



Project title: **Novel ways of managing tree crop fungal diseases:
Using precision diagnostic technologies to tailor
disease management strategies**

Project number: CTP_FCR_2018_1

Project leader: Thomas Heaven, University of Lincoln

Report: Annual report, Oct 2019

Previous report: NA

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Location of project: NIAB EMR

Industry Representative: [Megan McKertcher, Worldwide Fruit]

Date project commenced: 01 October 2018

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The results and conclusions in this report are based on an investigation conducted over a one-year period. The conditions under which the experiments were carried out and the results have been reported in detail and with accuracy. However, because of the biological nature of the work it must be borne in mind that different circumstances and conditions could produce different results. Therefore, care must be taken with interpretation of the results, especially if they are used as the basis for commercial product recommendations.

AUTHENTICATION

We declare that this work was done under our supervision according to the procedures described herein and that the report represents a true and accurate record of the results obtained.

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GROWER SUMMARY

Headline

Collection, culture and DNA extraction methods for studying apple scab and powdery mildew genetics have been established and optimised.

Background

Apple is among the most important fruit crops globally, ranked third in terms of annual production at 84.6 million tonnes (FAOSTAT 2014). Commercial apple cultivation is hampered by its susceptibility to a number of fungal pathogens. The most serious among these is apple scab caused by the pathogen *Venturia inaequalis*, where production losses can be as high as 70% in heavily affected orchards (Biggs 1990; MacHardy 1996). It is thought that apple producers in the eastern United States spend as much as 18.6 million USD per year on scab control alone (Cox 2015). Apart from scab the most common fungal disease found in UK apple cultivation is apple powdery mildew caused by *Podosphaera leucotricha* (Lesemann and Dunemann 2006). Currently, growers use a range of integrated pest management strategies to control this disease but remain heavily dependent upon fungicide use, applying pesticides throughout the season to limit damage to their crops (Roßberg 2003). However, this practice is unsustainable as fungicide resistant varieties have begun to emerge in both pathogen populations and increased restrictions on fungicide use are expected in the near future (Brent and Hollomon 1995; Lesemann et al. 2006).

Genomic resources for these two pathogens lags behind those available for the apple host or for other pathogenic fungi. There has long been significant interest in developing new varieties of apple combining the fruit quality of commercial cultivars with the superior disease resistance of wild species. However, whilst host resistance genes have been identified, corresponding pathogen virulence and avirulence genes, which confer disease or host defence respectively, remain unknown. Additionally the genetics behind fungicide resistance are not known. The objective of this project is to improve understanding of virulence in apple scab and mildew by identifying putative virulence and avirulence genes that determine isolate host specificity as well as mutations leading to fungicide resistance. This will inform future management strategies and breeding efforts.

Summary

In the first year of this PhD, techniques for collection, culture and DNA extraction from apple scab and powdery mildew were refined. The establishment of these methods will facilitate sequencing experiments to be performed in coming years beginning with the generation of the first apple powdery mildew genome and transcriptome assemblies. Subsequent comparison of genomes and transcriptomes will enable identification of virulence and fungicide resistance factors in the two pathogens.

- Samples of Scab were collected from indicator trees known to carry resistance genes
- Samples of mildew were collected from susceptible trees
- The identity of samples was confirmed by sequencing of the ITS region for each.
- Several methods for extracting DNA from the two pathogens were trialled for their effectiveness and DNA extractions performed on a number of isolates

Financial Benefits

This report summarises the work carried out in the first year of a four-year project, and so there are no direct financial benefits yet. Upon completion this project will provide key information for the precision diagnosis of the two diseases to strain level allowing the effects of management strategies to be tracked and modified to increase yield.

Action Points

- There are no grower actions points at this stage of the project