

Final Project Summary

Project title	Exploring the genetic and mechanistic basis of resistance to take-all disease in wheat		
Project number	RD-2012-3777	Final Project Report	SR40
Start date	01/05/13	End date	30/09/16
AHDB Cereals & Oilseeds funding		Total cost	

What was the challenge/demand for the work?

Take-all, caused by the soil-borne ascomycete fungus *Gaeumannomyces tritici*, is a root disease that devastates wheat production worldwide. Current control measures consist of partially effective chemical seed dressings as well as cultural methods such as crop rotation and the later sowing of wheat crops which are predicted to be at risk. Host plant resistance to take-all is not currently utilised as a form of control of take-all, yet it is considered as the most favourable form of control against plant pathogens due to social, economic and environmental reasons. The most recent estimate of an average annual UK yield loss from the disease is 5-20% but is considerably more when the severity of the disease is high, with the annual cost for UK farmers thought to be up to £60m.

The future of take-all control relies upon an integrated management strategy due to the complex nature of the environmental factors that affect the severity of the disease. Two of the main themes explored within this PhD project have focused upon two differing control strategies against take-all disease, identifying genetic resistance to take-all disease in the diploid *T. monococcum* wheat as well as exploring the potential of building up natural populations of the take-all suppressing fungi *Phialophora* spp. under a first wheat as a potential suppressant of take-all in a second wheat. The development of such future control strategies for plant pathogens is vital due to the diminishing pool of plant protection products available because of legislation and resistance, as well as the difficulty of developing fungicides for soil-borne diseases.

How did the project address this?

Within the host plant resistance strand of the project, two 3rd wheat field trials were conducted to phenotype the diploid einkorn wheat *Triticum monococcum* MDR037 (susceptible) X MDR046 (resistant) mapping population for susceptibility to take-all disease. Genetic mapping analyses were carried out to identify the genetic regions associated with take-all resistance. Additionally, two 3rd wheat field trials were conducted to further characterise the 25 most take-all resistant hexaploid wheat varieties. This would generate datasets by which to prioritise/identify genotypes with consistent resistance responses for further genetic analyses in the future. The relationship between upper root function and the level of take-all infection was also addressed for three of the take-all resistant

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varieties and two take-all susceptible varieties with the aim of identifying whether soil moisture sensors could be used as a non-destructive discriminatory tool for field screening of varieties for take-all infection. This was carried out by inserting soil moisture sensors into individual field plots and measuring the soil water content throughout the field season to explore whether the sensors could differentiate between a healthy root system and a take-all diseased root system.

The second approach of the project was to explore the potential of *Phialophora* fungi to colonise elite wheat genotypes/soil as a biological control method against take-all disease. To address this, a 1st wheat field trial was conducted to explore the ability of *Phialophora* fungi to colonise the adult roots of elite winter wheat varieties on the AHDB Recommended List (RL) as well as the ability to build-up the natural populations of *Phialophora* species in the soil under the first wheat elite varieties. A UK *Phialophora* isolate collection was also gathered from across the Rothamsted Farm to carry out seedling pot bioassays to screen the ability of *Phialophora* species to colonise the seedling roots of different cereal species with known susceptibilities/resistances to the take-all fungus. Next-generation genome sequencing for three *Phialophora* species was also carried out with the aim of determining genes or regions of uniqueness in each of the three *Phialophora* genomes for future species-specific diagnostic assays.

What outputs has the project delivered?

The two 3rd wheat field trials screening the diploid *Triticum monococcum* MDR037 (S) X MDR046 (R) mapping population revealed a good spread in susceptibility to take-all within the population. In both field trials MDR046 was less infected than MDR037. This provides the first insights in the potential genetic basis of resistance in a *T. monococcum* mapping population. The two 3rd wheat field trials revealed that one line had a consistently low level of take-all infection across the two field seasons. Whilst the genetic basis of resistance has not currently been identified, an initial quantitative trait loci (QTL) analysis has been carried out and a QTL has been found for the analysis with 2014 take-all data, yet the QTL is not consistent across the years and has not been found for the analysis with the 2015 take-all data and more recent 2016 take-all data.

Evaluation of the relationship between take-all infection and soil moisture did not find a consistent relationship between the level of take-all infection and the level of soil moisture and therefore preliminary results suggest that soil moisture sensors solely at a depth of 15 cm could not be used as a discriminatory tool for field screening wheat varieties for take-all infection.

This project revealed the first indication that elite wheat varieties on the AHDB RL differ in their potential to build-up *Phialophora* spp. under a 1st wheat crop. Although the findings are only represented by one field season and therefore care must be taken when interpreting the results, the

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current findings are highly promising and a repeat field trial will be assessed to provide a comparison across a separate field season. There does not appear to be any interaction between *Phialophora* colonisation of the roots and the nabim groups or year of release of the elite wheat varieties or any clear relationship with parentage.

A working pot bioassay protocol to screen the ability of *Phialophora* spp. to colonise the roots of cereal genotypes has been devised from the AHDB summer bursary project in 2014. Although the pot bioassay revealed similarities between *Phialophora* colonisation and take-all infection of cereal varieties, rye indicated a significantly lower level of colonisation of an unnamed *Phialophora* sp. during the seedling stage.

A UK *Phialophora* isolate collection was gathered and from this an isolate representing each of the three *Phialophora* spp. was sequenced and the genomes were assembled and annotated. Genome comparisons revealed poor completeness values across the three *Phialophora* draft genomes compared to the *Ggt* genome. Although there were differences in the coverage and the extent of assembly across the three genomes, these are the first *Phialophora* reported draft genomes and they provide the first glimpse into the similarities that *Phialophora* spp. have with the closely related take-all fungus. The draft genomes will allow a species-specific diagnostic assay to be developed in the future, which could allow *Phialophora* species to be detected in the farmers' fields.

Who will benefit from this project and why?

Results from a QTL analysis could provide novel information that will allow wheat breeders to explore whether it is possible to introgress the *T. monococcum* resistance to take-all into commercial wheat varieties. Wheat breeders could also utilise the ability of certain commercial winter wheat varieties to build-up *Phialophora* fungi in future breeding programmes. The farming community could also use the information gathered on the ability of elite winter wheat varieties on the 2013/2014 RL to build-up *Phialophora* species under a 1st wheat crop to aid in decision making when growing a 2nd wheat as a practical solution to manage take-all disease. The 1st wheat field trial data are also intended to be written-up as a scientific paper and published, aiding the scientific community. In addition, the genomes for the three *Phialophora* species will be published online. This will allow other researchers in the scientific community to access this information and use it for sequencing analyses.

If the challenge has not been specifically met, state why and how this could be overcome

The genetic basis of resistance to take-all has not currently been identified. The genotyping data were returned at the end of the project. Due to time constraints, data analysis was not included in the final project report. The data are currently being analysed and genetic maps are being constructed along with QTL analyses with the phenotyping data from the two 3rd wheat field trials. In addition, the

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mapping population was screened in the 2015-2016 field season, outside of this project, and will be included in the genetic analyses to help validate any identified QTLs from the two previous field seasons.

Identifying a relationship between the upper root function and the level of take-all infection across take-all resistant and take-all susceptible wheat varieties was not successful with inconsistencies across varietal plots in soil water content and the level of take-all infection. There was also little difference in the level of take-all infection across the susceptible take-all varieties and the moderately resistant take-all varieties. Although the plots were small, the level of take-all inoculum within a plot can vary and could have led to some of the obscurities in the data. Another limitation was that only one sample point at the end of the season was assessed for take-all levels. If plant samples were taken throughout the spring and summer months, a direct correlation with soil water for individual dates would account for weather conditions on the build-up of take-all.

How have you benefited from this studentship?

I was able to participate in a number of knowledge transfer activities, in particular I attended national conferences, arable events such as Cereals and PhD symposiums, which allowed me to develop my communication skills as well as allowing me to network and meet industry representatives.

The studentship also allowed me to apply for an AHDB Undergraduate Research Bursary, allowing me to gain skills in designing and managing an additional research project. I also developed and gained confidence in my time-management skills and the bursary provided me with the opportunity to gain skills in teaching and supervising an undergraduate student.

Lead partner	University of Nottingham/Rothamsted Research
Scientific partners	Rothamsted Research
Industry partners	AHDB Cereals and Oilseeds, Agrii
Government sponsor	BBSRC

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