

**WGIN management meeting**

**20th October 2009, University of Nottingham**

**MINUTES**

**Attendees:**

Neil Paveley, Paul Verrier, Nick Gosman, Peter Jack, W. J. Angus, Jim McVittie, Kim Hammond-Kosack, Sarah Holdgate, Mike Grimmer, Lesley Smart, Ruth Gordon-Weeks, John Foulkes, Andy Phillips, David Feuerhelm, Malcolm Hawkesford, John Snape, Stephen Smith, Simon Griffiths, Peter Shewry, Claire Fremann, Peter Werner, Reshmi Geyi, Dan Godfrey, Elke Anzinger

**Apologies:**

James Melichar, Andy Greenland

**Welcome – Peter Shewry**

**Simon Griffith: Research Update on Objective 2, 3 and 4 - tools and resources**

*Power Point presentation (001SG WGIN October 2009 UNo)*

Additional information on NILs:

Now is a good time for any suggestions on NILs. We can consider them now and still get results within WGIN2.

Q: Why did you choose Maris Dove?

A: James Brown has used this variety in the LINK programme Breeding for improved resistance to *Septoria triticae* (BIRST).). There is DArT data on this variety that can be used to compare to Paragon and so maximise polymorphism.

Q: How do you bulk?

A: We don’t bulk, we keep the plants separate.

Q: How far have you got with DArT analysis on Koga x Paragon?

A: The effect of 7A has been mapped. We are still waiting for DArT data on height.

Koga is known for late flowering, but in the field it showed late initiation. There should be a nice way of genetically mapping the gene quickly.

Additional information on Watkins collection:

During WGIN1 most effort on the Watkins collection was spent on collation, eliminating heterozygosity and phenotyping.

NIAB wishes to map dwarfing genes in the Paragon x JIC synthetic SSD population.

During WGIN 1 we did hand harvesting, but we would like to bulk in larger quantities. We are carrying out this work under WGIN and hope to fund the analysis of the material with BBSRC support.

Additional information on A x C:

We are using a programme called Threadmapper for quality control. Threadmapper is available as an online web tool at: <http://cbr.jic.ac.uk/threadmapper>

Q: How many markers have you put on the map so far?

A: We have 500 – 600 polymorphic markers and have placed around 350 on the map

Luzie Wingen is currently assessing Germinate, Cropstore, and ISIS (CGIAR). This assessment is for in-house purposes at the moment and it is not planned to place it anywhere.

Additional information on WGIN staff at JIC:

The former John Innes Genome laboratory services at JIC have now been embedded in individual departments at JIC, genotyping is now led by Crop Genetics.

**Lesley Smart: Research update on objective 7 - insect resistance**

*Power Point presentation (002 LS WGIN October 2009 UNo)*

Q: Are you using SR39 and SR120 only?

A: No, 7-8 lines have been chosen.

Q: Why are you using Spark x Rialto?

A: Studies have already been carried out in Argentinia with the cereal pests Russian wheat aphid and with Greenbug on this population. The UK cereal aphids *Sitobion avenae* and *Rhopalosiphum padi* are from the same tribes and may respond in a similar way.

Q: How much effort would it take to test a larger sample?

A: A huge effort. Aphids would need to be bulked up. Preference tests are very labour intensive.

Q: Are there any UK field experiments?

A: No. We can try a field test. However you need big plots because of the patchy distribution of the aphids. It is difficult to quantify the effects.

Comment: In the laboratory test you use young plants. What relevance does that have to the field?

A: Both UK cereal aphid species can colonise the crop in the autumn when plants are small.

Comment: It would be interesting to map variation.

A: Biotypes have been defined under artificial conditions in an Argentinean study. Details on the Argentinean study have been published (Castro A M, Tocho E F, Tacaliti M S, Vasicek A, Gimenez D O, Börner A and Snape J W (2009) Gene discovery in recombinant doubled haploid populations for breeding wheat resistance against aphids. Proceedings of the 11th International Wheat Genetics Symposium, Brisbane, Australia, August 2008: Vol 3 pp 721-723.)

**Malcolm Hawkesford: Research update on objective 8 - NUE and NUE linked QTLs**

*Power Point presentation (003 MHawkesford WGIN October 2009 UNo)*

Additional information – diversity trial:

We need to discuss the availability of seed of the Hereward x Malacca NILs in time for the 2012 and 2013 trials (we will need large quantities by Oct 2011).

We drilled the diversity trial last week.

For the 2008/2009 diversity trial sowing we replaced seven varieties with
6 A x C DH and with Marksman. The A x C lines were chosen based on NUE parameters.

We have a good BBC film clip on the diversity trial that should be put on the WGIN website. Elke will add it to the website – Elke is this on your still to do list?.

Additional information – A x C traits:

The N levels used for the AxC field trial were high in 2007 but low in 2008 and 2009. We plan two more years with high N levels.

I am open to suggestions on the traits studies, especially if help is provided.

We have now mapped QTLs for senescence.

We have been mapping QTLs but they need to be validated. The data are based on only one trial at high N and 33 trials at low N but are giving interesting leads for the future.

A manuscript has been prepared on the N use efficiency of the lines grown in WGIN1.

Comment: Please alert us when it becomes available.

A: Yes, we will.

Q: How are the data from the Diversity trial to be used?

A: By identifying the underpinning genes and then validating them. There is useful information on stability.

Q: What population will you be using for future studies?

A: Both the diversity trial and the AxC population will be used for gene expression analysis. In future we will do more work on the A x C trial.

Q: Do you want to take the diversity trial any further (ie new crosses)?

A: This is not planned as part of WGIN, but we have robust data which could form the basis for decisions on such crosses.

Comment 1: We need smart screens.

Comment 2: Yes, but even with smart screens it will still be labour intensive. Working with mapping populations is very labour intensive. Only now after three years do we have enough data for analysis.

Q: Do you have any data on the AxC population on NUE, NUp and NUtE and how they relate?

A: Analysis is in progress, but data has not been calculated yet.

Q: Will the diversity trial be continued for another five years?

A: Yes, but we can change the germplasm used.

Comment: It is useful to have a core set of lines, but we can reduce the size of this. The core set includes six lines for the new IPA grant on grain N. Some lines are also useful for Andy Phillip’s studies on height and harvest index. Other lines are appropriate to study yield and quality and some lines show extremes of traits.

Q: Do you see as much variation in the A x C population as in the diversity trial?

A: Maybe even slightly more variation in the A x C population.

A dataset by Peter Barraclough will be ready soon to go on the website.

**John Foulkes: Research update on objective 9 – drought tolerance**

We (UoN and JIC) need to decide in consultation with BWB within the next few months which DH population to use in the 2010/11 field trials at SB and JIC.

16 cultivars in the have been sown in two irrigation treatments (fully irrigated and rain fed) 2009/10 experiment located at Sutton Bonington Farm, UoN. The 16 varieties have also been sown on a second unirrigated site in 6 m plots on a light blowing sand at Bunny farm, UoN..

In earlier work at Nottingham outside WGIN in the Beaver x Soissons population transgressive segregation for 12/13 C isotope discrimination has been shown by a PhD student Aravinda Kumar. We are just submitting a paper on this.

Results of the PhD work showed higher yields under drought were associated with a higher 12/13C isotope discrimination indicative of an ability to access water under drought as the plant keeps stomata open longer during grain filling.

**Kim Hammond-Kosack: Research update on objective 10 – Take-all disease and objective 11 – Introgression of extreme Septoria resistance from *T. monococcum* into hexaploid wheat**

*Power Point presentation (004 KHK WGIN October 2009 UNo)*

Take all – *T. monococcum* and Watkins field tests: We have naturally mixed populations of take all in the field. We will select lines by a process of elimination. In year 1 all the Watkins lines were grown under 3rd wheat conditions and no chemical treatment was added. This gave Richard Gutteridge a chance to assess for other diseases. Data on this will soon be ready to go on the website. We have arranged for Chris Burt (PhD Student at JIC in Paul Nicholson’s group) to check his new QTL markers for known sources of eyespot resistance, on the lines with low eyespot disease scores in this trial once our statistical analyses are completed.

*T. monococcum* displays good traits for bread making quality and disease resistance.

Oats are a non-host for take all.

Diversity trial: We now want to find the QTLs f conferring differences in take-all inoculums build up in 1st wheats..

Q: Has DArT shown that there is a variation in *T. monococcum* take-all infectivity depending on the geographic origin of the *T. monococcum* line?

A: The Take-all fungus thrives under moister soil conditions and unless you have GPS data on the origin you will not know whether the accession came from a wet or dry habitat. So we are not sure how useful the DArT data would be for this approach. But we do intend to screen all the *Tm* accessions already in our collection taken from the same regions where we have already identified lines showing resistance to take-all. This would be done in pot tests in the first instance.

Q: Where will your studies on take all resistance in *T. monococcum* lead to?

A: We want to find out the genetic basis of resistance and find scorable traits.

Q: When you cross take-all resistance from *T. monococcum* into hexaploid wheat, will it stand up?

Comment: Take all is a monoculture disease – was the selective pressure in the old times right to fit into this?

A: A look- alike root infection pathogen may exist in natural ecosystems and the resistance identified could potentially be affected against more than one pathogen. In the HGCA-BBSRC funded PhD project we will explore whether the resistant *T. monococcum* accessions also confer resistance to *Magnaporthe oryzae* - the rice blast fungal pathogen which is known to infect hexaploid wheat roots and cause disease. An additional comment from Richard – the take-all fungus is found in many natural ecosystems where it can infect and cause disease on numerous grass species.

Comment: Five weeks flowering differences were observed when the different *T. monococcum* lines were grown in small pots for the crossing experiments. However, in the field trials all the *T. monococcum* lines all flowered within a few days of each other and so are unlikely to have an effect on take-all epidemic development.

Comment – we have not seen any obvious differences in root development between susceptible and resistant *T. monococcum* lines in the absence of presence of the take-all fungus

**Peter Shewry: Subcontractor Projects**

*Power Point presentation (005 PShewry WGIN October 2009 UNo)*

We had five applications, three that would cover the whole £50,000.—budgets individually and two smaller ones. Two applications were on drought, one on Nitrogen, one on acrylamide precursors and one technological proposal.

The selection panel will be chaired by Peter Shewry, unless someone else from the management group wants to come forward. – ‘No comments received on this.’

On the selection panel will also be Defra representative, and we also require two independent assessors. Peter Jack would agree to be on the panel and I would suggest Graham Jellis or Jim McVittie as the fourth member.

It was agreed for Peter Jack to be on the panel and to ask Graham Jellis to be the fourth panel member.

Q: Who at Defra is now looking after WGIN?

A: Kath Bainbridge has been promoted and no replacement has been assigned yet. We will continue to liaise with Kath until a replacement has been appointed.

**Paul Verrier: A community resource for wheat functional genomics – cross searching databases**

*Power Point presentation (006 PVerrier WGIN October 2009 UNo)*

The Monogram website provides long term infrastructure. The website of any closed cereal project can be hosted on Monogram. For example the Wheat Big Picture website is now on the Monogram server. Alternatively a website can be embedded into Monogram Web and we will update it on your instructions. For embedded web sites, you can have your own user privileges so that you can have private areas of your web site.

The Monogram website is searchable and you can add information (data, publications, events, news, vacancies etc.) by clicking on the Add New tab providing you have logged into the site (and have therefore registered).

If you have data to be included in the parallel search mechanism that you want to make available to the community please contact Gary Barker or Paul Verrier.

A QTL & marker database exists for Brassicas. This has been funded by BBSRC projects. We could set up a system for other crops that allows people to enter their various markers and QTLs, but initially someone has to put everything together and curate the data. Alternately we can have a self-curating mechanism where submitters curate the data.

Comment: Curating historic data is impossible for wheat. If a system could be put into place we can enter new data from now on.

The Brassica site has several levels of closure, which makes it possible to make selected data available to specific users only.

Comment: I’ve asked for a system like this to be put in place for two years, but nothing has happened so far.

Q: How are QTLs presented?

A: We have a consensus map structure and a proforma of how to present data, as used for Brassicas.

Comment: The French are creating a consensus map on wheat.

Comment: Someone needs to propose a format so data can be presented in the same form. Two or three volunteers are required to define a standardised nomenclature for traits.

It was proposed that a small working party should define the marker and QTL data requirements (John Snape, Peter Jack, Simon Griffiths & Paul Verrier). these could then be used as a basis to create a Monogram resource for wheat markers of various types.

Comment: 454 data – short contigs are likely to represent most genes that are useful to the wheat community. Would you like to relate these to other plants (Brachypodium, maize etc.) via an Ensembl or Gbrose/jBrowse environment?

A: Yes.

Reply: We just add tracks and obtain the data.

Comment: the Brachypodium genome sequence (9x version) is now public.

Comment: The existing DArT data sets on hexaploid wheat should be collated and put on the MONOGRAM website. This would be a very useful resource to the community and would also stop duplication of effort.

Elke to follow up on this by sending an e-mail to all on MM list and the Stakeholder mailing list , if they have generated DArT marker data in any project for hexaploid wheat and if so which lines. This can be the start to help Paul achieve this.goal ASAP

**AoB:**

East European wheat workshop:

John Snape is organising a workshop with East European wheat breeders with the Institute of Field Crops in Novi Sad in Serbia. Eastern European countries have a strong background in wheat breeding and genetics. We intend to invite wheat scientists from Serbia, Croatia, Czech Republic, Hungary, Rumania and Bulgaria. The host in Serbia will be Boris Kobiljsky who specialises in markers and wheat breeding. John has submitted a grant proposal to BBSRC that should cover the costs of 12 UK representatives (from JIC, RRes, ADASADAS, NIAB and the University from Nottingham). The breeders are invited but would have to cover their hotel and travel costs (approx. £200,-- for the return flight, £50,-- for transfers and about £80,-- for the hotel). Food will hopefully be provided.

The workshop will take place around the 18-21st May and last four days including two travel days. Anyone interested in the workshop please contact John Snape.

Crop Improvement Club:

The crop Improvement club now has nine business members and will be funded on a 9 (BBSRC)/1 (industry) basis. The Scottish government is also a funding partner. There will be a call for projects next year.

Quality workshop:

Peter Shewry is planning a quality workshop for later this year or early in 2010. Please contact Peter if you are interested.

A x C workshop:

Q: Is it possible to obtain information on the pedigrees of Avalon and Cadenza?

A: Donal O’Sullivan has asked the same question. I think he has pedigrees for Cadenza.

Comment: Avalon is not well represented in new lines, only Avalon sisters are.

Comment: It is better to look at a larger set once you have selected a region.

Q: Is there a database of DArT markers?

A: Keith Edwards was going to make one.

Comment: Peter Denzel is working on a consensus map for 20 crosses. WGIN lines will be represented.

Comment: It is better to use SSRs for checking.

Acknowledgement of the use of WGIN resources and datasets:.

WGIN Disclaimer : WGIN is a publicly funded project and the data and resources it generates are freely available to the research community, providing that the use of any WGIN data and resources are acknowledged.