Meeting Report
10th International Congress on Molecular Plant-Microbe Interactions
Madison Wisonsin July 10-14, 2001

University of Wisconsin in Madison was the venue of the 10th MPMI meeting. The MPMI meeting has always been a key event in the world of plant-microbe interactions, and this year's conference was no exception. Emphasis as always was placed on recent scientific contributions and advances in the field of molecular plant-microbe interactions and functional genomics in different phytopathosystems.

The conference attracted over 1000 scientists from all fields of plant pathology with more than 680 posters. The organising committee has made a fantastic job in managing the events during this congress in addition to the provision of communication facilities (e.g. free e. mail and internet access) and organically-grown food during the meals. This has provided those who attended the meeting with an excellent opportunity to gain insight into many aspects of molecular plant-microbe interactions not accessible in their normal working environment. In this context, I found it extremely useful for the poster presentation of my PhD work and for the opportunity to discuss the latest advances in the field.

The meeting featured talks by internationally-recognised and highly-reputed speakers from all over the world. Topics covered during the talks included: recognition of pathogens by plants, plant-virus interactions, rhizobium-plant interactions, plant-fungal interactions, local/systemic resistance, plant-nematode interactions, defence signal transduction, ecology and population biology of plant-associated microbes, cell biology of plant-microbe interactions, functional genomics and biotechnology.

The meeting kicked off by a very interesting talk presented by Prof. David Baulcombe (The Sainsbury lab, UK) on the use of viral induced gene silencing (VIGS) as an efficient functional genomic tool for high throughput cloning and of host genes. VIGS is a process whereby virus infection causes sequence specific down-regulation of plant RNA(s) sharing homology with the infecting virus. This technique has been used to identify genes required for *Rx* and *Pto*-mediated disease resistance in tomato and tobacco. Candidate proteins such as SGT1 and HSP90 were isolated by this screen and were shown to be required for resistance.

In the recognition of pathogens by plants session the talk by Roger Innes (Department of Biology, Indiana University) caught my attention. Innes's talk focused on the identification of novel genes involved in the incompatible interaction between *pseudomonas syringae* in Arabidopsis (RPS5/AvrPphB). The *pbs1* mutant of was isolated causing susceptibility to *pseudomonas syringae* DC3000/*avrPphB*. Interestingly, the PBS1 gene contains a serine/threonine protein kinase domain with 65% similarity to Apk1a kinase. Interestingly, PSB1 phosphorylates the RPS5 protein (a typical LZ-NBS-LRR resistance protien that is involved in recognition of AvrPphB). In the local/systemic resistance session, talks by Xinnian Dong (The Biology Department, Duke University) and Terry Delaney (Department of Plant Pathology, Cornell University) were exquisite. They are both independently isolated the NIM1/NPR1 gene as an important switch that positively regulate systemic acquired resistance (SAR) signal transduction pathway. However they used two different approaches: biofungal resistance assay against the biotrophic oomycetes *Peronospora parasitica* (Delaney) and BGL2-GUS screen (Dong). Both groups have presented their recent work involving the screen for suppressors of nim1 (son) and

sunpressors of npr1 inducible/constitutive (sni/snc). Dong isolated and cloned *SNI1* (a negative regulator of SAR and *SNC1* and they were shown to encode a novel protein and an R gene, respectively. Morover, Delaney has presented his lab efforts to isolate novel components in SAR independent resistance (SIR) pathway. In this regard he is using mutagenised *nim1* plants to screen for mutants that display increased susceptibility to the normally avirulent *Peronospora parasitica* isolate. It is fascinating to know how powerful these strategies could be in uncovering novel components in completely novel pathways.

In the defence signal transduction session, a very interesting talk given by Daniel Klessig (Rutgers' Waksman Institute) on the role of salicylic acid (SA) and nitric oxide (NO) in disease resistance. He ponted out to the discovery that the salicylic acide binding protein 3 (SABP3) is a chloroplastic protein with 100% homology to the enzyme carbonic anhydrase (CA) of tobacco. *In vitro* radiolabelling assays revelaed that SABP3 binds to SA and this does not affect its CA activity. Overexpression of SABP3(CA) was shown to protect yeast from oxidative stress whereas deletion of this gene resulted in oversensitivity to hydrogen peroxide.

The icing on the cake of this meeting came at the last talk in the functional genomics and biotechnology session given by John Ryals (Ciba Plant Biotechnology, NC) on systems biology. His talk focused on the data gathering process and how industrialized institutions are being built where genes are being analysed at unprecedented rates. This is enabled by the huge financial investments, revolution in knowledge-based computing systems and organization and data mining in order to convert information into biological knowledge. A functional discovery process include: gene discovery, mutant generation, phenotype profiling, gene expression profiling, metabolic profiling and data mining. In the so-called "plant phenotype factory", each mutant generated is characterized for at least a 150 different traits including: timing of growth stage, seedling structure and development, rosette structure and development, influorescence structure and development, floral structure and development, fruit trait, seed trait and yield trait. As to the metabolic profiling at least 2000 genes are studied with full finger prints generated for each gene in response to different factors. It is of vital importance for these information to be available to public use in order for benefits and gains to be achieved at all scientific fronts.

Finally, attending this meeting has indeed enabled me to interact with fellow scientists in the field and to be able to present my work. There are numerous lessons for me to be learned. And due to space limitation I will not be able to elaborate. One important implication of attending this meeting, is that now I am able to discuss my PhD work with a much better knowledge and understanding of the field. Moreover, I am now much more updated with the latest advancements and progress in the field.

Last but not least, I would like to thank the Renei Bequest Committee for their generous support without which I wouldn't have been able to participate in such an important annual meeting.

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