



# **Grower Summary**

**Engineering tolerance to *Botrytis cinerea* in soft fruit crops**

**CTP\_FCR\_2020\_11**

**Project title:** Engineering tolerance to *Botrytis cinerea* in soft fruit crops

**Project number:** CTP\_FCR\_2020\_11

**Project leader:** Dr Charlotte Nellist (NIAB), Dr Helen Cockerton (NIAB EMR), Prof Matthew Dickinson (University of Nottingham), Assoc Prof Tim Robbins (University of Nottingham)

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**Previous report:** NA

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**Location of project:** NIAB

**Industry Representative:** Harriet Duncalfe, Berry Gardens

**Date project commenced:** 01/10/2020

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# 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.

Finlay Bourquin

PhD Student

NIAB

Signature  Date 27/10/21

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# GROWER SUMMARY

## Headline

Investigating the molecular mechanisms behind *Botrytis cinerea* infections of different strawberry organs. The results obtained during this PhD will increase our understanding of this pathosystem and could lay the groundwork for producing *B. cinerea* resistant strawberry plants.

## Background

*Botrytis cinerea* is an extremely virulent necrotrophic plant pathogen. It is responsible for causing fruit rot in strawberries. Strawberries are an exceedingly valuable soft fruit crop with almost 9 million tonnes being produced globally in 2019<sup>1</sup>. In the same year, the value of strawberry production exceeded \$2.5 billion in the US<sup>2</sup> and £350 million in the UK<sup>3</sup>. Not only are strawberries a high value crop, they also have numerous benefits for human health; they contain high levels of vitamin C and phenolics like anthocyanins<sup>4</sup>, which have been shown to reduce the risk of many disorders including cancers, cardiovascular diseases and diabetes<sup>5,6</sup>.

*B. cinerea* is particularly concerning since there are a myriad of factors that make it difficult to control. It can initiate disease through primary infection (infecting the flowers) and secondary infection (infecting the fruit receptacles)<sup>7</sup>. It can infect all of the above ground parts of a plant, including the seeds<sup>8</sup>, through various sources of inoculum such as overwintering sclerotia (hardened mass of mycelia), mycelia from neighbouring plants and conidia<sup>9</sup>. It has a quiescent stage of infection where it appears asymptomatic<sup>10</sup>, enabling it to become established in plants and ultimately leading to pre- and post-harvest crop losses. Currently, the most effective control methods are fungicides. Unfortunately, *B. cinerea* is able to recurrently develop resistance to different fungicides, with the number of multi-pesticide resistance phenotypes increasing in *B. cinerea* populations across different countries<sup>11,12</sup>. Moreover, there are growing concerns from the public about fungicide residues on crops and in the environment<sup>13</sup>. It is clear that novel control methods are paramount to prevent the spread of this fungus.

In order to develop novel control methods, it is crucial to understand the mechanisms behind the *B. cinerea*-strawberry pathosystem. This project aims to examine susceptibility and resistance factors in strawberry and virulence factors in *B. cinerea*.

## Summary

This project aims to elucidate some of the mechanisms behind *B. cinerea*'s success as a strawberry pathogen. To do this pathogenicity tests are being developed to examine

differences in virulence between 31 *B. cinerea* isolates, these tests will be conducted on strawberry leaves, fruits and flowers to capture the mechanisms this fungus uses for infection. To date, preliminary pathogenicity tests have revealed  $5 \times 10^5$  spores/ml is the optimum spore concentration for discerning differences in virulence between isolates. Optimising these pathogenicity tests on the different strawberry plant organs is currently ongoing.

To study how *B. cinerea* causes disease, isolates will be subjected to UV radiation, inducing random mutations throughout their genomes. The isolates will then undergo pathogenicity tests to examine changes in virulence; any isolates that exhibit a change in virulence will be genome sequenced in order to identify the responsible genomic loci. This will reveal certain mechanisms that *B. cinerea* is using to cause infection.

In order to examine strawberry susceptibility or resistance factors to *B. cinerea*, an ethyl methanesulfonate (EMS) population of *Fragaria vesca* plants will be produced; this is a population of plants that will have random mutations in their genomes. *F. vesca*, unlike *Fragaria x ananassa*, is a diploid and therefore is a less complex organism to study. These plants will be screened for changes in susceptibility or resistance to *B. cinerea* using the developed pathogenicity tests; plants of interest will have their genomes sequenced to identify genomic areas involved in successful infection. This will reveal targets to examine in the cultivated strawberry (*Fragaria x ananassa*). This knowledge will lay the groundwork for future research to produce *B. cinerea* resistant strawberry plants. Since *F. vesca* is the dominant subgenome of cultivated strawberries<sup>14</sup>, this work may have implications for the horticultural industry. This could occur if desirable genomic loci detected in *F. vesca* are conserved in the cultivated strawberry. A potential avenue could be the production of selective markers for breeding or genetic modification depending on legislations. Either of these avenues could lead to the future production of *B. cinerea* resistant strawberry cultivars.

## **Financial Benefits**

There are no financial benefits to report. However, the potential results from this work could aid in developing more resistant strawberry plants and hence reduce harvest losses for growers and consumers.

## **Action Points**

This is the first year of this project, currently there are no action points to suggest.