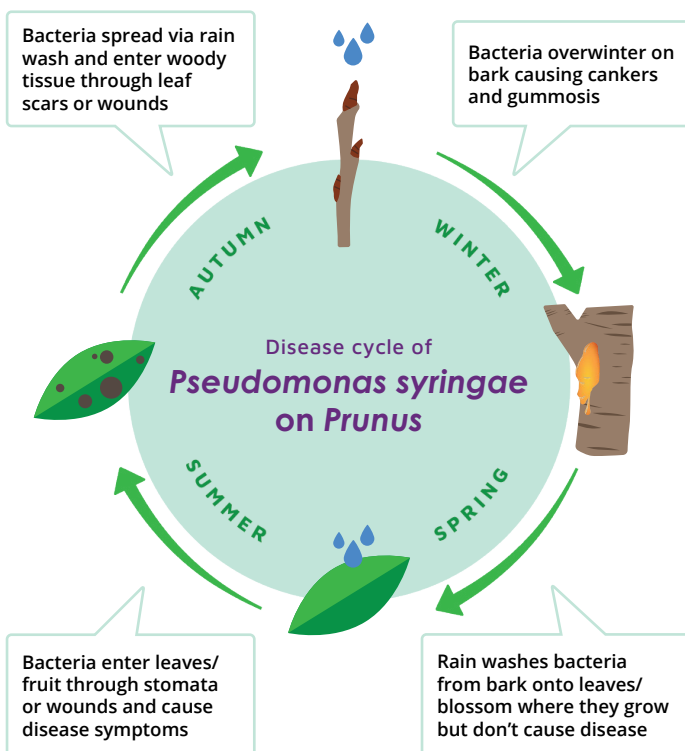




Bacterial canker symptoms on cherry

UNDERSTANDING PATHOGENICITY TO PREDICT AND PREVENT BACTERIAL CHERRY CANKER



Why do some bacteria cause cherry canker and not others?

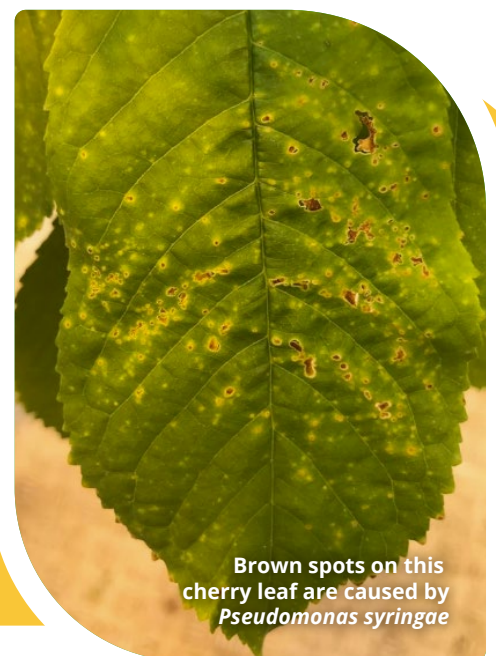
Prunus is an economically important tree genus including cherries, plums, and peaches. Bacterial canker of *Prunus* is mainly caused by strains of the bacterium *Pseudomonas syringae*. Symptoms include oozing or gummy areas of bark, and brown spots or holes on leaves. There are no effective chemical treatments. To contain the disease infected parts or whole trees need to be destroyed. Better ways to monitor and predict disease are needed to reduce tree losses.

Key to this is understanding how *Pseudomonas syringae* bacteria become pathogenic. The community of microbes (microbiome) living naturally on the *Prunus* leaves includes a huge variety of *Pseudomonas syringae* bacteria. Some of these are pathogenic, some are not. Pathogenicity (the ability to cause disease) may emerge when natural gene transfer happens between different strains in the leaf microbiome.

This research used genetic sequencing and AI to predict pathogenicity

Using high-throughput genome sequencing we examined the microbiome of farmed cherry trees and nearby wild trees. This revealed all the different strains and the relationships between them. We then studied the frequency of genes for known pathogenicity factors within the strains. Machine learning was used to predict the potential of the bacteria to cause disease in horticultural crops.

We also explored the role of viruses (bacteriophages) in gene transfer. This work involved investigating the transfer of virulence genes between bacteria both in the lab and in the plant.



Brown spots on this cherry leaf are caused by *Pseudomonas syringae*

Discoveries

Our research has shown that the bacteria which cause *Prunus* canker disease are diverse and constantly evolving.

- 🔍 A remarkable variety of both pathogenic and non-pathogenic *Pseudomonas syringae* variants were found living in and around orchards. There was significant variation between different regions, perhaps due to climate.
- 🔍 *Pseudomonas syringae* bacteria can receive virulence genes from other bacteria mediated by naturally occurring viruses called bacteriophages. This may drive the evolution of new pathogens.
- 🔍 Machine learning was used to analyse the genome of isolated bacterial strains, identifying numerous potential pathogens which contain virulence genes.
- 🔍 In the short-term monitoring, prevention and possibly biological control should be combined to rapidly react to emerging threats. Breeding for resistance remains a long-term goal.
- 🔍 Cultivation techniques including the use of polytunnels and nitrogen fertilisers may reduce the incidence and severity of disease, although research is ongoing.



Recommendations

To reduce the impact of bacterial canker disease we recommend a focus on monitoring, prediction and prevention.

- 🌿 More emphasis on monitoring the microbiome, especially in woodlands and non-agricultural land.
- 🌿 Greater use of artificial intelligence to rapidly identify emergent pathogens and predict outbreaks.
- 🌿 Increased collaboration between researchers, growers and land managers for monitoring and sharing information.
- 🌿 Focus on good husbandry to keep plants healthy and minimise disease impact.
- 🌿 Fund research on cherry resistance mechanisms and virulence gene transfer in other species.



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This document is based on this and other research:

Hulin MT, et al., Genomic and functional analysis of phage-mediated horizontal gene transfer in *Pseudomonas syringae* on the plant surface. *New Phytologist* (2023) 237:959–973 <https://doi.org/10.1111/nph.18573>



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