

**WGIN Management Meeting  
25<sup>th</sup> March 2013 @ KWS-UK, Thriplow**

**Draft Minutes**

**Attendees:**

Peter Shewry (Chair), Kim Hammond-Kosack, Malcolm Hawkesford, David Cooper, John Foulkes, Thomas Joliffe, Simon Berry, Stephen Smith, Peter Jack, Cath Mumford, Dhan Bhandari, Keith Edwards, Vanessa McMillan, Luzie Wingen, David Feuerhelm, Matt Curtain, Simon Griffiths, Sue Freeman, Matt Kerton, Ed Byrne (Minutes), Jacob Lage.

**Apologies:**

Chris Tapsell, Suzanne Thrussell

**Welcome** – Peter Shewry

**Actions from last meeting**

AxC workshop scheduled for this week at JIC  
All other actions completed prior to the meeting

**RESEARCH UPDATES**

**1) Objectives 2, 3, and 4 (Simon Griffiths) Presentation SG 001**

Simon provided an overview of resources with a focus on bread-making functionally of the Malacca x Hereward NILs.

Topics covered include:

- QTL and trait development
- Germplasm collections
- Segregating populations
- Markers including COS markers
- Mutant populations (Paragon)
- NILs

Bread making data had been obtained previously through a previous DEFRA link project ([add project No Simon or Peter](#)) involving several millers and breeders. This project focussed on the “spiral white” bread making process.

QTL data was shown: Bread-making traits tend to have low heritability and low correlation between years which causes issues for QTL LOD significance levels; the reanalysis of this data set was no exception.

Currently the NILs (whole population) are in the ground at the JIC (1m<sup>2</sup> plots) and RRes (3 x replicated 3m<sup>2</sup> plots). Metabolomics screening has been done on this material with a view to look at the non-protein components that may

provide clues to the source of low-protein quality characteristics. [But surely this level of phenotyping has not been funded through WGIN?](#))

Peter Shewry aims to also run the MxH NILs material through a lipid-omics platform. [Again is this WGIN funded or not. Please clarify](#)

Any association analysis will have to rely on existing baking dataset as there are no resources to undertake further baking tests.

### Questions

Q. Why choose Spiral White baking process over e.g. CBP – [in full please](#) ?

A. Spiral White tends to pull out differences in baking quality traits in contrast to the CBP which tends to equalize/homogenize the differences

## **2) Objective 8 – NUE (Malcolm Hawkesford) Presentation MH 002**

Malcolm mentioned that there was not much new data to report and that his presentation would focus on data analysis over the recent highly contrasting seasons .

The AxC population was not drilled last autumn due to poor seed quality and bad weather at drilling time.

### Diversity Trial

The diversity project now has many years of data (2004 to 2013), with a set of 16 core lines and an additional rolling set of lines which currently include lines relevant to WUE and Take-all projects. For this coming season, 2 new lines (AC Barrie and Cocoon) have been included. Trial drilled 13<sup>th</sup> October 2012.

In more recent years, the diversity trial has been grown in a standardised experimental design/treatments which has helped analysis.

An analysis of the dataset was presented:

- Yield increased initially with increasing level of N but no yield gain was detected between 200 and 250 kg/ha and above
- Low yielding lines tended to perform better under low N input
- GxE across years has a larger effect than genotype
- Yield stability across years was presented showing that there was no correlation for yield between some years

The diversity population is providing a useful tool for developing NIRS calibration sets. This work is ongoing.

### AxC trial

Traits measured include flowering time, height, yield and straw N (Good segregating characteristics). However, despite this good trait data, QTL suffer from instability and disappear in different years.

### Root analysis

Malcolm gave an update on the image analysis of “paper germinated” seedlings. Root QTL are stable under glasshouse based phenotype screens, and match many of the QTL from the traits measured in the field; distinct root QTL also exist. Paper in-press, due out online shortly. [Malcolm please add in full details of paper here](#)

Some AxC height NILs have been looked at as possible candidates for root QTL but there are also QTL which are not linked to plant height.

In general the taller genotypes also have longer roots

### Looking forward

- Evaluate modern diversity trial
- Field phenotyping methods
- Cross interaction between yield/roots/NUE/WUE.

### Questions

Q. Are the pleiotropic effects clustering on AxC map, e.g. overlap with root QTL and height?

A. Yes, clustering due to pleiotropic effects is apparent, but other traits other than root length e.g. lateral branching, do not appear to have lead to clustering.

Q. Is this analysis just identifying root:shoot ratio; has this been looked at?

A. Yes, there is a root:shoot effect which is linked to *rht* mutants. However, the focus is the many additional QTL observed.

### **3) Objective 10: Take-all disease (Kim Hammond-Kosack) Presentation KHK 003**

KHK introduced Vanessa McMillan as the replacement for Richard Gutteridge at Rothamsted.

Following a summary of the pathogenesis of take-all, an outline of the *Triticum monococcum* Take-all trial was presented. The trial is now in its 4<sup>th</sup> year and includes a range of *T. monococcum* lines based on the index of Take-all severity; high, intermediate or low infection severity. A publication describing the coding of the lines relative to Genebank names is available (contact Kim for further details).

Initially, two sets *T. monococcum* populations were speculatively developed; only 1 turned out to have interesting contrasting parental phenotypes and was subsequently carried forward. The segregating populations are now at the F6 generation (n=76) and include reciprocal pollen donor population to mitigate against the possibility of maternal inheritance of the resistance trait. The population will be analysed using the “pot test” procedure this coming season and an in-house qPCR test that detects Take-all DNA in plant tissue.

Take-all inoculum build up in the *T. monococcum*'s A small selection of the *Tm* accessions that show either root resistance or no resistance to the take-all fungus were also tested for their ability to cause Take-all inoculum build up when grown in a 1<sup>st</sup> wheat situation in the field. The *Tm* genotype with a high level of root resistance, was still able to build the take-all inoculum in the soil. Also the low take-all inoculum builder (Cadenza) is full susceptible to take-all root disease. Therefore the two traits, namely root tissue resistance and low take-all inoculum build up in soil appear to be controlled by distinct mechanisms.

#### Looking forward

Current work is focused on introgression of resistance trait from *T. monococcum* lines into Paragon (ph1). Previous attempts to introgress directly into hexaploid wheat (4 genotypes) halted when the F1 plants failed to produce any pollen and /or flowering tillers.

#### Questions

Q (comment). It was noted that introgression work is only just re-starting with only 8 months left on the project

Q. Is using *ph1* material the correct approach? Since *T. monococcum* is the A genome progenitor, introgression should work on regular material via an amphidiploid.

A. this 1<sup>st</sup> approach involving embryo rescue was tried in 2009-2011 and failed due to lack of viable pollen from the F1 plants.

Ian King has been consulted on this and suggested this ph-1 approach was suitable.

#### **4) Objective 9 Drought Tolerance (John Foulkes) Presentation IF 004**

John described his experiment using isotope screens to investigate WUE at the leaf level. An overview of the technique and a summary of data were presented. Main message from the presentation is that WUE is related to photosynthesis which is correlated with flag leaf specific weight (density).

2012 season proved to be very difficult to get good drought QTL data due to poor weather and lodging. The trial was re-sown last autumn.

Luzie then presented an update on the QTL analysis which showed several leaf-curl QTL lining up with grain m<sup>2</sup> QTL.

Flag-leaf Specific weight and the ranking of QTL correlations could be topics for discussion at the next meeting. – **ACTION ITEM**

### Questions

Q. Could early stage traits be detectable using leaf specific weight?

A. Potentially yes

Q. What was the size of the panel?

A. 18 varieties

### **GENERAL UPDATES**

#### **5) DEFRA update (David Cooper)**

David Cooper gave an overview of the strategy and topics currently being discussed in the political arena. Consideration could be given to:

- WGIN3 should not be an extension of previous work and that clear water should exist between e.g. WGIN2 and WISP.
- Topics high on the political agenda include those promoting Economic Growth e.g. adding value to the food chain; increasing export; sustainable intensification.
- Project could address areas where the market has failed (“market failures”) and should not shy away from topics involving GM crops and breeding per-se.
- Although not specifically targeted at the WGIN3 proposal, an additional topic on the political agenda is plant health and resilience, including emerging disease/changing disease status e.g. the increasing importance of cereal aphids.
- The notion of a Network is outdated and the role of WGIN as a “platform” which has established “leads” means WGIN is in a favorable position.
- A “bottom up” approach of WGIN is regarded as a good example, where the agenda and innovative ideas being influenced by the breeders/end users at an early stage.
- Ian Boyd is new DEFRA head
- Due to timing of proposal and funding of potential WGIN3, we should apply for short extension of 3-4 months within WGIN2 (i.e. the end of the financial year), with specific milestones

It was pointed out that the process for application for funds has changed and now, in the first instance, an expression of interest is required as opposed to a full proposal.

The expression of interest would outline a general direction and could be submitted to DEFRA, perhaps in the form of an appendix to the WGIN2 final report. DEFRA would then invite interested parties to submit a detailed proposal in the direction of the expression of interest. It was advised against making bids larger than previous successful awards.

#### **6) Breeder meeting feedback (Jacob)**

An outline of the main discussion points from the Jan 2013 was provided. The breeders felt the traits being looked at were important and the WGIN had provided a good set of resources. The breeders saw high value in maintaining the good rapport/ networking opportunities that has been established between academics and breeders through WGIN so would be supportive of WGIN3. The breeders commented that additional resources, for example. MAGIC populations from NIAB could be incorporated into WGIN3. Other new and existing mapping population wheat resources were also discussed.

Improvements could be made to communication between the breeders and academics and delays in the delivery of data generated through WGIN projects were highlighted as a significant concern. There was also some concern about how to separate resource development between WISP and WGIN.

#### **7) Potential areas for WGIN3**

The potential new areas for WGIN3 to focus on were as follows:

- Yield stability, building on findings from WGIN2
- Bread making wheat with lower protein content
- Continued development on the *T. monococcum* introgressions
- Biotic stresses

Additional suggestions/comments included:

- Diversity of disease resistance (e.g. for rusts)
- Economic assessment/quantification of traits which could involve an economist

**Action: Kim and Simon to start developing proposal for WGIN3. Mail-shot to be sent to all breeders with early ideas for WGIN3**

#### **8) Stakeholders meeting 2013**

Potential topics/speakers include:

- Waterlogging tolerance
- Farmers yield
- **Yield Stability - this came out at the lead topic**
- Emerging diseases
- Hybrids (linked to stability)
- Emerging technology (e.g TALENS)
- RRes GM trial

Panel discussion (5 members) – the focus of the discussion will be farm orientated

**9) AxC workshop**

This is scheduled for Wednesday 27<sup>th</sup> and currently has around 30 participants.

**10) WGIN newsletter**

The newsletter is out at end of April should include SID4 report. A call was made for information/papers for the report.

**11) Next WGIN meeting**

Scheduled for the end of June/ beginning of July (Post Cereals event), date was tentatively set for Wednesday the 3<sup>rd</sup> July.

Keith Edwards was invited to give a presentation on ideas for creating a website to host the new wheat genome and marker data sets.

Location now decided - Rothamsted with a pm WGIN field tour and a cream tea at the adjacent Rothamsted manor post the field tour.

**12) AOB**

Suzanne has been working on the new WGIN website and has made an area available under 'resources/results' for deposition project data. It should be possible in the future to make this area secure.

Simon Griffiths mentioned that the wheat review should be out before the stakeholders meeting

Stakeholder meeting - **Wednesday 4<sup>th</sup> December 2013 at RRes, Harpenden.**