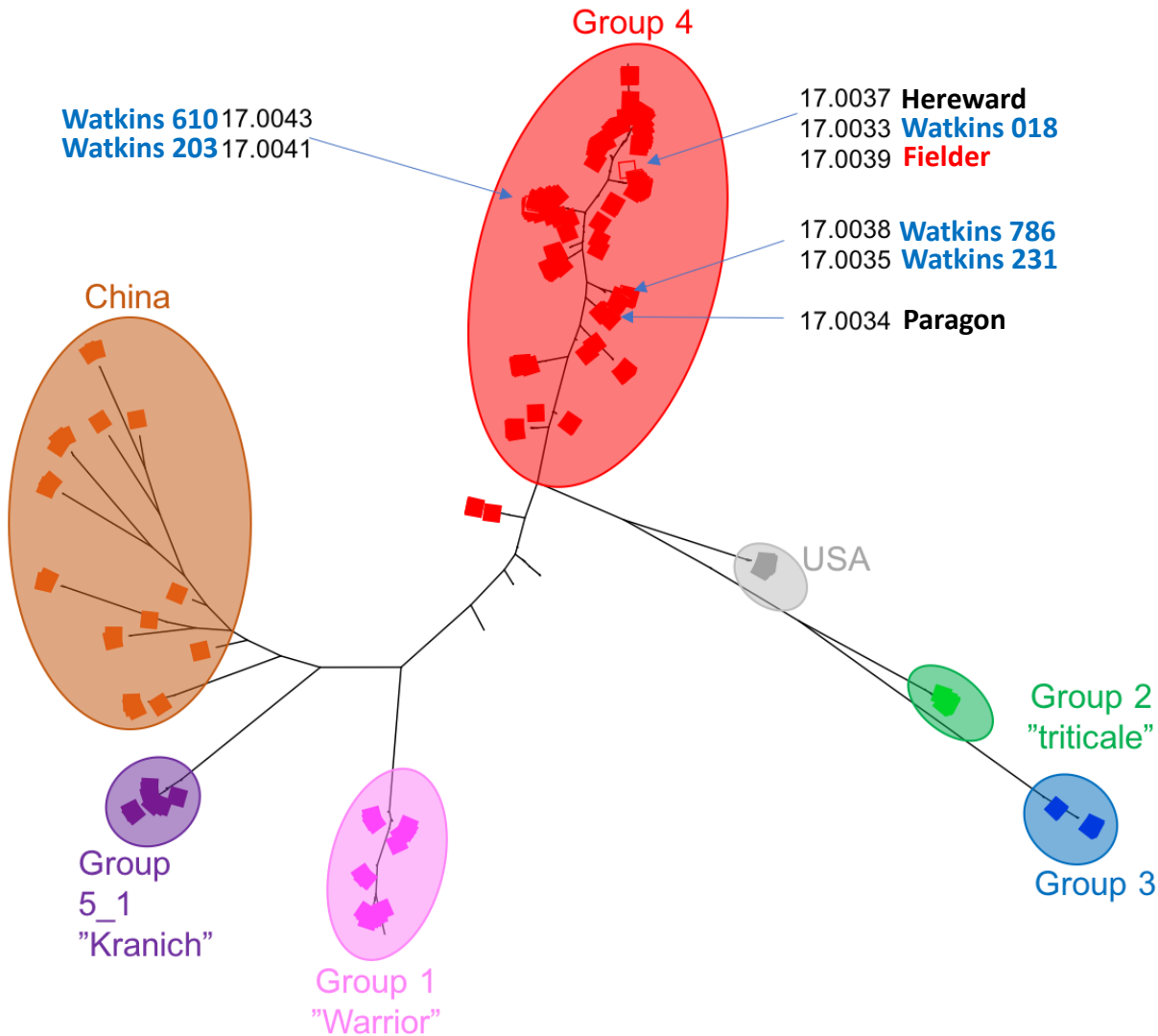
Warrior-type races dominant across UK in 2015, 2016 and 2017

2017 field trial – samples submitted to "Field Pathogenomics" pathogen surveillance programme

# All samples from 2017 field trial belong to Group 4



ROTHAMSTED  
RESEARCH

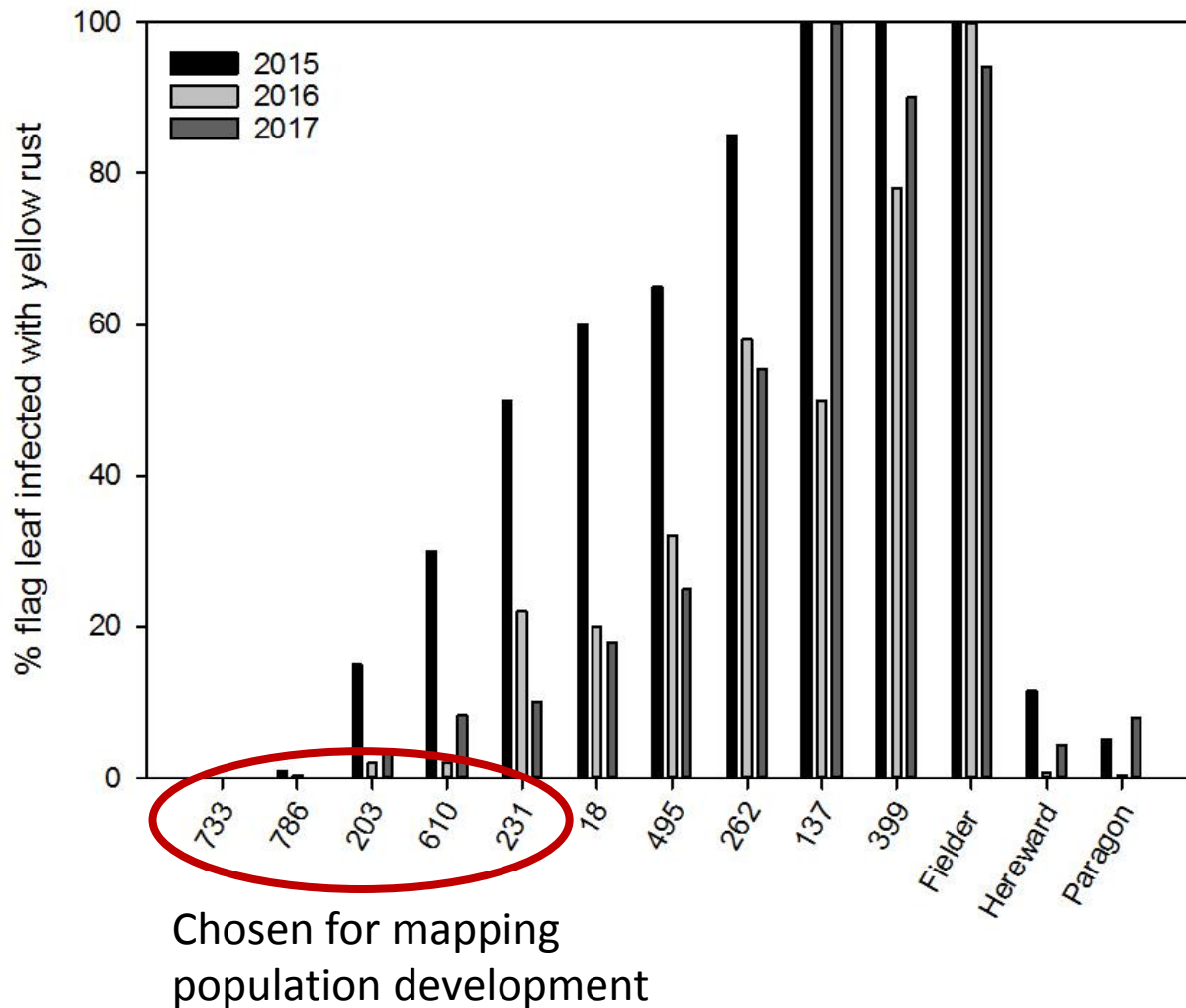


Group 4 is the dominant genetic group of YR in the UK

# Watkins mapping population development



ROTHAMSTED  
RESEARCH



Chosen for mapping  
population development

# Watkins mapping population development



ROTHAMSTED  
RESEARCH

Accession Number	Growth habit	Country of Origin	Ears crossed	F <sub>1</sub> grains	Crossing
203	Winter	India	8	31	Field 2015
231	Spring	Hungary	8	54	Field 2015
610	Spring	Yugoslavia	6	33	Field 2015
733	Spring	Iran	6	49	Field 2015
★ 786	Spring	USSR	10	108	Glasshouse 2016

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

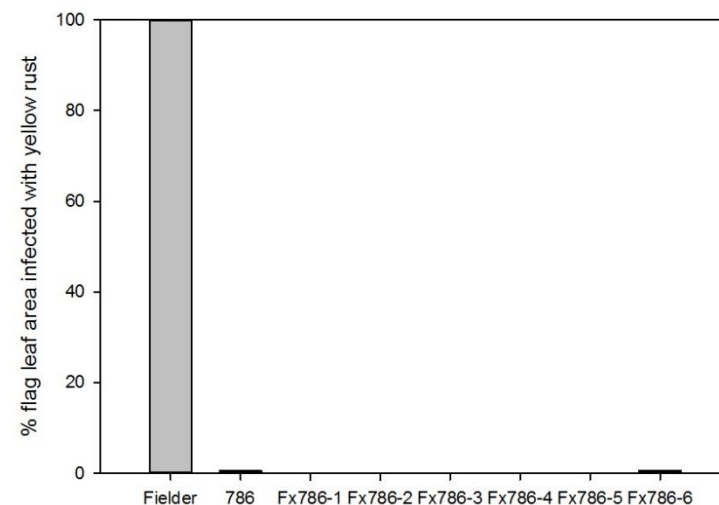
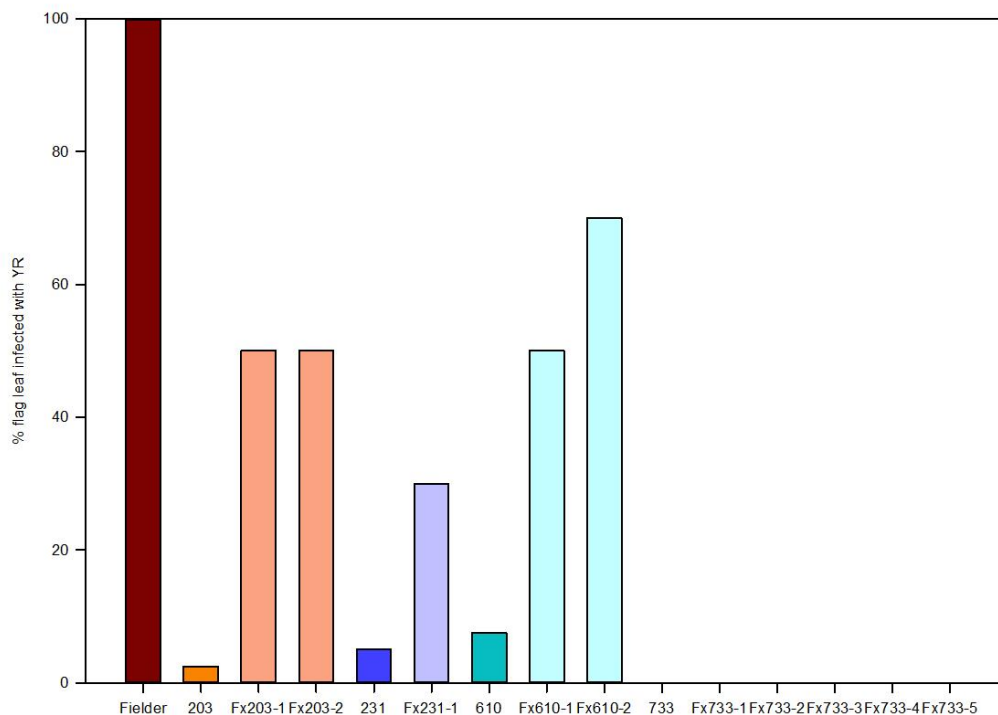
Watkins genotypes to be phenotyped for seedling resistance at NIAB in March 2018  
(Blue 7, Red 24 and Kranich race to be tested)

# Genetics of resistance – F<sub>1</sub> generation



ROTHAMSTED  
RESEARCH

- F<sub>1</sub> grain included in field trial in 2015/16 (W203, W231, W610, W733) or 2016/17 (W786) to study inheritance



- Dominantly inherited resistance for W733 and W786
- Intermediate resistance phenotypes for F<sub>1</sub> of W203, W231 and W610

# Genetics of resistance – F<sub>2</sub> generation

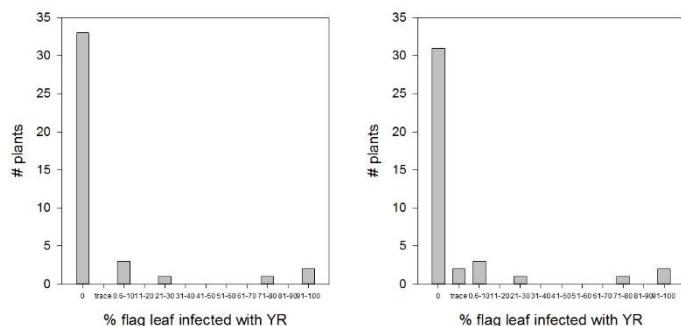
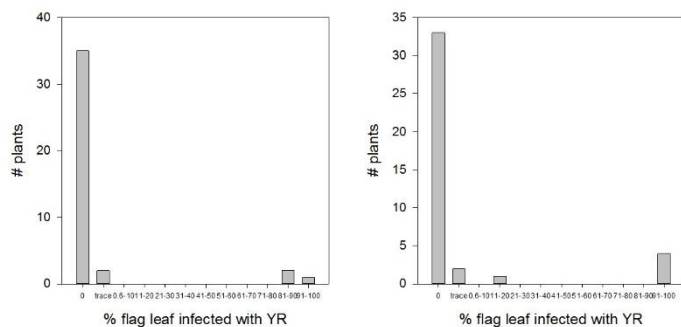


ROTHAMSTED  
RESEARCH

- F<sub>2</sub> grain included in 2016/17 field trial (W203, W231, W610, W733)

Complete resistance : Fully Susceptible  
No sporulation : > 90% YR

Fielder x W733



132 R : 9 S  
14.7 R : 1 S

Two unlinked dominant loci

But some intermediate phenotypes:  
Neighbouring plants with lots of inoculum  
Other minor effect loci affecting overall plant physiology

Should give 3 R : 1 S ratio in backcross

# Genetics of resistance – F<sub>2</sub> generation



ROTHAMSTED  
RESEARCH

- F<sub>2</sub> grain included in 2016/17 field trial (W203, W231, W610, W733)
- Fielder x W203, Fielder x 231 and Fielder x 610 (with intermediate F<sub>1</sub> phenotypes) all gave more complex segregation ratios

## Fielder x W203

24 R : 37 I : 19 S

1.2 : 1.9 : 1

Large number of intermediates

**Should give 1 I : 1 S ratio in backcross**

## Fielder x W231

16 R : 29 I : 35 S

1 : 2 : 2

Weakest parental resistance

Skewed towards fully susceptible phenotype

Suppressor locus from Fielder?

## Fielder x W610

30 R : 14 I : 32 S

2 : 1 : 2

Lack of intermediate phenotypes

Interaction effect with other loci?

610 physiological later maturing variety

# Genetics of resistance – BC<sub>1</sub> and F<sub>2</sub> generations



ROTHAMSTED  
RESEARCH

## BC<sub>1</sub> populations

backcross	harvested
203	145
231	169
610	171
733	175

- Include F<sub>1</sub> plants and parental genotypes to benchmark the phenotype of known hets – confirm if we see variation in hets due to potential suppressor alleles

## F<sub>2</sub> FxW786 populations

Fx786 F <sub>1</sub> Plant	F <sub>2</sub> harvested seed
1	579
2	610
3	605
4	251
5	No seed
6	335

- Field trial drilled 16<sup>th</sup> October 2017 in Long Hoos 6/7



# Resistance to Septoria– 2017/18 Field Trial



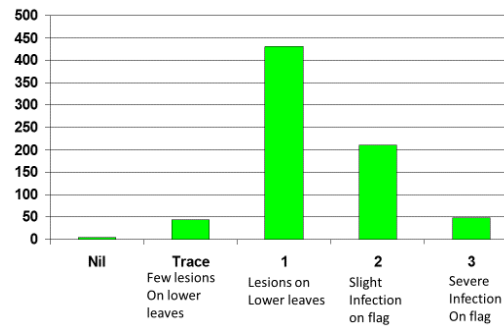
ROTHAMSTED  
RESEARCH

Replicated field trials with Watkins landraces (51 genotypes with nil or trace disease in 2008), CIMMYT material from international septoria nursery programme (50 genotypes), hexaploid wheats with known Stb resistance genes and controls (31 genotypes)

Av Treatment Av



Watkins 2008 Field Trial  
Septoria Infection score



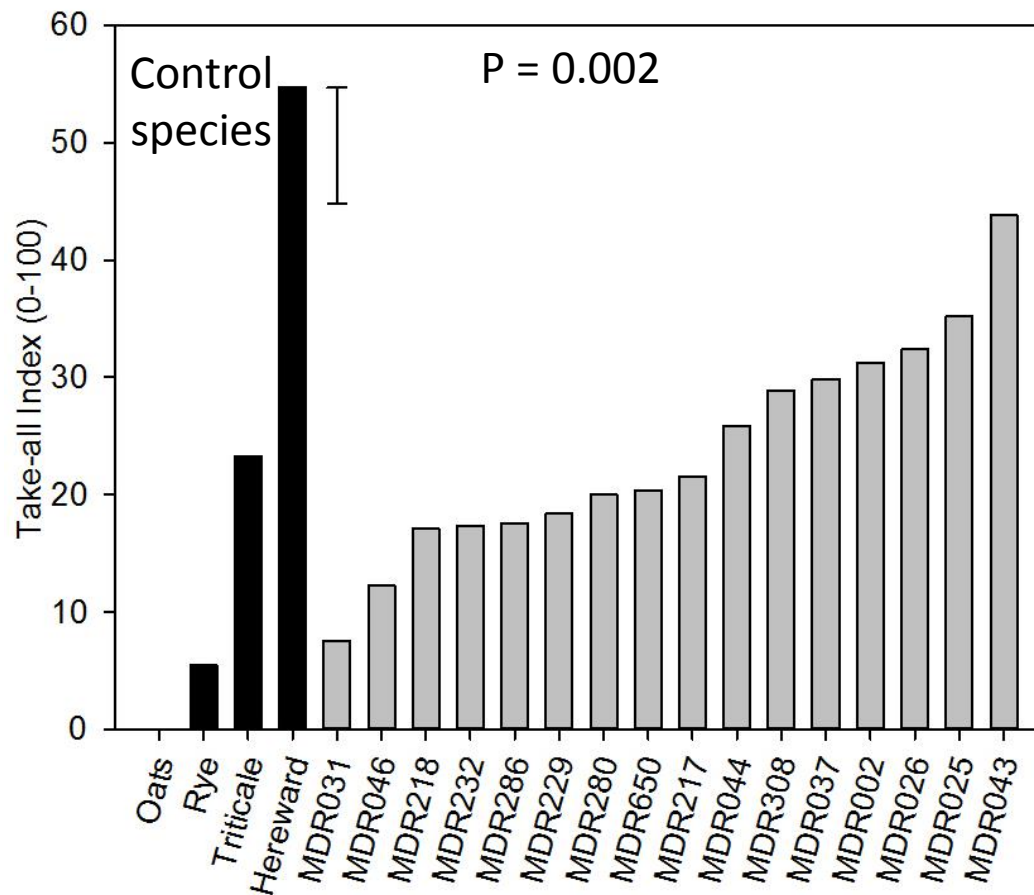
- 2 replicates of each genotype, spreader rows of Avalon
- Fungicide regime to control rusts and irrigation in spring if required
- Above ground plant phenotypes to be recorded – plant height, flowering, leaf senescence
- Visual disease assessments to be carried out at several dates during growing season
- Leaf samples also to be taken for analysis using ImageJ software  
% necrotic leaf area, pycnidia size and density

# Resistance to take-all disease in *Triticum monococcum*



ROTHAMSTED  
RESEARCH

- 3<sup>rd</sup> wheat field trials 2006-2011 (WGIN 1 and 2)
- **34 *T. monococcum* accessions (AA diploid genome)** tested over 5 years



## F<sub>2</sub> Tm cross progeny numbers:

Parentage		Estimated F <sub>3</sub> progeny number
<b>MDR031 (R) x MDR043 (vS)</b>	31 ears from 3 plants	450 ←
MDR031 x MDR229	16 ears from 1 plant	320
MDR031 x MDR650	48 ears from 3 plants	900
MDR043 (vS) x MDR031 (R)	48 ears from 3 plants	960
<b>MDR043 (vS) x MDR046 (R)</b>	36 ears from 3 plants	750 ←
MDR229 x MDR031	94 ears from 6 plants	2000

Populations advanced by SSD from F<sub>4</sub> to F<sub>6</sub> for field phenotyping ←

# *Triticum monococcum*

## MDR031(R) x MDR043 (S) mapping population



ROTHAMSTED  
RESEARCH

- 516 F<sub>2</sub> seeds → 380 F<sub>6</sub> lines (0.5-33.5g of each available at F<sub>6</sub>)
- **129 lines** > 18 g seed selected for field trial + parents + Hereward control plots
- Plot size 4 rows x 0.6 m length, 80 seeds per plot, 3-5 reps per genotype
- **3<sup>rd</sup> wheat field trial** drilled in Claycroft on 6<sup>th</sup> Oct 2016
- Plant samples (3 x 20cm row lengths) taken July 2017 and currently being assessed



- Repeat trial drilled in Long Hoos 3 on 3<sup>rd</sup> October 2017

# Many thanks to



ROTHAMSTED  
RESEARCH

Kim Hammond-Kosack

## Undergraduate summer students

Erin Baggs

Eleanor Leane

Tessa Reid

Laurie Neal

Alex Chambers-Ostler

Leanne Freeman

Jamie Hawkesford

Ellen Farnham

Gail Canning - seed preparation

Mike Hammond-Kosack - crossing

Rodger White - statistics

RRes farm and glasshouse staff



# WGIN 3

## The WGIN Promotome Capture Experiment Update

WGIN MM 1<sup>st</sup> February 2018

Michael Hammond-Kosack

- Please note:

ALL Promotome slides removed because of  
the IWGSC pre-publication agreement

# **WGIN 3 Breeders Priority Traits Questionnaire (August – November 2017) (KHK)**

- Based around the 10 traits used for the promotome capture experiment plus additional traits identified by the WGIN team  
**107 sub-traits**
- Nine breeding companies contacted individually
- Outcome: high level of consistency between companies  
but also notable differences
- Summary of the top results (max score 30) on next page



# WGIN 3 Breeders Priority Traits Questionnaire (August – November 2017)

Resilience	Sustainability	Quality	Resource efficiency
<b>29* Septoria leaf blotch</b>	24* Lodging	<b>25* Specific weight</b>	23* Nitrogen
<b>29 BYDV</b>	24 Deep rooting	23 Grain protein deviation	
<b>28 Loss of chemistry</b>	24 Early root establishment	22 Pre harvest sprouting	
<b>25 Yellow Rust</b>	24 Floret fertility	22 Grain size	
24 Floral health - ergot	23 Yield stability	22 Grain filling rate	
24 Floral health - fusarium	23 Season independent yield QTLs	22 Grain filling duration	
23 Aphids	22 Context independent yield QTLs		
22 Bulb Fly	22 Sterility		
	22 Staygreen - canopy senescence		
	22 Stem Height		
	22 Spikelet fertility		
<b>* max value 30</b>	22 Ear size		