



Evidence Project Final Report

- **Note**

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- This form is in Word format and the boxes may be expanded, as appropriate.

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Project identification

1. Defra Project code

2. Project title

3. Contractor organisation(s)

4. Total Defra project costs (agreed fixed price)

5. Project: start date

end date

6. It is Defra's intention to publish this form.

Please confirm your agreement to do so..... YES

- (a) When preparing Evidence Project Final Reports contractors should bear in mind that Defra intends that they be made public. They should be written in a clear and concise manner and represent a full account of the research project which someone not closely associated with the project can follow.

Defra recognises that in a small minority of cases there may be information, such as intellectual property or commercially confidential data, used in or generated by the research project, which should not be disclosed. In these cases, such information should be detailed in a separate annex (not to be published) so that the Evidence Project Final Report can be placed in the public domain. Where it is impossible to complete the Final Report without including references to any sensitive or confidential data, the information should be included and section (b) completed. NB: only in exceptional circumstances will Defra expect contractors to give a "No" answer.

In all cases, reasons for withholding information must be fully in line with exemptions under the Environmental Information Regulations or the Freedom of Information Act 2000.

- (b) If you have answered NO, please explain why the Final report should not be released into public domain

Executive Summary

7. The executive summary must not exceed 2 sides in total of A4 and should be understandable to the intelligent non-scientist. It should cover the main objectives, methods and findings of the research, together with any other significant events and options for new work.

Work Package 1: Maintain and expand a network of UK researchers and stakeholders. WP1.1: Maintaining and improving the WGIN platform through regular meetings – *During WGIN 3 we have held 10 management meetings with the breeding companies and other significant parties working on wheat improvement as well as three large WGIN stakeholder meetings (n = 70-110 participants) held each November. The Nov 2017 was done jointly with the new BBSRC funded ISP Designing Future Wheat and involved a lot of new academics and industry participants. In addition, a joint GINs event was held at the JIC in Feb 2016 to showcase the overall achievements of the four GINs (n=150 participants + the press);* WP1.2: Maintain and update a website and add in new data types – *Updated throughout the project, immediately after each management meeting with all meeting minutes, presentations, new data sets and information on new publications;* WP1.3: Utilise the technologies available through collaborations (in UK and abroad) to maximise opportunities for UK wheat improvement. *The application of new technologies was particularly evident through the use at the University of Bristol Genomes Facility of the 35K wheat breeders array for many types of genotyping biparental populations, the T. monococcum collection and developing the new Avalon x Cadnza TILING path resource, via the use of the MYBaits technology for the large wheat promotome capture experiment and the extensive use of drone technology to assess the JIC spring drought trials, the take-all trials and the WGIN diversity trials;* 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) – *This was achieved through oral and poster presentations given at national and international meetings by all team members, tours of the WGIN trials to institute visitors, plot demonstrations and posters at the annula Cereals event held each July (Cambridgeshire and Lincolnshire), the publication of peer reviewed with press releases and specific interviews with journalists. Three WGIN Newsletter were produced and a 4th is in progress;* WP1.5: Establish industry-led forum to promote the uptake of newly characterised resources into associated projects. – *Although initial attempts were made in year 1 to establish an forum with the nine UK based wheat breeding companies, this proved too time consuming for them to continue.*

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 – *This was done throughout the project. Most of the seed distribution is now done via the JIC Germplasm Resource Unit to ensure Nagoya compliance and to ensure the correct MTA and receiver information is centrally recorded;* 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; [The highlights were XXX](#) 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, *The highlights were XXX* Improve the marker coverage for the genotype in the core Tm collection using the (BR) array – *This approach added ~900 markers for use in specific biparental crosses and permitted the 1st QTLs for take-all resistance to be mapped using two seasons of data. The entire collection of 263 Tm accessions was genotyped using the BR array and its structure determined*; WP2.4 New QTLs development for each of the traits identified in WP2.3 with a LOD > 3.0. *The highlights were XXX*

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 – *all successfully completed* 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. *This has been done and now XXX* WP3.3: Develop new T. monococcum introgression for take all resistance and septoria resistance using key accessions. *This has been achieved for both disease resistance traits using tetraploid T. durum (either Kronos or Hoh501) as the initial female crossing parent and then by backcrossing the F1 again as the female to hexaploid wheat (Paragon), because the F1 is male infertile. The Tm x Td F1 plants exhibit many traits from both parents and large grain were produced from the backcross to Ta*; 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) – *This was done by including soil moisture probes in the field trials, and using proxy measurements such as XXXX.*

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 – *5 accessions were shown to still provide an excellent level of foliar resistance to the new yellow rust races, xxxx; reevaluate T. monococcum collection for resistance to the Warrior race of yellow rust – the 1st year of field trialling of the collection of 294 Tm accessions revealed that all were fully resistant and therefore it was concluded that Tm is a non-host for the wheat attaching races of yellow rust. Post this negative result no further experimentation was done*, identify other suitable wheat collections that may provide new sources of variation for the traits of interest – *one slug resistant Watkins line was identified using a novel petri dish based assay, the evaluation of this line under field conditions will take place in WGIN 4.* WP4.2: Classify germplasm variants for a catalogue of crop-relevant genes, using high-throughput screens, add relevant information into CerealsDB data archive – *this was done using the Phenospec platform at the JIC and all nearly the data has been added into CerealsDB*; 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- *following discussions with the academic and industry communities in early 2016 this became a promoter capture experiment (a promotome analysis) for 1,395 genes. The experiment was deliberately delayed until the full genome of Chinese Spring became available in early 2017(IWGSC refseq1.0) to permit a set of promoter specific homoeologue selective baits to be made. The final large data set was received in November 2017 and after QA checking for accuracy was released to the academic project consortium members and the nine wheat breeding companies via a secure portal in March 2018. This experiment was 100% successful and provides a unique data set for use for multiple research and commercial purposes for ten different clusters of wheat traits.* As the IWGSC pre-publication agreement does not allow any details to be shown at present, we can however report here that the stringent specificity design of MYbaits resulted in homoeologue-specific capture for the A, B and D homoeologue promoters, and >90% of promoters had between 1000 – 2000bp sequenced. 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 – *all trials planned were successfully completed.* 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. *XXX* 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. *XXX*

Project Report to Defra

- As a guide this report should be no longer than 20 sides of A4. This report is to provide Defra with details of the outputs of the research project for internal purposes; to meet the terms of the contract; and to allow Defra to publish details of the outputs to meet Environmental Information Regulation or Freedom of Information obligations. This short report to Defra does not preclude contractors from also seeking to publish a full, formal scientific report/paper in an appropriate scientific or other journal/publication. Indeed, Defra actively

encourages such publications as part of the contract terms. The report to Defra should include:

- the objectives as set out in the contract;
- the extent to which the objectives set out in the contract have been met;
- details of methods used and the results obtained, including statistical analysis (if appropriate);
- a discussion of the results and their reliability;
- the main implications of the findings;
- possible future work; and
- any action resulting from the research (e.g. IP, Knowledge Exchange).

[See separate file for this detailed information.](#)

References to published material

9. This section should be used to record links (hypertext links where possible) or references to other published material generated by, or relating to this project.

Publications and other outputs

2018

Saintenac, C., Lee, W-S., Cambon, F., Rudd, J.J., King, R., Marande, W., Hélène Bergès, Phillips, A.L., Uauy, C., Hammond-Kosack, K.E., Langin, T., and Kanyuka, K. (2018) An evolutionary conserved pattern-recognition receptor like protein controls gene-for-gene resistance to a fungal pathogen in wheat. *Nature Genetics* **50**, 368–374, doi:10.1038/s41588-018-0051-x (with Rothamsted press release)

McMillan, V.E., Canning, G., Moughan, J. R.P. White, J.R.P., Gutteridge, R.J. and Hammond-Kosack, K.E. (2018) Exploring the resilience of wheat crops grown in short rotations through minimising the build-up of an important soil-borne fungal pathogen. *Nature Scientific Reports* (in press March)

Osborne, S.-J., McMillan, V., White R. and Hammond-Kosack, K. E. (2018) Elite UK winter wheat cultivars differ in their ability to support the colonisation of beneficial root-infecting fungi Phialophora. *Journal of Experimental Botany* (in press March)

2017

Acevedo-Garcia, J., Spencer, D., Thieron, H., Reinstädler, A., Hammond-Kosack, K.E., Phillips A.L. and Panstruga, R. (2017) *mlo*-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach. *Plant Biotechnology Journal* **15**, 367-378

- Simon, A. L., Wellham, P. A. D., Aradottir, G. I., Gange, A. C. (2017) Unravelling mycorrhiza-induced plant susceptibility to the English grain aphid *Scientific Reports* doi:10.1038/srep46497

2016

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 <http://dx.doi.org/10.1186/s12870-016-0849-6>

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

Harper, A., Martin, Trick, M., He, Z., H., Clissold, L., Fellgett, A., Griffiths, S., Bancroft, I. (2016) Genome distribution of differential homoeologue contributions to leaf gene expression in bread wheat *Plant Biotechnology Journal* **14**(5):1207-14. doi: 10.1111/pbi.12486

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

2015

Ma J., Wingen L. U., Orford S., Fenwick P., Wang J., Griffiths S (2015)

Using the UK reference population AvalonxCadenza as a platform to compare breeding strategies in elite Western European bread wheat. Molecular Breeding 35:70 <http://dx.doi.org/10.1007/s11032-015-0268-7>

From WGIN2 (not previously recorded, none of the authors were funded via WGIN)

G.J.Rebetzke, D.G.Bonnett and M.H.Ellis (2012)

Combining gibberellic acid-sensitive and insensitive dwarfing genes in breeding of higher-yielding, sesqui-dwarf wheats Field Crops Research Volume 127, 27 February 2012, Pages 17-25

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)

2017/ Q1 2018 – [still collating the data](#)

2016

Oral presentations

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.

2015

Oral Presentations

Kim Hammond-Kosack oral presentation on the WGIN project to ~50 MSc Plant Sciences Students University of Nottingham (Feb 215) at Rothamsted

McMillan VE – Monogram conference @ RRes, April 2015 on genetic control of take-all disease

Gia Aradottir presented "Searching for insect resistance in wheat", MonoGram 2015 29 April- 1 May 2015

McMillan VE – Rothamsted Research Day, May 2015 –on genetic control of take-all disease

Malcom Hawkesford plenary talk 22nd Sept International Wheat Meeting, Sydney Australia; including WGIN trials. The WGIN diversity trials continues to be a major testing ground for UAV technology for crop/trial monitoring.

McMillan VE – Rhizosphere microbiome workshop @ RRes, August 2015 – ppt on LowTAB trait

>McMillan VE - INIA-Rothamsted workshop Uruguay, September 2015 – ppt on LowTAB trait

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

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

Poster Presentations

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

Scientific Outreach

6th May Nabim; Malcolm Hawkesford oral presentation on trials and stability work

9th June CF Industries (USA) visit; Malcolm Hawkesford presentation of NUE and nutrient work

10-11th June Cereals 2015 – displays and presentation, on Take-all LowTAB and root resistance traits (V McMillan and Kim Hammond-Kosack) and Aphid Resistance (Lesley Smart)

18/19 June 2015 Wheat Initiative expert working group on NUE met at Rothamsted and visited WGIN field trials

New funding won (2015 to the present)

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)

New research projects and programmes

>Project Title: Aphid resistant wheat for the smallholder farmer in Africa

Funded by Technology Strategy Board: Agri-Tech Catalyst - Early Stage Feasibility - Round 4 Eligible costs estimated at £237,723; Rothamsted Research grant £71,923

Project title : Effector-directed approaches for improved disease resistance breeding in wheat. Funded by Syngenta £588,887. Sept 2016 to Dec 2018.

Pi Zhou (Earlham Institute, Norwich) - GP069JZ1Q CropQuant – The Next Generation Crop Monitoring Workstation for Precision Agriculture (£122,958.00) 2016 – 1 year

Pi Zhou (Earlham Institute, Norwich) - GP080JZ1M Eastern Agri-Tech Growth Initiative Grant Proposal (£49,075.00) 2016 1 year

Pi Zhou (Earlham Institute, Norwich) GP105JZ1B CropQuant - Next-generation cost-effective crop monitoring system for breeding, crop research and digital agriculture (£16,340.00) 2016 – 1 year

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.

Graham Moore (PI) with many coPIs at 8 institutes / universities, including Shewry, P, Hawkesford, M., Kanyuka, K, Aradottir, G and Hammond-Kosack, K at RRes and Griffiths, S at JIC. The BBSRC Institute Strategic Programme grant 'Designing Future Wheat, £16.5 million (April 2017 to March 2022).

Patent applications

Kostya Kanyuka, Cyrille Saintenac, 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.

PhD student Sarah-Jane Osborne (2012-2016) based full time at Rothamsted used many of the techniques developed for take-all research in WGIN 1 and 2 to complete a PhD on the Wheat root-take-all-Phialophora complex. This project was funded through the BBSRC – DTP University of Nottingham with additional funding from Agrii and HGCA.

PhD student Joseph Moughan (2013-2017) based full time at Rothamsted used many of the techniques developed for take-all research in WGIN 1 and 2 to complete a PhD entitled 'Uniting genetics and chemistry to reduce the severity of take-all root disease in commercial second wheat crops. Main supervisor RRes Kim Hammond-Kosack, co-supervisors RRes Vanessa McMillan . Academic Supervisor (University of Exeter) Chris Thornton. Funding source: Syngenta UK

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)

PhD student Petros Sigalas (supervisor Malcolm Hawkesford) fully funded by the French Chemical company Roullier, will be using the WGIN diversity trials from 2018 to 2022 to explore wheat tiller numbers.