

WGIN 3 Management Meeting 6th October 2017 @ Rothamsted

This was the ninth Management Meeting of the **DEFRA** funded **WGIN3**.

Minutes

Attendees:

Ruth Bryant (RB) (RAGT) (**chair**), Andrew Riche* (AR), Malcolm Hawkesford (MH), Vanessa McMillan* (VM), Gia Aradottir* (GA), Kim Hammond-Kosack*(KHK), Michael Hammond-Kosack* (MHK) (RRes), Simon Griffiths (SG), Clare Lister* (CL) (JIC), Dhan Bhandari (DB) (AHDB), Simon Berry (Limagrain), Jacob Lage (JL)(KWS), Sarah Holdgate (SH) (NIAB), Lucy James (LJ) (ADAS), Martin Cannell (MC)(Defra)

[*=gave oral presentation]

Apologies:

Peter Shewry (RRes), David Feuerhelm (Syngenta)

A. Welcome – Ruth Bryant

B. Presentations:

1. Review of minutes from April 20th 2017 (KHK)

Clare to add two URLs next week. Approved by all. To add to website.

2. Tools, resources, genotyping and phenotyping – (CL)

Details can be found in the presentation (**pp1-25**) on the WGIN website.

The Paragon Library consists of around 500 lines. All of these are available for field trials. This needs to be advertised to increase demand for this WGIN resource.

Components of Thousand Grain Weight (TGWT) need to be looked at, including

- degree of waxiness (increased in droughted part of trial),
- awns (more and longer in droughted part of trial),
- ear compactness (increased in droughted part of trial),
- tillering (reduced in droughted part of trial),

In 2017 the need for irrigation was overwhelming resources and irrigation was stopped in mid July.

In 2016 there was no drought at stage 31 (stem extension) when grain number is being determined.

C. MH – yield effect seems to be coming in when fully irrigated?

C. KHK – *Rht1B* is giving a yield penalty under irrigation.

Q. MH – yields higher in 2016, but generally quite low?

A. SG – units here are kg/plot and NOT tonnes/ha

C. VM – the 3N root proliferation could be explored at the seedling stage in pot tests.

3. Update on WGIN Diversity Trial 2017 (AR)

Details can be found in the presentation (**pp26-36**) on the WGIN website.

Data for uptake of 20 elements, including 8 key elements are available.

C. DBh – millers very interested in late (foliar) N application for breadmaking quality

N applied mid March, mid April and end of April. This was affected by the low rainfall, ie non-optimal uptake.

There is a general concern that high temperature at anthesis reduces yield.

Q. CL – what are the biological processes affected?

A. MH – mainly pollen abortion

The two hybrids (HyStar & HyLux) were harvested too late, resulting in lodging.

Q. KHK – why were hybrids included in trials?

A. MH – to assess stability over several years.

Changing the N regimes for the Diversity trials had been discussed at the previous MM. However, MH was adamant not to change these to preserve the continuity of the trials.

Q. DBh – has the lodging been scored?

A. AR – yes, both by degree of lodging and area involved.

C. DBh – therefore you could calculate yield potential.

Generally, to use the current UAVs for foliar disease scoring has proved difficult, the main problem being resolution. To increase resolution the drone would have to fly significantly lower, causing enhanced leaf movement causing lower resolution. A new lighter weight UAV has a more flexible camera with higher focal length (43mm vs 25mm) and this will increase resolution. It also has an ambient light sensor which can be used to automatically correct the images.

The current drone was used at the JIC drought trial at end of May and eight sets of images were taken in one day. But, unfortunately the pictures taken later in the day are not stitching together well.

C. MH – regarding mineral uptake, sulphur does not seem to track nitrogen. This is surprising.

4. Resistance to Aphids (GA)

Details in Presentation online (**pp37-41**).

R.padi shows a less pronounced shift to lower nymph weights than *Sitobian*.

MDR657 has now been dropped because no sustained effects could be observed.

MDR049 has been shown by Amma Simons (Ph.D. student) to be repellent to aphids and both a pre- and post-alighting effect could be observed.

C. KHK – all those MDR lines came from the Vavilov in the USSR and all of them were extensively phenotyped in various locations in the USSR. It might be useful to get back to them and ask for the phenotyping notes, to see whether any effect regarding aphids had been observed/ described.

C. GA – a PI at Oxford is looking at aphids +/- bacterial symbionts, and some of these were not able to grow on MDR045.

5. Resistance to Foliar Diseases (VM)

Details in presentation online (**pp42-71**)

Q. RB – have you tested yet for known yellow rust resistance genes?

A. VM – this will be done this autumn.

C. SH – no race changes observed for Brown Rust in the UK population.

C. SH – the new Yellow Rust UK population structure will be released midOctober by NIAB

Q. SB – how inbred are the Watkins lines?

A. SG – generally well behaved, all come from single seed descent

Q. RB – are there plans for genotyping the F₃ lines

A. VM – lines have been selected from F₃, but plans are to only select test crosses.

C. SG/SB – if we did bulk segregant analysis on 15 resistant and 15 susceptible on the Axiom array, we could quickly locate the chromosomes and do the SSR Marker analysis just on these chromosomes.

6. Update on Wheat Promotome Capture (MHK)

Details in presentation online (**pp72-116**).

All 1,385 promoter sequences were submitted to MYcroarray on May 10th 2017. Synthesis of stringent MYbaits was completed on August 24th. Chromosomal DNA extraction from all 96 wheat cultivars was completed in early September and samples received at MYcroarray in Ann Arbor on September 12th 2017. Library preparation and the

capture experiments are now in progress. It is envisaged that NGS sequences will be received at Rothamsted from mid November 2017.

Key outcomes so far include:

- **50 genes** were reassigned to different chromosomes (TGAC → IWGSC), in 32 cases completing the ABD Homoeologue sets
- Very specific primers identified **for each homoeologue**
- **71% of promoters** with >50% MYbaits coverage → **full 1700bp sequences expected** for ALL of these
- New **MITE** identified (let's call it **Taes WGIN**) – by aligning the homoeologous promoter/5'UTR sequences
- Good evidence for **differential homoeologous expression** in Chinese Spring – vindicating the WGIN approach of capturing individual homoeologues
- Chromosomes with highest densities for ALL Traits are 7D, 7A & 1D (243/1390)

C. SG/CL – we have not used all the baits, how could we ensure we used all of them in the future

Q. SB – can you search for specific motifs

A. CL – a motif search database provided by SoftBerry could be used for this.

Q. SB – where is all the raw data going to go? Could there be a BLAST function included?

A. MHK – need to think how best to achieve this.

Q. SG – if all three homoeologues were identical there would therefore be no probes

A. MHK – correct, but this would only affect 7-8% of sequences.

7. Stakeholder Meeting on November 30th 2017 (KHK)

It was agreed to

- 1) make all titles for presentations as snappy as possible – **and** add a short description in programme (2-3 sentences per talk)
- 2) shorten WGIN presentations to 25min including questions
- 3) extend the coffee break to 30min
- 4) for DFW have
 - a) 10min introductory talk by Graham Moore
 - b) 25 min for 'The Breeders' Toolkit' by Simon Orford
 - c) A selection of 10 min talks focussing on problems and how to solve them by
Laura Dixon (JIC),
Keith Edwards (Bristol U),
Andy Philips (RRes),
Alison Bentley (NIAB),
Vladimir Nekrasov (RRes)
Brittany Hazard (Quadrum Institute)
WP2.2 – solving septoria (RRes)
 - d) Include a Q&A session on DFW in general.

- 5) Not include a Panel Discussion this year. Especially regarding Genome Editing, it was felt to be a year too early.

8. New Defra Funding (MC)

Martin reported that the new round of funding has been approved by Defra for a longer period. The competition for funding will launch very soon and everyone on the BRAVO system will be notified directly. It is envisaged that the new funding will start seamlessly in February 2018 after the end of WGIN 3. WGIN breeders were encouraged to submit ideas for shaping WGIN4 to the PIs.

9. New publications, awarded grants and studentships using WGIN data and resources