

Meeting report

Pathogens: the plight of plants

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A report on the British Society for Plant Pathology Presidential meeting 'Plant pathogen genomics - from sequence to application', University of Nottingham, UK, 15-18 December 2003.

Over a hundred delegates, from several continents and from both academia and industry, were brought together to discuss plant pathogen genomics at the British Society for Plant Pathology's annual Presidential meeting, hosted by this year's president, John Lucas (Rothamsted Research, Harpenden, UK). The sessions covered the potential that genomics has for furthering knowledge in this field, updates on resources available for genome analysis and progress made to date in sequencing projects, as well as the emerging insights being made into the interactions between hosts and pathogens as a result of genome technology.

Twenty-five years of R-gene evolution

Richard Michelmore (University of California, Davis, USA) presented the Garrett Memorial Lecture, looking at the study of resistance (*R*) genes over the past 25 years and charting our growing understanding of them by likening it to stages of art history. Thus, the 'Classical' period represented the gene-for-gene hypothesis - which states that each resistance gene in a host plant interacts with just one avirulence (*Avr*) gene in the pathogen - and the idea that *R* genes evolve as clusters. 'Enlightenment' came from map-based cloning, and the 'Expressionist' period was characterized by expressed sequence tags and arrays; this period led to the realization that *R*-genes do not act alone but as components of macromolecular complexes. The 'Surrealist' period was identified as the comparative approach currently being taken by Michelmore's own group to investigate the evolution of specificity in plant-pathogen interactions, using the hosts *Arabidopsis*, lettuce and tomato. Their results suggest that

R-gene clusters have complex evolutionary histories, resulting from a range of genetic events that have taken place at these loci. The group aims to unravel the rate of occurrence and the relative importance of such events. Interestingly, they have found that even within an *R*-gene cluster (for example the major cluster in lettuce), some genes evolve slowly, with little sequence exchange between paralogs, whereas other genes frequently exchange sequence with paralogs; in the latter case, orthologs are rare. This has led Michelmore to suggest a division of *R* genes into two groups with different possible functions: fast-evolving type-1 genes, which detect variable pathogen ligands the loss of which give little fitness penalty for the pathogen, and the more slowly evolving type-2 genes, which detect prevalent stable ligands, these ligands having a fitness penalty if lost. Michelmore's 'Postmodern' period approaches the study of *R*-gene evolution in terms of artificial evolution of new specificities and the use of DNA shuffling to assess the roles of individual *R*-gene regions. To this end, his group has identified several different regions that are essential for R-protein action. In conclusion, Michelmore presented the conceptual changes that have come about over the past 25 years and showed how the gene-for-gene theory has developed into a complicated story of dual-speed *R*-gene evolution and of interactions involving proteins encoded by multiple *R* and *Avr* genes.

Two interesting talks covered the evolution of bacterial pathogens that infect plants. Jim Alfano (University of Nebraska, Lincoln, USA) demonstrated that the hypersensitive response in tomato - in which plant cells undergo programmed cell death in response to a pathogen - can be suppressed by expression in the pathogen *Pseudomonas syringae* pv. *tomato* DC3000 of specific effectors of the pathogen's type III secretion system; this effectively converts a virulent pathogen to avirulence. John Mansfield (Imperial College, Wye, UK) focused on mobility of avirulence genes in the genomes of different strains of *Pseudomonas syringae*. He discussed the idea that the effector functions of suppression of

the hypersensitive response and of basal resistance may not actually be that dissimilar, and that mobile effectors and pathogenicity islands have evolved within pathogens to perform both of these functions.

Fungal genome projects

Various genome projects were presented that are at widely differing stages of completion. Ralph Dean (North Carolina State University, Raleigh, USA) spoke about the progress made on the genome of the rice blast fungus *Magnaporthe grisea*. Currently, the complete nucleotide sequence of around 40 megabases is being anchored back to the genetic map, a process a year away from completion. Comparative studies suggest that 50-100 million years separate *M. grisea* and *Neurospora crassa*, the model filamentous fungus, and the *M. grisea* genome so far has revealed significantly more genes than *N. crassa* and around twice the number of secreted proteins. Comprehensive functional analyses of the *M. grisea* genome are now underway, using transcriptional profiling and genome-wide gene knockouts. The *M. grisea* genome story was also taken up by Nick Talbot (Exeter University, UK), who described comparative functional-genomic experiments taking place in his lab to identify novel pathogenicity genes. Traditional approaches to pathogenicity-gene discovery have focused on known genes in model fungal species and attempted to predict how their roles might be altered to provide pathogenicity. But this relies on pathogenicity genes being 'hijacked' genes, commandeered at some stage to take on new roles, rather than being entirely novel. His comparative-genomics approach seeks to identify the genes found only in pathogens and not in saprotrophs - which feed on dead tissue - and to use these as a basis for finding unique genes for pathogenicity.

Widening resources

The meeting also included several presentations from speakers whose work does not directly involve plant pathogens but nonetheless affects researchers attending the conference. David Denning (University of Manchester, UK) discussed techniques for studying the pathogenicity of the human pathogen *Aspergillus fumigatus*, an organism that can inflict both acute aspergillosis and a severe allergic reaction. Denning reported on the genome-sequencing project for this fungus, which is now almost complete. It is now known to carry approximately 9,500 genes, organized on eight chromosomes. Much can be made of comparison of this genome with that of the academic model organism *A. nidulans* and the biotechnologically useful *A. oryzae*. We wait with interest to see whether such cross-genome analyses provide insights into pathogenesis, the emergence of resistance, drug design, diagnostic indicators and even biodegrading enzymes.

The industrial perspective on high-throughput screening was eloquently presented by John Hamer (Paradigm

Genetics, Research Triangle Park, USA), who explored the applications that genomics could have in commercial crop protection. The continuing importance of chemicals in crop protection in a world climate that is suspicious of genetically modified organisms, together with the increasing cost of research, has prompted some large agrochemical companies to 'outsource' some of their discovery to specialist companies, and Paradigm Genetics fills this new niche. By intelligently coupling their high-throughput program of screening novel molecules with a 'chemical-genetic paradigm', in which libraries of plant-pathogenic organisms (beginning with *M. grisea*) are created and each gene sequentially knocked out and assayed with the novel molecules, they can generate potential targets as well as lead compounds with which to interest agrochemical industry partners.

Breaking stories

As with all meetings, the rumor of 'breaking stories' met with much curiosity. Here, excitement centered on work reported by Rebecca Allen from Jim Beynon's group (Horticulture Research International, Warwick, UK), on the interaction between the downy mildew oomycete pathogen *Peronospora parasitica*(*At*) and *Arabidopsis*. The *Arabidopsis RPP13* resistance gene encodes a protein of the coiled-coil:nucleotide-binding-site:leucine-rich-repeat (CC:NB:LRR) class. Analysis of this gene from 24 accessions of *Arabidopsis* revealed that *RPP13* is the most variable gene analyzed to date, and this extreme variation is focused within the leucine-rich repeats. To complement these studies, the group has mapped the segregation of the matching avirulence gene (*ATR13*) in a cross between two pathogen isolates, and they have successfully cloned the *ATR13* gene by mapping genes expressed *in planta* onto this population. This is the first avirulence gene cloned from the *P. parasitica*-*Arabidopsis* interaction. *ATR13* was shown to be under selective pressure, consistent with it being involved in an 'arms race' with *RPP13*.

Overall, the meeting was successful in gathering many members of the plant-pathogen community together. It provided a platform for talks covering both the progress made in this area over the past 25 years and the latest updates on genome projects, techniques and new discoveries, all of which provoked interesting and animated discussion amongst the delegates.