



## **Grower Summary**

**Characterising broad-acting resistance to bacterial  
canker of cherry and elucidating tissue-specific  
mechanisms of immunity**

**SF TF 170 CTP\_FCR\_2020\_4**

**Project title:** Characterising broad-acting resistance to bacterial canker of cherry and elucidating tissue-specific mechanisms of immunity

**Project number:** CTP\_FCR\_2020\_4

**Project leader:** Dr Richard Harrison, NIAB

**Report:** Annual report, 2021

**Previous report:** N/A

**Key staff:** Dr Glyn Barret, University of Reading

**Location of project:** NIAB, Cambridge

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

**Date project commenced:** 1<sup>st</sup> Oct 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.

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# GROWER SUMMARY

## Headline

This project seeks to characterise the genetics of resistance towards bacterial canker in cherry (*P. avium*). Initially, phenotyping experiments will be carried out on different wild and sweet cherry tissues. This will be followed by genotyping studies. This project will lead to the development of molecular markers, furthering progress towards identification novel sources of resistance and improved breeding strategies.

## Background

The cherry industry in the UK has seen a significant resurgence in recent years from producing ca. 1,000 ton in 2012 to >6,000 tons in 2019 (British Summer Fruits, 2019). High intensity orchards have helped to achieve this output but has also increased bacterial canker susceptibility through increased local abundance and transmission potential.

*P. syringae* disease is distributed widely throughout the world and the bacteria commonly exists as an epiphyte and is ubiquitous in the natural world, including rainwater, rivers, and soil (Morris *et al.*, 2013). It is an aerobic Gram-negative rod shaped  $\gamma$ -proteobacteria (1.5  $\mu\text{m}$  long and 0.7 – 1.2  $\mu\text{m}$  width), cells are motile exhibiting polar flagellum (Arnold & Preston, 2018). The *P. syringae* species complex is subdivided into >60 pathovars depending on which plant species it infects (Gutiérrez-Barranquero *et al.*, 2019). Diseases caused by *P. syringae* pathogenicity include annual crops such as tomato (causing bacterial spot), and beans (causing halo blight), as well as woody plants and trees including on horse chestnut (causing bleeding canker) and kiwifruit (causing canker) (Lamichhane *et al.*, 2014, Bartoli *et al.*, 2015).

The three main *P. syringae* clades responsible for canker in cherry are *P. syringae* pv. *syringae* (Pss), *P. syringae* pv. *morsprunorum* race 1 (Psm R1), and *P. syringae* pv. *morsprunorum* race 2 (Psm R2) these are located in phylogroup 2, phylogroup 3 and phylogroup 1, respectively (Hulin *et al.*, 2018, Taylor *et al.*, 1989).

*P. syringae* is able to infect in any season and cause lesions on all aerial plant tissues (leaves, fruit and blossom) and in autumn/winter seasons can infect dormant woody tissues through scars caused by mechanical and freeze/thaw damage. Symptoms include dead, sunken, water-soaked bark often accompanied with and gummosis as well as leaf shotholes.

Treatments such as copper-based biocides cause adverse environmental effects and not completely effective due to increasing copper resistance (McLeod *et al.*, 2017) and crop spraying has adverse ecological effects. Biological pathogen control attained through genetic

resistance is a key part for the global transition to sustainable agriculture (Sonmez & Mamay, 2018).

*P. syringae* pathogenicity is complicated due to the biochemical complexities derived from the multitude of virulence factors working in concert. In terms of defining host specificity the most important factor is the pathogen's effector/toxin repertoire. Other virulence factors include hormones (or hormone-like compounds), cell wall degrading enzymes, and exopolysaccharides (Xin, *et al.*, 2018). Plants have evolved a means for detecting these virulence factors and activating host defences.

Plant recognition receptors and NB-LRRs encoded by R genes, when triggered, activate downstream signalling enacting defence responses (Bucherl *et al.*, 2017, McHale *et al.*, 2006). A robust understanding of *P. syringae* effectors, effector interplay and corresponding resistance genes (R genes), may lead to the development of resistant cherry cultivars, greatly benefiting the cherry breeding strategies.

Biological control measures achieved through genetic understanding are much more financially—and ecologically favourable than the current chemical methods (Leung *et al.*, 2020). Therefore, the biochemical mechanisms and underlying genetics that determine the interaction between host recognition receptors and pathogen effectors are key to understanding resistance. Genomic, effector-informed, research has the potential to provide development of biological control through enabling accelerated breeding strategies and other potential control measures (Lenaerts *et al.*, 2019).

## Summary

- *P. syringae* is the causal agent of bacterial canker. This bacterium is ubiquitous with the environment and the species complex is vast with over 60 pathovars affecting many economically important crop species.
- *P. syringae* affects all areal plant tissues and can infect anytime throughout the year.
- Copper based treatments are becoming less effective due to increased resistance. Genetic solutions towards pathogen control are much more favourable and are key to the future transition to sustainable agriculture.
- *P. syringae* pathogenicity is complex and a range of factors affect host-pathogen interaction.
- The understanding of R gene-effector relationships is key to understanding genetic resistance towards *P. syringae* pathovars, and genomic research can facilitate

accelerated breeding strategies and has the potential to achieve continuous biological control.

### **Financial Benefits**

This is a 4-year project, no financial benefits can be reported at this stage in the project. However, this project will build knowledge towards genetically informed breeding strategies to avoid future bacterial canker tree loss.

### **Action Points**

At this stage of the project no action points can be recommended.

-recognition receptors. *Trends in Immunology*, 345–351.