



Epidemiology and Control of Potato Blackleg



Ashleigh Holmes, Sonia Humphris & Ian Toth
 The James Hutton Institute, Cell & Molecular Sciences, Errol Road, Invergowrie, Dundee, DD25DA
 Email: Ashleigh.Holmes@hutton.ac.uk

Blackleg, caused by *Pectobacterium* species, is an economically important bacterial disease of potato that threatens Scotland's seed industry.

Our group's work in the ENRA Strategic Research Programme aims to improve understanding of:

1. the epidemiology of the disease by investigating bacterial survival in the wider environment
2. its genetic diversity for improved diagnostics which will allow tracking of its spread in the field
3. potential control options for inclusion in IPM approaches to mitigate the disease

Understanding how *Pectobacterium* interacts with other plant species, such as weeds and cover crops, informs on potential sources of infection in the wider environment

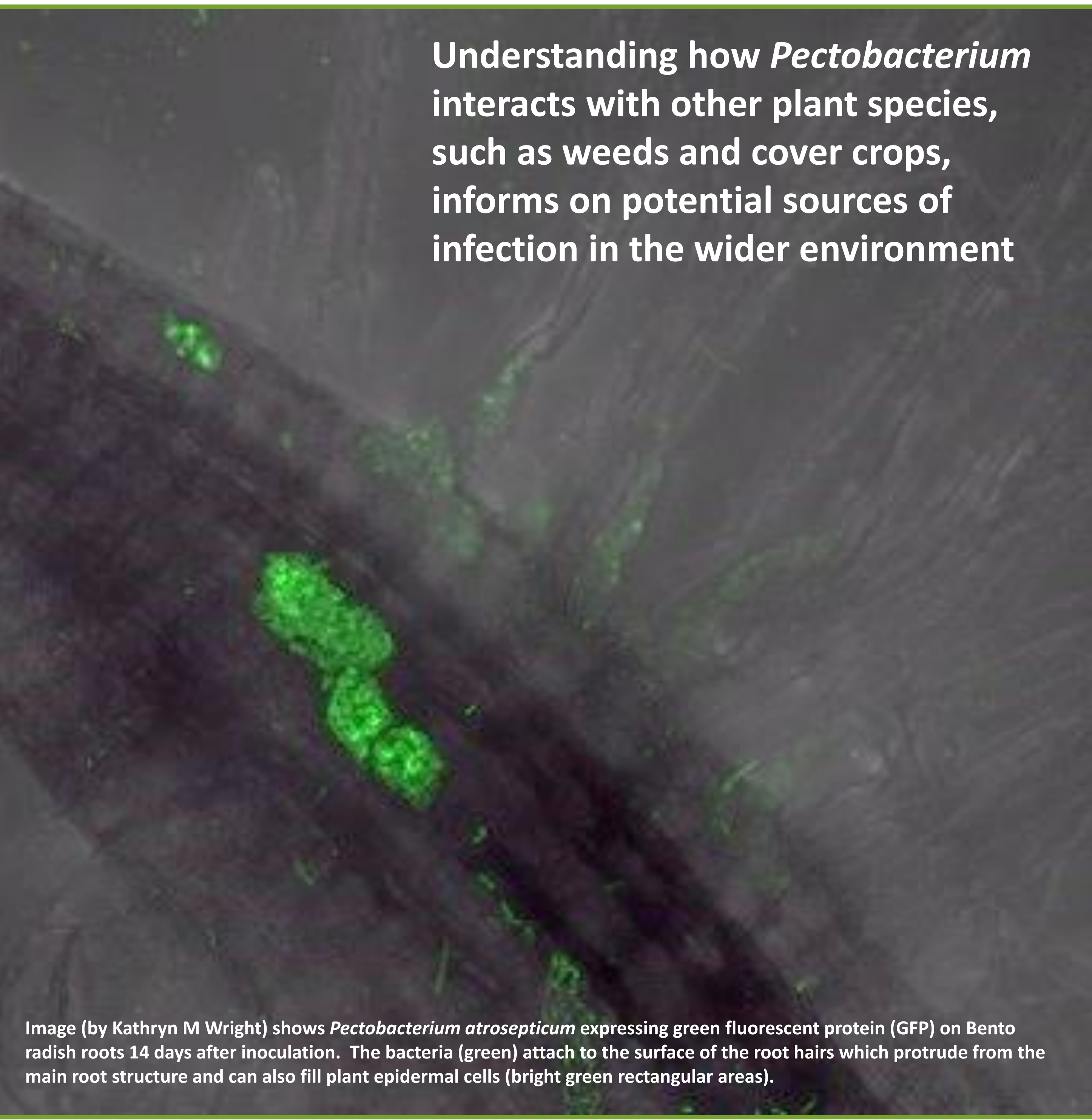


Image (by Kathryn M Wright) shows *Pectobacterium atrosepticum* expressing green fluorescent protein (GFP) on Bento radish roots 14 days after inoculation. The bacteria (green) attach to the surface of the root hairs which protrude from the main root structure and can also fill plant epidermal cells (bright green rectangular areas).

Future control options for Integrated Pest Management

There are no chemical control options for blackleg. Instead, disease control relies on a combination of methods including the use of seed certification schemes and following best practice standards to avoid contamination.

We are investigating the effects of soil amendments on blackleg disease progression and microbial communities present in the soil and surrounding potato roots (rhizosphere) (Figure 1).

Future work aims to understand whether microbial communities change with blackleg stress. Are there species present that can control disease by priming defenses or outcompeting *Pectobacterium*?

Linking with UKRI funded projects we are testing potential biocontrol applications:

- viruses (bacteriophages) that specifically target *Pectobacterium*
- synthetic microbial communities (SynComms)

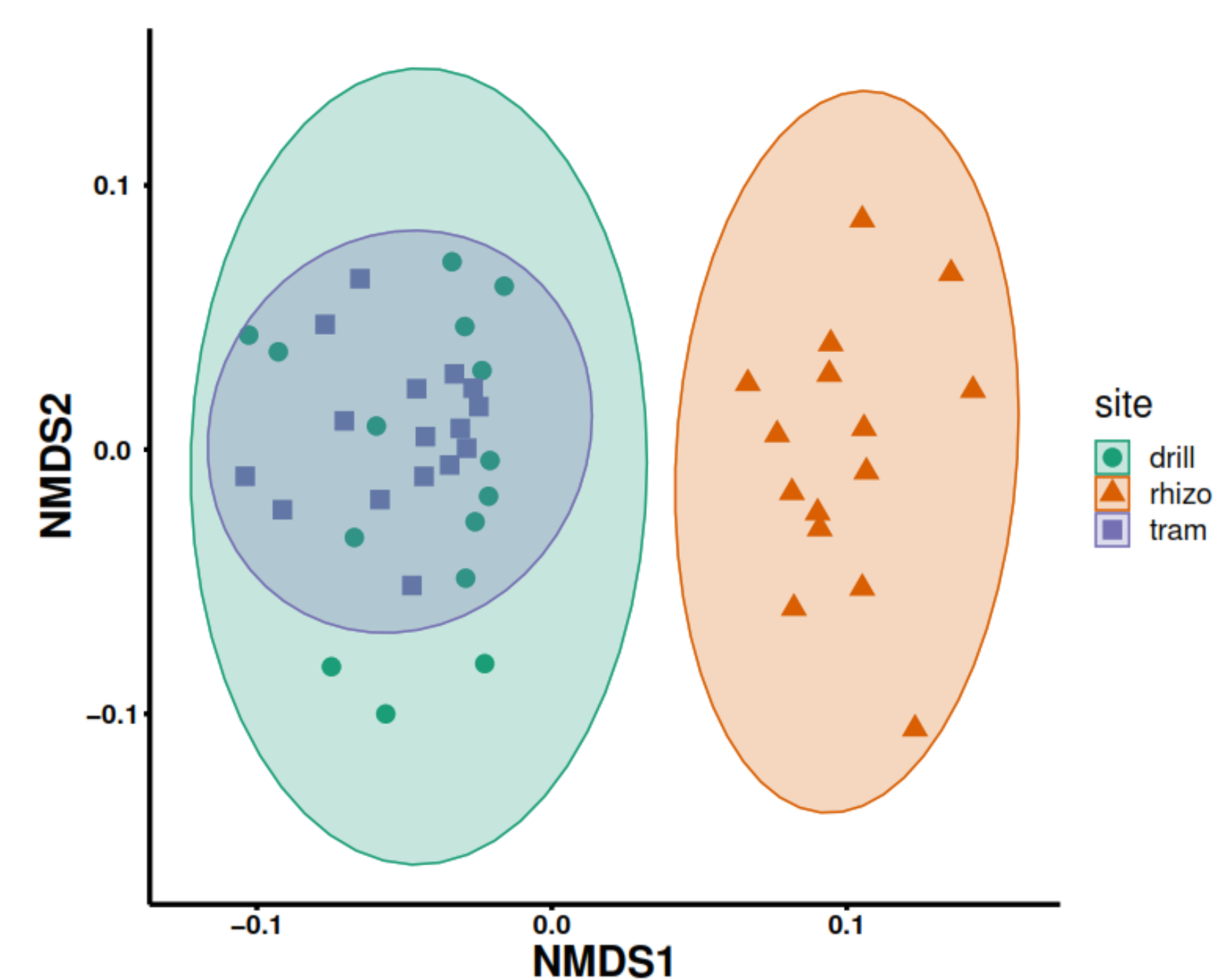


Figure 1: Comparisons of microbial communities as measured by 16S DNA amplicon sequencing from potato field drills, tramlines and potato roots. The microbial communities from the potato roots (orange) are diverse from the communities from the bulk soil sampled from the drills (green) and tramlines (blue).

Developing improved diagnostics

Using our resource of >150 whole *Pectobacterium atrosepticum* genome sequences, we are applying computational methods to examine the diversity across isolates from different geographical locations, sources and time periods to help track the pathogen in the environment and through the potato production system (Figure 2).

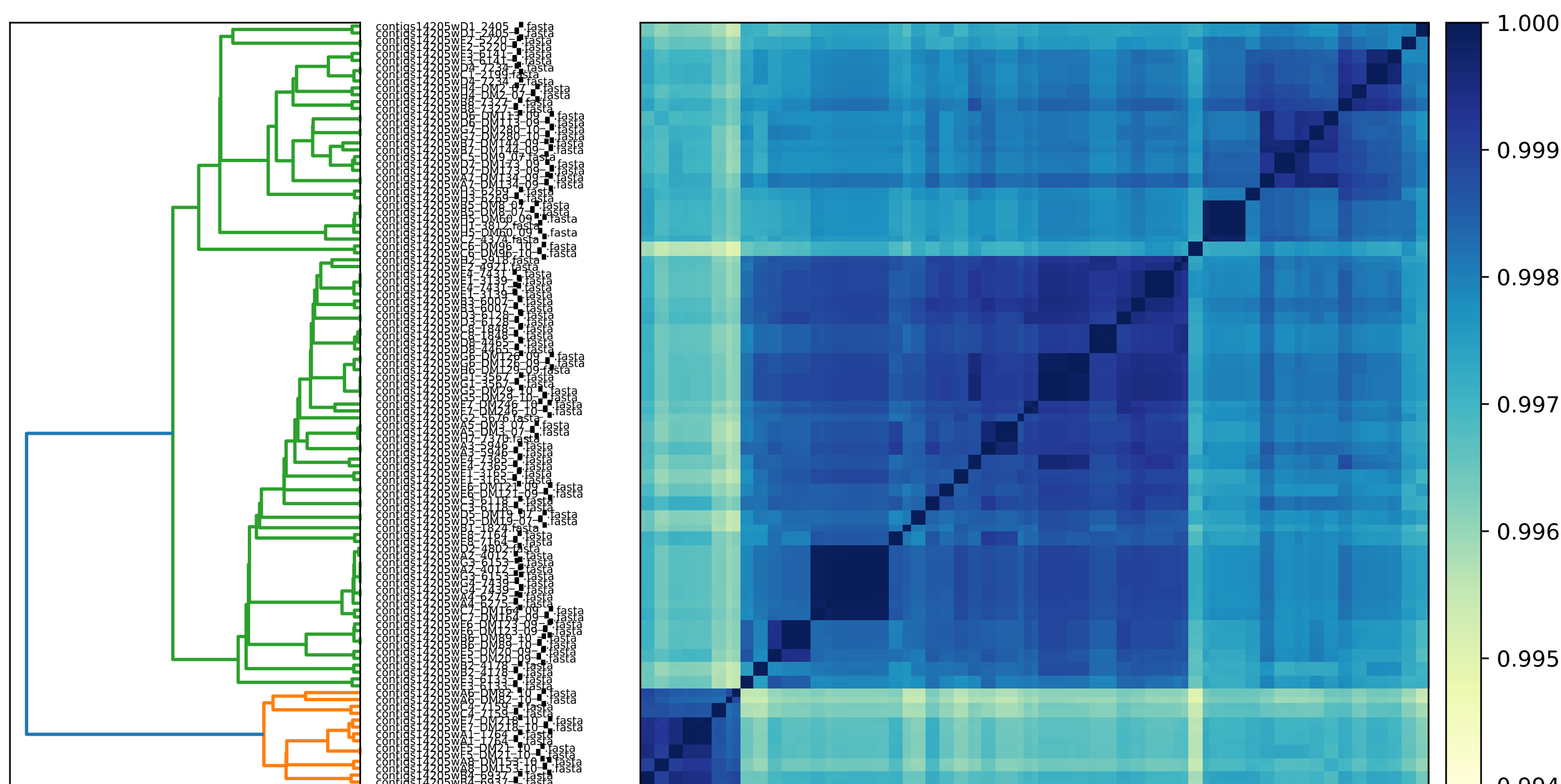


Figure 2: Heatmap of *Pectobacterium atrosepticum* genome similarity by k-mer content



Acknowledgements

This research was funded by the Scottish Government Strategic Research Programme (2022-2027) under projects JHI-A1-1 Epidemiology of Key Pests and Diseases, JHI-A1-2 Integrated Crop Protection and JHI-D3-1 Healthy Soils for a Green Recovery. Bacteriophage as biocontrol for blackleg is funded by Innovate UK (IUK10005717). Decision support tool for Blackleg (DeS-BL) is funded by BBSRC (BB/T010657/1).