



Annual/Interim Project Report for Period December 2015 to January 2017

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Project details

- Defra Project code CH0106
- Project title Wheat Genetic Improvement Network (WGIN) - Improving the resilience of UK wheat crop through crop genetics and targeted traits analysis
- Defra Project Officer Martin Cannell
- Name and address of contractor Prof. Kim E. Hammond-Kosack
Department of Biointeractions and Crop Protection
Rothamsted Research
Harpenden
Hertfordshire

Postcode AL5 2JQ
- Contractor's Project Manager Kim Hammond-Kosack
- Project: start date..... 20th February 2015
end date..... 31st January 2018

Objectives

7. Please list the objectives as set out in the contract. If necessary these can be expressed in an abbreviated form, indicate where amendments have been agreed with the Defra Project Officer giving the date of amendment.

Work Package A : Project management and finance [interim reports 1&2, finance report, Final report];
Work Package 1: Maintain and expand a network of UK researchers and stakeholders. WP1.1: Maintaining and improving the WGIN platform through regular meetings; WP1.2: Maintain and update a website and add in new data types; WP1.3: Utilise the technologies available through collaborations (in UK and abroad) to maximise opportunities for UK wheat improvement; WP1.4: Regularly disseminate of WGIN results, new technologies and resources information to the wheat research community and the wheat industry, and improve the potential for industry exploitation (including via WGIN Newsletters); WP1.5: Establish industry-led forum to promote the uptake of newly characterised resources into associated projects.

Work Package 2: Maintain archive and produce new and freely-available information resources for genetic improvement of wheat. WP2.1 Ensure availability and distribution of all archive WGIN as well as newly produced genetic and genomic data; WP2.2 Production of new disease trait data making them publicly available via the WGIN information site, including yellow rust, brown rust, Septoria tritici blotch, powdery mildew (when present in the field) and two species of aphids; WP2.3 Exploring in detail the genetic components of key traits including exploring the Paragon NILs, drought tolerance, yield and quality resilience (NUE, grain N and C content, grain minerals, canopy longevity), improve the marker coverage on key mapping populations and key Watkins lines using of Breeder (BR) array, Improve the marker coverage for the genotype in the core Tm collection using the (BR) array; WP2.4 New QTLs development for each of the traits identified in WP2.3 with a LOD > 3.0.

Work Package 3: Maintenance of existing wheat lines and accessions and creation of new ones, exploring new traits. WP3.1 Establishment/maintenance of Avalon-Cadenza population and other new populations and trials; complete the two mapping populations (to F6) for T.monococcum for take-all resistance and genotype, complete the F2 mapping populations for T.monococcum for aphid resistance, genotype the Pargon x Garcia population, regenotype the entire A x C extended population held at RRes using SSR markers to confirm seed stocks following field multiplication WP3.2: Development of new near isogenic lines in wheat; create the next generation A x C population. Use the available A x C NILS to create a minimal TILING path of individual C segment introgression into a Avalon background and individual A segment introgression into a Cadenza background WP3.3: Develop new T. monococcum introgression for take all resistance and septoria resistance using key accessions; WP3.4: Quantifying variation in below ground traits and the function of the root system, including specific Paragon A x C NILs, Paragon x Garcia population and WGIN diversity (all 1st wheat crops) .

Work Package 4: Broadening the genetic base for wheat improvement. WP4.1: Continue to identify novel sources of genetic variation within wheat germplasm with UK sustainability prospective, reevaluate 10 accessions from the Watkins collection for resistance to multiple foliar fungal pathogens; reevaluate T. monococcum collection for resistance to the Warrior race of yellow rust, identify other suitable wheat collections that may provide new sources of variation for the traits of interest WP4.2: Classify germplasm variants for a catalogue of crop-relevant genes, using high-throughput screens, add relevant information into CerealsDB data archive; carry out exome capture on a priority list of genes to be developed in conjunction with the breeders and UK academics, for up to 96 wheat genotyped WP4.3: Establishment/maintenance of field trials for traits such as: NUE, drought tolerance, vigour or others identified by stakeholders; see WP2 for the traits to be evaluated via these field trials WP4.4: Development of gene-specific marker data for the new traits by combining the data generated in WP 4.2 with the existing and newly generated field phenotyping data from WP 4.3. WP4.5: Analysis of the genetic bases of trait variation, assess the effects of variant genes. Make available the A x C NIL null genotypes (developed in WP 3.2) for subsequent physiological studies on any trait.

Summary of Progress

8. Please summarise, in layperson's terms, progress since the last report/start of the project and how this relates to the objectives. Please provide information on actual results where possible rather than merely a description of activities.

WP1.1 Four WGIN management meetings have been held (March, July, Oct and Jan17), one WGIN stakeholder event was held (RRes in Nov 2016) and another has been organised for Nov 2017. A successful application was submitted to BBSRC (in Dec 2015) for a joint wheat workshop in Turkey and a successful event was held in May 2016. WP1.2 The WGIN website has been updated with new datasets, the new project details and research partner details. WP1.3 The promotome capture technology and the AxC TILING projects have been explained and industry is now engaged. WP1.4 One newsletter was published. WP1.5 The industry-led forum was discussed again with the breeders but has not been implemented.

WP2.1 Specific seed stocks have been requested

Subset of paragon Library were requested by ADAS for their CINTRIN variety x N trial.

WP2.2 Production of new disease trait data making them publicly available via the WGIN information site
Ten Watkins lines have been field phenotyped for resistance to multiple foliar fungal pathogens across two field seasons (2014/2015 and 2015/2016). A third field trial is underway in 2016/2017. Five of the 10 genotypes exhibited moderate to high resistance against yellow rust across both field seasons conducted so far. Watkins 733 and 786 were most resistant to yellow rust with no sporulation visible on Watkins 733 across either field season. However, in contrast these two genotypes were heavily infected with brown rust in the 1st wheat trial site later in the 2016 season indicating that these lines do not possess multi-disease resistance against both rust species. Watkins 203 and 610 are the most promising genotypes for possessing multi-disease resistance with low disease scores against all three foliar pathogens (yellow rust, septoria and brown rust). Field crossing was carried out in summer 2015 between the partially resistant Watkins accessions and the fully yellow rust susceptible spring wheat cultivar Fielder. An F1 inheritance trial sown in spring 2016 revealed that the yellow rust resistance phenotype was dominantly inherited from Watkins 733 and semi-dominantly expressed in the F1 for Watkins 203, 231 and 610. An F2 field trial is currently underway to explore the inheritance of resistance in these crosses in more detail. All data is available via WGIN Management Meeting presentations on the WGIN website.

In autumn 2016 a third wheat take-all field trial was sown with replicated plots of an F6 mapping population developed by single seed descent between the take-all resistant Triticum monococcum accession MDR031 and the fully susceptible accession MDR043 (129 lines + parents). Plant samples will be taken during grain filling in summer 2017 and assessed for take-all root infection during autumn/winter 2017. Data will be uploaded to the WGIN website when available.

Work Package 2.2 Screening germplasm for resilience to aphids.

Phenotyping studies have revealed promising partial resistance in diploid wheat species, particularly Triticum monococcum, to the major cereal aphid pests the grain aphid, Sitobion avenae, and the bird-cherry oat aphid, Rhopalosiphum padi. Nymph production and survival were significantly reduced or absent on some resilient lines. Lines showing relatively strong resilience to both aphid species have formed the basis of this research in WGIN3. Crosses between the resilient lines MDR045, MDR049 and MDR657, and the susceptible MDR037 were generated and the F1 populations were tested in the laboratory based aphid screening bioassay, against both aphid species (results reported in previous interim report and in the February 2016 WGIN Newsletter). F2 and F3 populations have now been produced and have been or are being tested in the aphid screening bioassay, against both aphid species.

Results from assays with the F2 generations of all the crosses showed that there was no discernible effect on the number of nymphs produced by adult winged aphids of either species on the T. monococcum crosses when compared to an elite hexaploid control variety, Solstice. However, the weight gained by these nymphs over time on some of the lines was reduced compared to the control. Some of the F2 plants, particularly of the MDR037 x MDR049 crosses, had the best resilience against both aphid species when measured as nymph weight gain over time, although the response of S. avenae was the more promising. It was not possible to use standard statistical analytical methods on these trials as the plants are not fully segregated at this stage.

Since the best results were achieved with plants from the MDR037 x MDR049 crossing events, initial studies on the F3 generation have concentrated on this cross. Again, the difference in aphid performance, i.e. weight gain over time, on the T. monococcum compared to the hexaploid control is most evident for S. avenae. Interestingly, for both aphid species, performance on the separate crossings varies and may indicate slight genotypic differences between the original parental plants or could be due to plasticity in response amongst the aphids. These plants will now be taken to F4 with the aim of generating mapping populations. Trials with F3 plants from MDR037 x MDR045 and MDR037 x MDR657 are ongoing. Plant material has been collected for genotyping.

See WP 4.2 for the field evaluations for the various foliar diseases

Work Package 2.3 Exploring in detail the genetic components of key traits

The Diversity trial was increased to 30 varieties for 2015/16, still grown at the same four levels of nitrogen fertilisation and three-fold replication. All plots were sampled at anthesis, and the grain and straw yield were measured at final harvest. From the anthesis sampling and final yields, the biomass growth during the grain fill period was calculated, and all samples were analysed for N, P, K, Mg, Fe, Zn and other elements, allowing post anthesis mineral uptakes to be calculated. This was also done in 2014/15 and is planned for 2016/17. Therefore there should be three years of data for robust analysis.

Anthesis was scored manually and senescence kinetics measured weekly by hyperspectral reflectance.

The experiment was also used for developing workflows for processing images taken by Unmanned Aerial Vehicle (UAV), and it is now possible to extract plant height, canopy cover, canopy temperature and NDVI from UAV images.

The Paragon X Garcia drought trial was drilled in Oct 2015 (1st year) and October 2016 (2nd year). This consisted of 177 PxG RILs (which were selected to be Ppd sensitive) and also included Paragon, Garcia and the subset of Paragon Library NILs including Rht's (Height), Ppd's (DTEM), Staygreen mutant and Lr19 alien introgression. Four reps were drilled in each trial: two reps were additionally irrigated when required and two reps not irrigated. Traits scored were stage 31, booting, DTEM and height. Traits calculated were yield, TGWT and grains/m². Phenotypic data was used to QTL map traits. Periodic imaging of plots using an UAV was carried during growth to track senescence and compare the irrigated versus non-irrigated plots. Soil water content and matric potential, plus temperature, were measured using probes from DeltaT.

WP3.1 Establishment/Maintenance of Avalon-Cadenza population and other new populations and trials.

The two take-all T. monococcum mapping populations (MDR031 x MDR043 and MDR043 x MDR046) have been progressed by single seed descent in the glasshouse to the next generation (F6 stage).

Generation of lines carrying Rht8 + Rht-B1B or Rht8 + Rht-D1D in Paragon ongoing – these could facilitate development of high-yielding varieties targeting favourable and unfavourable environments, such as drought and low N.

Generation of nearly 30 new populations for studying yield stability in the UK, selected populations at F3. Will be taken to F5/F6 and aiming for ~400 lines in each population

WP3.2 A x C TILING path.

Genotyping was carried out on the 94 NILs, plus Avalon and Cadenza, using the Breeders Axion 35K Breeders Array. Data used to generate maps of the NILs used the current resources available. The NILs have been backcrossed to the recurrent parent to generate lines where QTL region and random segments have been separated.

WP3.3: Develop new T. monococcum introgression.

The introgression via direct crossing between T. monococcum and hexaploid Paragon containing the ph-1 pairing locus mutation was discontinued. This was because none of the F1 plants tested had either viable pollen or stigmas. Instead crosses between Tm lines MDR 308, MDR049, and MDR031 and two different durum lines, namely Kronos and Hoh301 were planned and started in autumn 2016.

WP3.4; Quantifying diversity in below ground traits and the function of the root system

Post-harvest 2015 and 2016 soil cores were taken from all varieties in the WGIN Diversity trial at the 200 kg/ha N rate to phenotype for the take-all build-up trait. These samples have been processed and assessed over the winter months. This has provided valuable information on the consistency of the phenotype over different sites and seasons and was analysed along with earlier WGIN diversity data within a BBSP funded summer bursary project in 2016 (June -Sept, 2nd year undergraduate student Rhiannon Brown under the supervision of two members of the statistics team at Rothamsted Research.

WP4.1: Continue to identify novel sources of genetic variation within wheat germplasm with UK sustainability prospective.

See WP2.2 for update on foliar disease resistance traits.

The RRes Triticum monococcum collection (263 accessions) was evaluated for susceptibility to yellow rust disease under field conditions. Overall the non-host reaction of the whole T. monococcum collection to yellow rust (reported in the previous interim report- milestone 7) restricts the use of the collection in follow-up association mapping studies. Instead work will focus on the more promising results from the Watkins foliar disease field trial reported in section WP2.2

WP4.2. Exome capture, renamed the promotome capture experiment. The discussions at the WGIN stakeholder meeting (April 2016) and the July 2016 MM focussed the project on the capture of sequence variation within 1700bp of the promoters of the A, B and D homoeologous loci of a finite number of nominated genes in 96 wheat cultivars and within 10 trait categories: (1) yield resilience, (2) grain quality, (3) grain development, (4) biotic stress – fungi and insects, (5) abiotic stress – drought, high temp, (6) nutrient use efficiency, (7) canopy development, (8) flower biology (9) root architecture and (10) recombination. Of a total of 15 scientists chosen as trait co-ordinators, 10 have not previously been directly involved with WGIN, thereby increasing the network. By mid December 2016, a total of 1355 Ensemble (TGACv1) gene IDs for all traits had been received. By mid January 2017, all promoter sequences had been extracted from the Ensembl scaffolds using Ensembl BioMart, and were on the verge of being sent to the company MYcroarray for design of MYbaits. However, because the imminent public emergence of the IWGSC refseq (v0.4 but in the end the current v1.0 was used) promised to not only be the gold standard of wheat sequencing but also would allow researchers to locate all WGIN trait genes physically on individual wheat chromosomes it was decided to re-extract all promoter sequences from IWGSC, beginning in February 2017. The 96 wheat cultivars were chosen by the WGIN Management Team, out of a total of 137 varieties suggested by WGIN scientists, WGIN breeders and also some of the trait co-ordinators. Seed for most varieties was obtained through the GRU (Mike Ambrose, germplasm resource unit at JIC) and Simon Orford (Watkins lines) with the remainder received from individual WGIN members. By the end of January 2017 all seeds had been received at RRes with the aim to sow and harvest leaves from seedlings for subsequent chromosomal DNA preparation.

WP4.3: Establishment/maintenance of field trials for traits such as: NUE, drought tolerance, vigour or others identified by stakeholders.

The 30 variety, 4 N level trial at Rothamsted 2015/16 provides data for on-going analysis of yield stability, yield components and NUE, along with mineral uptake and partitioning.

The Avalon-Cadenza population was grown in large plots with three-fold replication and one nitrogen level at Rothamsted 2015/16. The data is to be used to confirm results from previous years of the experiment.

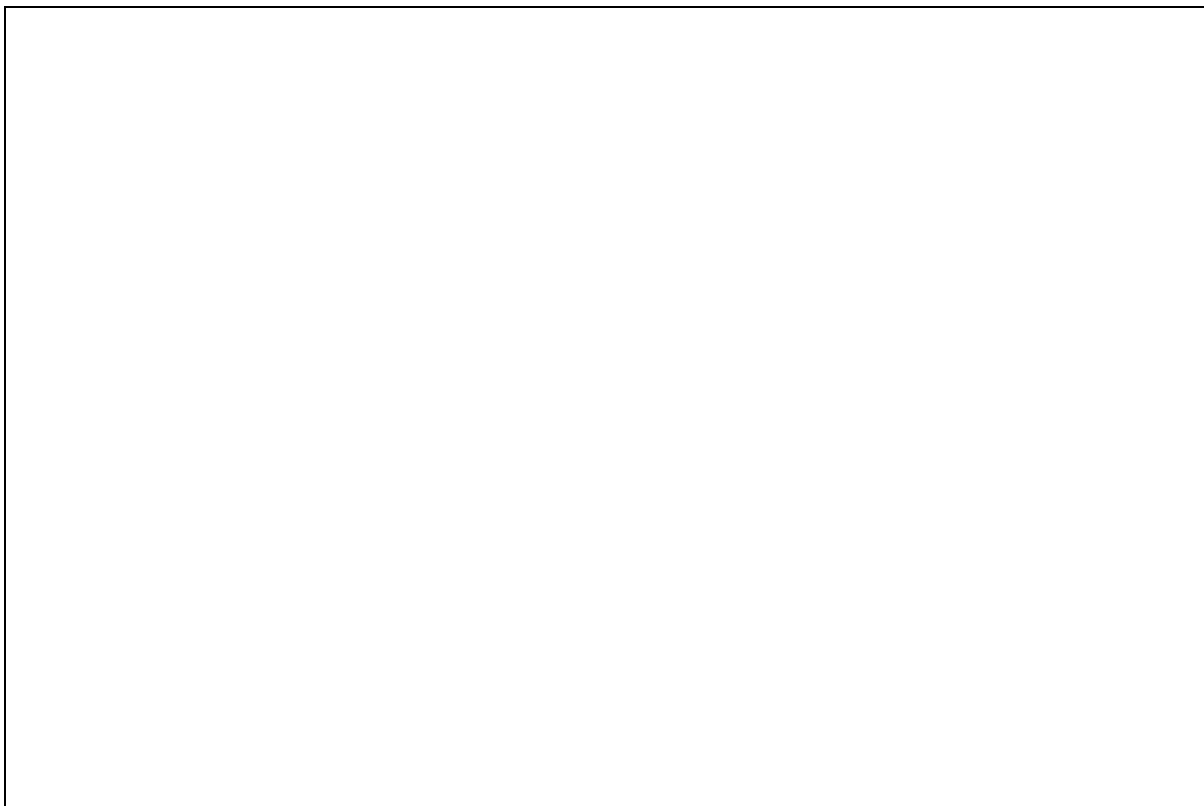
At the JIC, the subset of Paragon Library lines were drilled under the Phenospex Plant Eye Laser scanning platform in two randomised blocks of 16 plots in a N-trial. One treatment was applied to all plots with N (40 kg/h) then two subsequent treatments +/- additional nitrogen (250 kg/h). Differential responses to N application were observed in the PL lines.

Amendments to project

9. Are the current objectives appropriate for the remainder of the project? YES NO

If **NO**, explain the reasons for any change giving the financial, staff and time implications.

Contractors cannot alter objectives without the agreement of the Defra Project Officer.



Progress in relation to targets

10. (a) List the agreed milestones for the year/period under report as set out in the contract or any agreed contract variation.

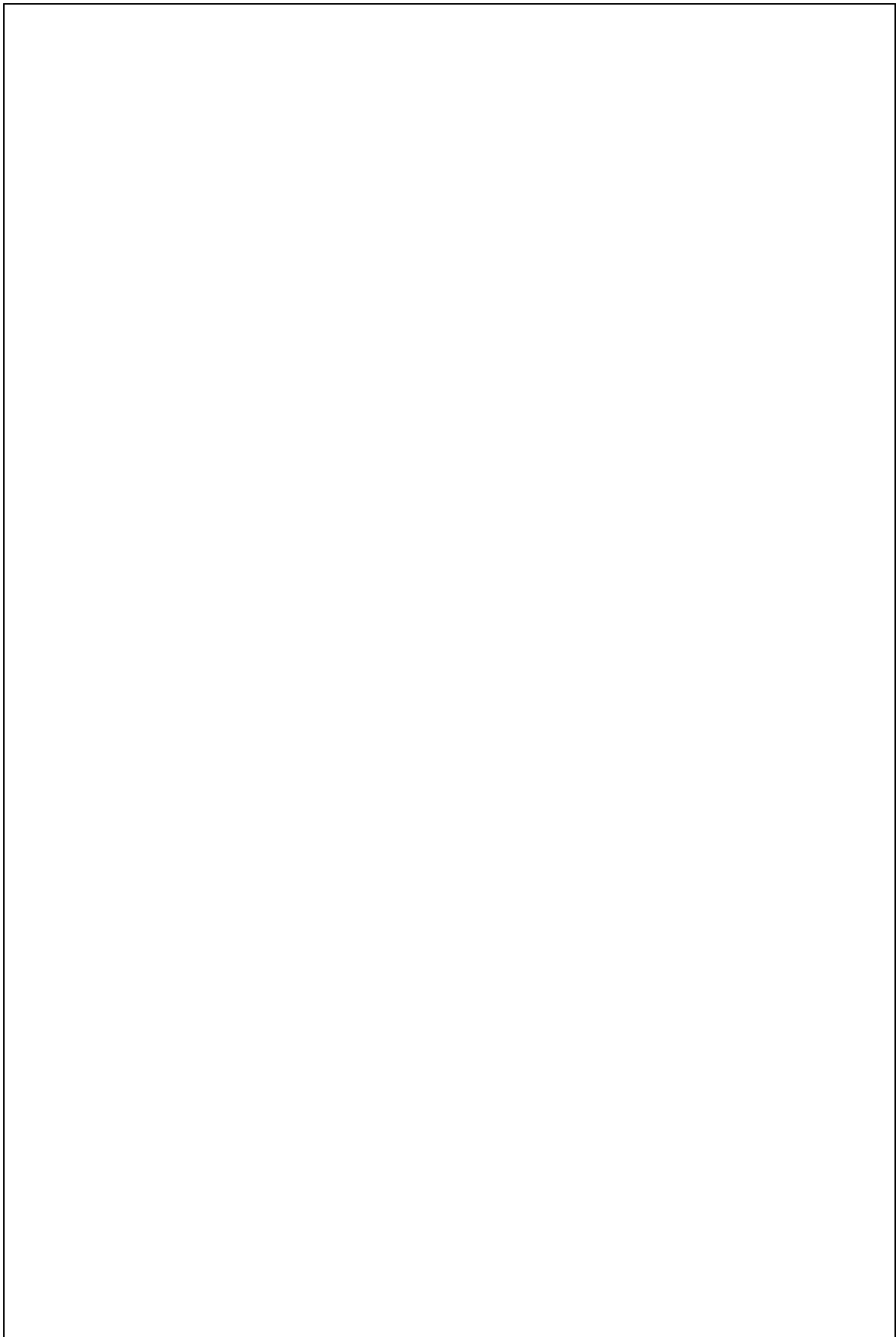
It is the responsibility of the contractor to **check fully that all milestones have been met** and to provide a detailed explanation when they have not been achieved.

Milestone		Target date	Milestones met	
Number	Title		In full	On time
1	First stakeholder meeting	(March 15)	Yes	YES
2	Development of new near isogenic lines	(February 15)		
3	Further maintenance and distribution of Avalon x Cadenza doubled haploid population.	(throughout project)	Yes	Yes
4	Genetic characterisation of Paragon mutants	(Feb 15)		
5	Identification of useful genetic variation in Watkins population.	(March 15)	Yes	Yes
6	Development of new mapping populations	(Apr 15)		
7	First Interim written report to Defra	(June 15)	Yes	late
8	Resistance to cereal aphids, information to establish the likely genetic basis of resistance to cereal aphid (Sept 15)	(Sept 15)	Yes	Yes
9	Development of new QTL for yield at low and high N input	(Aug 15)	Yes	Yes
10	Information on stability of yield and	(Sept 15)	Yes	Yes

	nitrogen use efficiency parameters for elite varieties			
11	Collection of data on variation in canopy longevity and nitrogen remobilisation	(Oct 15)	Yes	Yes
12	Evaluation of lines with good bread-making properties	(Dec 15)	??	??
13	Second stakeholder meeting	(Dec 15)	Yes	Yes
14	Second Interim written report to Defra/Project evaluation	(Jan 16)	This report	late
15	Improvement of water use efficiency and drought tolerance traits	(Feb 16)	Yes	Yes
16	Take-all disease, genetic basis, introgression of lines harbouring resistance	(Feb 16)	Yes	Yes
17	Introgression of extreme resistance to Septoria tritici from T. monococcum	(March 16)	Yes	Yes
18	Information on germplasm with new important traits.	(Apr 16)	Yes	Yes
19	Grain Archiving: from each plot of the annual diversity and Avalon x Cadenza field	(Summer 16)	Yes	Yes
20 and 21	Third Stakeholder meeting and 21. Report (Interim) (Jan 17)	(Dec 16)	Yes and This report	Yes + late report
MHarvest	RRes and JIC complete the 2016/2017 field season including field measurements, grain and straw harvests and various trait quantification.	(Aug-17)		
22	RRes - Complete UAV evaluations of foliar and root diseases, and canopy temperatures JIC - Complete field laser scanner image analysis of continuous canopy growth	(Sept 17)		
23	RRes - Complete the T. monococcum populations for the take-all and aphid resistance screening and genotyping JIC - Maintain the Avalon-Cadenza and Paragon-Garcia populations and other new populations /germplasm resources	(Sept 17)		
24	JIC - Genotype the Paragon Library on the 35K wheat breeders array (34K array)	(Sept 17)		
MSow	RRes and JIC complete the drilling of the 2017/2018 field trials	(Oct 17)		
25	Stakeholder event	(Nov17)		
26	Exome capture	(Dec 2017)		
27	SSR markers	(Dec 2017)		

28	Traits, LoD Scores	Dec 2017		
29	SSR and WAK markers Tm	(Jan 2018)		
30	Avalon x Cadenza CSSL Tiling and experimental QTL breeding using A xC	(Jan 2018)		
31	introgression	(Jan 2018)		
32	Existing and new data, combined analyses	(Jan 2018)		
33	Watkins Pathology	(Jan 2018)		
34	Insects	(Jan 2018)		
35	Final report	(Jan 2018)		

(b) Do the remaining milestones look realistic? YES NO
 If you have answered **NO**, please provide an explanation.



Publications and other outputs

11. (a) Please give details of any outputs, e.g. published papers/presentations, meetings attended during this reporting period.

Publications and other outputs

Aradottir, G.I., Martin, J.L., Clark, S.J., Pickett, J.A. & Smart L.E. (2016). Searching for wheat resistance to aphids and wheat bulb fly in the historical Watkins and Gediflux wheat collections. *Annals of Applied Biology* doi:10.1111/aab.12326

Farré A., Sayers L., Leverington-Waite M., Goram R., Orford S., Wingen L., Mumford C., Griffiths S. (2016) Application of a library of near isogenic lines to understand context dependent expression of QTL for grain yield and adaptive traits in bread wheat. *BMC Plant Biology* 16 161

Fenner H. Holman, Andrew B. Riche, Adam Michalski, March Castle, Martin J. Wooster and Malcolm J. Hawkesford (2016) . High Throughput Field Phenotyping of Wheat Plant Height and Growth Rate in Field Plot Trials Using UAV Based Remote Sensing, *Remote Sensing* 8(12), 1031, doi: 10.3390/rs8121031

Gardiner, L-J, Bansept-Basler, P., Olohan, L., Joynson, R., Brenchley, R., Hall, N., O'Sullivan, D.M. and Hall, A. (2016) Mapping-by-sequencing in complex polyploid genomes using genic sequence capture: a case study to map yellow rust resistance in hexaploid wheat. *The Plant Journal* 87, 403-419. No author funded by WGIN. This study used the A x C mapping population resource.

Greenslade A.F.C., Ward J.L., Martin J., Corol D.I., Clark S.J., Smart L.E., Aradottir G.I. (2016). Triticum monococcum lines with distinct metabolic phenotypes and phloem based resistance to the bird cherry oat aphid *Rhopalosiphum padi*. *Annals of Applied Biology* DOI: 10.1111/aab.12274

Mehrabi, Z., McMillan, V.E., Clark, I.M., Canning, G., Hammond-Kosack, K. E., Preston, G., Hirsch, P.R. and Mauchline, T.H. (2016) *Pseudomonas* spp. diversity is negatively associated with suppression of the wheat take-all pathogen. *Nature Scientific Reports* 6, e29905. With Rothamsted press release.

Jones H., Lukac M., Brak B., Martinez-Eixarch M., Alhomedí A., Gooding M., Wingen L., Griffiths S. (2016) Photoperiod sensitivity affects flowering duration in wheat *The Journal of Agricultural Science FirstView* 1-12.

Kowalski A., Gooding M., Ferrante A., Slafer G., Orford S., Gasperini D., Griffiths S. (2016) Agronomic assessment of the wheat semi-dwarfing gene *Rht8* in contrasting nitrogen treatments and water regimes *Field Crops Research* 191 150-160

PhD thesis

Sarah-Jane Osborne (submitted Sept 2016, successful viva Jan 2017) Exploring the genetic and mechanistic basis of resistance to take-all disease in wheat. SJO field phenotyped one T. monococcum mapping populations developed in WGIN. PhD Thesis University of Nottingham – Rothamsted Research DTP. Supervisors (main) and Vanessa McMillan (trainee) (RRes) and John Foulkes (UoN) Internal Examiner Professor Matt Dickinson and External Examiner Dr Matthew Cromey (formerly a senior Plant Pathologist in New Zealand specialising in cereal root diseases)

Oral presentations

Kim Hammond-Kosack, Jason Baverstock and Vanessa McMillan Hutchinsons conference in Peterborough on the 19th November 2015 on the tech stand for Rothamsted Research showcasing the WGIN project and Take-all research

Gia Aradottir, poster presentation on 'Searching for aphid resistance in wheat', English-French aphid Special Interest Group in Paris November 2015

Vanessa McMillan and Kim Hammond-Kosack - The Wheat Genetic Improvement Network – a public-private partnership project (2003-2017) NABIM – Dec 2015, London

Simon Griffiths

Plant and Animal Genomes, San Diego, USA Jan 2016 QTL Cloning Workshop

'Identification of Genes Controlling Earliness per se and Short Day Photoperiod Response in Bread Wheat'

Kim Hammond-Kosack- talked to NFU young farmers visit to RRes in February 2016. described the WGIN project and the 20:20 wheat project.

Kim Hammond-Kosack, WGIN: Wheat Genetic Improvement Network. A Public - Private Partnership Project started in 2003. Defra's Genetic Improvement Networks, Stakeholder event 'Uncorking the

genetic 'GINie' for British crops, The John Innes Conference Centre, Norwich Research Park, Norwich, 22nd Feb 2016

Sarah-Jane Osborne, Vanessa McMillan, Richard Whalley, John Foulkes and Kim Hammond-Kosack (10th March 2016). Exploring the genetic and mechanistic basis of resistance to take-all disease in wheat. Rothamsted Research PhD Symposium

Andrew Riche Measuring Crop Traits by Remote Sensing, presentation to group of West Herts Farmers, March 2016

Gia Aradottir, Biovision Alexandria, Egypt, Invited speaker. Title of presentation: The future of crop protection April 2016

Sarah-Jane Osborne, Vanessa McMillan, Richard Whalley, John Foulkes and Kim Hammond-Kosack (26th April 2016). Exploring the genetic and mechanistic basis of resistance to take-all disease in wheat. BBSRC DTP Spring School, University of Nottingham.

Gia Aradottir, Turkey-UK Workshop "Wheat Improvement: Opportunities for collaboration", delivered a presentation "Searching for insect resistance in wheat" May 2016

Vanessa McMillan – gave a talk to undergraduate students from the University of Hertfordshire, 3rd June 2016

Vanessa McMillan – gave a talk to farmers from the Kelloggs Origins programme, 2nd November 2016

Sarah-Jane Osborne, Vanessa McMillan, Richard Whalley, John Foulkes and Kim Hammond-Kosack (17th-18th November 2016). Exploring the genetic and mechanistic basis of resistance to take-all disease in wheat. AHDB Crops PhD Symposium, Stratford Manor Hotel, Stratford-upon-Avon.

Kim Hammond-Kosack ' Picky Plant Pathogens: Focus – Fusarium and take-all fungi, Nanjing Agricultural University, 21st November 2016

Gia Aradottir, presented current priorities for insect pests in wheat at the Wheat Initiative Expert Working Group on Durable Pest and Disease Resistance in Wheat Workshop in Minneapolis, USA November 2016

Vanessa McMillan – gave a talk on the WGIN project at the Procam Advanced Agronomy Seminar, 13th December 2016

Poster presentations

Sarah-Jane Osborne, Vanessa McMillan, Richard Whalley, John Foulkes and Kim Hammond-Kosack. Exploring the genetic and mechanistic basis of resistance to take-all disease in wheat. Defra's Genetic Improvement Networks, Uncorking the genetic 'GINie' for British crops, The John Innes Conference Centre. 22nd February 2016.

Vanessa McMillan, Gail Canning, Richard Gutteridge and Kim E. Hammond-Kosack. Identifying root resistance to the take-all fungus. Monogram Conference, NIAB, 12-14th April 2016.

Clare Lister JIC Breeders day June 2016 'WGIN3: Dissecting UK drought tolerance in Paragon x Garcia'

Scientific Outreach

Kim Hammond-Kosack – 'Is it all in the genes' Arable Farming write up of the Defra's Genetic Improvement Networks, Stakeholder event in Feb 2016

Vanessa McMillan, Joe Moughan, Sarah-Jane Osborne and Kim Hammond-Kosack Cereals 2016 event: plot and poster display on our take-all research by (June 2016)

Andrew Riche Farming in the future using UAVs to assist with crop research, presentation at BA Festival of Science, Swansea, Sept 2016.

New Funding won – including PhD projects, DTP rotation projects, overseas visitors

DTP2 PhD Studentship - Elizabeth Chapman (2016-2020) – "Balancing the genetics of source and sink to increase the productivity of bread wheat" Main Supervisor Simon Griffiths, JIC.

Nottingham DTP PhD: Amma Simon (2016-2020) Unravelling interactions between cereal aphids and ancestral wheat lines to elucidate mechanisms of aphid resistance. The student is based full time at Rothamsted research. Main supervisor Gia Aradottir, and additional supervisors Lin Field, Kim Hammond-Kosack and John Foulkes

DTP2 PhD studentship: (2015-2019) Deploying Effector And Genomics Approaches To Genetically Dissect Disease Interactions Between The Necrotrophic Fungal Pathogen *Parastagonospora nodorum* And Wheat (*Triticum aestivum*). Main supervisor James Cockram (NIAB), Co-supervisor Prof Richard Oliver (Curtin University, Perth, Western Australia).

DTP2 PhD studentship: (2016-2020) The genetic dissection of cereal root traits. Main supervisor Eric Obers (NIAB), co-supervisor James Cockram (NIAB)

Pi Zhou (Earlham Institute, Norwich) - GP069JZ1Q CropQuant – The Next Generation Crop Monitoring Workstation for Precision Agriculture (£122,958.00)

Pi Zhou (Earlham Institute, Norwich) - GP080JZ1M Eastern Agri-Tech Growth Initiative Grant Proposal (£49,075.00)

Pi Zhou (Earlham Institute, Norwich) GP105JZ1B CropQuant - Next-generation cost-effective crop monitoring system for breeding, crop research and digital agriculture (£16,340.00)

Peter Shewry, Malcolm Hawkesford and Till Pellny (Rothamsted Research) BBSRC Link Project “Developing novel types of low protein wheat for breadmaking” BB/N000854/1. January 2016-December 2019. This LINK project is supported by 7 x breeders; 6 x industry; 1 x non breeder (£319,000).

Agritech Innovation Centre – Crop Health and Protection – phase 2 of the bid. £2.6 million for Rothamsted for specialist equipment £1.6 million and 3 FTEs over 3 years. Total project £23 million over 3 years. Lead Fera York, other academic partners CABI, University of Newcastle and University of Cranfield. Eight core industry partners, including Bayer, Unilever, Tesco, Frontier and Wellcome Trust farms. From March 2016. Leads at RRes are Lin Field, Kim Hammond-Kosack, Paul Neve and Andrew Spencer.

Patent applications

Kostya Kanyuka, Cyrille Sainetnac, Florence Cambon, Wing-Sham Lee, Thierry Langin and Kim E. Hammond-Kosack Plant Fungal Resistance Gene (Wheat Stb disease resistance) – UK Patent Application No. 1522146.8. Submitted to the European Patent Office on 15.12.2015. Updated with new data Dec 2016 International Patent Application No PCT/GB2016/053929, February 2017. This project started in 2004 by using the WGIN original and extended Avalon x Cadenza DH mapping population to fine map the Stb6 gene. It has also screened and used mutants from WGIN Cadenza TILLING populations to confirm that Stb6 conferred resistance against specific Septoria isolates.

Training the next generation of wheat scientists

MSc project at Rothamsted: Student: Lucas Bruguier (2016) Developing molecular markers for BYDV in *Rhopalosiphum padi* and *Sitobion avenae* and testing how BYDV transmission differs for aphids feeding on susceptible and resistant wheat varieties. Supervisors: Gia Aradottir and Martin Williams
MSc student – (2016) Collaboration with Professor Charles Godfray and Dr Ailsa Mclean at Oxford University. The effect of aphid symbionts on aphid ability to feed on resistant and susceptible wheat varieties.

Nuffield student, (2016) supervised by Amma Simon (Rothamsted)

The 30 variety Diversity trial has been utilised by a PhD student in the Hawkesford group, assessing grain protein distribution in a subset of lines.

The diversity trial was also utilised by a 2nd PhD student, visiting the Hawkesford group at Rothamsted, in 2015/16, investigating the impact of foliar applied N on yield and quality characteristics.

A third PhD student, working with Dr Y Wan at Rothamsted has also utilised the Diversity trial, assessing low protein wheat quality.

A DTP- PhD student based full time at NIAB (2015-2019) is being training to explore fungal effector- wheat genotype interactions and is using the Paragon EMS, Chinese Spring x Paragon RILs (Main supervisor-Dr James Cockram) .

A DTP- PhD student based full time at NIAB (2016-2020) is being training to undertaking a genetic dissection of cereal root traits and is using Avalon x Cadenza NILs. (Main supervisor-Dr Eric Obers)

- (b) Have opportunities for exploiting Intellectual Property arising out of this work been identified?..... YES NO

If YES, please give details.

One to one discussion with commercial plant breeders during tours of WGIN field experiments were identified as two important ways to advertise the availability of germplasm resources and discuss new project ideas.

One UK patent was submitted was submitted in Dec 2015 and this was folowed by the PCT international filing a year later. The cloning of the 1st resistance gene against Septoria infection was achieved using two key WGIN resources, namely the Avalaon x Cadenza mapping population and the EMS Cadenza populations that was then turned into the TILLING population. The isolated Stb6 resistance gene is used commecially in Europe in most breeding programmes. The identification of this novel sequence linked to disease resistance opens up the opportunity to identify other Septoria resistance genes from wheat and related species.

- (c) Has any other action been taken to initiate Knowledge Transfer? YES NO

If YES, please give details.

During the planning of the Designing Future Wheat (DWF) ISP, discussions were held to potentially hold a joint annual Stakeholder event. These discussions have continued and the 1st joint stakeholder event will take place in Nov 2017.

Future work

12. Please comment briefly on any new evidence opportunities which may arise from the project.

Pathogen and Pest

The mapping populations developed in WGIN 3 between take-all resistant and susceptible Triticum monococcum genotypes will need to be evaluated over a further two seasons, to confirm the locations of the QTLs so far identified. The five mapping populations developed between foliar disease resistant Watkins landraces and the modern spring wheat cultivar Fielder are being used to explore the genetic basis of this trait. Individual yellow rust pustule samples will be taken from the repeated trials in 2017 to determine the pathogenomes of the races able to still partially colonise four or the five Watkins lines. This later activity will be done in conjunction with Dr Diane Saunders (JIC).

The 10 Watkins lines with resistance to multiple foliar disease will also be included in a Septoria only trial to eliminate the problem associated with susceptibility to yellow rust minimising the leaf area available for Septoria infections. To achieve this septoria only trial, a combination of fungicides are used to which all Septoria isolates are currently resistant but which are still effective at controlling the rusts.

Phenotyping the WGIN Diversity trial for the take-all build-up phenotype generates additional trait information across different sites and seasons. In the future these long-term datasets will be important to model the disease-weather relationship to understand take-all epidemic development and explore the cultivar x site interaction. In this regard, a PhD project has been devised and was re- submitted into the University of Nottingham DTP 2016-2017 round (Vanessa McMillan, Kim Hammond-Kosack, Frank Vandenbosch and John Foukes). A DTP rotation project on this topic will commence in Feb -April 2018 with a student registered at Nottingham.

Important knowledge has been gained in identifying resilience in wheat against cereal aphids. In the future, it will be important to develop a better understanding of the factors responsible for resistance which can be exploited in breeding resistant material for farmers. During this work a need to include the transmission of Barley Yellow Dwarf Virus to our screening has also become evident. Preliminary work

has already been done on this by an MSc student to prepare and test techniques for further work. This is because the transmission rate and plant tolerance to the virus is an important factor in securing wheat yield and are frequently asked for by farmers and breeders.

Nutrient Use efficiency

The 15 years of data from the WGIN diversity trial will now be collectively analysed to explore yield stability and yield resilience traits. This has also informed on specific parents to be included in developing future mapping populations for detailed analyses of these two main traits. Grain from this trial from both good and poor seasons will be evaluated in the new BBSRC LINK funded project, 'Developing novel types of low protein wheat for breadmaking' which is a major interest to breeders, millers and bakers. Many of the cultivars included in all 15 years of trialling have been included in the promotome capture experiment. In the future, this comparative sequence analysis may help to link specific phenotypic performance, and differences in seasonal performance to genes of interest to nutrient use efficiency and other key traits.

Drought tolerance

The 2nd year PxG drought trial will be scored and analysed in the same way as the 1st year trial. A 3rd year has also been drilled in October 2017.

- Use data and resources as background in a H2020 grant application
- Purchase small 'rain out' shelters together with BBSRC DFW programme for more precise control on selected PxG RILs
- Nominate selected PxG RILs for joint assessment with commercial breeding programmes

Exome / promotome capture

This large experiment has brought together a considerable community of UK scientists interested in a diverse array of traits. Many of these scientists have not previously been involved with WGIN. This massive data set once available will need to be placed in an easy access format that will allow for simple BLAST searches as well as provide for more complex queries. In the first instance, access will be restricted to those involved in the nomination of the traits and gene lists and the 96 cultivars selected. Discussions will also be held with the wheat breeders to find out the best ways to accommodate their analysis needs. This new resource and new knowledge is likely to stimulate the development of new projects to investigate specific traits and underlying mechanisms in greater detail with industry partners. New PhD projects are also envisaged.

A x C TILING population

Progeny from selected backcrosses will be genotyped to determine whether they carry the required chromosomal segments. Seed will be bulked for distribution.

- Increasing the visibility of this resource eg by working with EBI to display on Ensembl
- Identify regions missing in current collection and target.
- Secure PhD funding to further analyse epistatic interactions using this resource.

Other activities

The Diversity trial has been used for the continuing development of a UAV phenotyping platform. The trial provides an excellent, diverse, range of genotypes and biomass yields (due to the N levels), ideal for developing workflows for image processing.

- Increasing collaboration amongst WGIN partners in sharing phenomics resources and capabilities e.g. use of RRes UAV staff and equipment for JIC trials

Declaration

13. I declare that the information I have given is correct to the best of my knowledge and belief.

Name

Professor Kim Hammond-Kosack

Date

3rd November 2017

Position held

Deputy Head , Department of Biointeractions and
Crop Protection, Rothamsted Research

