

L. Torrance

Changes in the organisation and management structure of SCRI during 2005 have resulted in the formation of a new Plant Pathology Programme to investigate economically important pests and pathogens. The research covers a range of scales from the molecular and cellular to that of pest and pathogen populations. The overall aims are to understand disease processes and provide knowledge and strategies for crop improvement through durable resistance and sustainable disease control strategies. Much of the work is geared to improvement of potato, barley and soft fruit.

There are three major areas of research:

Plant response to pathogens To understand the cell and molecular mechanisms of disease resistance and susceptibility, to provide underpinning knowledge for durable disease resistance.

Pathogen genomics To conduct whole genome sequencing and comparative genomics to provide knowledge of effectors, mechanisms underlying pathogenicity, horizontal gene transfer and intraspecific variation.

Pest and Disease Management To understand mechanisms of pest and pathogen transmission, disease development and factors driving population change and evolution, to develop sustainable control strategies.

The programme has close links to the Genetics and Plant Environment Interactions programmes particularly through research on pest and disease resistance and survival of pathogens in managed ecosystems and we expect to develop and strengthen these links in future e.g. through the work described below on *Erwinia*.

Research highlights during the year include:

An unusual structure at one end of potato potyvirus particles Potyviruses are transmitted by aphids in a non-persistent manner and can spread readily in crops during the growing season; they have filamentous particles that are generally supposed to be assembled from many copies of a single type of coat protein. Using atomic force microscopy and immunogold labelling techniques we have demonstrated that filamentous helically-constructed particles of potyviruses, Potato virus Y and Potato virus A contain a novel and unusual structure at the virion end containing the 5'-end of the RNA. Such a structure contains virus-encoded proteins, VPg and helper component proteinase, and potentially plays key roles in different virus-encoded functions such as virus assembly/disassembly, movement and vector transmission (published in Journal of Molecular Biology).

Plant Pathology



A novel role of the nucleolar protein fibrillarin in plant virus systemic infection For many years, plant RNA-containing viruses were thought to replicate and assemble mainly in the cytoplasm of cells, but recently we have shown that a number of plant viral proteins such as the long-distance movement (ORF3) protein of Groundnut rosette virus (GRV), an umbravirus, enter the cell nucleus, and specifically target the nucleolus. These findings led us to propose the existence of a novel nucleolar function associated with regulation of plant macromolecular transport via the phloem, the long-distance transport system for the products of photosynthesis and nitrogen metabolism in plants. The mechanism of nucleolar involvement in the long-distance transport was elucidated: we found that the nucleolar protein fibrillarin is targeted by the viral ORF3 protein and relocated to the cytoplasm where it mediates assembly of transport-competent complexes containing viral RNA which then move through the phloem.

New role for virus triple gene block (TGB) movement proteins Intracellular localisations of fluorescent protein-tagged triple gene block (TGB) movement proteins of *Potato mop-top virus* (PMTV) and *Barley stripe mosaic virus* (BSMV) were examined by confocal laser scanning microscopy of living cells. We found differences in subcellular distribution of the TGB2 of the two different viruses which indicate subtle differences in the role and function of these proteins in virus movement. Moreover, we have revealed for the first time that the TGB2 of PMTV and the cysteine rich γ b protein of BSMV play roles in establishing replication complexes in chloroplasts.

Virally-expressed cDNA libraries provide novel protein localisations In a project funded by The Gatsby Foundation, we have successfully constructed virallyexpressed cDNA-GFP fusion libraries from *Arabidopsis* and *Nicotiana* sp., and used them to search for proteins that localise to different subcellular structures. In the last year, many novel proteins have been discovered. The data has been uploaded to ProtLocDB, a web-enabled database (http://bioinf.scri.ac.uk/cgi-bin/ ProtLocDB/home), which is publicly available and has been accessed by a number of labs worldwide.

Origin of siRNAs in response to virus infection in plants is described in the following article by C. Lacomme *et al.* (published in *Journal of Virology*).

VIGS-based functional characterization of genes associated with powdery mildew resistance in barley (see following article by C. Lacomme *et al.*).

Survival of *Erwinia carotovora* in managed systems Studies of the complete genome sequence of the potato blackleg pathogen *Erwinia carotovora* susbp. *atroseptica* (*Erwinia*) have led to the discovery of a binding protein delivered by a Type I secretion system that appears to be responsible for binding of *Erwinia* to the roots of brassica plants but plays no part in binding to potato roots. The presence of other genes (within the *Erwinia* genome sequence) that are often associated with root-dwelling organisms and which code for traits such as the ability to fix nitrogen, the breakdown of root exudates and the production of competition-reducing antibiotics further supports this hypothesis. Work is in progress to investigate whether such alternative hosts aid *Erwinia* survival in managed ecosystems for the subsequent contamination of high grade seed potatoes.

The first *Phytophthora infestans* avirulence gene As part of an international collaboration, the first avirulence gene, *Avr3a*, has been isolated from the late blight pathogen, *P. infestans*, which encodes a protein that is recognized by the potato resistance protein R3a (published in *Proceedings of the National Academy of Sciences, USA*). This presents the first opportunity to study gene-for-gene recognition and resistance mechanisms in the late blight pathosystem. Studies of allelic diversity in *Avr3a* are stimulating the development of novel disease resistance strategies.

Phytophthora infestans population studies A set of over 1000 *P. infestans* isolates from the UK, and other European states were screened using SCRI's SSR markers to examine the population structure. Together with EU collaborators we developed a data entry tool and database of over 10,000 isolates of *P. infestans* to collate EU-wide data on *P. infestans* populations. A training course on characterising *P. infestans* populations was held at SCRI. In addition, real-time multiplex PCR tests for *Phytophthora* species affecting forests were developed and the protocols are being tested by bodies responsible for UK statutory testing.

Demonstration that multiple independent horizontal gene transfer events from several different sources have driven the evolution of plant parasitism by nematodes Plant parasitism has arisen independently at least three times within the nematodes. Our work has shown that on each occasion important pathogenicity genes, most often plant cell wall degrading enzymes, have been acquired by horizontal gene transfer. Independent transfer events from bacteria to nematodes and fungi to nematodes have occurred during their evolution (published in *Biochemical Journal* and *FEBS Letters*)

Genotyping individuals of *Globodera pallida* (see following article by M.S. Phillips *et al.*).

PCN Management model Five hundred copies of the PCN management model developed at SCRI were released by the British Potato Council to growers and agronomists. The management model allows users to understand the principles governing yield loss and nematode population dynamics. By altering potato cultivar characteristics and cultural practices such as rotation, nematicide treatment etc. future trends in both yields and PCN population levels can be explored.

Climate change is expected to increase pest populations SCRI in partnership with SASA, Rothamsted Research and SAC are studying the ecology of one of the most important agricultural insect pests of potato, the peach-potato aphid Myzus persicae. Using molecular techniques that we developed to distinguish genotypes in ecological studies, we have established that there is a constant local population which is supplemented from time-to-time by insecticide resistant forms. We have found that the resistant forms appear to be subject to turnover depending on agricultural practice. With the help of local farmers we have elucidated some of the sources and conditions which maintain insecticide resistant forms in Scotland. In future we will study the underlying effects on potato virus epidemiology. The data generated from this work will provide a useful baseline, not only for changes in the ecology of an agricultural pest, but an insect species that is a widespread indicator of different ecosystems.

The Media Kitchen now managed by the Plant Pathology Programme delivers a wide range of sterile microbiological, mycological and plant tissue culture, media and disposable plasticware across the Institute and operates under ISO 9001:2000 accreditation. The 2005 user survey showed that 100% of respondents rated the service they received as 'good' or 'excellent'. The cost-effective service provides quality assured products (35,000 plates, 41,400 Items, 465,000 Eppendorf tubes and 2,156,000 tips supplied in 2005) and the daily delivery and removal of waste microbiological materials to researchers.