

Grower Summary

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

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Project leader:	Thomas Heaven, University of Lincoln
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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

High coverage genome assemblies have been generated for powdery mildew of apple, strawberry and raspberry. These are the first genomes available for strawberry and raspberry mildew and the first generated from a European apple powdery mildew sample. A population of apple scab segregating for fungicide resistance has been sequenced.

Background

To better inform the disease management strategies of growers there is an immediate need for improved diagnostic testing for disease. Specifically, a test is needed that provides a quick diagnosis at a low cost to growers, ideally simultaneously, for a panel of common diseases. This test also needs to be precise enough to identify key pathogen characteristics such as resistance to certain fungicides and virulence. One approach is a diagnosis by sequencing method which identifies genetic markers associated with resistance and virulence traits. Such a diagnostic could also be used to better track the effects of different planting decisions and agronomic practices, informing disease management over the longer term.

Among those diseases affecting UK horticulture are the fungal pathogens *Venturia inaequalis*, *Podosphaera leucotricha* and *Podosphaera aphanis*. These are responsible for apple scab, powdery mildew of apple and powdery mildew of strawberry, raspberry and blackberry respectively. Successful control of these pathogens is paramount for growers. Production losses can be as high as 70% in orchards affected by apple scab (Biggs 1990; MacHardy 1996) and powdery mildew has been rated as the most important aerial disease for UK strawberry growers (Calleja, 2011). Diagnosis by sequencing has been proposed for these diseases.

Unfortunately, the requisite genomic resources for diagnosis by sequencing of these pathogens lags behind those available for their respective host plants or for other pathogenic fungi. Indeed, there were no genome assemblies available for any *Podosphaera* species prior to 2020. The genetic basis for resistance to commonly used fungicides is not well understood in either scab or powdery mildew. Similarly, no virulence genes have been characterised that facilitate the suppression of a host's natural immune response. There is significant interest in developing new varieties combining the fruit quality of commercial cultivars with the superior disease resistance of wild species. However, in the past the resistance of cultivars has quickly been broken in field conditions, to prevent this from happening in the future, a better understanding of these pathogens is needed (Caffier et al. 2014, Caffier and Laurens 2005).

The objective of this project is to generate some of the first genomic resources for the study of apple, strawberry and raspberry powdery mildew. We aim to improve the 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 three years of this PhD, techniques for collection, culture and DNA extraction from apple scab and powdery mildew have been refined. These methods have facilitated DNA and RNA sequencing of the apple, strawberry and raspberry powdery mildew genomes. Comparison of these species genomes and transcriptomes will enable identification of key virulence and fungicide resistance factors. Additionally, 50 apple scab isolates displaying different levels of fungicide susceptibility have been sequenced enabling identification of fungicide resistance markers.

- Apple Scab was sampled from indicator trees known to carry resistance genes
- Apple Scab was sampled from problem orchards and confirmed to be fungicide resistant
- Fungicide resistant and susceptible strains of apple scab were crossed to generate a mapping population for the fungicide resistance trait
- A fungicide resistant population was sequenced
- Samples of powdery mildew were collected from susceptible apple, strawberry and raspberry plants
- DNA extraction and sequencing was performed on apple, strawberry and raspberry powdery mildew samples
- Genome assemblies were generated for apple, strawberry and raspberry powdery mildew
- RNA extraction and sequencing was performed on strawberry powdery mildew samples
- A mapping population of apple trees were scored for susceptibility to apple powdery mildew in 2020 and 2021

Financial Benefits

Apple growers are currently heavily dependent upon frequent fungicide applications to control disease in orchards. Without these products, outbreaks inflict serious crop losses of up to 70%. There is increasing pressure to reduce the use of such crop protection products. This

project lays the groundwork for diagnosis by sequencing of the two pathogens behind: apple powdery mildew and scab. This kind of rapid and precise diagnosis would allow the effects of management strategies to be tracked and modified, supporting the maximisation of yield whilst minimising the application of fungicides.

Action Points

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