



Grower Summary

**Identifying novel powdery mildew
susceptibility/resistance genes in strawberry**

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Project title: Identifying novel powdery mildew susceptibility/resistance genes in strawberry.

Project number:

Project leader: Dr Helen Cockerton

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Key staff: Professor Jim Dunwell

Location of project: NIAB EMR

Industry Representative: Harriet Dunclafe

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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

Analysing strawberry powdery mildew disease symptoms (*Podosphaera aphanis*) to identify key mildew resistance/susceptibility genes using a Genome Wide Association Study (GWAS).

Background

Strawberries are the major soft fruit produced in the UK, favored for its sweet fragrant taste. In addition to the strawberry containing compounds that have potential health benefits (Amil-Ruiz *et al.*, 2011). The introduction of tunnels benefited strawberry crops through protection from extreme weather conditions, extending seasonal production and improving yield. However a warmer, more humid environment the diseases such as powdery mildew can be more prevalent in warm and humid environments (Asalf *et al.*, 2013; Hall, Jin and Dodgson, 2019).

Podosphaera aphanis is a global pathogen, causing disease on strawberry. The symptoms of the disease include upward curling of the leaf edges and discolored patches as well as powdery white mycelium growth which can cover the leaf, flowers, and fruit. Infection of the fungus can impact on strawberry development causing misshapen and damaged fruit leading to severe yield loss due to unmarketable fruit (Hall and Jin, 2017; Hall, Jin and Dodgson, 2019).

Powdery mildew is mitigated by the application of stringent crop management practices and fungicide sprays. The fungicide sprays are applied at regular intervals using chemicals such as myclobutanyl or demethylation-inhibiting fungicide (DMI) (Carisse and Bouchard, 2010). However, the frequency of fungicide application can be restricted by regulations, as some products such as Brupirmate, Penconazole or Proquinazid can only be applied a few times a year. The restriction on applications reduces the possibility of insensitivity and fungicide resistance (Hall, Jin and Dodgson, 2019). For instance, sterol demethylation inhibitors (DMIs) fungicides like Penconazole are highly effective at controlling the disease and is commonly used in commercial fields. However, over time the powdery mildew fungus has developed resistance to these fungicides, current evidence suggests one mode of resistance

that has occurred is caused by mutations in the CYP51 gene (Sombardier *et al.*, 2010).

Summary

The first year of this PhD required the propagation of 350 different strawberry cultivars. Five replicate plants of each cultivar were propagated and transferred into the field. Genotypic data will be established through DNA extractions from each cultivar and genotyping will be conducted using the istraw35 Affymetrix SNP chip. Year 2 has consisted of collecting phenotypic data on leaves, year 3 will include phenotyping of the fruit and flowers. Phenotypic data has been gathered through scoring of disease symptom and imaging of leaves and fruit. The genotypic and phenotypic data will be used in a Genome Wide Association Study (GWAS). The GWAS will identify key Quantitative Trait Loci (QTLs) associated with disease resistance. Disease resistance in plants can be controlled by either a single gene or multiple alleles. Resistance genes are frequently found within QTL regions (Pu *et al.*, 2020). The QTLs are represented by molecular markers that correlate with the disease phenotype. Single nucleotide polymorphisms (SNPs) molecular markers are used due to their high frequency in the genome, ease of identification and cost-effective nature (Zhu *et al.*, 2008).

As part of a literature search, key genes associated with powdery mildew were identified. Bioinformatics tools were used to establish the evolutionary conservation of Mildew loci 0 (MLO) genes against available strawberry genomes from GDR (Jung *et al.*, 2014) - octoploid *Fragaria x ananassa* 'Camarosa' and diploid *Fragaria vesca*. These genes were concluded to have a high evolutionary conservation within the subspecies strawberry genome and therefore good candidates for gene editing. Using different methods of gene editing these genes will be disrupted to alter gene function and will be validated with pathogenicity tests.

Financial Benefits

No recommendations at this stage

Action Points

No action points are available at this stage of the project