# Grower Summary

**Genomics of fungal diseases in apple, strawberry & raspberry**

**CTP-FCR-2018-1**

Final report

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# Student Project No. CTP_FCR_2018_1

# Title: Precision diagnostic technologies in horticulture - exploring the genomics of fungal diseases in UK apple, strawberry, and raspberry production

Genomics of fungal diseases in apple, strawberry & raspberry

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## Industry Summary

The overarching objective behind this study was to progress towards in-field diagnosis-by-sequencing of UK horticultural pathogens. A need for improved surveillance, detection, and diagnostic tools in agriculture has been identified by the UK Department for Environment, Food and Rural Affairs. Rapid and precise diagnosis of pathogens is necessary for tailored, efficient, and sustainable disease management. Diagnosis-by-sequencing methodologies require a basic knowledge of pathogen genetics. To achieve this objective, this study investigated the genetics of three of the most serious pathogens in UK horticulture: *Venturia inaequalis*, which causes apple scab disease; *Podosphaera leucotricha*, which causes apple powdery mildew disease; and *Podosphaera aphanis*, which is the cause of powdery mildew disease of raspberry and strawberry.

Quantitative Trait Loci mapping was used to identify genetic regions associated with reduced susceptibility to tebuconazole in apple scab. This resulted in the identification of multiple distinct regions in the genome. One region was found close to the gene which encodes the target of azole fungicides, implying that altered expression of of this target contributes to resistance. A second region was found on a separate part of the genome.This second region could indicate that a second resistance mechanism, not related to the azole target gene, has developed in apple scab.

Genome assemblies were constructed for apple, strawberry and raspberry powdery mildew. These include the first genome assemblies for strawberry and raspberry powdery mildew and the first assembly for a European population of apple powdery mildew. Collection of field samples avoided difficulties maintaining powdery mildew cultures, whilst still yielding high-quality genome assemblies following stringent controls for purity. This method has the potential to be applied to other challenging plant pathogens which cannot be cultured easily. The genomic resources developed in this study will accelerate research into apple and strawberry powdery mildew. Additionally, unique effector genes were identified that determine which plants each pathogen can infect, these could support diagnosis-by-sequencing to the level of a particular race or host-adapted form within each species.

This research lays the groundwork for the development of sequencing-based molecular diagnostics for these species, allowing detection of the pathogens and fungicide resistance. Early detection enables growers to identify and respond to disease outbreaks before they become severe, thereby preventing crop damage and reducing the need for extensive spraying. Furthermore, enhanced diagnostic precision can help growers to determine the exact pathogen strain present in the crop, enabling the selection of effective agrochemicals for control and reducing the risk of resistance to these chemicals over time.