

Studentship Project: Annual Progress Report January 2020 to January 2021

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Project Title:	Fostering populations of arbuscular mycorrhizal fungi through cover crop choices and soil management		
Lead Partner:	NIAB / University of Cambridge		
Supervisor:	Dr Lydia Smith / Prof Uta Paszkowski		
Start Date:	08/01/2018	End Date:	07/09/2021

1. Project aims and objectives

The overall aim of this project is to quantify how cover crops influence colonisation and diversity of arbuscular mycorrhizal (AM) fungi and how this interaction influences crop growth and yield in field conditions. The study will utilise field-scale trials, as well as glasshouse experiments, to address the following project aims:

1. To assess the impact of cover crop species on soil health, including the diversity and abundance of AM fungi.
2. To quantify the effect of increased diversity and abundance of AM fungal species on crop yield, under a range of soil, inoculation and physico-chemical conditions.
3. To consider the impact of common farm practices, such as cultivation, nutrient application and use of herbicides, on AM fungal diversity and abundance.

2. Key messages emerging from the project

A UK wide assessment of AM fungal diversity (in collaboration with Fera's Big Soil Community) has shown that different farming practices, including crop species, cultivation choice, and fungicide applications can influence diversity of AM fungi in the soil.

This experiment has set the scene for further experimental work, including two fully replicated trials at Bawburgh and Morley, in Norfolk. The former investigates cover crop mixtures grown with, and without, a five species AM fungal inoculum sourced from Plantworks, the industry partner. In this reporting year, the same AM inoculum was tested on the same cultivar of spring barley in controlled glasshouse conditions. It was found that at an early time point, *Rhizophagus irregularis* was the dominant taxa colonising roots, which was correlated with a significant decrease in shoot biomass. High throughput sequencing (HTS) will be used to compare the dominant taxa colonising barley roots from the glasshouse and Bawburgh trials.

At the New Farming Systems (NFS) trial at Morley, a legume mix, or oat and radish cover crop have been grown as part of a long term rotation since 2007. Here, both of the cover crop treatments increased the root length colonisation (RLC) of barley by AM fungi, which could suggest either soil type specificity, or that multiple iterations of cover crops are required before quantitative benefits can be observed. At this trial, growth of cover crops decreased barley yield at the full and 50% nitrogen doses, but the leguminous cover

The results described in this summary report are interim and relate to one year. In all cases, the reports refer to projects that extend over a number of years.

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crop increased yields in the zero nitrogen application plots. This is likely to be due to increased soil nitrogen fixed by rhizobia associating with legume root nodules, as barley RLC was not a significant predictor of yield in this trial.

Applying these findings to the farm scale, an Innovative Farmers (IF) trial investigated the use of anaerobic digestate (AD) and cover crops, at four sites ahead of maize. The impact of the treatments on soil characteristics was recorded, with soil type differences apparent. Generally, application of AD increased available nitrogen in the soil profile, however it appeared to be leaching to the 30-60cm and 60-90cm horizons. Cover crops reduced N leaching into the lower soil horizons except at North Moor farm, where the cover crop treatment had the highest soil N. This was thought to be due to the site being waterlogged and did not represent an accurate treatment effect. Neither cover crops, nor application of AD influenced RLC or biomass of maize in this experiment, further suggesting the importance of multiple cover crops to achieve a quantitative benefit.

3. Summary of results from the reporting year

In this reporting year, there was considerable disruption to lab work caused by the COVID-19 pandemic. Nevertheless, two computational analyses have been undertaken, which will complement the original project aims.

Firstly, a phylogenetic analysis of the DNA sequence reads that did not match to AM fungi in the FERA trial aimed to identify previously undescribed species of AM fungi. Using pipelines adapted from the curators of the mycorrhiza specific MaarjAM database, three novel AM fungal taxa were identified: one *Glomus*, one *Paraglomus* and one *Ambispora* species. Analysis to describe which biotic and abiotic conditions influence the distribution of these species in UK agriculture is now being undertaken.

Later in the year, a collaboration with the Alan Turing Institute was formed to implement novel statistical methods for soil health analysis. A Latent Dirichlet Allocation (LDA) was applied to the FERA diversity data. The LDA is a Bayesian multinomial mixture model, which clusters AM fungal DNA reads into 'latent' or unobserved topics. The topics are fully generative and cluster AM taxa that show patterns of co-occurrence. Using latent factors as predictor variables, it is possible to correlate topics to biotic and abiotic conditions, or certain farming systems. This will identify indicators of certain soil health parameters, such as whether cultivations or fungicides had been applied to the field, or novel candidates for AM fungal inoculation. In this analysis, 30 latent topics have been identified, for which the analysis is ongoing.

Later in the year, a glasshouse trial was carried out to determine how each component of the five species AM fungal inoculum (used at the Bawburgh trial) influences AM RLC and biomass in Laureate spring barley. As outlined above, *Rhizophagus irregularis* was the dominant taxa colonising roots, and was correlated with a decrease in shoot biomass. However, discussion with other researchers in the field has suggested that the other components of the five species mix are slower growing and may increase their levels of colonisation later in the growing season.

4. Key issues to be addressed in the next year

Between now and the end of the PhD, the focus will be to complete the delayed molecular work, investigating how the various replicated trials influence mycorrhizal diversity. Microscopy work, including RLC of cover crop roots at Bawburgh, and Wheat Germ Agglutinin (WGA) staining of representative samples from across trials, will investigate phenotypic difference in fungal colonisation.

In the summer, project results will be disseminated to farmers and growers at events such as Cereals, and the Royal Norfolk Show, either in person or online. Following these summer events, the focus will be on writing the thesis for a timely completion in September 2021.

5. Outputs relating to the project

(events, press articles, conference posters or presentations, scientific papers):

Output	Detail
Presentation	NIAB Genetics and Breeding Seminar presentation (09/07/20)
Presentation	AFCP Eastern Region meeting (08/10/20)
Presentation	Endosymbiosis joint seminar (02/03/21)
Article	AHDB Arable Focus article, available at https://ahdb.org.uk/news/students-union-arbuscular-mycorrhizae-all-greek-to-me
Conference talk	2020 Maize Growers Association Conference (05/02/20)
Conference talk	AHDB PhD Studentship conference (26/01/21)
Conference talk	AHDB Agronomists conference (01/12/20)

6. Partners (if applicable)

Scientific partners	NIAB
Industry partners	PlantWorks
Government sponsor	