- **The next WGIN Stakeholders' Meeting will be held at Rothamsted Research, Harpenden on November 30th 2017**

Contents:

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), 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 (WGIN3). 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 inter-connected 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.

WGIN3 funding has now been extended to January 2018 by Defra.

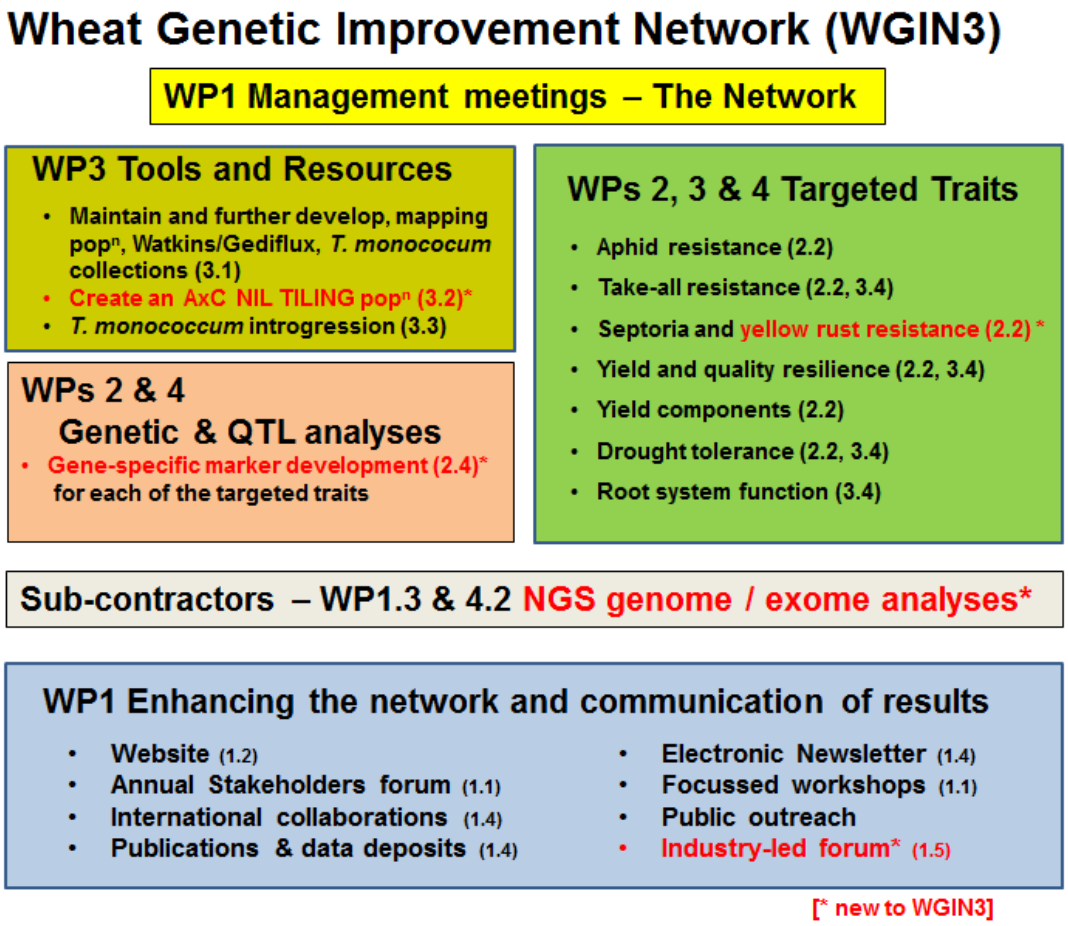

Figure 1: The new layout of WGIN3 with details of the four work packages (WP)

Section 2 Research Update

Developing New Resources for Wheat Gene Discovery (JIC)

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

The Avalon x Cadenza Doubled Haploid Population (AxC) was developed as part of WGIN1. The Avalon and Cadenza NILs derived from this population have validated QTL discovered in WGIN and beyond. We are generating a new resource which utilizes the random background in each NIL; each NIL has a 'foreground' segment from the donor, around the selected QTL, and additional random 'background' segments (see **Figure 2**). As high density, whole genome SNP screening is now a routine and cost effective technology, then screening a large number of the AxC NILs to determine the location and extent of the QTL foreground and the random background is feasible.

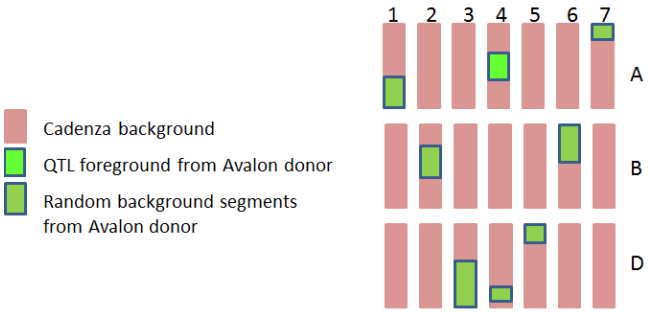

Figure 2: The QTL region (from Avalon on 4A in this *hypothetical* NIL) had been selected using flanking molecular markers, however additional Avalon chromosomal segments have also been randomly introduced into the Cadenza background.

In a pilot experiment eighteen of the AxC NILs 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 data from these eighteen NILs has been used to generate SNP marker maps, based on the AxC maps from Winfield et al (2015). The maps from the eighteen NILs and additional information are published on the WGIN homepage www.wgin.org.uk

We have used the Axiom® 35K Wheat Breeders Array at the University of Bristol Genomics Facility to screen over 90 NILs, from Cadenza or Avalon recurrent backgrounds. The position of the polymorphic Axiom SNPs (in the AxC NILs) has been aligned with the WGAv0.4 (NRGene) sequence assembly of Chinese Spring and this has allowed the generation of a 'graphical genotype' for each NIL (see **Figure 3**).

Each of the NILs has been crossed to the recurrent parent and the F_2 are now ready to be screened with markers for the specific background segments. 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 and the whole wheat community to select the lines containing their region of interest to make productive crosses.

Reference

Mark O. Winfield, Alexandra M. Allen, Amanda J. Burridge, 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* Volume 14, Issue 5, 1173–1315, doi: 10.1111/pbi.12485

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

WGIN has been involved in developing NILs in the genetic background of Paragon; this collection is known as the 'Paragon Library' (PL). 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. During 2017 more details of these lines will be made available on the WGIN website to encourage their use by the wheat community.

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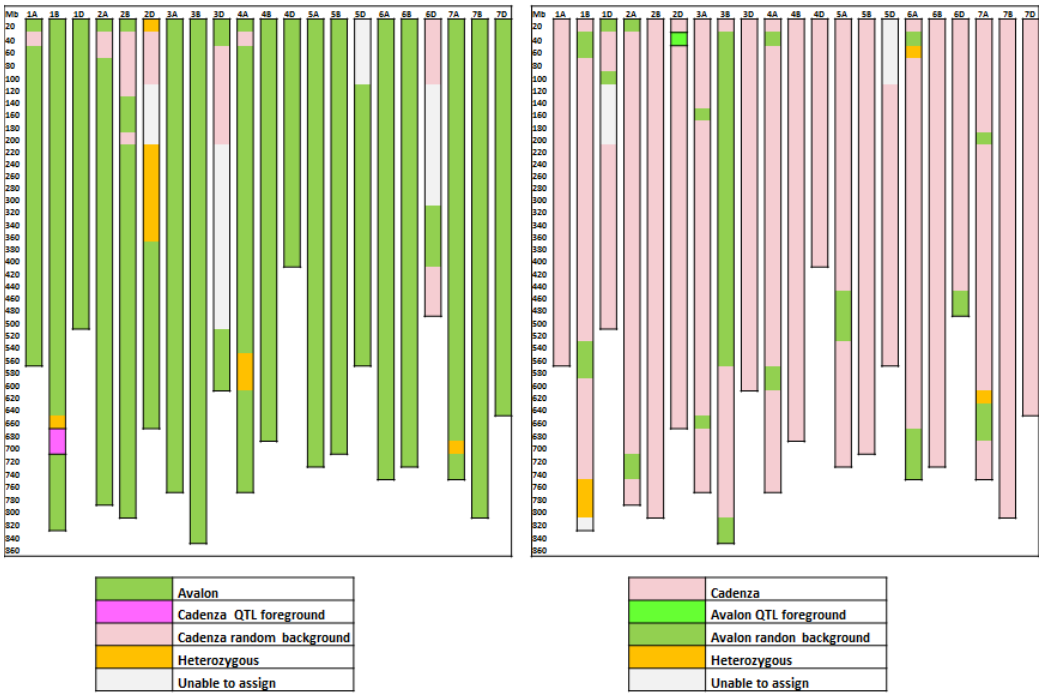

Figure 3: 'Graphical genotypes' of an Avalon NIL for 1B ear emergence (left) and a Cadenza NIL for 2D height (right). For each chromosome a representative genotype (see key) is shown for each 20 Mb region across the length of the chromosome, based on the WGAv0.4 (NRGene) sequence assembly of Chinese Spring

A subset of nine PL lines have been included in the Paragon x Garcia drought trials (see below). In addition seven of these have were sown under the Phenospex phenotyping platform in a nitrogen usage trial, in collaboration with Ji Zhou, Earlham Institute (EI), Norwich. The trial was drilled as two randomised blocks of 16, each with one rep +/- nitrogen. All plots received a preliminary treatment of 40 kg/h, and the +N plots had two subsequent treatments of 250 kg/h. The results show variation in nitrogen usage between the PL lines (**Figure 4**). The *Ppd* 1x and *Ppd* 2x results were affected by bird damage.

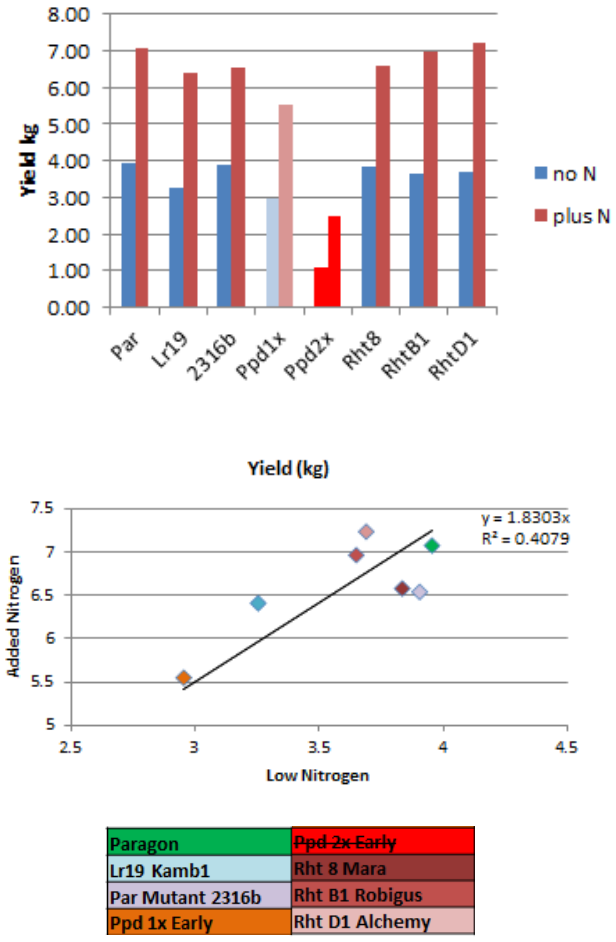

Figure 4: Yield data from Phenospex nitrogen usage trial from the 2015-2016 season at JIC field.

- **Informing multiple marker assisted selection for yield stability using the 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. Homozygous lines (**Figure 5**) are currently being bulked in 1 m field plots and will be scored for DTEM, Height, Yield and TGWT. A yield trial will be drilled in autumn 2017.

Figure 5: Double *Rht* mutants in a Paragon background.

In addition, we have made a winter Paragon by crossing in *VrnA1* + *VrnB1* from Malacca; this line has been shown to require vernalisation to flower. The winter Paragon has been crossed with *Rht8*, *RhtB1* and *RhtD1*, and F2 seed will be ready for drilling in 1 m field plots in autumn 2017.

- **Dissecting UK drought tolerance in Paragon x Garcia - WP2.3 & WP4.3**

Climate predictions suggest that the UK will have warmer and drier summers' so variable, and particularly low, rainfall is increasingly of concern to farmers. This is a particular problem in the south-east and east of England, which are the predominant wheat growing areas. Wheat yields in the UK are often limited by water deficit during critical early stages of crop development around stage 31 (**Figure 6**). Stage 31 is usually reached during April when rainfall can be especially low.

The Paragon x Garcia (PxG) population was produced within WGIN to specifically target UK drought and was developed from a DEFRA Link Project: LK0986: *Improving*

water use efficiency and drought tolerance in UK winter wheats (Eric Ober and colleagues).

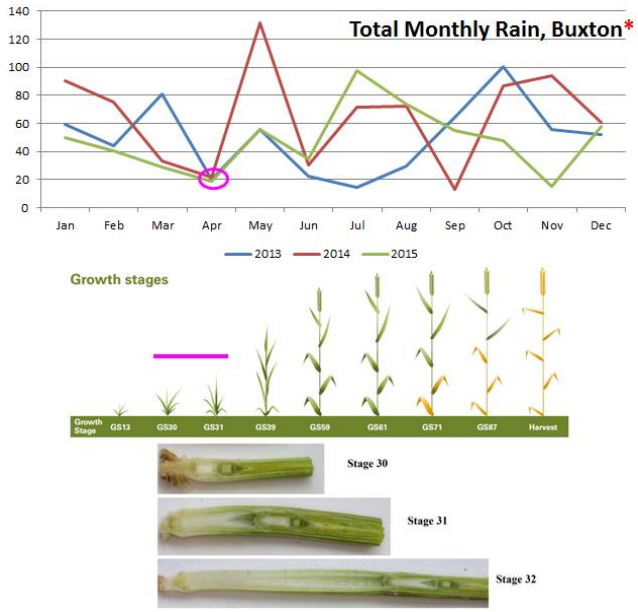

Figure 6: Monthly rainfall in Norfolk 2013-2015 (top). Sections of young wheat plants showing stages 30-32 (bottom). *Rainfall data courtesy of http://www.buxton-weather.co.uk/weather.htm. Buxton is 13 miles from the John Innes Centre.

The cultivar 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. Paragon is a UK spring wheat. There are a total of 351 PxG RILs and good genetic maps are available to allow QTL mapping.

From the days-to-ear-emergence (DTEM) data in a preliminary trial (2014-15) it was possible to identify those PxG RILs that are likely to be Ppd-sensitive, being the later-flowering lines. These were selected as to be most similar to UK wheat. These Ppd-sensitive RILs, along with nine lines from the Paragon Library (PL), and Paragon and Garcia controls, were used to set up a drought trial in autumn 2015. The trial consisted of two reps each, of all 200 lines, in non-irrigated and irrigated 6 m^2 plots (see **Figure 7**, left panel).

The plots were regularly screened overhead with the UAV, by Simon Orford, to monitor the plots, record lodging and the onset and progression of senescence, (**Figure 7**, right panel).

To correlate the quantitative response of the lines to the conditions during the growing season, temperature, water content and water potential data were collected from one irrigated and one non-irrigated plot, using soil measurement probes from DeltaT Devices Ltd. This commenced in early May and continued until harvest. Local climate data is also available.

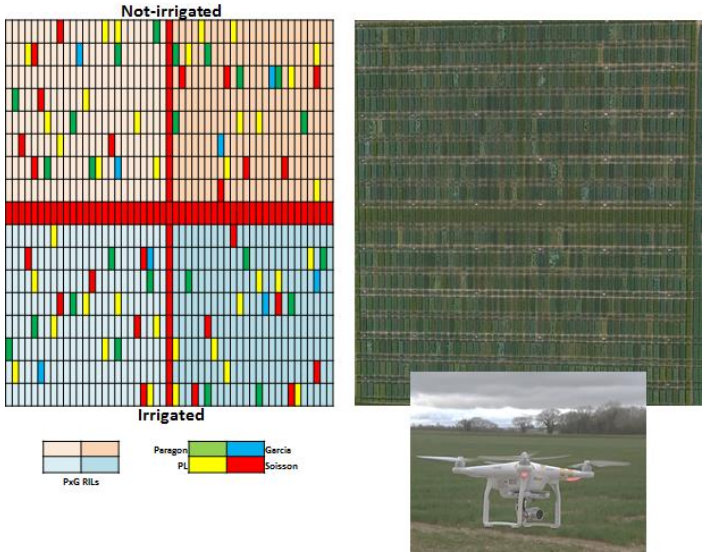

Figure 7: Field Plan for Paragon x Garcia Drought Trial (left) and aerial view of plots from UAV (right).

As it turned out this was a challenging year to perform a drought trial…. However, we are able to report some results! A number of traits were recorded; the dates at Stage 31, Booting and Ear Emergence, plus Height, Lodging, Senescence, Yield, Specific Weight, TGWT. Computational analyses of these quantitative data with the genetic data indicated a number of chromosomal regions where significant differences are observed in the PxG RILs and may indicate genes involved in drought response or tolerance (**Figure 8**).

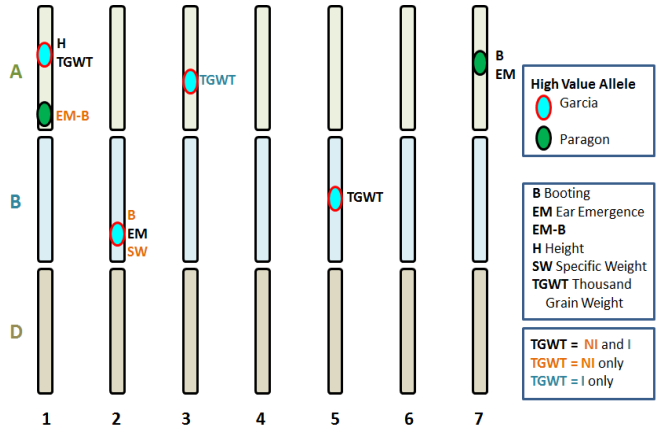

Figure 8: Diagram of the 21 wheat chromosomes showing the positions of possible drought-tolerant QTLs.

It is hoped that this large-scale, replicated drought trial, along with accurate water potential data, will 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.

The trial has been drilled again (autumn 2016) and what we need now is a drought! This has indeed now happened.

For further information of this aspect of the WGIN project contact Drs Clare Lister (clare.lister@jic.ac.uk), or Simon Griffiths (simon.griffiths@jic.ac.uk) at the John Innes Centre.

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

- **Developing a low altitude remote sensing capability using WGIN Field Trials**

Drones have been used at Rothamsted for the past three seasons to collect aerial images of the WGIN Diversity field experiment. During the growing season images are collected weekly. Three cameras are currently used, a normal Red-Blue-Green 24 mega pixel camera, a similar camera adapted to collect near infrared images and a 0.1 mega pixel thermal infrared camera. The drone is flown at 50m altitude, which gives a resolution of 1cm per pixel with the RGB and near infrared cameras. A flight route is planned at the start of each season for each trial and then on each occasion the same flight plan is uploaded and the UAV autonomously follows the same route, collecting images every second. The flights are planned so that there is an 80% overlap front-to-back and side-to-side for all images. This is done so that the images can be used in photogrammetry software and an accurate geo-located orthomosaic produced of each field experiment. A three-dimensional point cloud is also calculated from the photos.

Currently workflows have been developed to enable crop height, Normalised Difference Vegetation Index (NDVI), crop canopy cover and canopy temperature data to be automatically extracted from each plot of a field experiment. The height data is calculated from the point cloud data, and is as accurate as the traditional method of measuring crop height using a ruler on the ground. However, traditionally height data

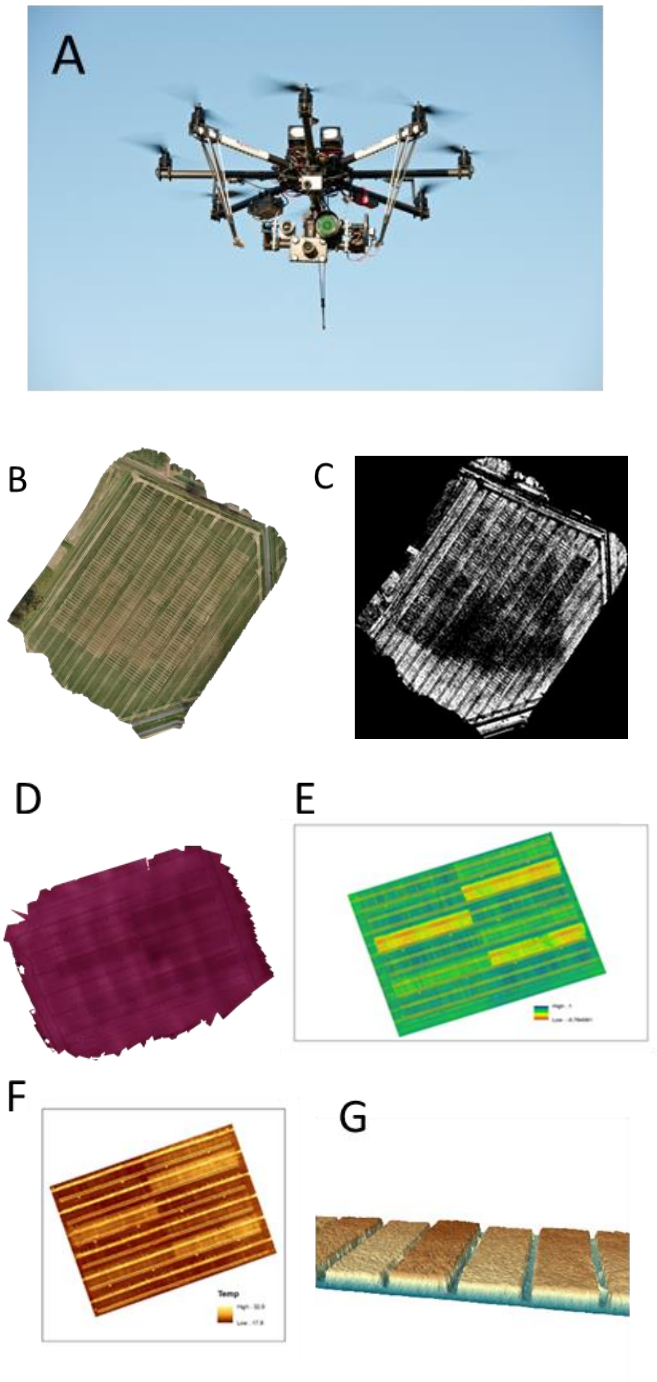

Figure 9: A) the Rothamsted UAV, B) a red-blue-green orthomosaic of the WGIN field trial at Rothamsted, c) a canopy cover mask calculated from image C, D) a near infrared orthomosaic, E) an NDVI image calculated from RGB and NIR images, F) a thermal image of the WGIN field experiment, G) a three dimensional image of some plots of the WGIN field experiment at Rothamsted.

has only been collected once, at the end of the season, but now the data can be collected weekly and thus we are able to measure the kinetics of canopy stem extension. NDVI can be used to give an estimate of canopy cover and hence crop growth; it is also possible to use this methodology to measure rates of canopy senescence and maturity.

Before NDVI or canopy temperature data can be extracted, the respective images need pre-processing to standardise the data within each image, to correct for changes in daily ambient conditions or even changes during the flight.

The canopy temperature data is being used for monitoring drought stress. As plants become drought stressed their stomata will close, reducing evapotranspiration, and as a consequence the leaf temperature will rise slightly. Therefore measuring canopy temperatures is used to compare different wheat lines and how they respond to drought. This is very difficult to measure with handheld thermometers as the small temperature differences are easily masked by changes in ambient temperature during the time to manually measure individual plots. Using a drone enables multiple plots to be measured at the same time, in the same photo, and therefore the temperature differences may be quantified accurately. Within the WGIN project a wheat mapping population is grown under irrigated and non-irrigated conditions at the John Innes Centre, and the drone will be used to collect canopy temperature data from this experiment in 2017.

For further information of this aspect of the WGIN project contact Andrew Riche or Malcolm Hawkesford at Rothamsted (andrew.riche@rothamsted.ac.uk, malcolm.hawkesford@rothamsted.ac.uk).

Reference

Holman, F H; Riche, A; Michalski, A; Castle, M; Wooster, M J; Hawkesford, M. High Throughput Field Phenotyping of Wheat Plant Height and Growth Rate in Field Plot Trials Using UAV Based Remote Sensing. REMOTE SENSING, Vol. 8, No. 12, 18.12.2016.

Key Trait: Resilience to Aphids (RRes)

- **Screening germplasm for resilience to aphids - Information to establish the likely genetic basis of resistance to cereal aphids (WP2.3)**

The aphid pests, *Sitobion avenae* and *Rhopalosiphum padi* (**Figure 10**) continue to threaten the yield potential of UK cereal crops by direct feeding damage and the vectoring of the disease, Barley Yellow Dwarf Virus. The available options for the control of cereal aphid pests however, are becoming ever more limited, with the introduction of restrictions on the use of some insecticides under a European directive and an increase in the occurrence of pyrethroid resistance in *S. avenae*. Heritable plant resilience to aphid attack is both economically sound and ecologically desirable, but to date phenotyping studies, developed and conducted in the preceding LOLA, WGIN and WISP projects (see articles on the WGIN website for full experimental methodology and results) showed little or no aphid resilience in elite hexaploid wheat varieties or Watkins collection wheat landraces. The development of aphid resilient wheat varieties would provide a sustainable alternative to pesticides.

Phenotyping studies have revealed more promising results with diploid wheat species, particularly *Aegilops tauschii, Ae speltoides* and *Triticum monococcum*, where nymph production and survival were significantly reduced or absent on some lines. The *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_1, F_2 and F_3 populations have been or are being tested in the laboratory based aphid screening bioassay, against both aphid species. The results of the aphid assays on the F_1 generations of the crosses were presented in the February 2016 WGIN Newsletter.

Results from assays with the F_2 generations of all the crosses showed that there was no discernible effect on the number of nymphs produced by adult winged aphids of either species on the *T. monococcum* crosses when

compared to an elite hexaploid control variety, Solstice. However, the weight gain by these nymphs over time on some of the lines was reduced compared to the control. Some of the F_2 plants of the MDR037 x MDR049 crosses in particular, had the best resilience against both aphid species (**Figures 11 & 12**), although the response of *S. avenae* was more promising (**Figure 12**). It was not possible to use standard statistical analytical methods on these data because the plants are not fully segregated at this stage. The data are therefore presented as a series of weight ranges (mg) to which the nymph weights have been allocated.

Figure 10: The bird cherry-oat aphid, *Rhopalosiphum padi* (left) and the grain aphid, *Sitobion avenae* (right)

These plants were taken to the F_3 generation and harvested. Of those which produced viable seed, lines exhibiting a range of aphid response from each of the crosses are now being tested in the phenotyping screen against both aphid species. Since the best results were achieved with plants from the MDR037 x MDR049 crossing events, initial studies have concentrated on those and data from the four MDR037 x MDR049 crosses (x4(3), x5(1), x11(3), and x17(1)) are shown in **Figures 13 & 14**. Again, the difference in aphid performance, i.e. weight gain over time, on the *T. monococcum* compared to the hexaploid control is most evident for *S. avenae* (**Figure 14**). Interestingly, for both aphid species, performance on the separate crossings varies and may indicate slight genotypic differences between the original parental plants or could be due to plasticity in response amongst the aphids. These plants will now be taken to F_4 with the ultimate aim of generating mapping populations. Trials with F_3 plants from MDR037 x MDR045 and MDR037 x MDR657 are ongoing. Plant material will ultimately be provided for genotyping.

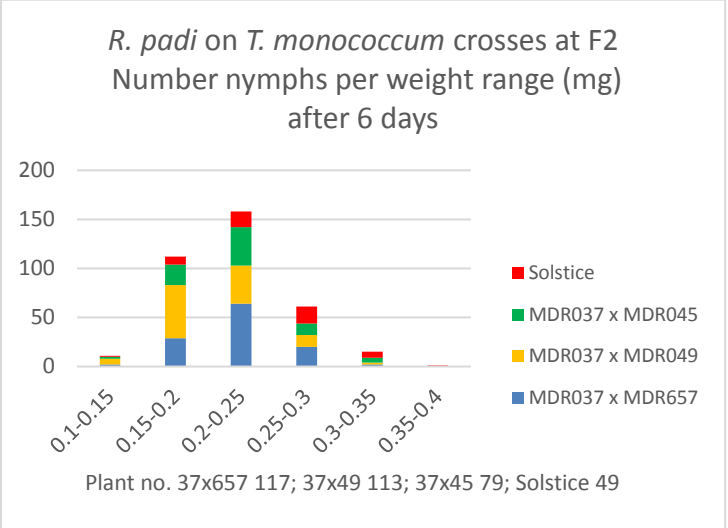

Figure 11: Number of *Rhopalosiphum padi* nymphs in different weight categories on F_2 plants of *Triticum monococcum* crosses compared to the hexaploid wheat variety Solstice.

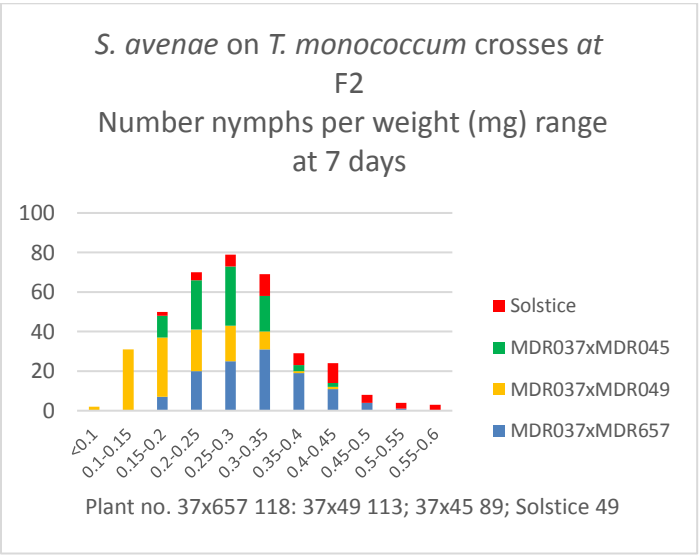

Figure 12: Number of *Sitobion avenae* nymphs in different weight categories on F_2 plants of *Triticum monococcum* crosses compared to the hexaploid wheat variety Solstice.

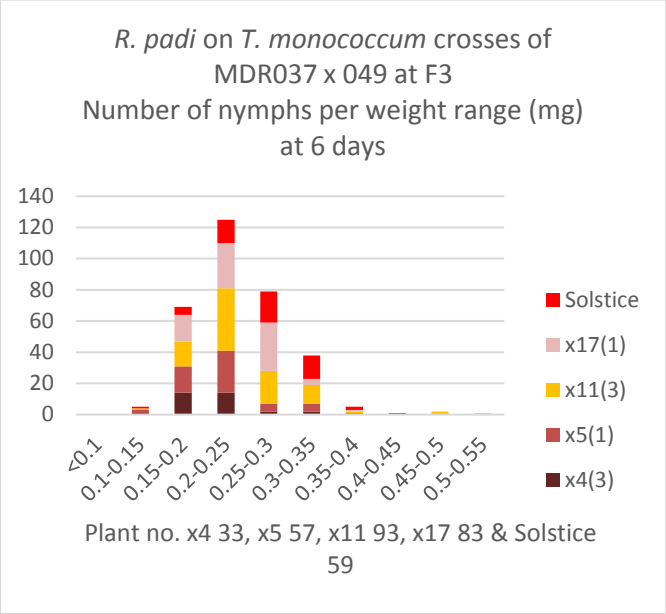

Figure 13: Number of *Rhopalosiphum padi* nymphs in different weight categories on F_3 plants of *Triticum monococcum* MDR037 x MDR049 crosses compared to the hexaploid wheat variety Solstice.

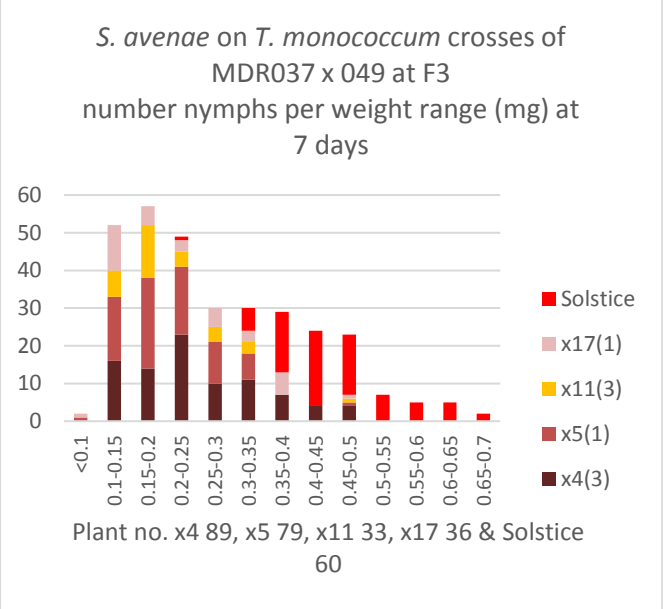

Figure 14: Number of *Sitobion avenae* nymphs in different weight categories on F_3 plants of *Triticum monococcum* MDR037 x MDR049 crosses compared to the hexaploid wheat variety Solstice.

For further information of this aspect of the WGIN project contact Lesley Smart or Gia Aradottir at Rothamsted (lesley.smart@rothamsted.ac.uk, gia.aradottir@rothamsted.ac.uk).

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

- **Exploring resistance of hexaploid wheat landraces to a broad spectrum of foliar infecting fungal pathogens**

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 yellow rust (*Puccinia striiformis*), powdery mildew (*Blumeria graminis*) and brown rust (*Puccinia triticina*). To avoid unnecessary fungicide applications, whilst protecting the yield potential of winter wheat and improving overall crop resilience, selection for host resistance to multiple foliar diseases is a high priority for the wheat breeding community.

In the WGIN 3 project the foliar disease resistance of 10 Watkins genotypes is being examined in replicated field trials on the Rothamsted Farm. Both 1st wheat (no take-all root disease) and 3rd wheat (high take-all root disease) field trials are being carried out to explore the interaction between take-all root infection and foliar disease resistance. The 10 genotypes were chosen for examination in replicated field trials in 2015, 2016 and 2017 based on their low disease scores against all 4 foliar fungal pathogens in a single replicate field trial of 740 Watkins genotypes conducted in 2008 (previously reported in WGIN Newsletter October 2008).

As reported in the previous WGIN newsletter (February 2016) yellow rust was the dominant disease which developed across the field trials in the 2015 field season. Five of the 10 genotypes exhibited moderate to high resistance against yellow rust. In repeat field trials in 2016 both yellow rust and septoria developed across the trial site in the spring, with brown rust developing later in the season. Yellow rust infection on the 10 Watkins genotypes showed a similar pattern to 2015 (**Figure 15**). Watkins 733 and 786 were most resistant to yellow rust with no sporulation visible on Watkins 733 across either field season. However, in contrast these two genotypes were heavily infected with brown rust in

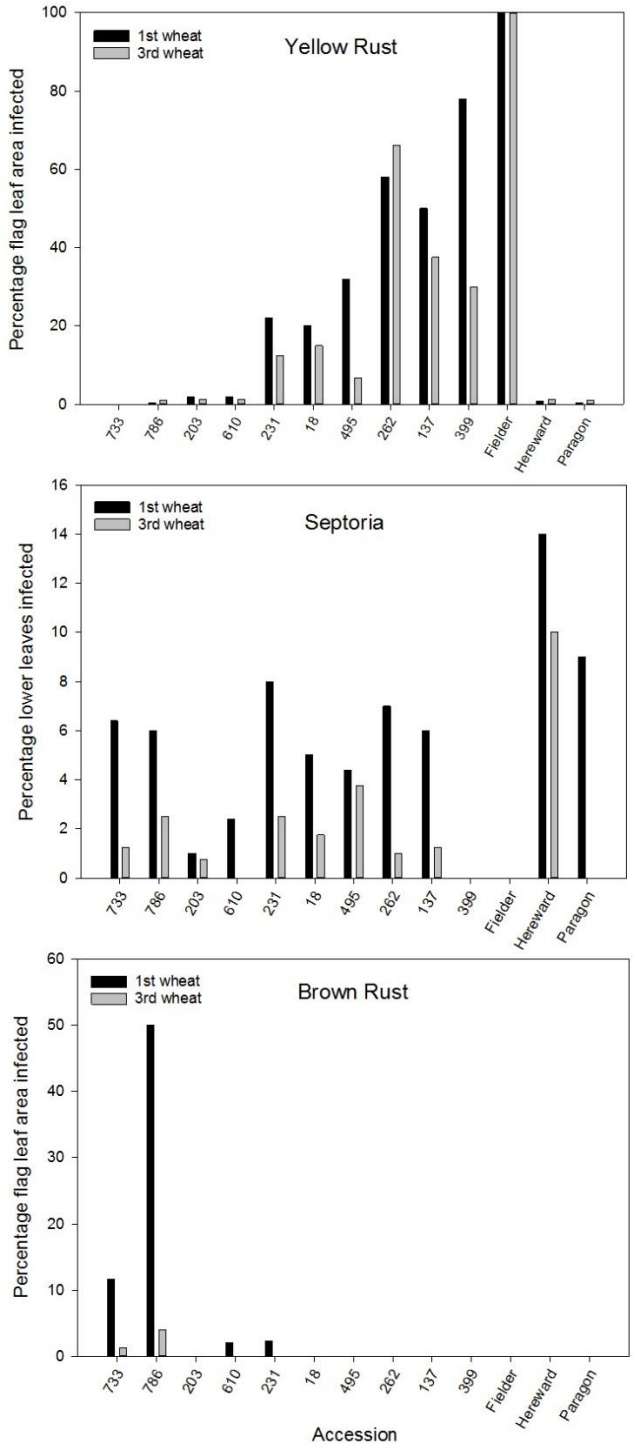

Figure 15: Yellow rust (upper panel), septoria leaf blotch (middle panel) and brown rust (lower panel) disease assessments in the 2016 field season. Yellow rust and septoria assessments were carried out on the 6th June 2016 on the flag leaf and lower leaves, respectively. On the 6th June 2016, all genotypes were at growth stage 57-61 (end of ear emergence to beginning of flowering) except Watkins 610 which was at GS 47 (booting). Brown rust was assessed on the flag leaf on the 22nd June 2016. Watkins 399 and Fielder were extremely susceptible to yellow rust so it was impossible to assess for septoria and brown rust.

the 1st wheat trial site later in the 2016 season indicating that they do not possess multi-disease resistance against both rust species (**Figure 15**). Watkins 203 and 610 are the most promising genotypes for possessing multi-disease resistance with low disease scores against all three foliar pathogens in the 2016 field trial (**Figure 15**). Watkins 610 was always at an earlier growth stage than the other genotypes within the trial which may have contributed to its low disease scores. For some genotypes with very high levels of yellow rust infection (Fielder and Watkins 399) is was impossible to assess for septoria and brown rust. The modern hexaploid wheat cultivars Paragon and Hereward were both very resistant to yellow rust, although there was some sporulation on both cultivars and evidence of extensive necrotic stripe formation on the leaves of Paragon. No brown rust was found on either cultivar. In contrast, both cultivars had clear evidence of septoria infections on the lower leaves. In general, there were lower levels of foliar disease infection in the 3rd wheat (high take-all) field site compare to the first wheat (no take-all) trial. However, follow up experiments in controlled environment conditions need to be carried out to confirm if this effect is conclusively due to an induced host response rather than a result of different foliar spore/disease pressures across the Rothamsted Farm which were unrelated to take-all infection.

- **Exploiting *Triticum monococcum* as a novel source of genetic diversity for improvement of hexaploid wheat**

Triticum monococcum is a diploid wheat species known as einkorn wheat which was cultivated during early cereal farming over 8000 years ago. The species is relatively widely found throughout Europe and the Middle East but has infrequently been used in wheat breeding.

In the earlier WGIN 1 and 2 projects a global collection of *T. monococcum* accessions were assembled at Rothamsted Research with the aim of identifying and characterising novel traits that could be used for the improvement of modern hexaploid wheat. As reported in previous WGIN newsletters a small number of accessions have been phenotyped for a range of traits including foliar disease resistance, aphid resistance,

take-all resistance, root penetration, grain texture and germination under salt and drought stress.

Recently 202 viable genotypes from the collection (from 35 countries of origin) were genotyped using the Wheat Breeders 35 K Array at Bristol University. In total, there were 1124 polymorphic SNP markers across the collection. Initial analyses reveal that there is some clustering of accessions based on their country of origin (**Figure 16**). For example, most accessions collected from Albania (red circles) or Spain (green stars) cluster closely together.

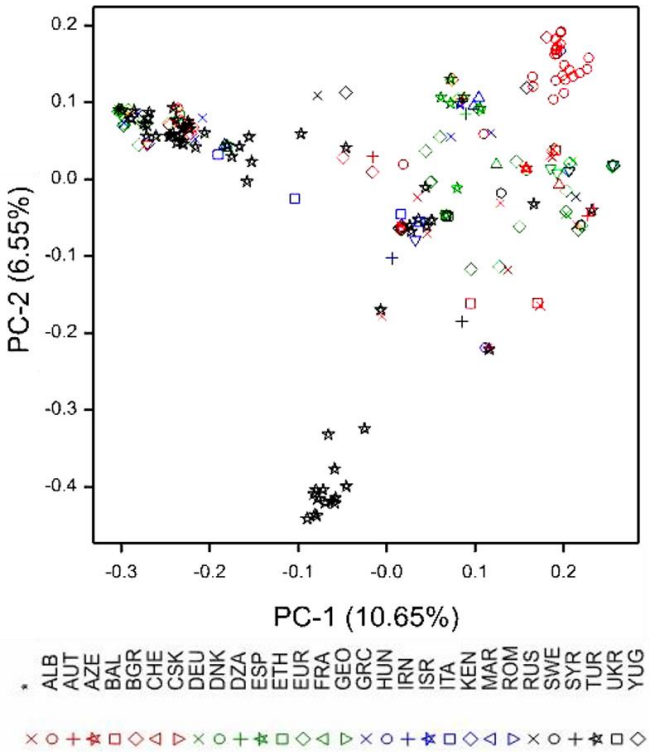

Figure 16: Principal coordinate analysis of 202 *T. monococcum* accessions based on 1124 SNP markers. The diagram shows the position of each accession in the space spanned by the first two coordinates of a relative Jaccard similarity matrix. The key for country of origin of each accession is shown in the legend.

Further analyses will shortly be carried out to explore the genetic structure within the collection in more detail and carry out marker-trait association analyses.

Various *T. monococcum* mapping populations have also been developed by single seed descent between accessions contrasting for traits of interest. Those currently being investigated are shown in Table 1. We are also testing various introgression strategies for transferring such traits into elite hexaploid wheat.

Table 1. *T. monococcum* mapping populations being used to facilitate genetic dissection of key traits.

T. monococcum mapping population	Generation	Trait of interest
MDR037 x MDR045	F_3	Aphid resistance
MDR037 x MDR049	F_3	Aphid resistance
MDR037 x MDR657	F_3	Aphid resistance
MDR037 x MDR229	F_6	Root penetration ability
MDR308 x MDR002	F_3	Septoria resistance
MDR031 x MDR043	F_6	Take-all resistance
MDR037 x MDR046	F_6	Take-all resistance

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

Section 3 Events

The next (15th) WGIN Stakeholders' Meeting will be held @ Rothamsted Research on **Thursday November 30th 2017**. Registration via Eventbrite is already possible either via the WGIN website (wgin.org.uk) or via this link https://www.eventbrite.com/e/15th-wgin-stakeholders-meeting-tickets-35456308774

Section 4 News

One Stakeholders' meeting was held in 2016, on November 30th at Rothamsted. This included talks by the principal WGIN scientists, a preliminary update on the **WGIN Promotome Capture** experiment (nb: to be revealed in the next Newsletter) as well as introducing the research of some of the trait coordinators for this

experiment, and finished with a very well received panel discussion on **Priorities for Wheat Grain Quality**, chaired by **Professor Peter Shewry**. The panel consisted of **Ian Foot** (Limagrain), **Sam Millar** (Warburtons), **Martin Savage** (NABIM) and **David Leaper** (Agrii).

This event was sponsored by RoCRE who provided delicious artisan breads, cheese and soup to sustain the participants.

Section 5 Publications 2016 to 2017

- Alba Farré, Liz Sayers, Michelle Leverington-Waite, Richard Goram, Simon Orford, Luzie Wingen, Cathy Mumford and **Simon Griffiths*** (2016) Application of a library of near isogenic lines to understand context dependent expression of QTL for grain yield and adaptive traits in bread wheat. **BMC Plant Biology** 16:161 DOI10.1186/s12870-016-0849-6
- Simon, A. L., Wellham, P. A. D., **Aradottir, G. I.**, Gange, A. C. (2017) Unravelling mycorrhiza-induced plant susceptibility to the English grain aphid *Scientific Reports* doi:10.1038/srep46497
- **Aradottir G. I.**, Martin J. L., Clark S. J., Pickett J.A., **Smart L. E.** (2016). Searching for wheat resistance to aphids and wheat bulb fly in the historical Watkins and Gediflux wheat collections. *Annals of Applied Biology* doi: 10.1111/aab.12326
- Greenslade A.F.C., Ward J.L., Martin J., Corol D.I., Clark S.J., **Smart L.E.**, **Aradottir G.I.** (2016). *Triticum monococcum* lines with distinct metabolic phenotypes and phloem based resistance to the bird cherry oat aphid *Rhopalosiphum padi*. *Annals of Applied Biology* DOI: 10.1111/aab.12274
- Mehrabi Z, **McMillan VE**, Clark IM, Canning G, **Hammond-Kosack KE**, Preston G, Hirsch PR and Mauchline TH (2016) *Pseudomonas* spp. diversity is negatively associated with suppression of the wheat take-all pathogen. *Scientific Reports*, 6., e29905
- Holman, F H; **Riche, A**; Michalski, A; Castle, M; Wooster, M J; **Hawkesford, M**. (2016) High Throughput Field Phenotyping of Wheat Plant Height and Growth Rate in Field Plot Trials Using UAV Based Remote Sensing. REMOTE SENSING, Vol. 8, No. 12, 18.12.2016.

For further information on any aspect of the WGIN project please go to www.wgin.org.uk or contact us at wgin.defra@rothamsted.ac.uk.

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Department for Environment Food & Rural Affairs

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