



Swede leaf with *Xanthomonas* symptoms

MITIGATING THE IMPACT OF XANTHOMONAS DISEASES ON CROPS

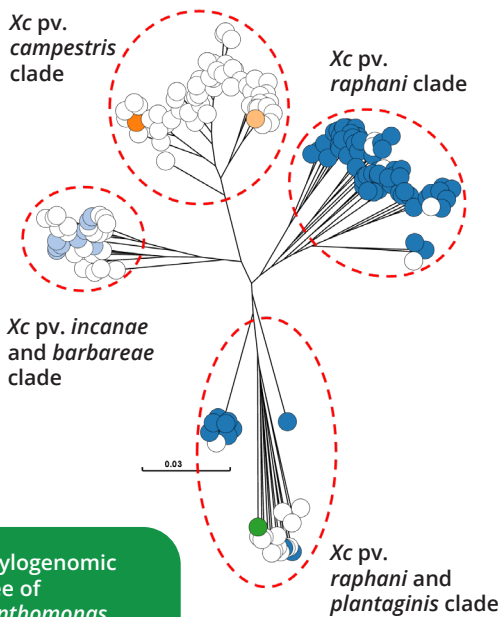


Xanthomonas includes diverse, widespread and damaging bacterial plant pathogens

Bacteria of the genus *Xanthomonas* can cause disease in more than 350 plant species including many economically important crops. For example, black rot, caused by *Xanthomonas campestris* pv. *campestris* (Xcc), is a major disease of brassicas like cabbage and cauliflower in the UK.

Climate change and plant imports are increasing the threat posed by other *Xanthomonas* species. Although currently absent or rare, diseases like bacterial leaf streak of maize (caused by *X. vasicola* pv. *vasculorum*), angular leaf spot of strawberry (caused by *X. fragariae*), and black rot of watercress (caused by *X. nasturtii*) are of significant concern to the UK.

Accurate diagnostics are essential for informed disease and biosecurity management. Large-scale whole genome sequencing of diverse *Xanthomonas* isolates can facilitate development of species, pathovar and even race-specific genetic markers. It can also identify novel species and aid taxonomic reclassification. For brassica improvement, genetically mapping black rot resistance can support breeding programmes.

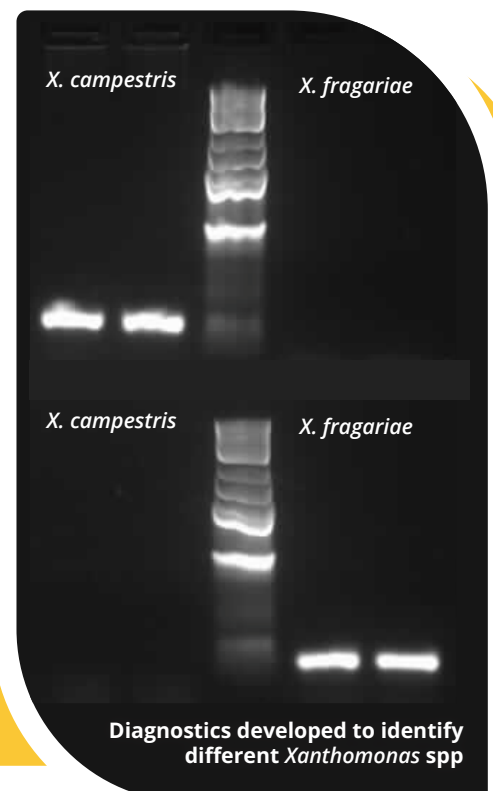


Phylogenomic tree of *Xanthomonas campestris*

Our research used genetic sequencing and imaging to better understand *Xanthomonas* infections and screened for disease resistance in brassicas, strawberry and maize

Whole-genome sequencing of ~1000 *Xanthomonas* isolates enabled detailed classification of relationships in the *Xanthomonas* genus. We identified novel species, made taxonomic reclassifications, and developed highly specific diagnostic markers which can discriminate species, pathovars or races.

Screening unique lines of *Brassica oleracea* (cabbage species) and *Brassica napus* (rapeseed and swede species) lines identified useful sources of resistance to Xcc. We also screened two *Xanthomonas* species considered to represent a real biosecurity threat to the UK; *X. fragariae* on strawberry varieties and *X. vasicola* pv. *vasculorum* on some popular maize varieties.



Diagnostics developed to identify different *Xanthomonas* spp

Discoveries

We have clarified the taxonomy and risks posed by various *Xanthomonas* diseases

- 🔍 We sequenced ~1000 diverse *Xanthomonas* isolates identifying new species, incorrect naming and taxonomic reclassification.
- 🔍 We developed PCR diagnostics at the level of species, pathovar and race for key *Xanthomonas* diseases providing new tools for biosecurity and crop management use.
- 🔍 Several *B. oleracea* and *B. napus* lines with race specific and broad-spectrum resistance were identified, including lines with combinations of resistance. The most promising lines have been crossed and we are currently screening to identify resistance-linked markers. This will be useful for breeding more resilient crops.
- 🔍 We developed novel tools to non-destructively visualise *Xcc* disease progression in brassica tissues. This revealed movement of *Xcc* from infected leaves to seeds, as well as demonstrate seed transmission to the next generation. We found no evidence for aphid transmission.
- 🔍 Maize bacterial leaf streak (*X. vasicola* pv. *vasculorum*) poses an imminent threat to UK and European maize crops as no resistance was found in popular varieties.
- 🔍 While angular leaf spot of strawberry (*X. fragariae*) is not of immediate concern, several popular UK strawberry varieties are very susceptible. Our diagnostics can help future disease management.

For more information contact:

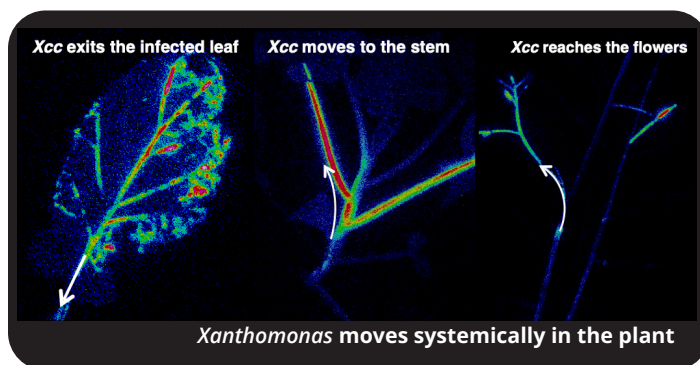
Prof Murray Grant - email: m.grant@warwick.ac.uk
or visit <https://bacterialplantdiseases.uk/xanthomonas-threats/>

To access the *Xanthomonas* genomic data visit PhytoBacExplorer <https://phytoexplorer.warwick.ac.uk/>

Recommendations

Our diagnostics can be deployed in both disease management and biosecurity to facilitate rapid identification and containment of diseases.

- 🌿 Encourage use of our diagnostic assays and genomic resources to detect different *Xanthomonas* pathogens.
- 🌿 Adopt and adapt our *Xcc* race-diagnostics to monitor diversity and evolution which in turn will help establish the effectiveness of varietal resistances.
- 🌿 Use resistance-linked molecular markers to incorporate our race-specific and broad-spectrum resistances into commercial crops.
- 🌿 Employ the imaging tools developed to gain a more detailed understanding of *Xanthomonas* virulence mechanisms.
- 🌿 Add bacterial leaf streak of maize (*X. vasicola* pv. *vasculorum*) to the Plant Health Risk Register and regulate it.



An interdisciplinary research consortium working together to understand bacterial plant diseases to protect UK farms, forests and gardens.

