Benign infections or damaging epidemics: the influence of biology, the environment and agricultural practice on vector-borne phytobacteria

Factors that contribute to some pests and diseases being serious problems in one location and not another are largely unknown. Identifying these factors is fundamental to better understand risks associated with introductions of pests and diseases into new environments via globalised trade of plants and plant products.



The bacterium 'Candidatus Liberibacter solanacearum' (Lso) is an emerging threat to a range of crops including potato, tomato, carrot and celery and is under statutory control in the EU. In potato Lso induces zebra chip, a damaging disease manifest by brown stripes in the tubers, which cause large losses in fresh and processing markets. The disease has spread quickly through the Americas and more recently into New Zealand. A genetically different sub-group (haplotype) of the bacteria causes a damaging disease of carrots in Scandinavia, Northern France and the Mediterranean basin. Whereas this haplotype can infect potato, disease in this crop is not evident in Europe. The disease is transmitted by psyllids, which are sap-feeding insects. The psyllid *Bactericera cockerelli* spreads Lso in the Americas and New Zealand, whilst two native species (*Trioza apicalis* and *Bactericera trigonica*) and possibly a third species (*B. nigricornis*) spreads the bacteria in Europe. In the UK the pathogen has been detected in carrots, weeds and in psyllids caught in insect traps. Despite the presence of the pathogen and competent vector species, the bacteria is not currently causing widespread crop damage in either potato or carrots.

The focus of this project is to better understand the factors that may contribute to Lso becoming a more important pathogen in the UK. Factors may include differences between Lso haplotypes, the geographical distributions and genetics variations of Lso haplotypes and psyllid vectors, landscape designs (such as weeds that surround crop fields), and agricultural practice/policy. The overall aim of the work is to investigate the complex network of Lso haplotypes, hosts and vectors in the UK landscape, focussing on carrots, related crops and apiaceous weeds.

Working within this system our objectives are to:

(i) Generate genome sequence information for Lso haplotypes and psyllids to understand genetic variations of the pathogens and vectors present in the UK, and use this information to develop rapid diagnostics tests;
(ii) Study the spatial and temporal distributions of Lso and psyllid vectors in crops and the surrounding environments;

(iii) Improve our understanding of vector host plant preferences and ability to transmit the bacteria;
(iv) Use ecological network analysis to build a comprehensive picture of the pathosytem;
(v) Use ecological and trade models to examine how future policy options (changes in the UKs tariff structure with trading partners and how UK habitats are managed) might alter this transmission risk. Ultimately the modelling will consider the systems readiness to withstand changes in risk and provide information on the drivers (biological, ecological and man made) that influence the potential of a pathogen to become a damaging disease-causing agent.

The outcomes will be of interest to government stakeholders working in Plant Health, where the research will provide insights into prioritising responses to Lso and other complex pests and diseases. The overall approach should improve our ability to predict risk and prioritise surveillance activity on the most damaging threats. For agri-food-environment, information on the impact of changes in land and crop management and approaches to assess this will help us to better understand the complex networks that exist and the impact of future environmental and trade policies. For industry, better understanding of emerging pathogens will help them to proactively manage this and future problems. Finally the interdisciplinary consortium will deliver innovative science of interest to academics in a number of fields.