

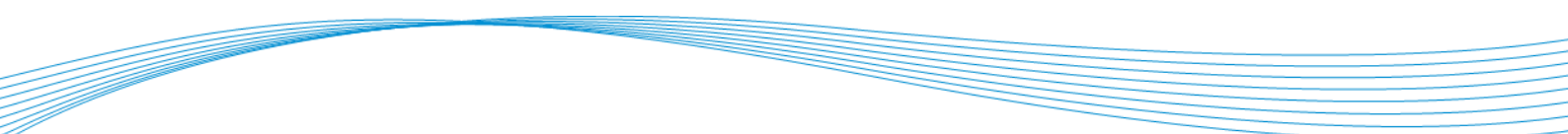


Grower Summary

**Investigating durable resistance to *Phytophthora*
cactorum in strawberry and apple**

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Final report



Final Report

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Student Project No. [AHDB project number]

Title: Investigating durable resistance to *Phytophthora cactorum* in strawberry and apple

Investigating durable resistance to *Phytophthora cactorum* in strawberry and apple

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1. Industry Summary

- **Headline**

- This project aims to identify sources of durable resistance to *Phytophthora cactorum* in strawberry and apple to integrate them in the UK breeding programmes.

- **Project summary and results**

Phytophthora pathogens are responsible for substantial damages to crops worldwide. One example is *Phytophthora cactorum* (*Pc*), which can cause disease in over 160 plant hosts, including such economically important crops as cultivated strawberry (*Fragaria x ananassa*; crown rot and leather rot disease) and apple (*Malus x domestica*; crown rot and collar rot disease). Previous work on identifying resistance to *Pc* in strawberry at NIAB EMR has identified several regions of the genome, which provide partial resistance. In comparison to strawberry, there is very little know about resistance to *Pc* in apple. Thus, the key aims of this project are to identify markers associated with resistance in apple and to elucidate the underlying molecular plant-pathogen interactions in both apple and strawberry plants.

An initial excised shoot assay screen (Luberti *et al.*, 2019) allowed for the identification of an existing apple population (M432) generated from the cross of parents 'M.27' and 'M.116', that segregates for resistance to *Pc*. Using the same artificial inoculation technique to allow for a larger number of replicates, the individuals in this population underwent two rounds of assessment for resistance/susceptibility in 2019 and 2020 leading to the identification of a putative resistance region on chromosome 6 of the apple genome. A total of 99 apple rootstock and scion accessions were similarly screened in 2020. This data led to identification of two genomic regions associated with resistance, on chromosomes 5 and 6 (within the same region identified in the M432 population). These results suggest resistance to *Pc* in apple may be controlled by a single major resistance region. In 2021, 126 individuals from another apple population (MCM007), which is closely related to M432, were screened to assess the predictive power of the resistance markers identified earlier in the study. A panel of representative individuals from the MCM007 population were then genotyped with the final aim of integrating these markers in the breeding pipeline.

To explore the response of the root system of each variety to infection and elucidate the mechanisms underlying resistance, the parental genotypes from M432 ('M.116' and 'M.27') were inoculated with *Pc* zoospores in a time-course experiment. These samples were sent for sequencing and the data was analysed to identify resistance/susceptibility gene candidates. Strawberry gene expression data, previously generated at NIAB EMR in a similar time-course experiment, was also analysed to identify infection related genes.

- **Conclusions**

- The data generated during this PhD project suggest the presence of a single major resistance region on the apple genome
- Markers for this locus have been selected and are being assessed
- Gene expression data from both strawberry and apple time course inoculation experiments show differences in the immune response between resistant and susceptible varieties, potentially revealing genes underlying resistance to *Pc*.