Mathematical modelling of phytopathogen-targeted secretion pathways

Supervisory team:
Main supervisor: Dr David Richards (University of Exeter)
Second supervisor: Dr Mike Deeks (University of Exeter)
Prof Christian Soeller (University of Exeter), Dr Stefano Pagliara (University of Exeter)

Collaborators: Prof Peter Winlove (University of Exeter)

Host institution: University of Exeter (Streatham)

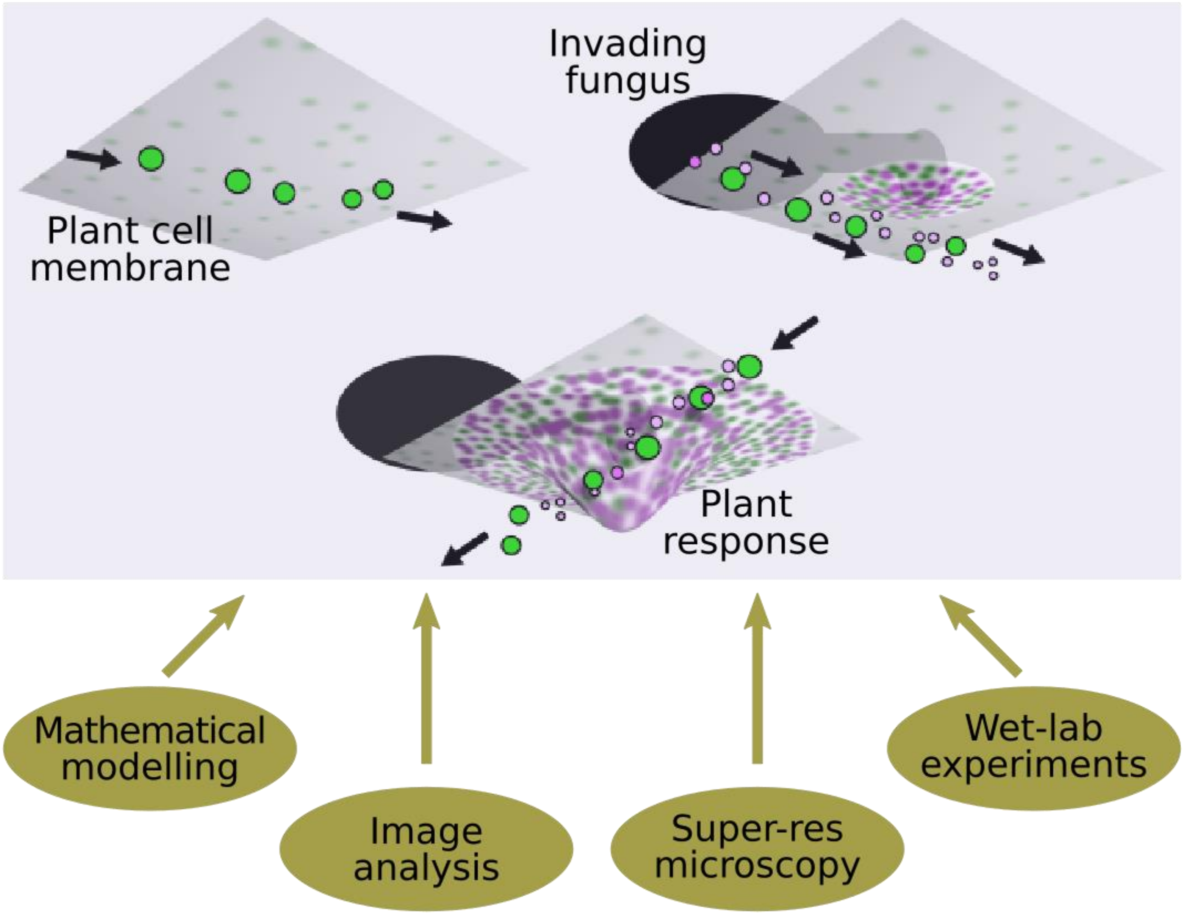
Project description:
Understanding how plants respond when pathogens attack is of vital importance. This is especially true since 90% of all calorie intake worldwide comes directly from crop plants. When these crops fail, such as during the historic potato famine in Ireland and the more recent Cassava famine in Uganda, millions of deaths can result.

During infection, plant cells move their immune defences to the site of infection with the aim of repelling the invader. However, it is not known how these immune defences are moved. Is the whole process due to passive diffusion or are more active mechanisms at work? Are the relevant molecules wrapped up in individual packages or can they jump from package to package? If questions like these are understood, then it may be possible to improve the plant immune response in order to develop stronger resistance and safeguard crop production for the future.

In this PhD project, you will examine the relative contribution of these (and other) behaviours during the plant immune response. You will achieve this using a multidisciplinary approach that combines mathematical modelling, image analysis, super-resolution microscopy and traditional biological wet-lab experiments. This combination of disciplines often leads to the best results and will allow you to learn a wide range of different skills and techniques. You are not expected to already know both mathematical modelling and wet lab techniques. Full training will be provided in both areas during the PhD. In particular, you will

- Design mathematical models of plant vesicle motion that include vesicle diffusion, protein exchange between nearby vesicles, active vesicle motion towards the infection site, and vesicle tethering. Other factors such as subdiffusion and confined diffusion will also be considered. These models will then be simulated on a computer using MATLAB or C++.
- Perform experiments with the plant Arabidopsis to obtain movies of motile vesicles labelled using fluorescent cargoes.
- Use super-resolution microscopy to better define the spatial distribution of trafficked material.
- Develop image analysis software to automatically extract and track vesicle position. This will allow quick, accurate analysis of movies from part 2, which will in turn inform the mathematical modelling.

This interplay between experiment and modelling is a key part of this project and will make for an exciting PhD.



Invading fungus
Plant cell membrane
Plant response
Mathematical modelling
Image analysis
Super-res microscopy
Wet-lab experiments