

February 2016

- **A Joint Stakeholder Meeting involving WGIN, OREGIN, VEGIN and PGIN will be held on February 22<sup>nd</sup> 2016 @ John Innes Centre, Norwich**
- **High Density Genotyping of 18 WGIN AxC Near Isogenic Lines – maps available on WGIN website NOW!**

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**Defra Wheat Genetic Improvement Network (WGIN): Improving the resilience of UK wheat yield and quality through crop genetics and targeted traits analysis**

**Section 1 Project Background**

The UK government is committed to more sustainable agriculture but this vision is facing an ever expanding range of environmental, energy and climate change challenges. Wheat is grown on a larger area and is more valuable than any other arable crop in the UK. The **Wheat Genetic Improvement Network (WGIN)** started in 2003. The overall aim of WGIN is to generate pre-breeding material carrying novel traits for the UK breeding companies and to deliver accessible technologies, thereby ensuring the means are available to produce new, improved varieties.

To achieve WGIN's goals, an integrated scientific 'core' has been established which combines underpinning work on molecular markers, genetic and genomic research, together with novel trait identification. The programme is managed by a team including representatives of the key UK research groups and breeders. They ensure the programme and its outputs are communicated to the wider scientific and end user communities, via a web site ([www.wgin.org.uk](http://www.wgin.org.uk)), a stakeholder forum, focussed

meetings and peer reviewed publications. WGIN liaises with equivalent operations overseas to ensure the programme is internationally competitive.

**This project**

**WGIN is now in its third phase** and will be funded by DEFRA until March 2017. The new WGIN project is entitled '**Improving the resilience of UK wheat yield and quality through crop genetics and targeted traits analysis**'. This project consists of four work packages (WPs) (**Figure 1**). WP1 focusses on further enhancing the networking and communication activities. The three interconnected research work packages (WP2, WP3 and WP4) focus on exploring a range of high priority traits for the UK wheat crop and then undertaking detailed genetic and quantitative trait loci (QTL) analyses (WP2 and WP4), maintaining and developing new genetic resources for the UK research community (WP3), and testing new tools based on next generation sequencing technologies for their applicability to wheat research (WP4).

WGIN provides genetic and molecular resources for research in other Defra projects and for a wide range of wheat research projects in the UK. The resources under development include wheat genetic stocks, mapping populations, molecular markers and marker technologies, trait identification and evaluation, genomics and bioinformatics.

The funded partners in Phase 3 of WGIN are the **John Innes Centre (JIC)**, **Rothamsted Research (RRes)** and the sub-contractors, the **Bristol Genomics Facility**, based within the University of Bristol and the company **MYcroarray**, based in Michigan, USA.

# Wheat Genetic Improvement Network (WGIN3)

## WP1 Management meetings – The Network

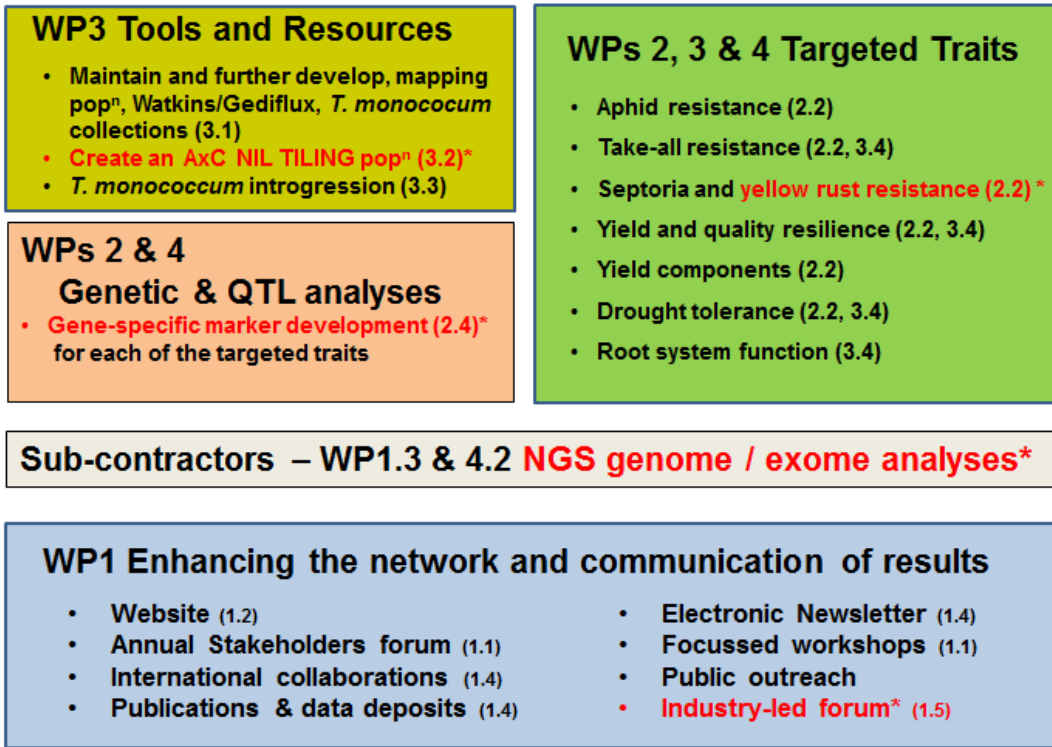


Figure 1: The new layout of WGIN3 with details of the four work packages (WP)

## Section 2 Research Update

### Developing New Resources for Wheat Gene Discovery (JIC)

#### 1) A Chromosome Segment Substitution Library (CSSL) for Avalon x Cadenza (AxC) (WP3.2)

The Avalon x Cadenza Doubled Haploid Population (AxC) was one of several developed to represent a broad spectrum of the variation present in the UK elite winter germplasm pool. The population is a Defra UK reference population and was developed as part of **WGIN1**. The Near Isogenic Lines (NILs) derived from this population have validated QTLs discovered in WGIN and beyond. Here we propose a new, unique, resource, utilising the average 12.5% random background in each NIL (**Figure 2**). High density, whole genome SNP screening is now a routine and cost effective technology for wheat. Therefore the screening of a large number of the AxC NILs, to determine the location and extent of both the QTL regions

and the random parental background, is feasible. We will use the Axiom® 35K Wheat Breeders Array to screen 94 NILs, 47 each from Cadenza and Avalon recurrent backgrounds. The genomic segments from the donor will

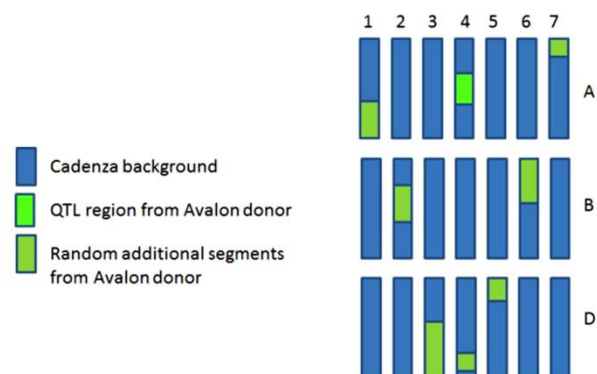


Figure 2: The QTL region (from Avalon on 4A in this *hypothetical* NIL) had been selected using flanking molecular markers, however additional chromosomal segments will also have been randomly introduced into the Cadenza background.

be positioned on the AxC genetic map and wheat pseudomolecules. Lines will be selected based on their background content and crossed to the recurrent parent, twice. Selected lines will then be self-fertilised and homozygous CSSLs selected. The desired final outcome would be a set of lines representing a whole genome 'tiling path' of Avalon or Cadenza, in a Cadenza or Avalon background, respectively. This set of lines would then be available to breeders to select the lines containing their region of interest to make productive crosses.

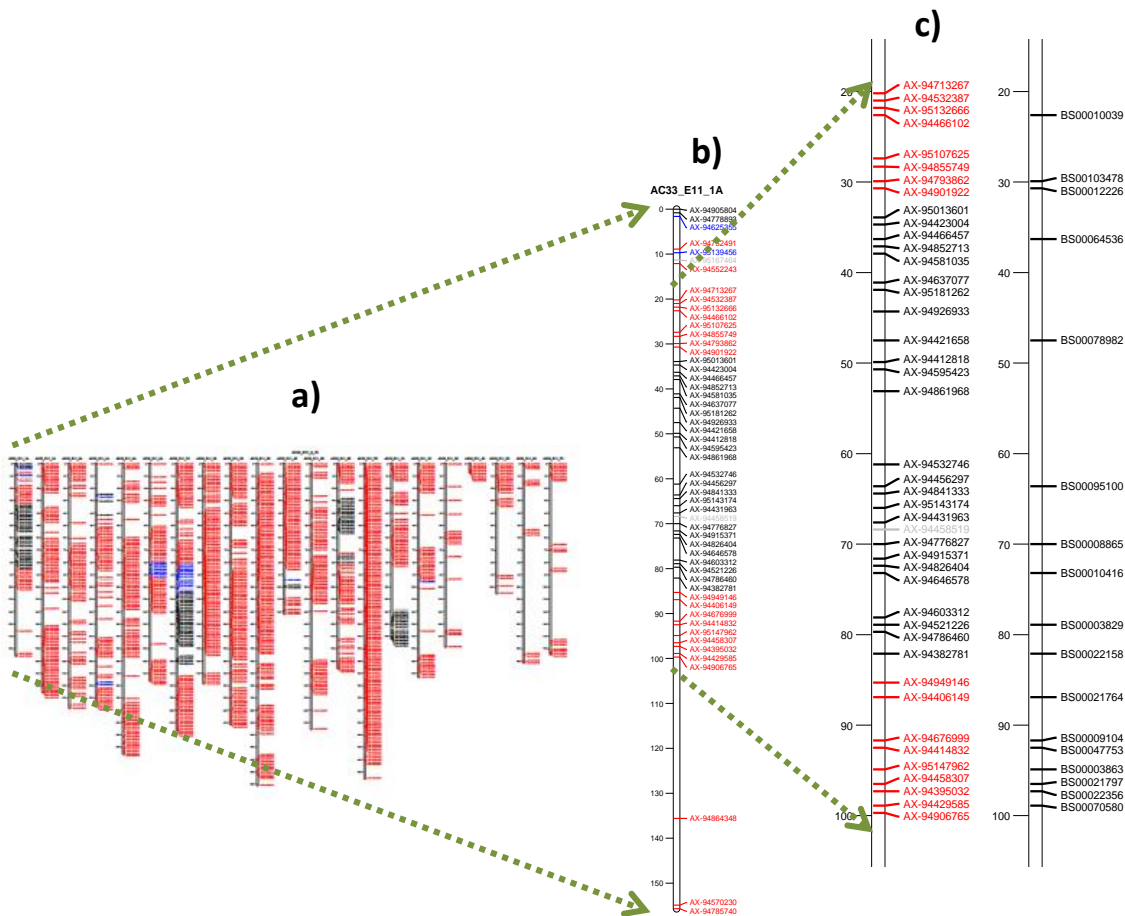
In a pilot experiment eighteen of the AxC NILs, representing most of the identified QTLs, were genotyped on the Axiom® HD Wheat Genotyping Array (a.k.a. 820K array), at the University of Bristol Genomics Facility. These data indicated the average of 12.5% random background in the NILs. The segregation data of these eighteen NILs has been used to generate SNP marker maps; the marker order being based on the AxC maps from Winfield et al (2015). **The maps from the eighteen NILs and additional information are now published on the WGIN homepage [www.wgin.org.uk](http://www.wgin.org.uk)** Excerpts from two of the maps are shown in **Figure 3**.

**Reference** Mark O. Winfield *et al* (2015) High-density SNP genotyping array for hexaploid wheat and its secondary and tertiary gene pool. *Plant Biotechnology Journal* doi: 10.1111/pbi.12485. [Epub ahead of print]

**2) Quantifying agronomic impact of WGIN target genes using the Paragon NIL library (WP2.3, WP3.2).**

**WGIN1** and **WGIN2** have been involved in developing NILs in the genetic background of Paragon; this collection is known as the 'Paragon Library'. The ability to analyse gene effects in a uniform genetic background will provide a unique insight into the potential breeding value of these genetic effects for UK breeding and agriculture.

Paragon NILs are now available for multiple alleles of *Rht-D1*, *Rht-B1*, *Rht8*, *Ppd-B1*, *Ppd-D1*, *Lr19*, *1BL.1RS*, 8 eps QTL, *Vrn1*, *Vrn3*, 3N, five grain shape QTL, 13 QTL from the Watkins collection (BBSRC WISP), and selected WGIN mutants.



**Figure 3: a) Complete SNP map of NIL AC33\_E11\_5\_10 (QTL for 1D DTEM). All 21 chromosomes are shown. b) Chromosome 1A of AC33\_E11\_5\_10. c) Section of chromosome 1A of AC33\_E11\_5\_10 showing the Axiom SNP markers and the BS markers from the University of Bristol Genomics Facility. Markers shown in black are from Avalon, in red from Cadenza, blue are heterozygous and grey unscored.**



Single rep, 1 metre plot trials of many of these lines have been carried out in 2013-2014 and 2014-2015 with Days to Ear Emergence (DTEM), Height, Yield and Thousand Grain Weight (TGWT) being scored. The first yield trial with a subset of the Paragon Library was drilled in spring 2015 (three replicates in 6m plots). This subset includes *Rht-D1*, *Rht-B1*, *Rht8*, *Ppd-B1*, *Ppd-D1*, *Lr19* and the 'Staygreen' mutant, plus Paragon control. The plots were scored for DTEM, Height, Yield and TGWT and showed the expected phenotypes in the relevant backgrounds, for example *Rht-D1*, *Rht-B1* and *Rht8* (Figure 4). This three rep, 6 metre plot, yield trial is being repeated, and was drilled in autumn 2015.

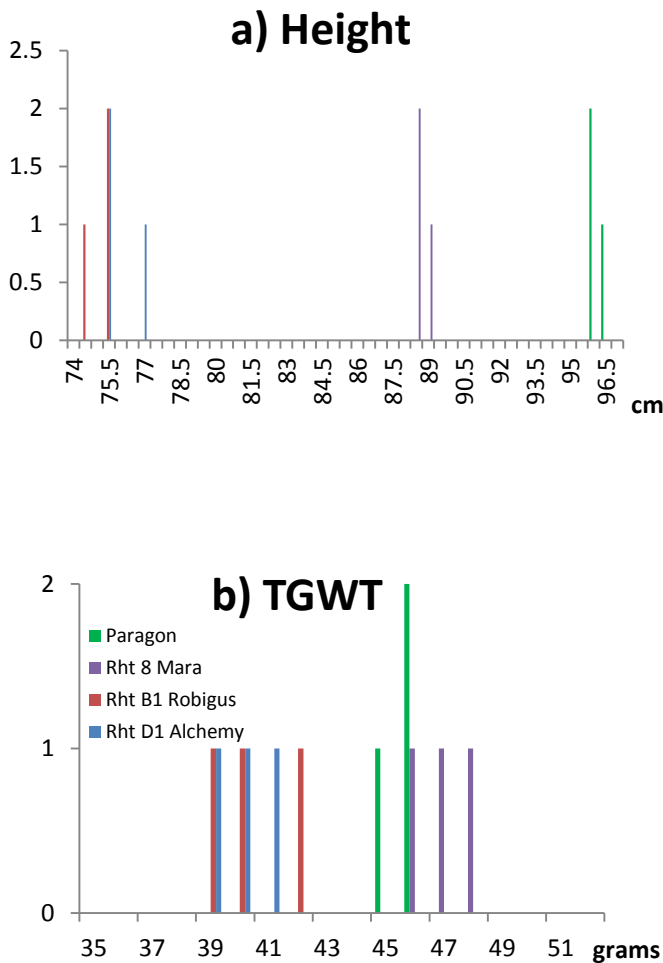


Figure 4: a) Height (cm) of individual reps of *Rht-B1*, *Rht-D1*, *Pht8* and Paragon in yield trial. b) Thousand Grain Weight (TGWT) (g) of individual reps of *Rht-B1*, *Rht-D1*, *Pht8* and Paragon in yield trial

The subset of Paragon lines have been included in the 2015-2016 Paragon x Garcia drought trial (see below). In addition most of these lines have been sown under the Phenospex phenotyping platform (Figure 5) in a nitrogen usage trial as two randomised blocks of 16, +/- additional nitrogen, in collaboration with Ji Zhou, TGAC, Norwich.



Figure 5: The Phenospex Phenotyping Platform at JIC with emerging Paragon lines (picture taken February 9<sup>th</sup> 2016)

### 3) Informing multiple marker assisted selection for yield stability using Paragon library (WP3.2)

There is an increasing amount of data showing which alleles can be selected together with desirable breeding consequences. To this end the following crosses were made; *Rht8* Mara x *Rht-B1* Robigus, *Rht8* Mara x *Rht-D1* Alchemy and *Rht-B1* Robigus x *Rht-D1* Alchemy. These crosses are being bulked and will be tested in 1 metre field plots in 2016-2017.

### 4) Dissecting UK drought tolerance in Paragon x Garcia - WP2.3 & WP4.3

The Paragon x Garcia (PxG) population was produced within **WGIN2** to specifically target UK drought. Variable, and particularly low, rainfall is increasingly of concern to farmers in the UK so looking for drought tolerant characteristics in non-UK wheat varieties could be highly beneficial. Garcia was chosen as it is grown in the Mediterranean climate of southern France and northern Spain and is therefore adapted to an environment where drought stress is commonplace.

There are **351 PxG RILs** and a good genetic map. A single-rep, 1 metre field trial was carried out in 2014-15 and the RILs scored for Days to Ear Emergence (DTEM), Height, Yield and TGWT. QTL mapping with these data revealed QTLs for all of these traits, only some of which being at known loci (data not shown).

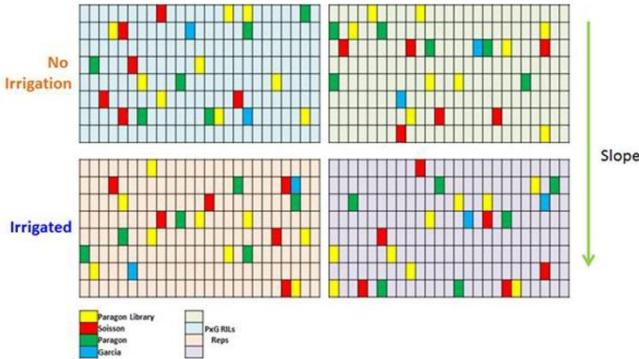
From the DTEM data it was possible to identify those PxG RILs that are likely to be Ppd-sensitive, being the later-flowering lines. These Ppd-sensitive RILs, along with a subset of the Paragon Library, and Paragon and

Garcia controls, were used to set up a drought trial in autumn 2015. The trial consists of two reps each, of all 200 lines, in non-irrigated and irrigated 6 metre plots (see **Figure 6**).

**Key Trait: Nitrogen Use Efficiency (NUE) and Quality QTLs linked to NUE (RRes)**

**The WGIN variety/N trial**

The WGIN variety/N trial (WGIN Diversity Trial) has been running annually since 2004, examining 58 varieties, 20 of which have been in the trial every year. An aerial view of the 2015 trial is shown in **Figure 7**. The trials received 4 levels of N (0, 100, 200 and 350 kg/ha) and yield and N uptake into grain and straw are measured thus allowing derivation of NUE parameters.



**Figure 6: Field Plan for Paragon x Garcia Drought Trial**

The plots will be scored for DTEM, Height, Yield and TGWT, and QTL mapping carried out, as previously. To accurately correlate the quantitative response of the lines to the conditions during the growing season, temperature, water content and water potential data will be collected from one irrigated and one non-irrigated plot, using soil measurement probes from DeltaT Devices Ltd. This will commence in early February and continue until harvest. Local climate data will also be available.

This large-scale, replicated drought trial, along with accurate water potential data, should help to dissect the response of wheat to drought stress and lead to the discovery of genes involved in this response. These genes could then be incorporated into breeding drought tolerant commercial wheat.

For further information of these aspects of the WGIN project please contact Drs Simon Griffiths ([simon.griffiths@jic.ac.uk](mailto:simon.griffiths@jic.ac.uk)) or Clare Lister ([clare.lister@jic.ac.uk](mailto:clare.lister@jic.ac.uk)) at John Innes Centre.



**Figure 7: Aerial view of WGIN Diversity Trial at Rothamsted in 2015.**

A summary of the yield data at 200 kg/ha N is shown in **Figure 8**. An overriding impact of season is apparent with 2008 and 2015 being amongst the best and 2010, 2011 and 2013 being low yielding years. Some varieties show greater stability than others. The highest yield obtained was 13.8 t/ha in 2015.

The WGIN Diversity experiment has proved a particularly useful resource for the development of new technology for aerial trial assessment (using UAV

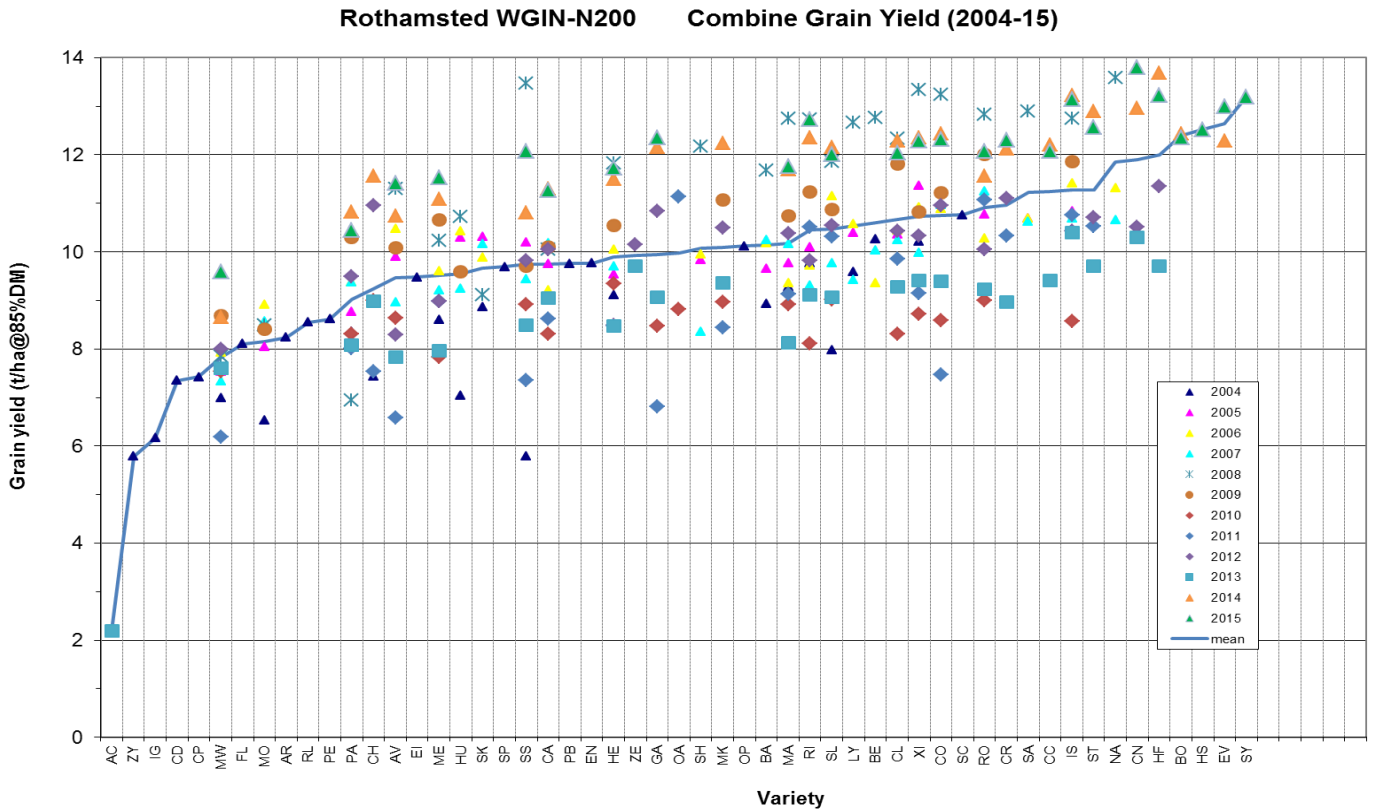


Figure 8: Summary of grain yield data for 200 kg/ha N treatment in the years of 2003 to 2014 for 53 varieties. All trials were conducted at Rothamsted (see WGIN website for the list of cultivars used in the complete set of diversity trials).

drones). Plot growth can be assessed by NDVI, thermal photography and by 3D reconstruction. A digital elevation model of the 2014 trial is shown in **Figure 9**.

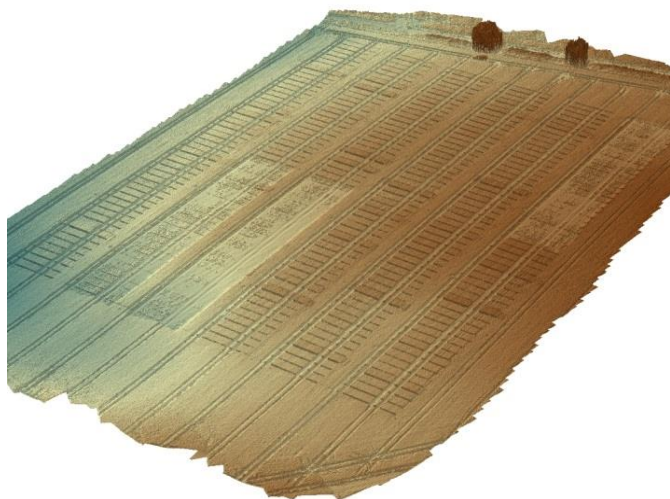


Figure 9: A digital elevation (surface) map of the 2014 WGIN Diversity trial. Data was collected by an UAV and an elevation model constructed from multiple overlapping photographs. Plot heights can be determined to within a few centimetres accuracy.

The trials have been exploited for a number of other studies including take-all studies, aerial phenotyping

technology testing (**Figure 10**) and grain quality projects. Several PhD students have sampled materials and data used within their projects.



Figure 10: The fully automated Phenotyping Platform @ RRes

The varieties examined previously but in the current trial are Avalon, Bonham, Cadenza, Claire, Cocoon, Conqueror, Cordiale, Crusoe, Evoke, Gallant, Hereford, Hereward, Hystar, Istabraq, Malacca, Maris Widgeon, Mercia, Paragon, Riband, Robigus, Skyfall, Stigg, Soissons, Solstice, Xi19, New for the 2016 harvest season are Evolution, KWS Lili, Reflection, RGT Illustrious and Hylux.



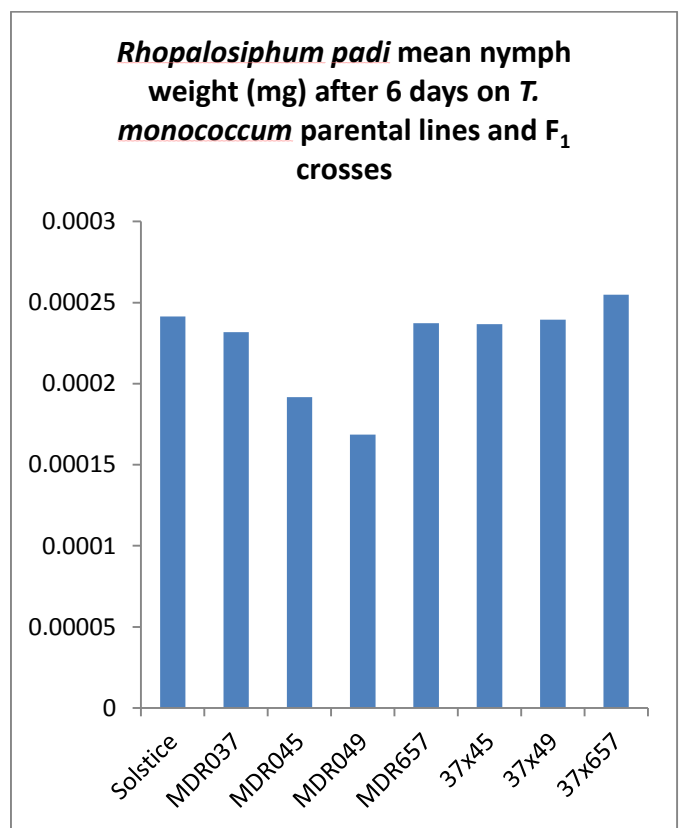
For further information of this aspect of the WGIN project please contact Dr Malcolm Hawkesford ([malcolm.hawkesford@rothamsted.ac.uk](mailto:malcolm.hawkesford@rothamsted.ac.uk)).

**Key Trait: Resilience to Aphids (RRes)**

The major aphid pests of UK wheat, the grain aphid, *Sitobion avenae*, and the bird-cherry oat aphid, *Rhopalosiphum padi*, vector Barley Yellow Dwarf Virus (BYDV), a serious disease causing severe yield losses, and also damage plant quality directly through feeding activity. Currently controlled by neonicotinoid seed treatments and autumnal pyrethroid applications, widespread resistance to pyrethroids has now been identified in UK *S. avenae* populations. This has focussed research to find alternative methods for aphid control. Wheat breeding has concentrated on yield and quality, but development of aphid resilient varieties would provide a sustainable alternative to pesticides.

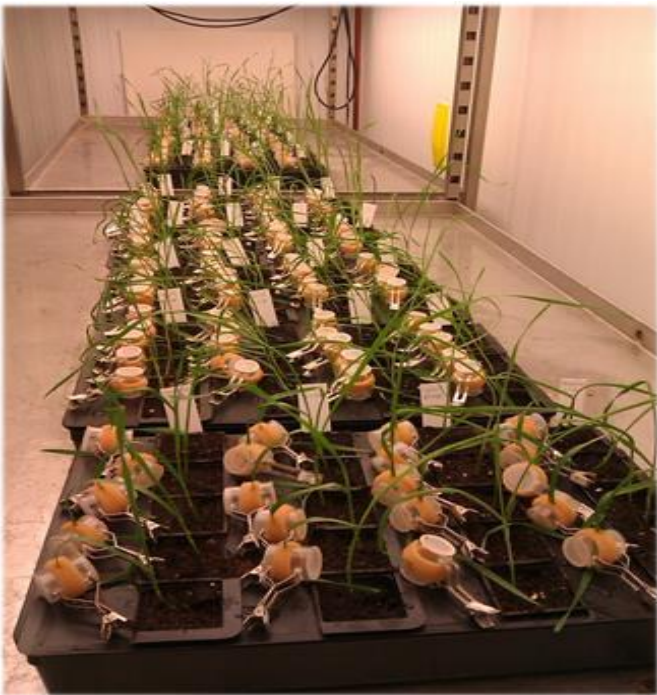
reduced or absent on some lines. These *T. monococcum* lines showed relatively strong resilience to both aphid species, and formed the basis of this research in **WGIN3**. Crosses between the resilient lines MDR045, MDR049 and MDR657, and the susceptible MDR037 were generated and the F<sub>1</sub> populations were tested in the laboratory based aphid screening bioassay, against both aphid species.

Analysis of results showed that *R. padi* mean nymph weight on the parental *T. monococcum* lines and crosses was not significantly reduced, and nymphs were produced on MDR045 and MDR657, which in previous screens had not supported nymphs (**Figure 12**). This could be due to the plants being older during this



**Figure 12:** Mean weight (mg) of *Rhopalosiphum padi* nymphs after 6 days on *Triticum monococcum* lines compared to the hexaploid cultivar Solstice, which acted as a standard in all trials.

phenotyping screen. In contrast, *S. avenae* nymph weights on the same lines showed some differences, with a significant reduction on MDR045 and MDR049 and on the F<sub>1</sub> plants from the MDR037 x MDR045 and MDR037 x MDR049 crosses, compared to the control (**Figure 13**). Thus there appears to be a separation in response between the aphid species on the *T. monococcum* crosses (see Presentations from 17/07/15 WGIN3 Management Meeting on the WGIN website for full experimental methodology and results).



**Figure 11:** Aphid phenotyping bioassay

Phenotyping studies (**Figure 11**), developed and conducted in the preceding LOLA, **WGIN2** and current WISP projects (see Presentations from 04/03/15 WGIN3 Management Meeting on the WGIN website <http://www.wgin.org.uk/information/meetings> for full experimental methodology and results) showed little or no aphid resilience in hexaploid elite or Watkins collection landraces, but more promising results with diploid species, particularly *Triticum monococcum*, where nymph production and survival were significantly

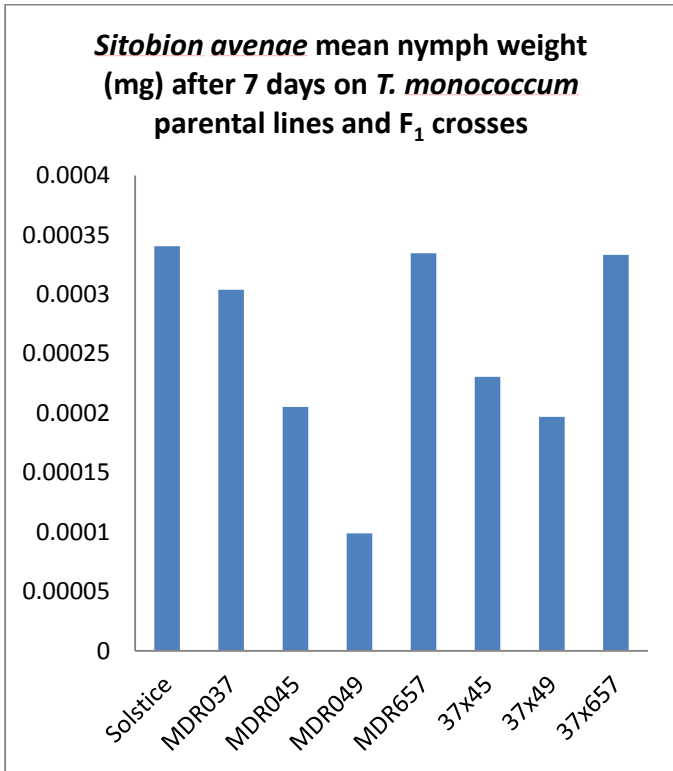


Figure 13: Mean weight (mg) of *Sitobion avenae* nymphs after 7 days on *Triticum monococcum* lines compared to the hexaploid cultivar Solstice, which acted as a standard in all trials.

These plants have now been grown through to the F<sub>2</sub> generation or backcrossed to the susceptible line MDR037. Seed from the F<sub>2</sub> generations are currently being tested against both aphid species in the phenotyping screen and further plant generations will be produced. The backcrosses will also be tested against the aphids in due course. Plant material will ultimately be provided for genotyping.

For further information of this aspect of the WGIN project please contact Lesley Smart at Rothamsted ([lesley.smart@rothamsted.ac.uk](mailto:lesley.smart@rothamsted.ac.uk)).

**Key Trait: Broad Spectrum Resistance to Foliar Infecting Fungal Pathogens (RRes)**

Winter wheat crops in the UK face major disease threats from a range of leaf attacking fungal pathogens. In the last decade Septoria leaf blotch disease, caused by *Zymoseptoria tritici*, has been most important foliar disease of winter wheat in Western Europe and the UK. The other predominant foliar diseases in the UK are brown rust (*Puccinia triticina*), yellow rust (*Puccinia striiformis*) and powdery mildew (*Blumeria graminis* f. sp. *tritici*). The lack of cultivars which have multiple high resistance ratings to all four of these foliar diseases means that farmers rely on chemistry applications for effective control. Winter wheat crops routinely receive 3

or 4 fungicide applications per annum to control foliar diseases. However, the emergence of pathogen isolates in the existing populations able to develop resistance to fungicides or overcome host resistance has created additional difficulties in trying to achieve effective disease control. For example multiple drug resistant strains of *Zymoseptoria tritici* are now found across the UK while serious outbreaks of yellow rust have occurred following the emergence of new races of *Puccinia striiformis* which are able to overcome host resistance. To avoid unnecessary fungicide applications and protect the yield potential of winter wheat, selection for host resistance to multiple foliar diseases is a high priority for the wheat breeding community.

In 2008, within the **WGIN1** programme, 740 accessions from the Watkins hexaploid wheat landrace collection were assessed for foliar disease and take-all root infection in a third wheat field trial on the Rothamsted Farm. This was a high take-all disease year with root infection early in the season. Under these conditions 10 Watkins wheat accessions were identified (**Table 1**) which were highly resistant to the foliar diseases yellow rust, brown rust, septoria leaf blotch and powdery mildew compared to the very susceptible controls. This potential multiple foliar disease resistance phenotype is a highly desirable trait.

Accession	Yellow rust	Brown rust	Septoria	Mildew
1190018	0	0	T	T
1190137	T	T	0	T
1190203	0	0	0	T
1190231	0	0	T (NS)	0
1190262	0	0	0	0
1190399	T	0	T	0
1190495	0	0	T	0
1190610	0	0	T (NS)	T
1190733	T	T	T	T
1190786	0	T	T	0
Controls	FS	FS	FS	FS

Table 1: Watkins 2008 foliar disease assessments; 0= no symptoms seen, T= trace infection, NS= no sporulation, FS= full sporulation.

In the **WGIN3** project the foliar disease resistance of these ten accessions is being re-examined in replicated field trials in both 1<sup>st</sup> wheat (no/minimal take-all) and 3<sup>rd</sup> wheat (high take-all) field trials (**Figure 14**). This will identify whether the foliar disease resistance in 2008

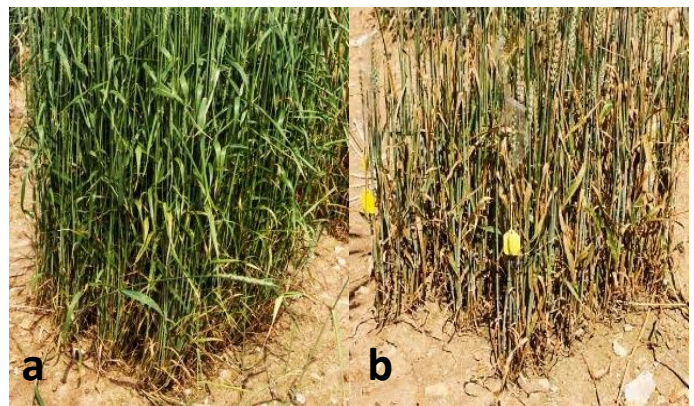


was an induced response to the early take-all root infection or whether these accessions are inherently resistant to foliar disease in a take-all disease free 1st wheat situation.



**Figure 14: Watkins hexaploid wheat landraces screened for resistance against multiple foliar fungal pathogen attack, 1<sup>st</sup> wheat field trial, June 2015.**

In both the 1st and 3rd wheat field trials in 2015 yellow rust was the dominant foliar disease that developed. Five out of the 10 Watkins accessions were highly susceptible to yellow rust in both the 1st and 3rd wheat field trials with flag leaf disease severity above 60 % in June 2015. This change in susceptibility of these accessions compared to 2008 indicates either that each genotype escaped disease in 2008 or more likely

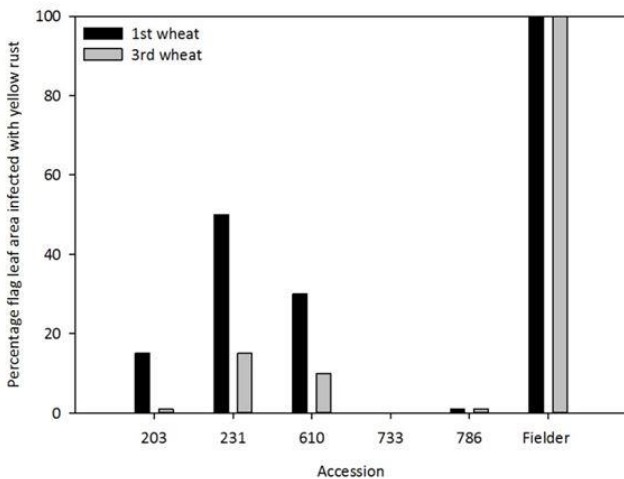


**Figure 16: Highly resistant Watkins accession 1190733(a) compared to the fully yellow rust susceptible spring wheat cultivar Fieldier (b) (June 2015)**

There is some evidence of an increase in host resistance in the third wheat site but this will be confirmed after assessment of root samples for take-all disease and full statistical analyses have been completed as well as in repeat field trials in 2016.

Field crossing between these resistant Watkins accessions and the fully susceptible spring wheat cultivar Fieldier was carried out in summer 2015 to begin developing mapping populations to dissect the genetic basis of disease resistance for plant breeding purposes. In autumn 2015 repeat 1st and 3rd wheat field trials were sown with the aim of phenotyping against other natural foliar disease infections in the 2016 field season. Due to the mild and wet winter there are already reports of septoria leaf blotch, powdery mildew, brown rust and yellow rust developing in wheat crops across southern England and all four diseases are present on the Rothamsted Farm.

For further information of this aspect of the WGIN project contact Dr Vanessa McMillan at Rothamsted ([vanessa.mcmillan@rothamsted.ac.uk](mailto:vanessa.mcmillan@rothamsted.ac.uk)).



**Figure 15: Moderate and high levels of host resistance against yellow rust infection detected in five Watkins accessions compared to the fully susceptible spring wheat cultivar Fieldier in June 2015**

reflects the dramatic shift in the yellow rust race structure between 2008 and 2015. The other five Watkins accessions still exhibited moderate to high resistance against yellow rust (**Figures 15 and 16**).

## Section 5 Events

A European Wheat Breeding workshop will take place from **23rd to 28th May 2016 in Konya, Turkey** (via Istanbul). The organiser in Turkey is Alex Morgunov (Turkey-CIMMYT, Ankara). The Thursday (26th May) has been marked for a tourist trip to Cappadocia. VISA applications can be done online. Please note that this workshop is NOT funded by WGIN. Peter Shewry has

applied for funding for 12 people (£700pp) from the BBSRC, but flights need to be booked early and before the outcome of the grant application is known. All people contacted so far have agreed to self-funding if need be. If interested please contact Peter Shewry ([peter.shewry@rothamsted.ac.uk](mailto:peter.shewry@rothamsted.ac.uk)).

## Section 6 News

Two Stakeholders' meetings were held in 2015.

- The first @ JIC on 16<sup>th</sup> April focussed on achievements of **WGIN1** & **WGIN2** and explained the aims of **WGIN3**.
- The second @ RRes on 20<sup>th</sup> November presented an overview of current wheat research within the UK not limited to WGIN, with a wide variety of presentations from Industry, Academia and Knowledge Transfer.

## Section 7 Publications 2014 to 2016

- Mauchline, T.H., Chedom-Fotso, D., Chandra, G., Samuels, T., Greenaway, N., Backhaus, A., McMillan, V., Canning, G., Powers, S.J., Hammond-Kosack, K.E., Hirsch, P.R., Clark, I.M., Mehrabi, Z., Roworth, J., Burnell, J., and Malone, J.G. (2015) An analysis of *Pseudomonas* genomic diversity in take-all infected wheat fields reveals the lasting impact of wheat cultivars on the soil microbiota. **Environmental Microbiology** 17:11, 4764-4778.
- Ania Kowalskia, Mike Goodingb, Ariel Ferranted, Gustavo Slaferd, Simon Orforda, Debora Gasperinia and Simon Griffiths (2016) Agronomic assessment of the wheat semi-dwarfing gene Rht8 in contrasting Nitrogen treatments and water regimes. **Field Crop Research** (accepted subject to changes)
- Alba Farre Martinez, Elizabeth Sayers, Michelle Leverington-Waite, Richard Goram, Simon Orford, Luzie Wingen, Cathy Mumford, and Simon Griffiths (2016). Dissection of Context Dependent QTL Expression in Wheat Using a Library of Near Isogenic Lines. **Genetics** (under review)
- Mark O. Winfield, Alexandra M. Allen, Amanda J. Burrige, Gary L. A. Barker, Harriet R. Benbow, Paul A. Wilkinson, Jane Coghill, Christy Waterfall, Alessandro Davassi, Geoff Scopes, Ali Pirani, Teresa Webster, Fiona Brew, Claire Bloor, Julie King, Claire West, Simon Griffiths, Ian King, Alison R. Bentley, Keith J. Edwards (2015) High-density SNP genotyping array for hexaploid wheat and its secondary and tertiary gene pool. **Plant Biotechnology Journal** doi: 10.1111/pbi.12485. [Epub ahead of print]
- Greenslade AFC, Ward JL, Martin JL, Corol DI, Clark SJ, Smart LE and Aradottir GI (2016) *Triticum monococcum* lines with distinct metabolic phenotypes and phloem-based partial resistance to the bird cherry-oat aphid *Rhopalosiphum padi*. **Annals of Applied Biology** in press

- G. A. Chope, Y. Wan, S. P. Penson, D. G. Bhandari, S. J. Powers, P. R. Shewry & M. J. Hawkesford (2014) Effects of Genotype, Season, and Nitrogen Nutrition on Gene Expression and Protein Accumulation in Wheat Grain dx.doi.org/10.1021/jf500625c | **J. Agric. Food Chem**
- Ellen F. Mosleth, Yongfang Wan, Artem Lysenko, Gemma A. Chop3, Simon P. Penson, Peter R. Shewry & Malcolm J. Hawkesford (2015) A novel approach to identify genes that determine grain protein deviation in cereals. **Plant Biotechnology Journal** 13, 625–635
- McMillan, V.E., Gutteridge, R.J. and Hammond-Kosack, K.E (2014). Identifying variation in resistance to the take-all fungus, *Gaeumannomyces graminis* var. *tritici*, between different ancestral and modern wheat species. **BMC Plant Biology** 14, 212

For further information on any aspect of the WGIN project please go to [www.wgin.org.uk](http://www.wgin.org.uk) or contact us at [wgin.defra@rothamsted.ac.uk](mailto:wgin.defra@rothamsted.ac.uk).

The contributors to this newsletter were: Kim Hammond-Kosack, Malcolm Hawkesford, Andrew Riche, Vanessa McMillan, Lesley Smart, Michael Hammond-Kosack (RRes); Clare Lister and Simon Griffiths (JIC).

