Swede leaf with *Xanthomonas* symptoms

MITIGATING THE IMPACT OF *XANTHOMONAS* DISEASES ON CROPS

Xanthomonas Threats Consortium

Xc pv. *campestris* clade

Xc pv. *raphani* clade

Xc pv. *incanae* and *barbareae* clade

0.03

Xc pv. *raphani* and *plantaginis* clade

**Phylogenomic tree of *Xanthomonas campestris***

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.
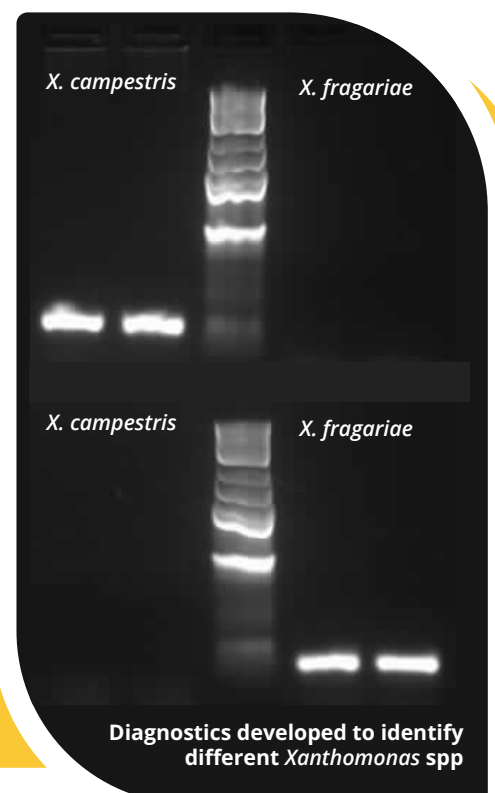
Accurate diagnostics are essential for informed disease and biosecurity management. Large-scale whole genome sequencing of diverse *Xanthomonas* isolates can facilitate development of species, pathovar and even race-specific genetic markers. It can also identify novel species and aid taxonomic reclassification. For brassica improvement, genetically mapping black rot resistance can support breeding programmes.
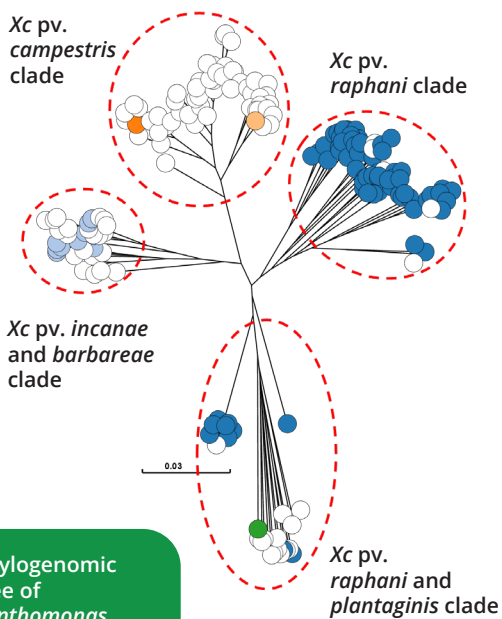
Our research used genetic sequencing and imaging to better understand *Xanthomonas* infections and screened for disease resistance in brassicas, strawberry and maize

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.

X. campestris

X. fragariae

X. campestris

X. fragariae

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 and revising taxonomic names.

- 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.
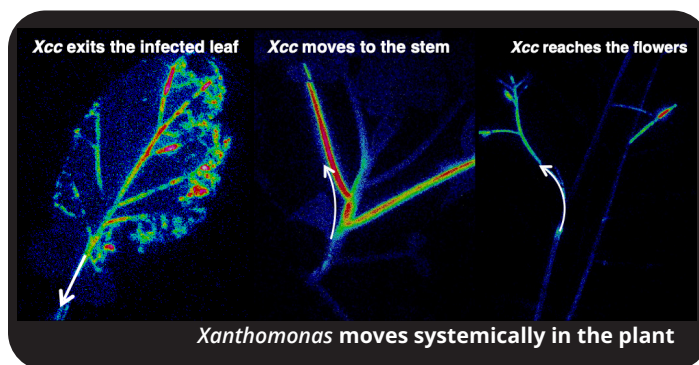
Recommendations

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.

Xcc exits the infected leaf   *Xcc* moves to the stem   *Xcc* reaches the flowers

Xanthomonas **moves systemically in the plant**

Bacterial leaf streak symptoms on maize

WARWICK
THE UNIVERSITY OF WARWICK

fera

UNIVERSITY OF EXETER

Bacterial Plant Diseases Programme

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

UKRI Biotechnology and Biological Sciences Research Council

UKRI Natural Environment Research Council

Scottish Government Riaghaltas na h-Alba gov.scot

Department for Environment Food & Rural Affairs