

WGIN

Stakeholder's Newsletter



November 2012

WGIN Field Visit to JIC 28th June 2012

The 10th WGIN Stakeholder meeting – 27 November 2012, RRes, Harpenden

Contents:

Project Background	Page 1
WGIN and other funders	Page 2
Resources and Archived Samples	Page 3
Subcontractor Projects	Page 8
News and Events	Page 8
Publications	Page 8
Stakeholders Meeting Agenda	Page 9

Defra Wheat Genetic Improvement Network – Improving the environmental footprint of farming 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. 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 (SNL) and since then many additional projects have been agreed (see [November 2010](#) SNL). 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.

Section 2. The ongoing relationship between WGIN and other major wheat research initiative supported by other UK funders

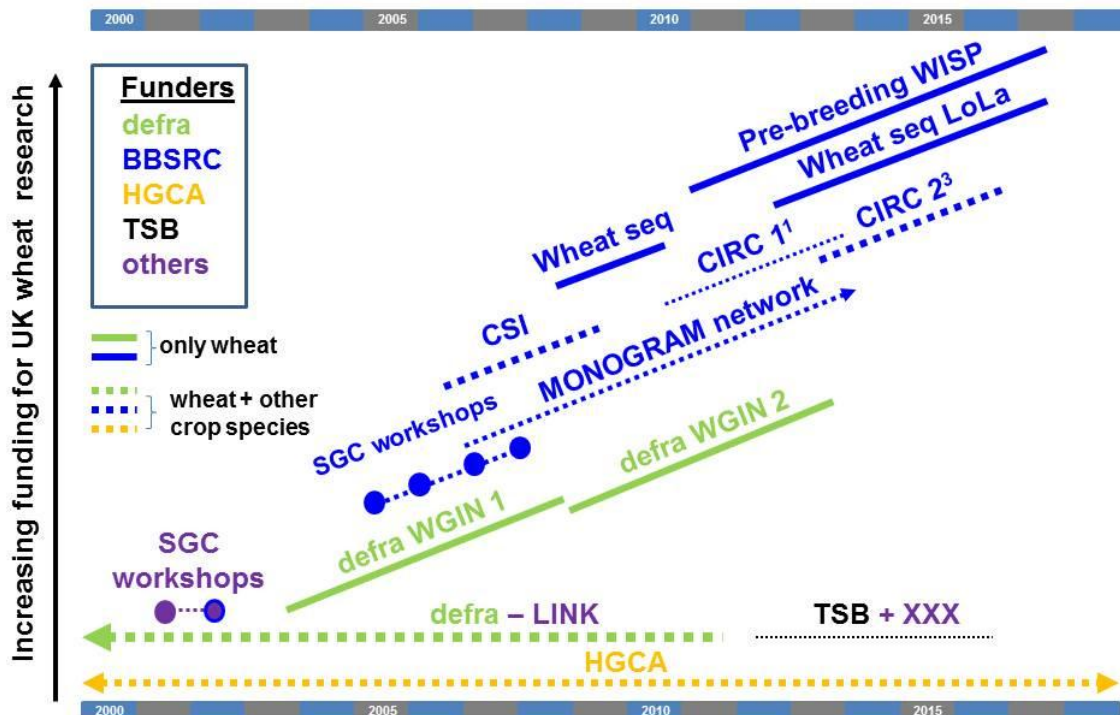
The WGIN is now regarded by Defra, the UK-internationally wheat research and wheat stakeholder community as a highly effective **NETWORKING PLATFORM** that provides four functions.

1. Access to IP free knowledge, techniques and resources
2. Seed funding for exploratory pilot projects
3. Fostering close links between the private sector (breeding and other companies) and academics to achieve new and challenging goals together.
4. Providing a focus for international collaborations involving multiple UK partners

The availability of these four interconnected functions for 9 years has resulted in significant use of WGIN data and genetic resources by the wider UK community, both within existing projects or increasing as part of new projects.

The diagram below illustrates the relationship between WGIN and the other major UK major initiatives supporting wheat research over the period 2000-2017. Prior to WGIN, research meetings with a wheat focus occurred rarely. The various Small Grain Cereals (SGC) workshops held in the early 2000s started to create a multi UK location academic research community that linked with industry. Thereafter the start of continuous WGIN funding and the establishment of the Networking Platform helped many in the UK wheat community to bid successfully into successive BBSRC initiatives, and/or to leverage additional funding from existing sources such as Defra–LINK, HGCA and, since 2011, new Technology Strategy Board funding. Unlike WGIN, most of these newly funded wheat projects have focussed on single topics, have been of limited duration, typically 2 or 3 years, and the data and resources generated have been subject to IP, and therefore unavailable to the wider UK wheat community. The recently funded BBSRC Pre-breeding WISP programme is the only other multi-location, long duration project (possibly funded for up to 6 years) to have emerged over this time-frame. However, although interactions with the UK- based wheat breeders occur within WISP, only minimal networking activities with the wider UK wheat industry are planned. **The funding of WGIN 3 (2013-2018) and the NETWORKING PLATFORM would be highly advantageous** to the UK wheat research community, fostering academic-industry partnership to tackle existing and emerging difficulties for the wheat crop and wheat products via genetic improvement.

The relationship between WGIN and the major funding initiatives supporting UK wheat research (2000-2017)



Section 3. Resources and Archived Samples

In this section of the Newsletter we are providing updates on the genetic resources and molecular techniques used and / or developed within the WGIN2 project. We are also providing information on the archived grain samples arising from the multiple years of field trials. In the [March 2007 Stakeholder Newsletter](#) full details are provided on the resources developed during WGIN1. If you would like to exploit any of these open access resources please contact [Simon Griffiths](#) (John Innes Centre) or [Kim Hammond-Kosack](#) (Rothamsted Research).

Avalon x Cadenza

The Avalon x Cadenza double haploid (DH) population is a reference for UK bread wheat developed within WGIN. WGIN genotyping data includes DArT and SSRs on 206 lines and allowing the genetic mapping of 351 loci all available on the WGIN website. KASPar (<http://www.kbioscience.co.uk/>) markers have been added to the mapping population by Keith Edward's team at the University of Bristol (Allen et al., 2011) and more information on this data will be appearing soon at <http://www.cerealsdb.uk.net/> and the WGIN website.

QTL analysis for field trial data 2005-2008 for the phenotypes, days to ear emergence, grain length, grain surface area, grain width, grain yield, straw fill and 1000 dehulled grain weight is available on the website showing the nearest markers and also as graphical representations. See Excel files "[QTL Results for phenotype data for the Avalon x Cadenza double haploid population June 2012 update](#)" and "[QTL summary for the above data June 2012](#)". Small numbers of seed for the mapping population are available from JIC on request please contact [Liz Sayers](#) (John Innes Centre)

Extending the 'Avalon x Cadenza' mapping population of doubled haploids (DH)

The original A x C mapping population generated in WGIN1 is now used for a wide range of phenotyping projects in the UK and also elsewhere. To assist with the fine mapping of genes and QTLs controlling traits of interest segregating in this population, funds were provided by the former director of RRes, Professor Ian Crute to increase the population size. Subsequently, WGIN2 funds were used to

multiply the newly generated A x C DH lines and to make small aliquots of seed for each line available to any interested UK plant scientist, wheat geneticist or breeder for research purposes. In total, 574 additional A x C lines are now available from RRes. Contact – [Kostya Kanyuka](#) and / or [Kim Hammond-Kosack](#).

The full details of how the new population was generated in 2008 and subsequently multiplied are given in the [May 2010 WGIN Newsletter](#).

In 2012, using BBSRC funding available within the Wheat Pre-breeding WISP Project, each line in the extended A x C population has been genotyped with KASPAR markers. This has resulted in 223 mapped loci being surveyed using approximately 10 evenly spaced probes for each chromosome. This genotyping was done by Sacha Allen and Keith Edwards at the University of Bristol.

In March 2013, the 2nd A x C workshop will be held – see [page 8](#) of this newsletter for full details.

New wheat populations

Several new wheat populations have been made at the JIC. A Chinese Spring x Paragon population with 287 recombinant inbred lines was created through WGIN and mapped with 350 KASPar markers under the BBSRC Crop Improvement club grant: '*Development and validation of a flexible genotyping platform for wheat*'. This data is being prepared for upload, again onto Cereals db and WGIN websites.

The Synthetic (JIC W5993) x Paragon recombinant inbred lines (RIL) population has 280 lines available. Genotyping is in progress using KASPar markers, and will be available on the WGIN website by the end of 2012.

A population specifically targeted to the question of drought tolerance in the UK is Paragon x Garcia. These parents were chosen based on the outputs of a UK LINK project: '*Improving water use efficiency and drought tolerance in UK winter wheats*'. This RIL population is less advanced. At present with 350 lines at stage F₄ seed.

Near Isogenic Lines (NILs)

The Near Isogenic Lines (NILs) previously developed using MAS (Marker Assisted Selection) are now described. Further production of crossing is underway in autumn 2012.

Avalon x Cadenza NILs:

There are 400 AxC lines BC₂F₄ (Backcross 2 Filial 4) and 100 AxC lines at BC₂F₃ to be drilled in the field in 3 reps of 5.75m² plots 2012/13. These trials have two functions. Firstly we will determine whether we have used marker assisted selection to move single QTL into uniform genetic backgrounds and that the phenotypic effect of the gene underlying the QTL is still detectable. WGIN has already achieved this in small (1m²) plots, but the trials this year will use larger plots allowing the realistic assessment of grain yield effects. Secondly we will understand some of the wider agronomic implications of variation at these single genes on a wide range of traits and, eventually, in response to different environments such as drought and low nitrogen. The specific genetic effects under investigation are listed below:

NILs in the UK winter bread making variety Avalon:

1B heading / late, 1D heading early, 2A height / short, 2D height / tall, 2D height yield, 3B height / short, 5A yield, 6A height, 6B height, 7B and 7D yield.

NILs in the UK alternative variety Cadenza:

1B heading early, 1D heading, 2D height, 2A height /tall, 2D height, 3B height and yield, 6A height, 6B height and heading have also been tested. Yield plots using same parameters for 3B NILs were harvested in 2012.

The number letter combinations refer to wheat chromosomes. The word to the trait of interest (height, heading, yield).

Grain Size NILs:

The grain size NILs are derived from Shamrock x Shango at 7A, Avalon x Cadenza at 3B and 5A and Paragon populations for each. They have continued through to mainly BC₃ this year.

Lr19 NILs:

An alien chromosome segment carrying the rust resistance gene *Lr19* from *Agropyron elongatum* is being followed in 2 sets of crosses, Oasis, Kamb1 and Wheatear x Paragon to BC₄ and Oasis, Kamb1 and Wheatear x Alchemy to BC₃, grown again due to poor seed production. WGIN interest in this segment is based on the fact that, apart from disease resistance, this introgression appears to benefit yield and resource use in some environments. Does it confer any benefit in the UK?

Malacca x Hereward NILs:

A range of bread-making functionality traits for baking quality will be tested for, including loaf

volume and cell number. Bulking up in the field this year from BC₃F₂ material and test baking from harvest 2014. These NILs were based on QTL discovered in the breadmaking functionality LINK project.

EMS Mutated Paragon and Cadenza

In WGIN1, seed treatment with the mutagen ethylmethanesulphonate (EMS) was used to generate novel variation throughout the wheat genome. At JIC the selected variety was Paragon, whilst at RRes the variety Cadenza was used. Following mutagenesis, the surviving viable seed was used to generate an initial M₂ population and both DNA and M₃ seed samples were archived.

At JIC, the M₂ mutagenised Paragon population was then taken rapidly to the M₅ generation using the single seed descent (SSD) method, and then was field phenotyped at the M₆ generation.

At RRes, the M₂ mutagenised Cadenza population was taken to the M₃ generation and archived. In addition, in collaboration with the EU HEALTHGRAIN programme, 3,750 lines were taken to M₆ and evaluated in the field for a wide variety of characters. These analyses revealed variation in plant height, time of ear emergence, ear glaucosity, ear shape, fertility and resistance to several diseases (Rakszegi et al., 2010, Euphytica 174, 409-421). Detailed phenotype data is available on request from [Andy Phillips](#) (RRes).

DNA samples from the RRes Cadenza population have been used extensively for gene-based mutation screening (TILLING) using a variety of PCR-based methods. This resource continues to be used within BBSRC and other projects to generate novel alleles in various traits of interest, including starch biosynthesis and gibberellin signalling (Botticella et al., 2011, BMC Plant Biol 11; Sestili et al., 2010, Molecular Breeding 25, 145-154). In a subsequent project funded by BBSRC, 2,200 M₂ lines of the Cadenza population were grown to generate high quality DNA stocks for distribution as a TILLING resource. In collaboration with Cristobal Uauy at JIC and Jane Coghill at the University of Bristol, a novel high-throughput TILLING protocol based on sequence capture was also developed. Capture-based sequencing of the gene space in at least 1000 of the Cadenza EMS lines will be carried out as part of a LOLA ("Triticeae Genomics for Sustainable Agriculture") led by Jane Rogers at TGAC, which will facilitate mutation screening *in silico*.

TILLING- Targeting Induced local Lesions IN Genomes – See [March 2007](#) WGIN Newsletter for outline details of this technique and McCallum CM et al. (2000) Plant Physiol. 123, 439-442.

	M2 pop ⁿ size	DNA (generation)	Other generations available as seed	Estimated Mutation frequency
Paragon		M2	M5/M6	
Cadenza	4,500	M2	M3/M6	~35 mutations/MB

Table 1: Summary Table EMS Mutated Paragon and Cadenza

Watkins Collection

Full Details of this unique 1930s winter and spring wheat collection can be found in the presented slides, [Dr Luzie Wingen gave at the Nov 2010 Stakeholders Meeting](#), and by contacting [Simon Griffiths](#).

The *Triticum monococcum* resources

T. monococcum is a diploid wheat ($2n=2x=14$, A^mA^m genome), also referred to as einkorn wheat, which is closely related to hexaploid wheat. Although domesticated 8000 years ago and dominating early human farming activity, *T. monococcum* has been infrequently used in wheat breeding. Wheat genetic improvement often relies on the enlargement of gene pools by introducing novel traits from closely-related germplasm. A core collection of 30 *T. monococcum* accessions is maintained at Rothamsted Research. These core accessions were genetically purified from landrace stocks originally obtained from the Vavilov Institute in St Petersburg, Russia. This core collection has already been extensively genotyped (SSR and DART marker analysis) and phenotyped primarily for various biotic and abiotic stress traits and some grain quality traits (Jing et al., (2007) Journal of Experimental Botany 58, 3749-3764, Jing et al., (2008) New Phytologist 179, 1121-1132).

A further 482 individual *T. monococcum* genotypes (accession numbers - MDR500-MDR642 and MDR650-MDR710) have been acquired from other global collections and small quantities seed stocks are available for each genotype. Phenotyping and genotyping of this larger collection is far more limited.

To assist in genetic analyses, a limited number of F₁ seed is available for a total of 63 crosses. In addition, 7 mapping populations have been advance to at least the F₃ generation.

To provide additional variation, several mutagenised *T. monococcum* populations are available at either the M1 or M3 generations, following two types of mutagenic treatments. Namely, accession MDR50, treatment EMS, generation M3, MDR308 - 0.3 % EMS – M1, MDR308 - 0.4 % EMS – M1 and M3, MDR308 - 0.5 % EMS – M1 and M3 and three MDR308 ion-beam treated (IBT) populations; 2N, 5N, 8N exposure rates.

T. monococcum is a wheat species suitable for phenotyping under UK field conditions and is usually hand sown into shallow drills in the autumn. However, extreme care needs to be taken when selecting the herbicide regime to ensure the plants are not severely damaged.



Fig2 - *T. monococcum*(A^m A^m, 2n=2x=14) a cultivated diploid einkorn wheat

Grain and Straw Samples in the Avalon x Cadenza Field Trials

The double haploid Avalon x Cadenza mapping population (204 lines) along with the two parental lines have been grown since 2007 in replicated trials at defined N rates (high and low applications). In all cases, soil cores were taken in February/March to assess residual soil N. Grain and straw yield and N contents, long with parameters including crop height, flowering time, post anthesis canopy longevity, TGW and in some cases, grain mineral content have been measured. In addition dried and milled grain and straw from all trials has been archived, and some fresh grain samples from each plot have been stored in a sealed box at -20°C for selected years. Samples are available upon request.

Harvest Year	Site	N-Level (kg/ha)	Trial Number
2007	Rothamsted, Black Horse	200	719
2008	Rothamsted, Bones Close	100	817
2008	Woburn, Farfield/Lansome	100	851/2/3
2009 ^x	Rothamsted, Fosters/Summerdells	100	903/904
2010	Rothamsted, Black Horse	200	1036/7
2011	Rothamsted, Great Harpenden 1	200	1103
2012 ^{*x}	Rothamsted, Bones Close	50	1202
2013 ^{*x}	Rothamsted, Black Horse	50	1319

Table 2: Avalon x Cadenza Trials

^{*} Funded outside of WGIN
^x No grain samples available



Fig 3 – Avalon x Cadenza Mapping Population Trial, 2011 – Great Harpenden 1 @ 200 N-Level

Grain and Straw Samples From the Nitrogen-Variety Field Trials (Diversity Trial)

For each of the varieties listed in table 3 ([see page 7](#)), and for each year indicated, a 1 kg grain sample has been dried to 12% moisture content and then stored in a sealed box at -20°C. For each variety all the experimental replicates for each N regime used are available. Small grain samples can be requested from the seed archive at Rothamsted Research for any experimental purpose via the WGIN e-mail address wgin.defra@rothamsted.ac.uk. In addition, dried and milled grain and straw are available in small quantities for all varieties and treatments in all years.

Table 3: Diversity Trial Wheat Varieties - 2009-2013

Variety	Nabim	Rationale	Years of trials (harvest year)
A C Barrie		Canadian re wheat. Disease sensitive, Tall, High grain N, Low yield, spring type	13
Avalon	1	WGIN DH parent; Low NupE & NutE (D*), high TAB	09/10/11/12/13
Cadenza	2	WGIN DH parent; Best NupE (W*), low TAB	09/10/11/12/13
Chablis	2	SPRING variety (previous grown in 2004 trial) as very N-responsive variety	10/11/12/13
Claire	3	Biggest area on RL; WGIN DH parent; Good second wheat	09/10/11/12/13
Cocoon	3	Tall variety, high yield, 2010 introduction, eyespot and rust resistant	13
Conqueror	4	New Grp 4, very high yielding	12/13
Cordiale	2	Good second wheat. BBSRC Quality project	09/10/11/12/13
Crusoe	2		11/12/13
Gallant	1	new claimed high yield and high protein type	10/11/12/13
Hereford	4	Feed (not on RL), high yield, brown rust susceptible, possible low take-all build-up and good resistance, multi-trait	12/13
Hereward	1	Best protein on RL; benchmark bread variety. BBSRC Quality project	09/10/11/12/13
Hurley		Low NupE & NutE in 2004 WGIN trial	09
Istabraq	4	Best yield on RL; Distilling cultivar; In LINK 'GREENgrain'; Good second wheat. BBSRC Quality project. WUE trial	09/10/11/12/13
Malacca	1	Biggest Group 1 area; DH choice; Low NupE, high NutE (W*). BBSRC Quality project	09/10/11/12/13
Marksman	2	new for 2009, PRS request for BBSRC Quality project	09/10/11/12/13
Maris Widgeon	1	Tall (rht), old cultivar	09/10/11/12/13
Mercia	1	Low NupE & NutE (D*); Low Canopy N requirement; In IGF micro-array. WUE trial. RHT series	09/10/11/12/13
Oakley	4(hard)	Hard milling type. Highest yielding wheat on RL.	10/11/12
Paragon	1	Spring variety; WGIN mutagenesis population; High NupE (W*)	09/10/11/12/13
Riband	3	WGIN DH parent; Distilling cultivar; In LINK 'GREENgrain'; High NutE (W*)	09/10/11/12/13
Robigus	3	Best Group 3 yield; Best NUE, high NupE & NutE (D*); Good second wheat. WUE trial	09/10/11/12/13
Stigg	4?	Carries dicoccoides, High disease resistance, shows the 'stay green' character	11/12/13
Soissons	2	WGIN DH parent; Early maturing; High NupE, low NutE (W*)	09/10/11/12/13
Solstice	2	Biggest Group 2 area; DH choice; Worst NupE (W*)	09/10/11/12/13
Xi19	1	Best Group 1 yield; High NUE, NupE, NutE (D*); Low NupE (W*). BBSRC Quality project. WUE trial	09/10/11/12/13
Zebedee	3	High WUE, group 3, Multi trait	12/13
AxC line 181		new in 2010	10/11
AxC line 112		new in 2010	10/11
AxC line 127		new in 2009 – good early export from leaves	09/10/11/12
AxC line 82		new in 2009 – slow early export from leaves	09/10/11/12

N.B Further data on previous years (03-08) can be found in the [May 2009](#) Newsletter

* (D) – defra Desk Study (A study of the scope for the application of crop genomics and breeding to increase nitrogen economy within cereal and rapeseed based food chains. AR0714)

*(W) – WGIN field Data

Section 4. Sub-contractor projects

A total sum of £50K was set aside in WGIN2 to fund two sub-contractor projects predominantly for two main purposes. Firstly, to enhance the value of the main projects by involving other parties that will provide novel technology and/or novel phenotyping expertise on related traits, for example root structure. Secondly, these funds could be used to extend promising results arising from finishing LINK projects that will benefit their commercial exploitation by the UK wheat breeders and/or ideas resulting from discussions with the breeders. The following projects were selected in October 2009 following an approved application process:

Non-destructive screening of WGIN Paragon mutants for grain NUE traits - Richard Weightman, ADAS (1 year)

- [Project Information](#)
- [Final Report](#) + [Data](#)

Exploring the use of $\Delta^{18}\text{O}$ and total mineral ash content in wheat as a new tools for phenotyping wheat with respect to water inputs – John Foulkes, University of Nottingham (2 years)

- [Project Information](#)
- [Interim Report](#) + [Presentation](#)

Section 5. Events

10th WGIN Stakeholders Meeting – 27th November 2012

The 10th WGIN Stakeholders Meeting will take place on 27th November 2012 at Rothamsted Research. As in previous years, an afternoon panel discussion will take place centred around the topic "**Changing Disease Patterns**". Please see [agenda](#). If you are interested in contributing a question, please contact us on wgin.defra@rothamsted.ac.uk.

Avalon x Cadenza Workshop – 27th March 2013

This is currently being organised by [Simon Griffiths](#) and will take place on the above date at John Innes Centre, Norwich, to permit all researchers currently working with this mapping population to come together and discuss their findings and future intentions. If you are

interested in using the A x C population in the future or your research currently involves its use, please contact us at wgin.defra@rothamsted.ac.uk

Section 6. News

New Cultivar for Broadbalk

Broadbalk is the longest running agricultural experiment - duration of 169 years. About 2 years ago Rothamsted sought advice from some of the UK wheat breeders about changing the variety because this is usually done +/- every 10 years. Hereward had been grown for the last 17 years. Following detailed discussion this year, the decision was taken to change to a modern high yielding breadmaking wheat which is likely to be grown for some years. The winter wheat, Crusoe (RL, new 2012), was selected to be the replacement because this variety has good yields, high protein, high disease resistance and slightly later maturity.

Farhana Amin – Moving on

Dr Farhana Amin became defra's main contact for the WGIN project in August 2010, a role previously held by Dr Katherine Bainbridge. Farhana was very recently promoted. Many congratulations. Since September 2012, Farhana's new role at defra is within the Soil Team as the manager of their Research and Development portfolio. We thank Farhana for all the help, guidance and support that she has given to WGIN over the past 2 years. We wish her all the very best in her new role at defra. Defra is currently searching for a scientist with genetics training to fill the vacant post.

Section 6. Publications

Better Crops With Plant Food: A Publication of the International Plant Nutrition Institute (IPNI) XCVI (96) 2012, No. 3, Hawkesford, M.J

<http://www.ipni.net/publication/bettercrops.nsf/issue/BC-2012-3?OpenDocument&toc=1>



10th WGIN Stakeholders Meeting
27th November 2012, RRes
FINAL Programme



- 10:00 Arrival and coffee
- 10:15 Welcome – *Peter Shewry, RRes*
- 10:20 Wheat Market Update – *Susannah Bolton, AHDB*

The Wheat Genetic Improvement Network

- 10:40 WGIN: Overview and update on RRes WGIN research – *Kim Hammond-Kosack, RRes*
- 11:00 Drought Tolerance – *Pedro Carvalho, UoN (John Foulkes Lab)*
- 11:20 Rotation Trial – Take-all Root Disease – *Vanessa McMillan, RRes (Richard Gutteridge's Replacement)*
- 11:40 Coffee

End user developments

- 12:00 Update on Global Wheat Genebanks and Information Systems and recent developments at the Germplasm Resources Unit– *Mike Ambrose, JIC*
- 12:20 Development of genome-wide SNP-based markers in hexaploid wheat – *Sacha Allen, University of Bristol (Keith Edwards Lab)*
- 12:40 Lunch with **posters on wheat research**
- 13:45 Technology Strategy Board Funding initiative on “phenotyping” – Opportunities for Wheat – *Kim Hammond-Kosack, RRes*

Wheat initiatives

- 14:00 The Crop Improvement Club – Selection of Wheat Projects
 - Phenotyping root function in wheat - *Richard Whalley RRes*
 - Developing a Cereal Fertility Pipeline for wheat - *Jose Fernandez Gomez (Zoe Wilson's Lab), Nottingham*
 - The role of lipids in determining gas bubble retention and stability in wheat dough - *Peter Shewry RRes*
- 14:30 Integrated Biorefining Research and Technology Club (IBTI Club) – *Peter Werner (KWS)*
- 14:40 Bio break

Emerging Disease Patterns

- 15:00 Introduction to Discussion panel on “Emerging Disease Patterns” – *Judith Turner, Fera*

Discussion Chair: Peter Shewry, RRes

Panellists:

- Judith Turner, Fera (Crop Monitor Survey)
- Neil Paveley, Crop Pathology Lead, ADAS
- John Lucas, Cereal Pathologist, RRes
- Andrew Watts, Chairman of the NFU Combinable Crops Board
- David Feuerhelm, Plant Breeder, Syngenta

- 16:30 Tea and finish

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

The contributors to this newsletter were: At Rothamsted Research: Kim Hammond-Kosack, Malcolm Hawkesford, Wing-Sham Lee, Andy Phillips, Kostya Kanyuka, and Suzanne Thrussell. At the John Innes Centre: Simon Griffiths, Cathy Mumford, and Susan Freeman. At defra: Fahana Amin and David Cooper..

