



Speaker Abstracts

Applications of Plant Pathology: From Field to Clinic

Insight in phytohormone-induced gene regulatory networks reveals unknown defence controllers

Saskia van Wees, Utrecht University, The Netherlands

In nature, plants are subject to attack by a broad range of harmful pests and pathogens. To survive, plants have evolved sophisticated immune signalling networks that enable them to mount an effective defence response upon recognition of invaders. Plant hormones, especially salicylic acid (SA) and jasmonic acid (JA), emerged as core players in the orchestration of the signalling networks that underlie activation of plant defence responses.

The SA and JA pathways cross-communicate, providing plants with a highly flexible regulatory capacity to finely tune their defence responses against the attacker at hand. Moreover, a previous encounter with an attacker or with a beneficial microbe can prime plants to activate a faster and stronger SA- or JA-dependent defence response. We take a systems approach to advance our understanding of the regulation of SA- and JA-induced defence responses. We performed high-resolution RNA-Seq time series of SA- and JA-treated *Arabidopsis* to build dynamic gene regulatory network models. This allowed us to uncover novel regulators of the individual hormone-induced responses. Soon, we will work on identifying regulators of hormone signal integration and of defence priming.

The significance of these novel regulatory components is validated by molecular and genetic analyses and by bioassays using pathogens and insects. Understanding how plants shape their hormone-induced pathways to effectively defend themselves against different harmful organisms will identify strategies for breeding agricultural crops with a cost-efficient resistance to improve yield and reduce the need for pesticides.

Plant pathogen genomes: blueprint, recipe, opportunity?

Leighton Pritchard, The James Hutton Institute, UK

Microbial genome sequences are cheaply and readily available. In some ways they are the most informative assay available for an organism, but in other ways they are highly cryptic. A pathogen's genome in principle could tell us nearly everything about its biology, but in practice they currently do not. I will describe how genomic and related computational analyses inform pathogen studies at the James Hutton Institute, connecting with policy and potential industrial applications, as well as delivering insight into pathogenicity. I will describe work at the Hutton on baseline plant pathogen diversity in Scotland, genome-based diagnostics and classification, and selection of engineering targets for industrial biotechnology, and outline what I hope will be useful future directions for genome-enabled biology in understanding plant pathogens and interactions between them and their hosts.

Breakdown of plant-derived dietary carbohydrates by the human gut microbiota

Petra Louis, The Rowett Institute, University of Aberdeen, UK

The human large intestine is colonised by a highly diverse microbial community, the gut microbiota, whose activities are intricately linked to human health. Dietary carbohydrates originating from plant-based foods that cannot be digested by the human host in the upper gut (so-called non-digestible carbohydrates, NDCs) are the main energy source for the microbiota. They are fermented to various end products, in particular the short-chain fatty acids acetate, propionate and butyrate, which have health-promoting effects. NDCs constitute a wide range of different carbohydrate types from plant cell walls and storage



polysaccharides. Different gut microbes vary in their capacity to degrade the different NDCs, thus creating a complex network of cooperative and competitive metabolic interactions. The efficient degradation of particulate NDC fractions appears to be highly dependent on keystone primary degraders, which make more soluble breakdown intermediates available to the wider microbial community. For example, *Ruminococcus bromii* is a keystone species for starch degradation. This seems to be due to highly efficient extracellular multi-enzyme complexes (so-called amylozymes) that facilitate effective degradation of more recalcitrant resistant starches and that are not found in other known starch degraders in the human large intestine. Cross-feeding between different microbes does not only take place at the carbohydrate level, but also via fermentation products, for example, lactate, which can be utilised by certain propionate- and butyrate-producing bacteria.

The impact of the host microenvironment on plant disease development

Gail Preston, University of Oxford, UK

One of the most fundamental questions in the study of plant disease is the question of what factors determine whether a pathogen thrives, persists or dies during its interaction with its host? The bacterial pathogen *Pseudomonas syringae*, which causes a wide range of economically important plant diseases, colonises the apoplastic compartment that surrounds plant cells. It is therefore the biochemical and biophysical properties of the apoplastic environment that determines whether *P. syringae* successfully colonises host plants. This seminar will discuss how analyses of apoplast composition can be combined with analyses of pathogen metabolism and gene expression to investigate how the microenvironment inside host tissues affects the outcome of infection, and how this knowledge can be used to improve disease control.

Early detection of fungicide resistance in crop pathogens

Fran Lopez Ruiz, Centre for Crop and Disease Management, Curtin University, Australia

Fungal diseases are yield and quality limiting factors for agriculture worldwide. Chemical control together with cultivar resistance, are the two major disease management tools available for growers nowadays but, are we breaking them? The future of these tools is unclear as the overuse of fungicides, combined with the lack of sound integrated disease management (IDM) strategies, has created the perfect environment for fungicide resistance evolution.

Fungicide resistance is spreading and new cases of resistance are being identified each year. The development of sensitive, fast and cost-effective methods for the detection of fungicide resistant populations will be vital yet it continues to be the bottleneck for the development of anti-resistance management strategies tailored to suit individual growers. One of the main challenges continues to be the lack of quantitative mobile detection methodologies for the in-situ analysis of fungicide resistance.

Since 2015, populations of the barley diseases net type of net blotch and spot type of net blotch (*Pyrenophora teres* f.sp. *teres* and *Pyrenophora teres* f.sp. *maculata*, respectively) resistant to demethylase inhibitor (DMI) fungicides have been identified in Australian barley crops. The characterisation of the resistance revealed different target site mutations that lead to a combination of reduced fungicide binding and increased target overexpression. The implications of new laboratory and field based molecular detection methodologies for the management of fungicide resistance in the field will be discussed.



Making the unknown known: The application of diagnostic technologies in plant health virology

Adrian Fox, Fera Science, UK

Due to the obligate nature of viruses, plant virology has always been an early adopter of new diagnostic technologies. Until recently, the main diagnostic technologies applied in plant health laboratories were targeted and specific requiring *a priori* knowledge of the pathogens likely to be associated with a given host and symptom.

With the advent of Next-Generation Sequencing (NGS), the ability to detect the pathogens associated with plant diseases of unknown aetiology is becoming routine. The application of such approaches has resulted in an almost exponential increase in the number of previously uncharacterized viruses now being reported. Whilst these discoveries have led to a deeper understanding of the diversity of the plant virome, the greatest challenge for plant health authorities in applying NGS now lies in differentiating between the pathogenic, commensal, or even mutualistic viruses. Pathogen characterisation in support of plant health risk assessment is a laborious process requiring demonstration of causation, host range studies, vector transmission studies and baseline surveillance. Some of these considerations can be addressed through experimental set up, or through follow-up volume testing, whilst others may take months or years of additional research.

An overview of the development of NGS for frontline plant virus diagnostics will be illustrated with case studies highlighting the opportunities and challenges of deploying NGS in a plant health/biosecurity setting.

Impact of taxonomy on identification and detection of plant pathogens in the Enterobacteriaceae

Carrie Brady, University of the West of England, UK

The aim of taxonomy is to circumscribe taxa into monophyletic groups which are reflective of their genotypic, genomic and phenotypic characteristics. This can be difficult to put into practice especially for members of the family *Enterobacteriaceae*, where many species are phenotypically and phylogenetically closely-related despite representing genera from both clinical and plant hosts.

Over the years, numerous enterobacterial strains have been wrongly identified and species erroneously assigned at the genus level creating many taxonomic issues. There is also a blurred distinction between plant-pathogenic and clinical bacteria as several enterobacterial species are polypathogenic, meaning their taxonomy should not be studied separately. It is often necessary to clarify the taxonomy of causal agents of novel plant diseases before attempting to design a rapid identification or detection technique.

Multilocus sequence analysis (MLSA) scheme, based on short sequences of four protein-encoding genes, has provided a robust and reliable alternative to 16S rRNA gene sequencing for taxonomic and phylogenetic studies of plant-pathogenic and –associated enterobacteria. Concatenated analyses of *gyrB*, *rpoB*, *infB* and *atpD* gene sequences have resolved taxonomic issues within the genera *Pantoea*, *Tatumella*, *Brenneria* and *Dickeya*; supported the classification of many novel species and reassigned numerous strains to the correct species and genus.

Proving pathogenicity in polymicrobial pathosystems



Sandra Denman, Forest Research, UK

Causality of tree diseases attributed to primary pathogens is proven experimentally through successful completion of Koch's Postulates. In complex disease syndromes, cause and effect is more difficult to prove experimentally because the 1 pathogen = 1 disease model is not suitable for multifaceted, polymicrobial diseases. Oak declines are well documented, complex disease syndromes.

Acute oak decline, which is characterised by weeping stem patches with underlying innerbark necrosis and the presence of larval galleries of the native buprestid *Agrilus biguttatus*, serves as a good model to develop an appropriate suite of tests that would provide compelling, empirical evidence of causal roles for key organisms consistently associated with the disease.

We propose a novel template for acquiring proof of a causal role where classical methods combined with molecular technologies are used to link microbes and gene function.

The view from the sick bed: what plant health clinics tell us about diagnostics and healthcare delivery

Eric Boa, University of Aberdeen, Scotland

Plant, animal and human health sectors have many common features and face similar challenges, from accurately and quickly diagnosing diseases to delivering effective healthcare. Yet scientists and health practitioners working across these sectors have limited opportunities to share knowledge and evidence of what works best.

Diagnosis of pathogens is an obvious area for cross-sectoral collaborations, but there are other topics to consider. My talk will draw upon personal experiences, and those of colleagues, in establishing a global network of plant health clinics and strengthening plant health systems in mostly low-income countries in Africa, Asia and Latin America.

I will discuss how those of us working in agriculture have attempted to learn from human health, and how our results might in turn provide insights for improving healthcare delivery in other sectors. I will illustrate my talk with examples of diseases affecting banana, cocoa, maize and other key crops and discuss surveillance and rapid responses to new disease outbreaks.

The rise of zoonoses has encouraged collaboration between animal and human health through weighty initiatives such as One Health and EcoHealth. The minimal ostensible risks posed by plant diseases to human and animal health have done little so far to foster any significant involvement by plant health professionals. Yet the human and animal impact of plant losses and reduced quality of produce are huge. I will explore how we can foster closer collaborations between all health sectors and reap the wider benefits of "positive cross-infection".

Plant metabolomics & pathogen interactions

John Draper, Aberystwyth University, Wales

The field of plant metabolomics is the study of all metabolites that make up the plant metabolome. With the metabolome forming the interface between a plants genes expression and the environment, it can be indicative of the underlying molecular changes occurring during stress conditions such as pathogen interactions. The application of both fingerprinting and profiling mass spectrometry techniques can provide wide overview of the plant metabolome.



Laboratory based, integrative omics experiments of the model annual grass species *Brachypodium distachyon* and its interaction with rice blast fungus *Magnaporthe oryzae* have provided insight into the substantial system wide reprogramming that occurs during the pre-symptomatic infection phases in both susceptible and resistant interactions. The utility of metabolomics for woody perennial species in the field are also being shown by current investigations into oak decline syndromes such as Acute Oak Decline (AOD). This requires further considerations for sample collection such as tissue type as well as spatial and temporal variability to ensure reproducibility.

Decline syndromes are complex disease phenotypes to which a number of biotic and predisposing abiotic factors contribute. There is the potential for the application of metabolomics to these problems, not only as tool for investigating the molecular perturbations that occur in perennial species during pathogen interactions, but also to provide future diagnostic tools to monitor health status and even as a predictive tool for long term management strategies.