Next WGIN Stakeholder meeting – 17 November 2010, RRes, Harpenden

Contents:

Defra Wheat Genetic Improvement Network – Improving the environmental footprint of farming through crop genetics and targeted traits analysis

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. Established in 2003, the Wheat Genetic Improvement Network (WGIN) arose directly from a realisation in the early 2000s that over the preceding two decades there had been a widening disconnection between commercial plant breeding activities and publicly funded plant and crop research. 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. An integrated scientific 'core' which combines underpinning work on molecular markers, genetic and genomic research, together with novel trait identification, are being pursued to achieve this goal. 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, a stakeholder forum, focused meetings and peer reviewed publications. WGIN liaises with equivalent operations overseas to ensure the programme is internationally competitive.

The initial WGIN project ran for five years (2003-2008) and achieved considerable scientific success. In addition, the sustained networking activities and the availability of datasets generated by the project led to the establishment of many new wheat genetic improvement projects, including some funded jointly by the public sector and industry. Those funded by early 2008 were summarised in the May 2008 Stakeholders Newsletter and since then several additional projects have been agreed. There is no doubt that WGIN has a direct and significant impact on re-establishing the relationship between commercial plant breeding activities and public funded plant and crop research. However significant hurdles remain which currently prevent commercial implementation of much new research which should help to reduce the energy requirement and environmental impact of the UK wheat crop.

This project

The new WGIN Core Project started in 2008 to provide 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 initially funded partners are the John Innes Centre, Rothamsted Research and The University of Nottingham but support has been allocated for sub-contracted projects which were awarded in open competition during 2009.

Objective 2: Near Isogenic Lines (JIC)
Precise genetic stocks for the dissection of key agronomic traits in the UK

The WGIN team at JIC are close to completing the production of very precise genetic materials that are designed to study individual components of genetic variation for UK wheat one gene at a time. These lines are produced by the multiple rounds of crossing and selection with the aim of producing a series of lines for which most of the genetic content is derived from one variety, and just a small segment of chromosome from another. This material allows us to ask the question 'How has this particular gene helped UK breeders to achieve the gains they have?' In some cases the gene will not seem to have a beneficial effect. Does it need to be selected along with others? To address these questions the lines, known as Near Isogenic Lines (NILs) are produced in the genetic backgrounds of the two parents that were used to discover them in the first place; Avalon and Cadenza, the WGIN double haploid (DH) mapping population and the UK reference mapping population. The chromosomal regions used to produce NILs can be seen in figures 1 to 4.

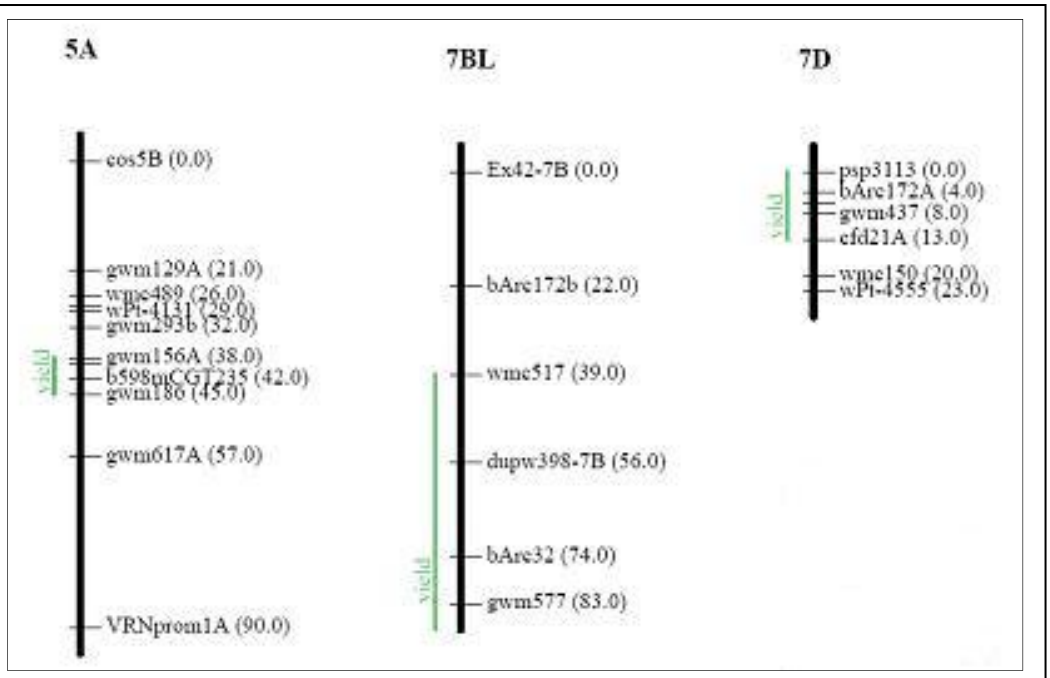

Figure 1: Mapping 3 loci controlling yield in the Avalon x Cadenza DH population

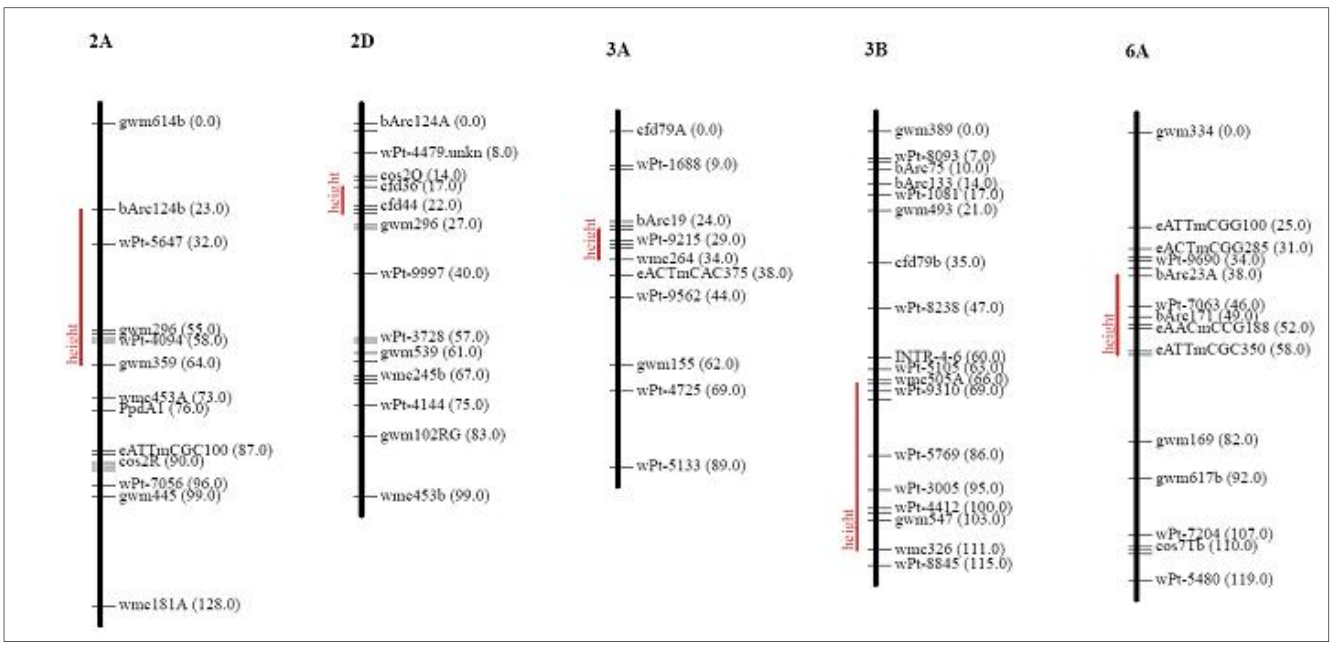

Figure 2: Mapping 5 loci controlling height in the Avalon x Cadenza DH population

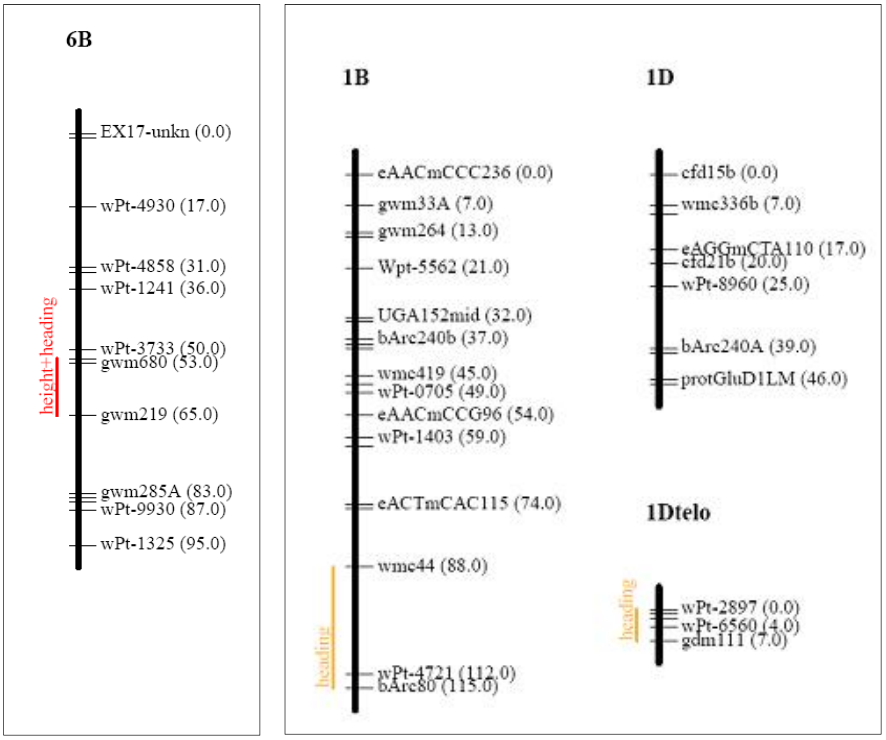

Figure 3 (left): Combined height and heading locus on Chromosome 6B, and Figure 4 (right): two heading loci on chromosome 1

They were selected to understand what controls height, heading date, and grain yield. We hope that they will also be useful in understanding other genes that may be present in the selected regions.

Focus on Objective 3 at RRes: Extending the 'Avalon × Cadenza' mapping population of doubled haploids (DH)

F_1 seeds of the 'Avalon × Cadenza' and reciprocal 'Cadenza × Avalon' crosses were provided to PLANTA (Einbeck, Germany) and in July 2008 > 1000 putative DH plants were returned. All these plants were vernalised and then grown to maturity under glass at Rothamsted Research. More than 30 grains were recovered from 484 plants, whereas 98 plants produced only 1-10 grains. DNA was prepared from each plant. During 2009-2010 growing season, the former 484 lines were bulked up in the field on ex-fallow land (two 75-cm rows per line / 15 grains per row). Most of the lines produced more than 140 g seed.

These will be used for an additional bulking-up on larger 1.8-m x 6-m plots during 2010-2011 growing season. The lines that produced 70-140g seed will be bulked-up on 1.8-m x 3-m plots. Very encouragingly, only 17 DH lines produced less than 70g seed. These lines will be hand sown in smaller plots comprising three-four 50-cm rows. The 98 plants which initially only produced 1-10 grains, have already been bulked up under glass and between 100 and 3000 grains were obtained. All these lines will be hand sown this autumn on small plots comprising three-four 50-cm rows. Phenotypes observed during the 2009-10 field season included variation in senescence date (Figure 5) variation in height and variation in ear colour (green / yellow) (Figures 6 and 7 overleaf).

Small quantities of seed from the 484 DH lines grown in the field in 2009-2010 are now available upon request for small research projects. However, to create a long term resource for the UK, DNA will be prepared from each line that is growing in the 2010-2011 season either in 1.8-m x 6-m or 1.8-m x 3-m plots. Subsequently, all seed requests will come from this harvest. The rest of the lines (115) will become available in 2012.

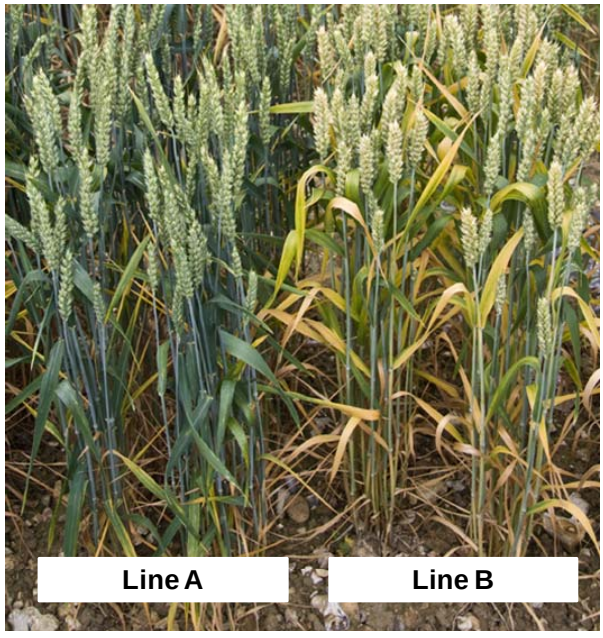

Figure 5: Variation in senescence date

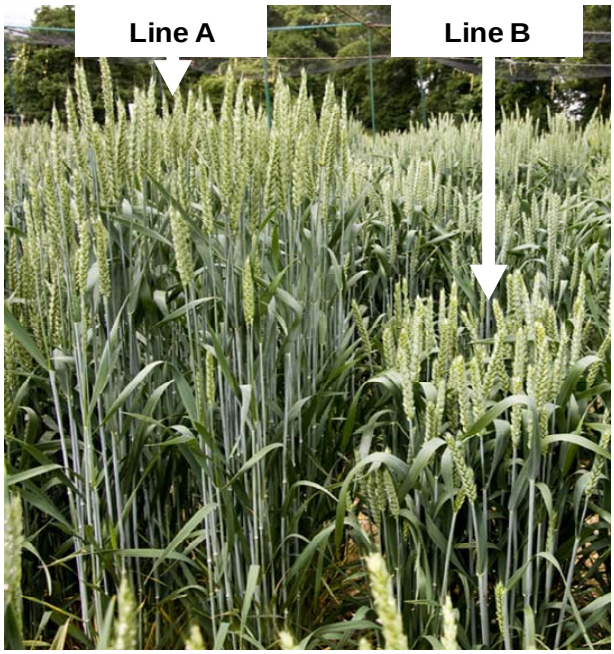

Figure 6: Height variation

Figure 7: Variation in ear colour

Objective 8: Improvements of nitrogen use efficiency and quality QTLs linked to NUE: dissecting NUE and quality traits and QTLs (RRes) D**iversity trial**

This year's harvest was compromised by dry weather during flowering time and adverse weather conditions during harvest (Figure 8). The 2010/11 diversity trial will be grown at a nitrogen regime of four nitrogen levels (0. 100, 200 and 350 kg N/ha) in a triplicated trial. It was planted this autumn with 25 varieties at Meadow at the Rothamsted farm (Table 1). Two of the double haploid lines were removed (the high/low NUtE lines) and two new commercial elite varieties were added (Stigg and Crusoe). These two varieties represent a source of material which has been derived from the use of Triticum dicoccoides. With high levels of disease resistance - particularly to *Septoria tritici* these represent novel germplasm. Both have a 'stay green effect'. Crusoe includes a dicoccoides segment associated with non-glaucousness, stay green and higher yield in UK environments (Simmonds et al 2008, Euphytica). This segment is being dissected in detail at JIC. Stigg is a candidate for the 2011 Recommended List and Crusoe has been promoted to Recommended List Trials for 2011.

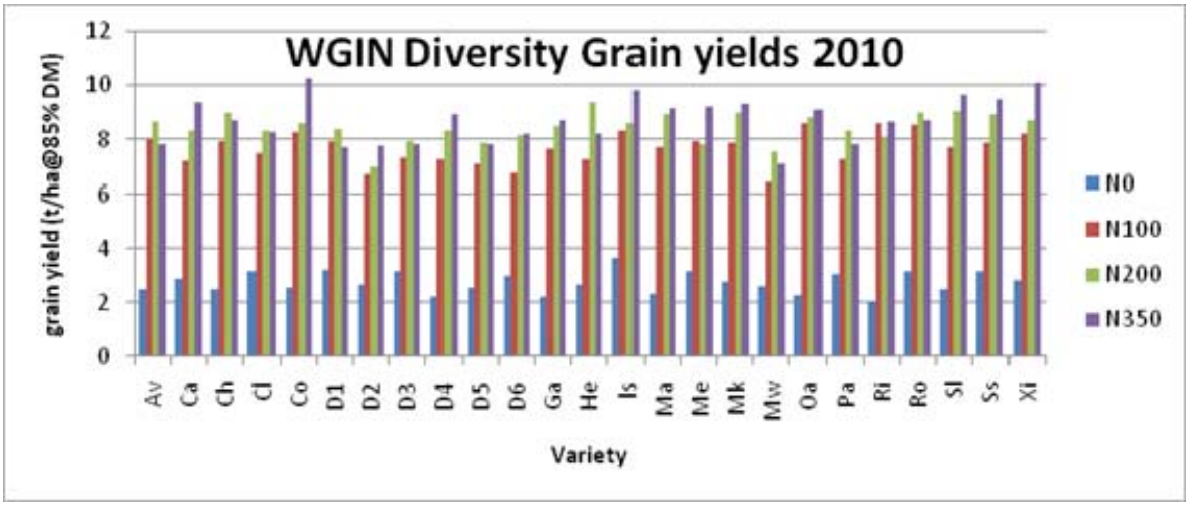

Figure 8: Grain yields, WGIN diversity trial 2010

Wheat varieties for WGIN-NUE 2010/11		W=WGIN data, D=desk study		
Variety	**Nabim**	**Rationale**	**Previous years of trials (harvest year)**	**Number of years in trial**
1. Avalon	1	WGIN DH parent; Low NupE & NutE (D), high TAB	2005-2010	6
2. Cadenza	2	WGIN DH parent; Best NupE (W), low TAB	2004-2010	7
3. Chablis NEW 09/10	2	SPRING variety (previous grown in 2004 trial) as very N-responsive variety	2004 and 2010 only	2
4. Claire	3	Biggest area on RL; WGIN DH parent; Good second wheat	2005-2010	6
5. Cordiale	2	Good second wheat. BBSRC Quality project	2006-2010	5
6. Crusoe NEW 10/11	2			
7. Gallant NEW 09/10	1	new claimed high yield and high protein type		
8. Hereward	1	Best protein on RL; benchmark bread variety. BBSRC Quality project	2004-2010	7
9. Istabraq	4	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat. BBSRC Quality project. WUE trial	2005-2010	6
10. Malacca	1	Biggest Group 1 area; DH choice; Low NupE, high NutE (W). BBSRC Quality project	2004-2010	7
11. Marksman	2	new for 2009, PRS request for BBSRC Quality project	2009 and 2010 only	2
12. Maris Widgeon	1	Tall (rht), old cultivar	2004-2010	7
13. Mercia	1	Low NupE & NutE (desk); Low Canopy N requirement; In IGF micro-array. WUE trial. RHT series	2004 and 2006-2010	6
14. Oakley NEW 09/10	4 (hard)	Hard milling type. Highest yielding wheat on RL.		
15. Paragon	1	Spring variety; WGIN mutagenesis population; High NupE (W)	2004-2010	7
16. Riband	3	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W)	2004-2010	7
17. Robigus	3	Best Group 3 yield; Best NUE, high NupE & NutE (D); Good second wheat. WUE trial	2005-2010	6
18. Stigg NEW 10/11				
19 Soissons	2	WGIN DH parent; Early maturing; High NupE, low NutE (W)	2004-2010	7
20. Solstice	2	Biggest Group 2 area; DH choice; Worst NupE (W)	2004-2010	7
21. Xi19	1	Best Group 1 yield; High NUE, NupE, NutE (D); Low NupE (W). BBSRC Quality project. WUE trial	2004-2010	7
22. AxC line 181		new in 2010	2010	1
23. AxC line 112		new in 2010	2010	1
24. AxC line 127		new in 2009	2009, 2010	2
25. AxC line 82		new in 2009	2009, 2010	2

Table 1: Wheat varieties sown for the WGIN diversity trial 2010/11

Objective 10: Take-All disease (RRes)

A. Take-all inoculum build–up in the soil

Work within the WGIN 1 project showed that wheat cultivars differ in their ability to build-up the take-all fungus in soil when grown as a first cereal crop. A manuscript presenting these findings has been prepared and accepted for publication (McMillan *et al*. (2010) Plant Pathology, in press). The galley proof of this article has been placed on the WGIN website.

The two wheat cultivars Avalon and Cadenza have consistently shown contrasting abilities to build-up the take-all fungus in the soil. These two cultivars are the parents of a large mapping population of doubled haploid (DH) lines which had already been shown to segregate for height and flowering time and are being evaluated for their Nitrogen Use Efficiency (NUE) within the WGIN programme (Objectives 3 and 8). We reported in the WGIN October 2009 Newsletter that from one of the experiments a significant correlation (R = 0.9245) between the take-all patch score, associated with the differential inoculum build-up of the different A x C lines during the previous year, and yield of the second wheat. Further analysis of this data using the numerous genetic markers available has revealed two possible major quantitative trait loci (QTLs) controlling the low take-all inoculum build-up (LowTAB) trait (Figure 9). In 2009, soil cores were taken from all 204 A x C line plots to assess their TAB potential and to gain further information on these QTLs. This year was conducive for take-all inoculum build-up, as indicated from other sites at Rothamsted, but unfortunately take-all failed to develop on the site where 204 A x C lines were grown. The roots of the bioassay plants showed symptoms of *Phialophora* spp. (Figure 10) and previous work, at Rothamsted, has shown that the presence of these fungi can delay the development of the take-all disease which may explain the lack of inoculum build-up in this field. This year we have again taken soil cores from all 624 plots in the A x C experiment for TAB to further study this trait.

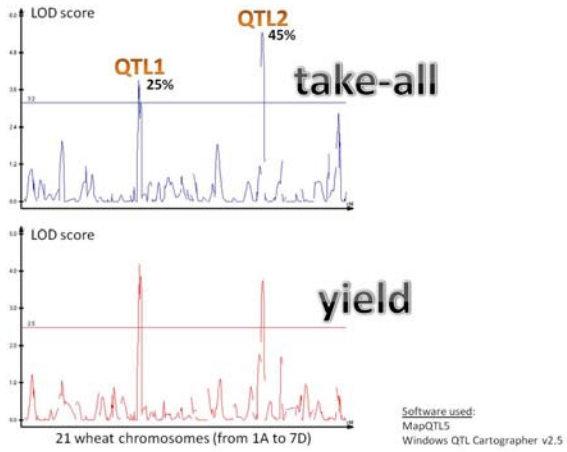

Figure 9: QTL analysis of field data from the Double Haploid (DH) lines oversown with Oakley. Above: Take All disease at the roots. Below: grain yield harvested

In addition, five years of new funding has recently been obtained from the Technology Strategy Board (TSB) as part of a special initiative called 'New Approaches to Crop Protection'. The new TSB project entitled 'Protecting Second Wheat through the Reduction of Take-All Inoculum Build Up', acronym LowTAB, (Project No TS/I001050/1) aims to identify and track the presence of this newly discovered trait in the pedigrees of the current elite wheat breeding germplasm pool used by the UK breeders. This new knowledge on the trait in current and future wheat cultivars should help farmers and farm advisors to reduce the risk of take-all by selecting a low TAB first wheat cultivar when deciding to grow consecutive wheat crops. *Phialophora* spp. with lobed hyphopodia colonise both the root and stem bases, whereas *Phialophora graminicola* only infects the roots. Roots appear light – medium brown in colour and under microscopic examination characteristic swollen cells are evident. These cells usually occur singularly or in small groups. Disease symptoms caused by *Phialophora* species can therefore be readily distinguished from those caused by the take-all fungus. *Phialophora* infections do not affect plant growth or development.

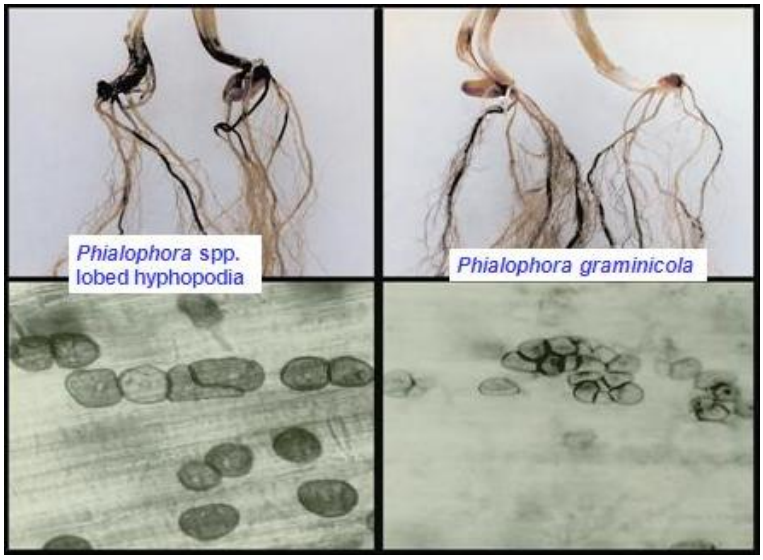

Figure 10: Colonisation of wheat roots by *Phialophora* spp.

B. Resistance to take-all in wheat

Take-all assessments of the Watkins and improved Gediflux collection for 2009 have been completed. Some lines have shown only slight take-all in both 2008 and 2009. The overall take-all disease pressure in both trial years was good and all the control plots gave data sets anticipated. For the 2010-2011 field season, a total of 540 lines will be sown again in the alpha design Watkins / Gediflux trial, this includes the 83 new Watkins lines received from JIC in 2009.

C. Resistance to stem base diseases

In 2008 the Watkins / Gediflux trial receive no fungicide treatments. As a consequence several stem base diseases developed. The details of these stem base diseases assessments are on the web site. Eyespot was the most common stem base disease. In the control plots 77% of the straws were affected, 44% in the moderate or severe category. Some of the Watkins lines had only slight infection and appeared to be relatively resistant to the disease. These lines, 45 in total, together with some fully susceptible lines were further assessed for the presence of known disease resistant genes by Chris Burt at JIC (see article below).

Eyespot Resistance in the Watkins Collection, Chris Burt and Paul Nicholson, JIC

Eyespot is an economically important stem base disease of wheat caused by two closely related species of fungi, *Oculimacula acuformis* and *Oculimacula yallundae* (Figure 11). However, there is a shortage of resistances available for use by plant breeders. The only resistances used in commercial cultivars of wheat are: *Pch1* from the wild relative *Aegilops ventricosa; Pch2* derived from the French variety Cappelle Desprez; and a gene on chromosome 5A, also from Cappelle Desprez.

To identify novel resistances to the disease, 740 lines from the Watkins collection were grown in a field trial at Rothamsted Research in 2009 (Figure 12) and were scored for eyespot stem penetration by Dr. Richard Gutteridge. From this data a group of 45 highly resistant lines and a group of 33 highly susceptible lines were identified. It is possible that the resistance in these lines may be due to currently known resistances, so DNA from the resistant and susceptible lines identified in the field trial were tested for the presence or absence of *Pch1, Pch2* and the 5A gene, using DNA markers that are known to be genetically linked to the resistances.

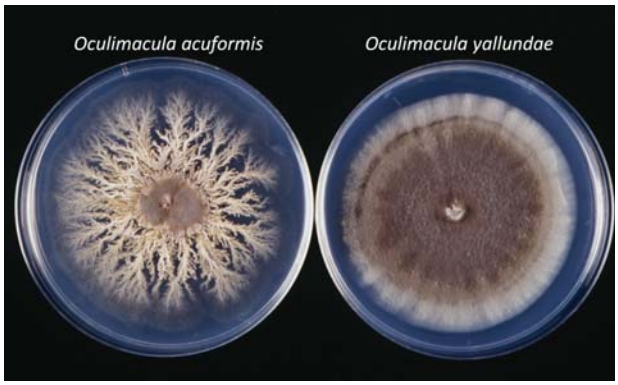

Figure 11: Eyespot causing fungi *Oculimacula acuformis* and *Oculimacula vallundae*

Figure 12: Watkins collection field trial at Rothamsted Research in 2009

Pch1 was not found in any of the tested lines. However, this was expected as the material was collected in the 1930's, whilst *Pch1* was not introduced into wheat until 1967. *Pch2* was found in 2 of the 45 resistant lines and 5 of the susceptible lines, and overall its presence was not found to be associated with resistance. Although this may seem unexpected, previous studies have shown that *Pch2* is not always effective at the adult plant stage and may not provide a significant level of resistance when tested in a field trial. In comparison, the chromosome 5A gene was found to be present in 5 of the highly resistant lines but was not present in any of the susceptible lines. Over the resistant and susceptible groups, this resistance gene appears to increase the level of resistance to eyespot. Interestingly, from the 45 resistant lines, 38 have no known resistance genes suggesting that there are novel sources of resistance within the Watkin's collection.

Further work is required to re-test the resistant and susceptible groups more accurately in controlled tests in glasshouses or growth rooms to both *O. yallundae* and *O. acuformis* species of the pathogen. In addition, a genetic mapping population has been developed between the resistant Watkin's line 827 and the eyespot susceptible spring wheat cultivar Paragon. Providing this resistant line demonstrates high levels of resistance in the repeat tests, this population could be used to identify the genetic locations of novel resistance genes.

Use of WGIN data:

A limited survey was conducted earlier this year to find out how WGIN data is being used. Table 2 below lists recently approved projects that have used WGIN data in their grant application. It has been acknowledged that WGIN data was useful in the GREEN GRAIN project. There are plans to use information from WGIN NUE in the Fr7 NUE-CROPS project. WGIN data is also used for educational purposes in the course on "Quantitative Methods in Plant Breeding", which is taught annually by Ian Mackey at NIAB. We are interested to hear from anyone using WGIN data. If you do, please e-mail us on **wgin.defra@bbsrc.ac.uk**.

Principal Investigator	Andy Phillips	Andy Phillips	Kim Hammond-Kosack
Co-PIs	Alison Huttly, Jane Ward	Cristobal Uauy, JIC	Industry PI Sarah Holdgate
PI location	RRes	RRes	RRes
General Research Topic	Wheat grain colour	TILLING in wheat	Take All
Sponsor	BBSRC	BBSRC	
Project type	Committee B	BBR Fund	TSB
Project Title	Investigating the role of flavonoid biosynthesis in coat-imposed dormancy to facilitate the breeding of white-grained varieties of wheat	Provision of TILLING resources and platforms in wheat.	Protecting Second Wheat through the Reduction of Take-All Inoculum Build Up', acronym LowTAB
Project Code	BB/H012362/1	BB/I000607/1	TS/I001050/1
Duration	01/09/10 to 31/08/13	01/09/10 to 31/08/11	5 years
Funding amount (total)	£602,358	£220,302	£120,000
New posts created	yes	yes	no
Purchase of new equipment	no	no	no
UK collaborators	Dr. Peter Jack, RAGT. Dr. Cristobal Uauy and Dr. John Flintham, JIC.	Dr. Cristobal Uauy, JIC	RAGT, Limagrain, KWS
Overseas collaborators	NA	Dr. Luca Comai, UC Davis, USA	NA
WGIN input	Cadenza EMS population	Cadenza EMS population and TILLING platform	Take-All findings and Avalon x Cadenza DH population map

Table 2: Use of WGIN data in successful grant applications

Forthcoming events:

WGIN Stakeholders Meeting
17 November 2010, RRes
Programme

10:00 Arrival and coffee
10:15 Welcome – *Peter Shewry, RRes*
10:20 The wheat market – an international perspective - *Michael Archer, HGCA*

The Wheat Genetic Improvement Network

10:40 WGIN: Overview and update on RRes WGIN research – *Kim Hammond-Kosack, RRes*
11:00: Genetic diversity of the Watkins collection – *Luzie Wingen, JIC*
11:20 Water and heat stress throughout the crop cycle - *John Foulkes, University of Nottingham*
11:40 Coffee

End user developments

12:00 100% UK wheat – *Paul Molyneux, Hovis*
12:20 Wheat quality requirements – *Simon Penson, Campden BRI*
12:40 Bioethanol production – *David Maxwell, Vivergo*
13:00 Lunch / Poster session (posters on wheat research)

Wheat initiatives

14:00 The Crop Improvement Club – *Simon Bright, BBSRC*
14:20 Wheat sequencing project - *Gary Barker, University of Bristol*
14:40 Wheat LoLa - *Graham Moore, JIC*
15:00 CIMMYT 'wheat yield consortia' – *Martin Parry, RRes*
15:20 Bio break

Farm level yields

15:30 Discussion panel on UK wheat field yields lagging behind breeders projections

Discussion Chair: Peter Shewry, RRes
Panellists:

- Chris Bean, technical director, United Agri Products
- Ian Blackhouse, National Farmers Union Combinable Crops Board
- Roger Sylvester-Bradley, principle research scientist, ADAS
- Tim Isaac, regional advisor, Country Land and Business Association Limited Eastern Region
- Richard Law, farmer
- Ian Mackay, statistical geneticist, NIAB
- Richard Summers, wheat breeder, BSPB/RAGT

17:10 Tea and finish

For further information on the WGIN project please see www.wgin.org.uk or contact us at wgin.defra@bbsrc.ac.uk.

The contributors to this newsletter were: At Rothamsted Research: Kim Hammond-Kosack, Malcolm Hawkesford, Richard Gutteridge, Kostya Kanyuka and Elke Anzinger. At the John Innes Centre: Simon Griffith, Luzie Wingen, Simon Orford, Chris Burt and Paul Nicholson..

.