Plant Pathology

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Plant pathology research provides underpinning knowledge to support sustainable agricultural production systems. We aim to understand, using molecular, cellular and whole plant techniques, mechanisms of plant resistance and susceptibility and discover how parasites evolve to overcome plant defences. Our applied science to detect pests and pathogens and to monitor and to predict changes in pathogen populations is conducted in collaboration with agencies or growers.

Advances in genome sequencing (pathogen and plant) combined with bioinformatics analysis and functional genomics techniques are being exploited to accelerate the discovery and characterisation of novel genes and processes. This year, research on *Pectobacterium atrosepticum* has shown the power of these approaches with the discovery of novel systems to enable this bacterium to survive in the absence of potato in managed ecosystems. This work has deepened our understanding of quorum sensing. With the first draft of the *Phytophthora infestans* genome now available, we anticipate similar strides to be made with this severe potato pest and substantial funding from EU and BBSRC has been won to pursue this. Research on plant viruses has revealed new insights into the importance of nuclear trafficking in virus replication and movement.

Climate change is of considerable worldwide concern and this year we have produced a report that identifies potential changes in disease profiles in Scottish crops, particularly the threat posed by pests and diseases whose spread is currently limited by the cooler temperatures of Northern Britain. This study will influence the direction of future programme research. New developments also include collaborations with colleagues in EPI programme on the survival and spread of soil-borne microorganisms in the environment.

More detail of our research can be found on the Plant Pathology Programme's pages on the SCRI website.

Research highlights include:

Demonstration of a role for plant ALY proteins in RNA silencing RNA silencing is a defence mechanism that

targets RNAs of invading pathogens for destruction. Two of the four plant nuclear protein ALYs become localised in the cytoplasm when the cell is infected with *Tomato bushy stunt virus* (TBSV) or when only the P19 protein is expressed, suggesting that plant ALY proteins are involved in the RNA silencing process.

Enhanced resistance to viruses by manipulation of disease-response genes It seems that while the HCPro gene is able to suppress the RNA silencing-mediated defence against virus infection, it stimulates other anti-viral defence systems. So, broad defence against a range of plant viruses could be achieved by down-regulating the expression of defence genes. The RDR1 gene from potato has been cloned and sequenced and its role in regulating virus infection in potato is being assessed.

Involvement of sub-nuclear bodies in plant virus systemic infection (See following article by Sang Hyon Kim *et al*.)

New insights into *Potato mop-top virus* (PMTV) movement Recent co-localisation experiments with fluorescent-tagged plant endosomal markers show that movement proteins localise in patches at the plasma membrane and associate with endosomes. Cell-to-cell movement of infectious virus particles requires movement proteins. Endocytic trafficking may be important in the uptake and delivery of virus by its soil–borne vector, *Spongospora subterranea*.

Targeting of *Tobacco mosaic virus* movement protein to plasmodesmata requires the actin / ER network Although movement protein is frequently seen associated with microtubules it has been shown that the microtubules are not required for targeting to the plasmodesmata.

New golgin protein identified An eighth possible *Arabidopsis* golgin, a homologue of the mammalian Golgi protein p115, localises to Golgi stacks and interacts with *Arabidopsis* Rab1 homologues in a yeast two-hybrid assay.

AtGRIP accumulates in the *trans*-Golgi network Using immuno-gold labelling and electron microscopy, the localisation of three novel *Arabidopsis* golgin candidates has been analysed in detail.

Progress in understanding how some strains of *Raspberry bushy dwarf virus* (RBDV) overcome resistance Some RBDV isolates capable of overcoming the resistance provided by the *Bu* gene carried by some raspberry cultivars have been found in England and elsewhere. SCRI's ability to infect raspberry plants with cloned infectious non-resistance breaking RBDV will form the basis of a rapid and efficient procedure to screen new germplasm for additional sources of resistance to the virus.

VirD2 protein mutants increase efficiency of gene transfer The VirD2 protein has been shown to be a substrate for a plant caspase-like protease activity (PCLP) in tobacco. It has been demonstrated that mutagenesis of the VirD2 protein to prevent cleavage by PCLP increases the efficiency of reporter gene transfer and expression.

Release of a first assembly of the *P. infestans* genome sequence SCRI are involved in the genome project through supply of our large insert BAC library. The sequencing effort is led by the Broad Institute, Cambridge, MA, USA (www.broad.mit.edu/annotation/genome/phytophthora_infestans/Home.html).

Functional genomic analyses of *P. infestans* genes We have identified a novel transmembrane protein that is localised to the appressoria and haustorial membrane. Appressoria are preinfection host penetration structures, and haustoria are biotrophic structures formed early in infection and likely to be used in nutrient extraction from the host. Silencing of this gene decreased *P. infestans* pathogenicity.

P. infestans effector protein *Avr*3a transport into host cells depends on a conserved RXLR-EER motif (See following article by Stephen Whisson *et al.*).

P. infestans populations There is concern about the potential for increased incidence of the sexual oospore stage of the late blight pathogen. Genetic analysis using markers is providing key data to explain how the population and the nature of the primary inoculum is

changing. This data feeds into the BPC's Fight Against Blight Campaign and a longer-term study on how pathogen populations evolve, research on the mechanisms of *P. infestans* pathogenicity and breeding for blight resistance.

The first phytotoxin and its mode of regulation have been identified in *Pectobacterium atrosepticum* *P. atrosepticum* (formerly known as *Erwinia carotovora* subsp. *atroseptica*) attacks plants through the production of large quantities of plant cell wall degrading enzymes via a cell density dependent regulatory process called quorum sensing. We have recently shown that a phytotoxic compound called coronafacic acid is required for virulence on potato and its mode of action appears to be in suppressing host resistance.

Disease risk assessment for soil-borne potato diseases (see following article by Alison K. Lees *et al.*).

RanBPM gene family identified in nematodes Expression analysis has shown that all family members (encoding proteins similar to RanBPMs) examined to date are expressed in the dorsal oesophageal gland cell of *Globodera pallida*, suggesting a role for these proteins in the host-parasite interaction.

Chorismate mutase (CM) plays key role in nematode infection Studies on a secreted chorismate mutase using RNA interference, a mechanism for RNA-guided gene silencing, have revealed that this protein is important for normal development of the nematode. The most significant effect is on adult females, which have the greatest nutritional requirements, suggesting the CM is important in inducing or allowing normal establishment of the feeding site.

Production of a cDNA library from a parasitic stage of *G. pallida* Nematodes from various stages of infection from potato roots were isolated and high quality RNA extracted to make a representative cDNA library. Preliminary analysis has revealed the presence of candidate pathogenicity and avirulence genes.

Quantitative molecular diagnostics (QMD) for nematodes QMD have been developed for the potato cyst nematodes *G. pallida* and *G. rostochiensis.* QMD have also been produced for the virus vector nematodes *Paratrichodorus pachydermus* and *Trichodorus similis* and the virus associated with these species, *Tobacco rattle virus*. These tests were devised for use in a pre-planting soil test with funding from the British Potato Council.

Rapid method for DNA analysis of suction trap aphids SCRI is one of four suction trap sites in Scotland (see www.sasa.gov.uk/seed_potatoes/aphids/index.cfm). These traps sample migrant flying aphids. The numbers and types of each species caught in the traps are used to formulate advice to farmers on the frequency of pesticide applications. We have developed a rapid method for extracting DNA from current and historical trap samples so that DNA fingerprinting can be used to identify subtypes and insecticide-resistant forms.