

Xanthomonas plant diseases: mitigating existing, emerging and future threats to UK agriculture

Brassica cultivation is a multi-billion dollar industry worldwide and *Xanthomonas* is a bacterial plant pathogen that can infect more than 350 plant species including many brassicas. This multidisciplinary project brings together experts in microbiology, genomics, pathology, imaging, molecular biology and risk assessment to take one of the first large scale integrated studies of the plant pathogen *Xanthomonas campestris* (*Xc*), using approaches involving large scale genomic sequencing, in planta imaging and screening for pathogen resistance using a unique set of brassica diversity lines. The objectives are to enhance knowledge and support effective breeding and deployment of appropriate control strategies for *Xanthomonas* in the UK and other countries that face similar challenges.



Our central focus is on black rot of crucifers (*Xc* *pv.* *campestris* or *Xcc* for short) which can attack all cultivated brassicas. *Xcc*, is a seed-borne vascular (the tissue that allows water and nutrients to flow) disease and probably the most important disease of vegetable Brassicas (*Brassica oleracea*; e.g. cabbage, cauliflower, broccoli, Brussels sprouts and kale) in the world. *Xcc* also infects *B. napus* (oilseed rape, swede), *B. juncea* (mustards) and *B. rapa* (turnip, Chinese cabbage). It is therefore really important. *Xcc* can cause complete crop loss, though in the UK it usually leads to reduced quality and marketability.

There are two main problems with *Xcc*. First, as with most bacterial phytopathogens, there is no simple chemical interventions, unlike for fungal pathogens. Traditional bactericides such as copper oxychloride are being withdrawn from sale. Secondly, and one key driver of this proposal, there is virtually no resistance in commercial *Brassica oleracea* varieties - this has probably been bred out. So we are going back to wild relatives and are fortunate that Warwick's UK Vegetable Germplasm collection maintains more than 6000 brassica accessions. Obviously this is far too much to deal with, but we recently (with Defra funding) generated what we call Brassica diversity fixed foundation sets (DFFs). These are designed to capture the majority of the genetic variation in a population of homozygous lines which can then be screened for resistance to *Xcc*. This project will use DFFs for *Brassica oleracea*, *Brassica napus* and also interfertile C genome crop wild relatives. We are also fortunate to have the largest collection of *Xanthomonas* isolates in Europe (~ 1,000) as well as the UK's most knowledgeable *Xanthomonas* pathologists Dr Joana Vicente on board.

We will sequence more than 900 *Xanthomonas* isolates from this collection so we can address some of the key challenges in the field, such as what makes a pathogen, what are the key genes a *Xanthomonas* pathogen needs to deploy to cause disease on specific plants and how the pathogen changes over time. A major output of this work will be a large set of diagnostic markers that can be used to identify specific pathovars of *Xanthomonas*, even in the field!

We will couple these studies to understanding how the pathogen infects and multiplies in the plant using two complementary imaging approaches, fluorescent/bioluminescent reporters and the plant endogenous chlorophyll fluorescence - which changes as disease progresses. We also aim to ask the questions, can we use a beneficial soil fungus to protect from *Xcc* disease and can insect pests such as aphids transmit the disease in the field following feeding on infected plants? One of the real concerns in a global community is incursions of pathogens. So aside from the diagnostic work proposed, we will also undertake a detailed risk assessment on a devastating *Xanthomonas* disease of maize, which is rapidly spreading in the US and causing over 50% of losses in some regions. This assessment will also consider risks to other crops considered potentially "at risk".