## Plant Pathology

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Work in the Plant Pathology Programme has continued to exploit pathogen genomics and comparative genomics resources to advance our research. This approach has been highly fruitful in shaping new hypotheses to address basic research questions and emerging issues of substantial importance to science policy.

A new area of research on the survival of human enterobacteria on plants was established with the appointment of Dr Nicola Holden. Contamination of leafy vegetables and other plants by human enterobacteria such as Escherichia coli O157:H7 and Salmonella *typhimurium* is becoming more frequent and evidence is accumulating that these pathogens can persist in association with plants posing considerable risks to human health. Within the PP programme, comparative genomics of enterobacterial pathogens of plants such as Pectobacterium atrosepticum (causing black leg of potato) has been a highly productive source of new information leading to new hypotheses of how human enterobacteria bacteria may survive on plants, for example, through horizontally-acquired islands of genes that are transferred between species. Dr Holden will help to help drive forward studies to investigate the adaptation of bacteria to different environments to address this problem.

We continue to attract competitive research income to extend and add value to our research and notable grants awarded this year include Paul Birch and colleagues who were successful in obtaining £536,000 grant from the BBSRC Crop Science Initiative to exploit the Phytophthora genome sequence for novel targets for potato resistance. In addition, SCRI nematologists are members of the consortium that has secured funding from BBSRC to sequence the genome of *Globodera pallida* at the Wellcome Trust Sanger Institute – opening the door to apply modern genomics technologies to control this important nematode pathogen of potatoes.

During the year Paul Birch was appointed to a personal chair in Plant Pathology equally funded by the University of Dundee and SCRI. John Jones was appointed Guest Professor at The University of Ghent, Belgium and is Chair of EU Cost Action 872 'Exploiting genomics to understand plant–nematode interactions'



In December, an external peer review was conducted to assess the Quality of Science produced by the programme; this included presentations, review of publications and individual interviews. Overall, the report was positive and highly complimentary with the review team concluding that PP research is predominantly of an internationally competitive standard with high strategic value to Scottish agriculture and the UK economy. The review involved a substantial amount of work by our administrative assistant Lesley Young in the preparation of documents. I would like to take this opportunity to thank the review team and Lesley Young for their work on our behalf.

## Research Highlights include:

Work in the *Phytophthora infestans* group led by Paul Birch and Steve Whisson has discovered a translocation signal in virulence proteins from *P. infestans* (the cause of late blight disease), that is required for delivery of these proteins into the plant cell. This finding advances our knowledge of how the late blight pathogen can establish infection in potato cells. The finding has broad significance because the signal is also conserved among other oomycete pathogens and distantly related organisms such as the malaria parasite (Whisson et al., 2007, Nature 450, 115).

In work funded by the BPC, David Cooke, Alison Lees and colleagues have conducted a detailed survey of *P. infestans* from disease outbreaks in GB potato crops. This showed a marked increase of the A2 mating type of the pathogen with most of the change being due to a single clonal lineage. Work is now underway to examine the implications of this change to the effectiveness of current disease management strategies based on host resistance, fungicide application and minimisation of primary inoculum sources.

Genomics technologies have been instrumental to lan Toth and colleagues in the bacteriology group in identifying key virulence factors involved in the later stages of potato infection by *Pectobacterium*. We now know that factors involved in manipulating potato resistance inside plant cells are produced at the same time as plant cell wall degrading enzymes, which attack the plant cells from the outside. This dual factor attack may be necessary for a successful infection and offers further targets for control. A transcriptomics approach linked to plant pathogenicity testing has been used to determine the complete quorum sensing regulon of *Pecto bacterium*, linking many known and putative virulence determinants to this master regulator of pathogenesis.

Strategic research on plant caspases has led to novel findings showing that the Agrobacterium tumefaciensencoded VirD2 protein (a key element in Agrobacteriummediated plant transformation) is a genuine target for plant caspase fragmentation. These findings have allowed Misha Talianksy and his colleagues to develop novel platform technology for Agrobacteriummediated gene transfer (plant transformation) based on a protection of the VirD2 protein from caspases (Reavy et al., 2007 Plant Cell Reports 26, 1215). In addition, the Taliansky group research on virus movement has revealed novel interactions between virus movement proteins and plant nucleolar proteins called Cajal Bodies. The groundnut rosette virus ORF3 interacts with fibrillarin (a component of Cajal Bodies) and studies showed that this interaction was essential for systemic infection of plants (Kim et al., 2007, PNAS 104, 11115; Kim et al., 2007, EMBO J 26, 2169).

In collaboration with John Carr at the University of Cambridge, Peter Palukaitis and colleagues found that the 2b gene of a severe strain of cucumber mosaic virus caused developmental virus-like symptoms when expressed transgenically in Arabidopsis thaliana, while the 2b genes of mild strains did not. The effects on development correlated with inhibition of microRNA (miRNA) turnover, but not on suppression of small interfering RNA (siRNA)-mediated RNA silencing, which occurred with all three 2b genes tested. Thus, the induction of symptoms is not necessarily a direct consequence of RNA silencing suppression. The Palukaitis group also investigated whether transgenic plants that express genes under the control of the cauliflower mosaic virus (CaMV) 35S RNA promoter would facilitate recombination of the CaMV viral genome into plant genomes. Four plant species (tobacco, oilseed rape, A. thaliana and Nicotiana benthamiana) were investigated and the data obtained do not support this hypothesis. Moreover, transgenic plants containing a 35S RNA



Dr David Cooke at work in a potato plot at SCRI

promoter also did not facilitate the seed transmission of CaMV from infected plants to their progeny. In addition, it was shown that infection of transgenic plants of the same four species by a mild CaMV strain did not suppress expression of the transgene or affect the stability of the transgene. In combination with other reports, this work shows that CaMV infection leading to suppression of the expression of transgenes driven by the CaMV 35S RNA promoter is highly dependent on both the host and the virus strain combination.

Work on potato mop-top virus (PMTV) movement in collaboration with Dr Eugene Savenkov on sabbatical leave from the Swedish University of Agricultural Sciences has revealed a number of novel findings including the rod-shaped particles of PMTV appear to be polar and contain the coat protein readthrough domain and TGB1 movement protein at one extremity, and that this association is essential for long distance movement of virions. The role of movement protein TGB2 was examined and in addition to its known association with cellular membranes in the secretory and endocytic pathways to facilitate movement it also targeted chloroplasts to facilitate virus replication and/or pathogenicity. We found specific interactions between TGB2 and lipids important in signal transduction and lipid raft formation, suggesting that TGB2 plays key roles at different stages of the virus 'life cycle'.

The three accompanying articles feature research findings on new viruses in raspberries; analysis of EST sequences from cDNA libraries of the virus vector aphid *Myzus persicae* and analysis of over 4000 *Globodera pallida* ESTs from two life stages that has revealed novel secreted proteins.