IS-MPMI Reporter
April 2002
International Society for Molecular Plant-Microbe Interactions

## IN THIS ISSUE



**IS-MPMI REPORTER DEADLINE**

**Deadline for submitting items for the next issue is June 14, 2002.**

Submission of materials as electronic files, either on disk or as e-mail attachments, will speed processing. Please submit black-and-white or color photos generated from negatives. If your image was created digitally, please submit a laser print of the image and a disk containing the electronic graphics file (.tif and .eps formats are preferred).

For more information on submitting electronic images contact Kayleen Larson at klarson@uslink.net.

**Send items to:**

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## Update on MPMI by the Editor-in-Chief

Recent issues of *MPMI* show that the journal is doing very well in many respects. For example, the speed of the review process has become more visible by publishing the submission date as well as the acceptance date in the manuscripts. Furthermore, it is certainly a lively (and colorful!) journal that is in the vanguard of new developments in molecular biology. The high quality of the past year's manuscripts provides reason to believe that the citation index impact factor of the journal will be still better than our 1999 rating (when we had a respectable impact factor of 3.3, just below the 3.7 rating of the *Journal of Bacteriology*). To back up this optimism, it can be noted that the Prestige Factor™ of MPMI for 2001 has a value of 118 as compared to 113 for that of *J.Bacteriol.* and 67 for *Plant Mol. Biol.* (www.prestigefactor.com). Following the editorial meeting in St. Paul last year, the editorial board has implemented several policy changes, some of which I would like to highlight in this letter.

- **Introduction of the Spotlight section.** For this section, the senior editor (after consultation with the EIC) selects manuscripts that present results which represent major scientific breakthroughs in a particular field or that present novel results which are of special interest to a broad readership. In order to stimulate the submission of such manuscripts, the following priorities have been set for these papers: (1) first priority in handling the manuscript by the editor with the goal of completing the review process within two weeks, (2) first in line for printing so that the paper can be published within four months after submission, and (3) first priority for representation on the cover of *MPMI*. Although the normal procedure is for the editor to select spotlight manuscripts from regularly submitted manuscripts, authors should feel free to suggest their paper as a possible spotlight paper and are even encouraged to ask in advance for the opinion of the handling editor and editor-in-chief, based on an abstract of the paper.
- **Discontinuing the Note format.** The original intention of the note format was to provide a way to publish highly novel findings at an earlier stage of research. This function of the note format is now taken over by the Spotlight section. An additional advantage of the note format was that the submission of short manuscripts was stimulated. However, short manuscripts can also be accommodated easily in the normal format. For that reason, the editors would like to encourage submission of short manuscripts presenting high quality research of exceptional novelty. When results of such research are mainly of a technical nature, the technical advance section can provide accommodations for them.
- **The submission of Review manuscripts is strongly encouraged**. The editor-in-chief has personally taken charge of handling review manuscripts and also is actively soliciting submissions of review manuscripts. Please let me know whether you have suggestions for reviews or would like to suggest other people who might be interested in writing a review.
- **The style of the publications has been changed as of January of this year.** I hope that you agree with me that these changes are an improvement. Some of the changes include (1) rules before and after the author and affiliations lines, (2) smaller margins to accommodate more text per page, and (3) the addition of an Author-Recommended Internet Resources section, which will need your input to make it a success. With the still increasing scientific impact of internet resources, I am sure that authors will not find it difficult to recommend useful links for this section, including data presented on their own homepage.

More details of these and other changes can be found in the *MPMI* report on the IS-MPMI*net* website (www.scisoc.org/ismpmi/MPMIreport.htm).

I want to conclude by thanking the other members of the editorial board and the associate editors for all their hard work in the past year. In your future submissions to MPMI, please keep in mind that these individuals are not paid for doing this demanding job, and therefore, their dedication to having manuscripts reviewed with such great speed is really admirable.

**Herman Spaink**, Leiden
*MPMI* Editor-in-Chief

## IS-MPMI Annual Meetings

One of the major responsibilities of the IS-MPMI Board is the organization of biennial congresses. It is encouraging to see how volunteers are available every time to do a formidable job.

### Some updates:

**Madison 2001**
**Sally Leong** and her crew did an excellent job. They made the Congress both scientifically and financially an enormous success. Publication of the Proceedings is foreseen in March 2002. Sally, thanks on behalf of the Society!

**St. Petersburg 2003**
**Igor Tikhonovich** and his team are working hard on the technical and scientific organization. Presently St. Petersburg is being renovated. In addition to great science you should not miss the opportunity to visit St. Petersburg with its unique Hermitage museum and cultural events. Also, in one night you can travel to Moscow by train. Igor will also organize tours.

**Puerto Vallerta 2005**
**Fédérico Sanchez,** assisted by **Isabel López-Lara, Otto Geiger** and **Carmen Quinto**, will organize this meeting in the modern Pacific beach resort Puerto Vallerta. More info will soon be published in the *IS-MPMI Reporter*.

**Europe 2007**
We have already a very serious candidate for a beautiful site in Europe. Since the final decision will be made at the 2003 Board Meeting I cannot give you details.

**Exchange of Illustrations for Teaching Purposes**
During the Madison meeting **Igor Tikhonovich** approached me about the possibility of making slides of all presentations available to all participants. Igor will work out this idea in the framework of the St. Petersburg 2003 meeting. Independently, **Christian Boucher** brought up a similar idea about PowerPoint files of posters.

These discussions inspired me to propose the following idea. Many of us prepare slides for teaching purposes that are reasonably up-to-date but do not carry unpublished information. It requires a lot of reading and other work. We could help each other enormously when each of us is willing to make available five slides, which cover the major aspects of our expertise. They should be specifically prepared for teaching purposes and may require a brief legend/explanation. Further suggestions and questions:

- the name of the author on the slide should guarantee quality
- contributors receive a free CD-Rom with all collected illustrations
- non-contributors can purchase the CD-Rom at a reasonable price (which on the other hand should be sufficiently high to elicit contributions and get a free copy of the CD-Rom!)
- who is willing to contribute?
- who is willing to act as an editor?

Please send your comments by email to ugtenberg@rulbim.leidenuniv.nl

**Ben Lugtenberg**
President IS-MPMI

### Calendar of Events

**XXIst International Carbohydrate Symposium**
*July 7-12, 2002, Cairns, Australia*
Full details and online registration are now available on the home page at http://www.ics2002.uwa.edu.au.

**International Union of Microbiological Societies Congress (joint meeting of the Xth International Congress of Bacteriology and Applied Microbiology, Xth International Congress of Mycology, and XIIth International Congress of Virology)**
*July 27-August 1, 2002, Paris, France*
www.iums-paris-2002.com

**XXVIth International Horticultural Congress.**
*August 11-17, 2002, Toronto, Canada*
www.ihc2002.org

**13th Australian Nitrogen Fixation Conference**
*September 24-27, 2002, Adelaide, South Australia, Australia*
Theme: Fixed nitrogen in sustainable farming systems. The program will cover a broad range of aspects of biological nitrogen fixation.
For details contact: Dr. Peter Murphy, Department of Plant Science,Waite Campus, The University of Adelaide, PB 1 Glen Osmond, South Australia 5064, AUSTRALIA, Tel: +61 8 8303 7262 Fax: +61 8 8303 7109 Email: peter.murphy@adelaide.edu.au

**3rd Asia-Pacific International Mycological Conference on Biodiversity and Biotechnology (AMC 2002)**
*November 4-8, 2002, Kunming, China*
Contact: amc2002@china.com

**8th International Congress of Plant Pathology** (ICPP2003)
*February 2-8, 2003, Christchurch, New Zealand*
"Solving Problems in the Real World", Contact: Helen Shrewsbury, Professional Development Group, PO Box 84, Lincoln University, Canterbury, New Zealand (shrewsbh@lincoln.ac.nz). Registration details and other information is available on the ICPP2003 website http://www.lincoln.ac.nz/icpp2003/.
The Final Circular for ICPP2003 will be released in December 2001, and will be distributed to those who have completed Registration of Interest details.

# People

**Mary S. Connolly** (PhD) defended a thesis entitled "The Molecular and Cellular Responses Of The Soybean Pathogen, *Phytophthora sojae*, to Calcium, Isoflavones, and Host Tissues" under the direction of **Paul F. Morris,** Biological Sciences, Bowling Green State University. Mary was awarded an NSF post-doctoral fellowship in microbial biology and has moved to the University of Dayton to work with **Jayne Robinson**. Her project on how nitrogen fixing bacteria react to plant signal mimics also involves collaborations with **Dietz Bauer**, Ohio State University, Columbus, OH, and **Barry Rolfe** Australian National University, Canberra.

**Zhonghua Wang** has nearly completed his PhD degree thesis on "Ecological risk assessment and food safety evaluation of Bt rice" under the direction of Professor **Yingwu Xia** at Zhejiang University, P.R. China. He has recently joined the laboratory of Molecular Plant Pathology at USDA-ARS, Dale Bumpers National Rice Research Center, Stuttgart, Arkansas as a visiting scientist. He is involved in dissecting signal transduction pathways of plant disease resistance using the rice blast system as a model under the supervision of Dr. **Yulin Jia**. Zhonghua's M.S. thesis was from the Molecular Genetics and Crop Improvement Center, and titled "Studies on the inheritance of transgene in the progenies of Bt rice crossed to conventional rice varieties and its field performance" under the guidance of Professor Yingwu Xia at the Institute of Nuclear Agricultural Sciences (INAS), Zhejiang University, P. R. China.

**Pratibha Singh** has successfully completed her PhD on "Host Specific SV-toxins produced by Stemphylium vesicarium causing brown spot of European pear" under the direction of Professor **Keisuke Kohmoto** at Tottori University, Japan as a Monbusho Scholar. She has recently joined the laboratory of Molecular Plant Pathology at USDA-ARS, Dale Bumpers National Rice Research Center, Stuttgart, Arkansas as a postdoctoral research associate. Her present responsibilities include studies on understanding molecular mechanisms of host-parasite interactions of rice blast (Magnaportha grisea) and sheath blight (Rhizoctonia solani) diseases of rice under the supervision of Dr Yulin Jia. Pratibha completed her B. Sc Ag. & A. H and M. Sc. in Molecular Biology and Biotechnology, thesis titled "Studies on inheritance and molecular genetics of host specificity in Pyricularia grisea, blast fungus" under the guidance of Dr **Uma Shankar Singh**, professor of plant pathology, G. B. Pant University of Agriculture & Technology, Pantnagar, India.

**Dr. Christopher Lawrence** recently joined the faculty as an assistant professor of molecular biology/ genomics at Colorado State University, Dept. of Bioagricultural Sciences and Pest Management. Dr. Lawrence is using the *Arabidopsis thaliana-Alternaria brassicicola* interaction as a model system to study the interaction between plants and necrotrophic fungal pathogens. His functional genomics-based research addresses the interaction from both sides, studying the genetic basis of resistance and susceptibility in the host as well as pathogenicity mechanisms employed by the pathogen. Contact information: Dept. of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523-1177. email: clawrenc@lamar.colostate.edu

## Theses Submissions

The following theses on the theme of Interactions between Plant and Biotic Agents were recently submitted to the Graduate School Experimental Plant Sciences (EPS) in the Netherlands.

**D.M.J.M. Duijsings**
Analysis of the transcription initiation mechanism of tomato spotted wilt virus. Prof.dr. **R.W. Goldbach** (promotor); dr. **R.J.M. Kormelink** (co-promotor), WU, Wageningen, 21 December 2001, 112 pp.

Tomato spotted wilt virus snatches capped leader sequences of suitable host mRNAs and uses them to prime transcription of the viral genome. To further identify the requirements for host leaders to function as cap donors Alfalfa mosaic virus (AMV) RNAs were tested as specific cap donors during a co-infection with TSWV of Nicotiana benthamiana, or offered as (mutable) 35S-driven cDNA constructs to transgenic N. tabacum p12 plants infected with TSWV. RT-PCR amplification and sequence analyses of chimaeric AMV-TSWV mRNAs obtained strongly supported a single basepairing requirement between cap donor and viral template and a cleavage preference for nucleotide position 16 from the cap structure. Base pairing not only occurred with the 3' ultimate residue of the viral template but also, though less efficient, with the penultimate or antepenultimate residues. To further identify and characterize cis- and trans-acting elements involved in cap-snatching a Vaccinia virus-T7 expression system was developed which enabled reconstitution of transcriptionally active viral ribonucleoproteins entirely from cloned cDNAs, as succesfully demonstrated with the expression of a reporter (luciferase) gene in vivo.

**A.B. Meijer**
Membrane-anchoring interactions of bacteriophage major coat proteins. Prof.dr. **T.J. Schaafsma** (promotor); dr. **M.A. Hemminga** (co-promotor), WU, Wageningen, 23 May 2001, 102 pp.

**People (Theses Submissions)** *continued on page 4*

The major coat proteins of the filamentous bacteriophages Pf3 and M13 are stored in the inner membrane of the cell during the reproductive cycle. In this process, protein-lipid anchoring interactions are important for the formation of the correct structure of these proteins in the membrane, enabling fast and efficient phage assembly. The focus of this thesis is on the role of domains and specific amino acids on the position of these proteins in the membrane. Both proteins are studied using site-specific probing using fluorescence and ESR spectroscopy. This biophysical approach provides information about the relative depth and dynamics of specific sites of the protein in the membrane. In previous structural views of the membrane-bound state of the M13 coat protein, the protein is thought to be in an L-shape, in which the N-terminal arm of the protein is positioned along the membrane surface. The spectroscopic studies described in this thesis show that the amphipathic N-terminus of the protein is not firmly associated with the membrane surface, but is also present in a more extended configuration. It is demonstrated that the hydrophobic amino acids in the N-terminal arm play an important role in the topology of the helix at the membrane surface. Furthermore, it is found that at the C-terminal side of the helical transmembrane domain, the charged lysines and hydrophobic phenylalanines are involved in strong anchoring interactions with the membrane interface region. These amino acids affect the location of the entire helical transmembrane domain. The results of a site-specific probing study on the Pf3 major coat protein reveal striking similarities with those obtained from the M13 major coat protein. Both proteins exhibit a strong structural coherence, in spite of the low primary sequence homology. Therefore, the tertiary structure of the Pf3 major coat protein should closely resemble the membrane-bound structure of the M13 coat protein. Apparently, domains of amino acids, which are comparable in physico-chemical characteristics, but lack sequence homology, are able to assemble in a structural coherent manner. In conclusion, the relatively simple coat proteins are positioned in the membrane via a complicated set of protein-lipid interactions provided by individual amino acids as well as domains of amino acids.

**T.W. Prins**
Identification and functional analysis of Botrytis cinerea genes induced during infection of tomato. Prof.dr. **P.J.G.M. de Wit** (promotor); dr. **J.A.L. van Kan** (co-promotor), WU, Wageningen, 17 October 2001, 114 pp.

The thesis describes the cloning and characterization of Botrytis cinerea genes that are differentially expressed during the infection of tomato leaves, as compared to growth in vitro. Methods that were used to isolate such genes comprised Differential Display RT-PCR, differential hybridization of a genomic library of B. cinerea, a modified subtractive hybridization RT-PCR method and PCR with degenerate primers. The genes that were cloned by these methods encoded ubiquitin, Glutathione S-Tranferase, an aspartic protease and a number of partial gene fragments encoding proteins with unidentified function. The expression of several genes was studied in planta and in vitro. Gene replacement was performed for the Glutathione S-Tranferase and the aspartic protease gene. No reduction in virulence was observed in mutants, as compared to the wild type recipient strain.

**T.E.M. Abbink**
Molecular analysis of N gene-mediated resistance to tobacco mosaic virus. Prof.dr. **J.F. Bol** (promotor); dr. **H.J.M. Linthorst** (co-promotor), IMP-LU, Leiden, 6 June 2001, 111 pp.

One of the mechanisms by which plants defend themselves against pathogens depends on a highly specific gene-for-gene interaction in which a plant resistance gene product directly or indirectly recognizes an avirulence protein of the pathogen. In the case of Tobacco mosaic virus (TMV), which triggers such a defense reaction after inoculation in tobacco plants equipped with the TMV-resistance gene N, the avirulence protein was identified. Agroinfiltration experiments identified the helicase domain of the replicase proteins as the minimal fragment with elicitor activity. Using the yeast Two-Hybrid system, a number of cDNA clones were isolated that encoded tobacco proteins that interacted with the TMV-helicase domain. Surprisingly, none of the encoded proteins corresponded to the product of N or were involved in N-mediated resistance. However, silencing of the genes for two of the proteins (an AAA protein and the catalytic subunit of the oxygen-evolving complex (OEC) of photo system II), influenced the susceptibility of the plants to infection with TMV and other viruses. Silencing of the OEC gene, as well as inhibition OEC activity, enhanced virus replication, indicating that uncompromised photosynthesis is required for basal defense against virus infection. Interestingly, infection with TMV, but not with AMV or PVX, reduced the expression of the OEC gene. This suggests that TMV has developed a strategy to counter this basal resistance mechanism.

**C.C. Anker**
Prehaustorial and posthaustorial resistance to wheat leaf rust in diploid wheat. Prof.dr. **P. Stam** (promotor), dr. **R.E. Niks** (co-promotor), WU, Wageningen, 20 June 2001, 96 pp.

The thesis describes (i) An inventory of pre- and posthaustorial resistance to wheat leaf rust (Puccinia triticina) in the three diploid wheat species Triticum monococcum, T. boeoticum and T. urarte and (ii) The inheritance of prehaustorial restance to wheat leaf rust. T. monococcum was almost completely resistant whereas T. boeoticum and T. urarte were completely susceptible. The association between species identity and leaf rust reaction in diploid wheat and the combination of pre- and posthaustorial resistance in T. monococcum resemble nonhost resistance

of cereals to inappropriate rust species, suggesting that T. monococcum is a nonhost for P. triticina. An existing mapping population of RILs as well as a new one, both derived from a cross between a susceptible T. boeoticum and a resistant T. monococcum genotype were used to locate QTLs for pre- and posthaustorial resistance on the genome. Remarkably, some QTLs had pleiotropic effects, controlling both pre- and posthaustorial resistance. This indicates the existence of a possible new class of resistance genes in diploid wheat, next to the known classes of hypersensitivity genes and prehaustorial resistance genes reported in barley and cultivated wheat.

**R.A.L. van der Hoorn**
The Cf-4 and Cf-9 resistance proteins of tomato: molecular aspects of specificity and elicitor perception. Prof.dr. **P.J.G.M. de Wit** (promotor); dr. **M.H.A.J. Joosten** (co-promotor), WU, Wageningen, 31 October 2001, 136 pp.

Resistance genes Cf-4 and Cf-9 of tomato confer recognition of the AVR4 and AVR9 elicitor proteins, respectively, of the pathogenic fungus Cladosporium fulvum. To examine these resistance genes in more detail, an efficient, quick and reliable transient expression system was employed, based on infiltration of Agrobacterium cultures into tobacco leaves. Using this assay, the specificity determinants in Cf-4 and Cf-9 proteins were elucidated through extensive domain-swap analyses. In addition, a novel resistance gene, 9DC, was discovered that confers AVR9 recognition in wild tomato species (among others Lycopersicon pimpinellifolium). The Cf-9 gene likely evolved through intragenic recombination between 9DC and another homolog. Both domain-swap analyses and the discovery of 9DC indicate that specificity in resistance proteins is mainly determined by a few of the variant residues. Extensive variation between resistance genes most probably serves as a rich reservoir from which new resistance genes can evolve through different recombination processes.

**K. Horsman**
Somatic hybrids of Solanum tuberosum and species of the Solanum nigrum-complex and their backcross progeny. Prof.dr. **E. Jacobsen** (promotor), WU, Wageningen, 14 May 2001, 104 pp.

Fusion experiments were performed between diploid (2n=2x=24) or tetraploid (2n=4x=48) potato genotypes and four species belonging to the S. nigrum complex. All five accessions of the four species of the S. nigrum-complex were able to form fusion hybrids with at least one of the potato genotypes. It was shown that the ploidy level as well as the genotype were factors that influenced the somatic combining abilities. Almost half (373) of the 761 somatic hybrid plants performed well in vitro, which was in striking contrast with their performance in vivo, but only 60 genotypes were vigorous in the greenhouse and were able to flower. Somatic hybrids of the fusion combinations of S. nigrum complex (+) 2x potato of S. nigrum-complex (+) 2x potato were used in backross experiments. First and second generation backcross progeny with S. nigrum could easily be obtained. Self-fertility was already restored in one of the BC1 genotypes. Only backcrosses with tetraploid potato resulted in seed containing berries. Two BC1 genotypes were obtained after 5000 pollinations from which 505 ovules were cultured of which one was vigorously growing genotype and in the greenhouse, and flowered abundantly. This BC1genotype was again crossed with tetraploid potato and also in this generation the success rate was low. Over 5000 pollinations resulted in 1750 berries from which over 3000 ovules were obtained. Twelve plants germinated from these ovules, which were not as vigorous in vitro and in vivo as the BC1 parent. Some of the BC2 genotypes were used for further backcrosses but no BC3 plants could be obtained. It can be concluded that traits from S. nigrum have become available for the cultivated potato with the aid of protoplast fusion. However, introgression of these traits by repetitive backcrossing with potato is much more complicated then initially expected although it seems to be possible.

**C.C. Huang**
How do plant species defend themselves against Oidium lycopersici; mapping of monogenic and polygenic resistance in Lycopersicon species.Prof.dr. **P. Stam** (promotor); dr. **W.H. Lindhout** (co-promotor), WU, Wageningen, 25 April 2001, 163 pp.

The thesis describes: 1) Resistance mechanism of tomato and some other crop plant species against O. lycopersici, a causal agent of the recent outbreaks of tomato powdery mildew; 2) Host range and genetic variation of the pathogen; 3) Inheritance analysis of resistance in wild tomato accessions including L. hirsutum G1.1560 and G1.1290, L. parviflorum G1.1601 and L. peruvianum LA2172; and 4) Mapping of monogenic (in G1.1560 and G1.1290) and polygenic (in G1.1601) resistance. It has been found that: 1) Resistance to O. lycopersici in Lycopersicon species is mainly associated with hypersensitive response. 2) Tobacco may be an alternative host of O. lycopersici. 3) Tomato powdery mildew isolates from different continents are very similar to each other, suggesting a single origin of these (field) isolates. 4) Resistances in G1.1560 and G1.1290 are monogenic and dominant. The two resistance genes Ol-1 and Ol-3 are both mapped between markers SCAF10 and H9A11, and are genetically not distinguishable from each other. 5) Resistance in G1.1601 is polygenic. Three QTLs for the resistance have been identified. 6) Resistance in LA2172 is monogenic and dominant. The corresponding resistance gene is designated Ol-4.

**People (Theses Submissions)** *continued on page 4*

**L. Qin**
Molecular genetic analysis of the pathogenicity of the potato cyst nematode Globodera rostochien-sis. Prof.dr. **J. Bakker** (promotor); dr. **J. Helder**, dr. **G. Smant** (co-promotors), WU, Wageningen, 5 October 2001, 99 pp.

One of the fundamentals of this thesis is the development of a new strategy to identify pathogenicity factors from the potato cyst nematode Globodera rostochiensis. cDNA-AFLP technology was used to compare mRNA pools from five highly synchronous different developmental stages. Visualisation of the expression patterns of thousands of genes allowed us to select for genes predominantly expressed in infective juveniles (the first selection criterion). A number of genes specifically expressed in the dorsal glands belong to a RanBPM (Ran-Binding Protein in Microtubule organization)-like gene family. The proteins encoded by these genes are probably secreted by the nematode into plant cells and might be involved in syncytium induction by changing the dynamic instability of microtubules. In addition the first expansin gene outside land plants was identified. The C-terminal half of the protein encoded by this nematode gene shares significant homology with plant b expansins, whereas the N-terminal half appears to be a family II cellulose-binding domain, which is specific for bacterial cellulases. Expansin activity was found in the infective second stage juveniles.This nematode expansin presumably facilitates the intracellular migration through plant roots by loosening plant cell walls.

**M.C. Vaz Patto**
The genetics and mechanism of avoidance of rust infection in Hordeum chilense. Prof.dr. P. Stam, prof.dr. **A. Martin** (promotors); dr. **R.E. Niks** (co-promotor), WU, Wageningen, 8 May 2001, 121 pp.

In a collection of 88 accessions of Hordeum chilense the level of avoiding rust infection, morphological and agronomic traits, habitat of origin and AFLP fingerprint, together with their associations suggested the existence of three distinct subspecific taxons within H. chilense. The role of the cuticular wax layer in infection avoidance appeared to be the covering of the stomatal apparatus, causing overgrowth by Puccinia hordei germ tubes. An F2 population derived from two distinct H. chilense accessions with contrasting levels of avoidance was used to construct a molecular marker linkage map (AFLP). On this map three QTLs involved in avoidance and three other QTLs controlling stoma density were located.

**V.G.A.A. Vleeshouwers**
Molecular and cellular biology of resistance to Phytophthora infestans in Solanum species. Prof.dr. **P.J.G.M. de Wit** (promotor); dr. **F.P.M. Govers**, dr. L.T. Colon (co-promotors), WU, Wageningen, 5 January 2001, 136 pp.

Late blight, caused by the oomycete Phytophthora infestans, is the most devastating disease of potato (Solanum tuberosum) world-wide. In wild Solanum species, various types of resistance are present. A set of Solanum species was examined for the cellular and molecular aspects of the resistance response. Diverse resistance mechanisms to P. infestans appeared to operate at various levels in these plants. The hypersensitive response (HR) was always associated with resistance, and the effectiveness of the HR correlated with resistance levels. The ubiquitous association of the HR in all types of resistance suggests that numerous R genes are present in Solanum. Phylogenetic analyses of Pto homologues from Solanum indicated that this R gene-like family is ancient and diverse. In addition to specific R gene-based resistance, basal levels of non-specific resistance were noted. Within species, constitutive mRNA levels of various pathogenesis-related genes correlated with nonspecific resistance to P. infestans, suggesting that basal levels of systemic acquired resistance (SAR) may vary between the Solanum genotypes.

**M.M. Camacho Carvajal**
Molecular characterization of type 4 pili, NDH-I and PyrR in rhizosphere colonization of Pseudomonas fluorescens WCS365. Prof.dr. **E.J.J. Lugtenberg** (promotor); dr. **G.V. Bloemberg** (co-promotor), LU, Leiden, 11 April 2001, 147 pp.

The work presented in this thesis is aimed at providing a better understanding of, and a more detailed insight into, the bacterial physiology exhibited in he rhizosphere, thereby focusing on novel traits of Pseudomonas fluorescens WCS365 involved in competitive root tip colonization. It was shown that both nuo and ndh of P. fluorescens WCS365, encoding NADH-I and II respectively, are expressed in the rhizosphere but that only NADH-I is important for competitive root tip colonization. In addition, a functional PyrR, a regulator of pyrimidine biosynthesis, was identified to be required for competitive root tip colonization. By performing targeted mutagenesis on pilA and pilT, we were able to show that type 4 pili of WCS365 are involved in rhizosphere colonization and in biofilm formation on polyvinyl chloride (PVC). Furthermore, lacZ was used as a marker to compare root colonization of tomato and Arabidopsis thaliana and to monitor gene expression in the rhizosphere.

**I. Kuiper**
Molecular characterization of root colonizing Pseudomonas strains for rhizoremediation. Prof.dr. **E.J.J. Lugtenberg** (promotor); dr. **G.V. Bloemberg** (co-promotor), IMP-LU, Leiden, 6 November 2001, 168 pp.

The use of pollutant degrading bacteria to restore contaminated sites is often limited by a poor distribution of the bacteria through soil and their low metabolic activity. In this thesis a novel enrichment procedure is

described which selects for bacteria able to degrade naphthalene and to colonize grass roots. The latter property enables these bacteria to use nutrients present in the root exudate and to penetrate layers, which are normally impermeable for bacteria. Using this method Pseudomonas strains PCL1444 and PCL1445 were isolated. PCL1444 degrades naphthalene during very efficient grass root colonization. In addition, PCL1444 has the highest growth rates on the major carbon sources in the grass root exudate, glucose and succinic acid, and shows the highest transcription of the naphthalene catabolic genes on these carbon sources. PCL1445 grows on intermediates of the naphthalene degradation pathway, secreted by PCL1444, and forms mixed colonies with PCL1444 in the presence of naphthalene on grass roots. In addition, PCL1445 produces two biosurfactants, which decrease the formation of biofilms on PVC and disrupt existing biofilms.

**J. Ton**
Rhizobacteria-mediated induced systemic resistance in Arabidopsis - Molecular-genetic basis of induced resistance in relation to basal resistance.Prof.dr. **L.C. van Loon** (promotor); dr. **C.M.J. Pieterse** (co-promotor), UU, Utrecht, 16 March 2001, 136 pp.

Induced resistance is manifested upon challenge inoculation as a stronger and faster activation of defenses compared to non-induced plants, and was shown in Arabidopsis to constitute an enhancement of salicylic acid (SA)-dependent basal defenses in the case of pathogen-induced systemic acquired resistance (SAR), and of jasmonic acid (JA)/ethylene-dependent basal resistance in the ase of rhizobacteria-mediated induced systemic resistance (ISR). Mutants impaired in salicylic acid, JA- or ethylene synthesis or perception are more susceptible to pathogens resisted by SA-dependent and JA/ethylene-dependent defenses, respectively, and cannot mount an induced resistance response against these pathogens. Several enhanced disease susceptibility (eds) mutants fall within these categories. Non-inducibility of ISR in Arabidopsis accessions RLD and Ws-0 was associated with reduced sensitivity to ethylene. This trait is conferred by a single gene (isr1) that also functions in basal resistance against bacterial speck disease.

**F.P. Drijfhout**
Studies towards the sex pheromone of the green capsid bug.Prof.dr. ***Æ.* de Groot** (promotor), dr. **T.A. van Beek** (co-promotor), WU, Wageningen, 23 May 2001, 152 pp.

The Green Capsid Bug, Lygocoris pabulinus (L.) (Heteroptera: Miridae) is a serious pest in fruit orchards, which is difficult to control. Former research has revealed that males are attracted by females and in this project the chemical nature of the sexpheromones has been investigated. Several methods like a Thermo Desorption System coupled to a gas chromatograph, Solid Phase Micro Extraction and Stir Bar Sorptive Extraction have been used to isolate and separate the chemical substances which are emitted by the insects. Two ioassays, the vibration assay and a Y-track olfactometer have been used to test the activities of the extracts. Extracts were analyzed using coupled gas chromatography-mass-spectrometry (GC/MS) and coupled gas chromatography and electroantennography (GC-EAD). Extracts of male and female legs contained several compounds with (Z)-9-heptacosene and (Z)-9-pentacosene as the main components respectively. The ratio of (Z)-9-heptacosene and (Z)-9-pentacosene was 5:1 in the extracts of female legs and 1:5 in extracts of male legs. GC-EAD experiments revealed that compounds like hexyl butyrate, (E)-2-hexenyl butyrate, (E)-4-oxo-2-hexenal, and (Z)-9-pentacosene and to a lesser extend also 1-hexanol, hexyl acetate, nonanal, (Z)-3-hexenyl butyrate and (Z)-7-pentacosene gave positive responses in EAG tests. A synthetic 5:1 mixture of (Z)-9-heptacosene and (Z)-9-pentacosene elicited vibration behavior in male L. pabulinus, indicating the important role of these compounds in the live of these bugs.

## Invitrogen Corporation Offers New Research Funding Program.

Invitrogen Corporation has created "The Research Tools Development Grants Program," designed to help enable investigators to develop innovative tools for use in life science research, including discovery, development, and commercialization. The program is open to new and established investigators working in academics, not-for-profit institutions, and for-profit companies such as start-up biotechs. Funding can range from $25,000 to$100,000 and are generally for a 1-year duration. Total funding of this program is $5 million per year. Invitrogen is providing the Grants on a quarterly basis; each quarter we will request grant proposals for a specific field of interest.

For the first quarter of 2002, we are seeking grant applications in the general area of Enzymes for Molecular and Cell Biology. For the second quarter we are interested in the area of Functional Analysis, i.e., tools to understand how genes and their corresponding proteins function and interact *in vitro* and *in vivo*. Future quarterly fields of interest for 2002 include: separations & purification and amplification, labeling & quantitation. Additional information on this program is available at our web site (www.invitrogen.com) or by contacting David Odelson at grants@invitrogen.com or at 800-955-6288 x 66140 (760-476-6140).

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*MST12* Regulates Infectious Growth but not Appressorium Formation in the Rice Blast Fungus *Magnaporthe grisea*. G. Park, C. Xue, L. Zheng, S. Lam, and J.-R. Xu. Pages 183-192. Publication no. M-2002-0131-01R.

Efficient Infection of *Nicotiana benthamiana* by *Tomato bushy stunt virus* Is Facilitated by the Coat Protein and Maintained by p19 Through Suppression of Gene Silencing. F. Qu and T. J. Morris. Pages 193-202. Publication no. M-2002-0118-03R.

Mutation of Three Cysteine Residues in *Tomato yellow leaf curl virus-China* C2 Protein Causes Dysfunction in Pathogenesis and Posttranscriptional Gene-Silencing Suppression. R. van Wezel, X. Dong, H. Liu, P. Tien, J. Stanley, and Y. Hong. Pages 203-208. Publication no. M-2002-0122-01R.

Differential Expression Patterns of an Acidic Chitinase and a Basic Chitinase in the Root Nodule of *Elaeagnus umbellata*. H. B. Kim and C. S. An. Pages 209-215. Publication no. M-2002-0212-01R.

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*Azoarcus* Grass Endophytes Contribute Fixed Nitrogen to the Plant in an Unculturable State. T. Hurek, L. L. Handley, B. Reinhold-Hurek, and Y. Piche. Pages 233-242. Publication no. M-2002-0118-01R.

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*Dm3* Is One Member of a Large Constitutively Expressed Family of Nucleotide Binding Site–Leucine-Rich Repeat Encoding Genes. K. A. Shen, D. B. Chin, R. Arroyo-Garcia, O. E. Ochoa, D. O. Lavelle, T. Wroblewski, B. C. Meyers, and R. W. Michelmore. Pages 251-261. Publication no. M-2002-0125-01R.

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Tombusvirus P19-Mediated Suppression of Virus-Induced Gene Silencing Is Controlled by Genetic and Dosage Features That Influence Pathogenicity. W. Qiu, J.-W. Park, and H. B. Scholthof. Pages 269-280. Publication no. M-2002-0219-03R.

Functional Analyses of the *Pto* Resistance Gene Family in Tomato and the Identification of a Minor Resistance Determinant in a Susceptible Haplotype. J. H. Chang, Y.-S. Tai, A. J. Bernal, D. T. Lavelle, B. J. Staskawicz, and R. W. Michelmore. Pages 281-292. Publication no. M-2002-0215-01R.

Molecular Determinants Required for the Avirulence Function of AvrPphB in Bean and Other Plants. A. P. Tampakaki, M. Bastaki, J. W. Mansfield, and N. J. Panopoulos. Pages 292-300. Publication no. M-2002-0219-01R.

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A Signal Transfer System Through Three Compartments Transduces the Plant Cell Contact-Dependent Signal Controlling Ralstonia solanacearum hrp Genes. B. Brito, D. Aldon, P. Barberis, C. Boucher, and S. Genin. Pages 109-119. Publication no. M-2002-0114-01R.

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## 2003 Meeting to be Held in St. Petersburg

The XI International Congress on Molecular Plant-Microbe Interactions will take place on July 18-27, 2003, in St. Petersburg, Russia. All congress activities will take place at the "Pribaltiyskaya" hotel. Congress information will be displayed at http://www.arriam.spb.ru. The local organizing committee is headed by:

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# 40th Congress of the Southern African Society for Plant Pathology.

**Dave Berger**, Associate Professor, Botany Department, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria. dberger@postino.up.ac.za

Plant Pathology research in Southern Africa has a long and distinguished history, and this provides a strong foundation for the growing interest in Molecular Plant Pathology in the region (http://www.saspp.co.za). The discipline is thriving as demonstrated by the 40th Congress of the Southern African Society for Plant Pathology held in January 2002 at the Dikhololo Game Ranch near Pretoria in South Africa. The congress – a "not to be missed" annual event for local plant pathologists – was organized this year by the Forestry and Agricultural Biotechnology Institute (FABI) of the University of Pretoria http://www.up.ac.za/academic/fabi/.

Invited keynote speakers from overseas laboratories are a special feature of each congress. This year, the Ethel Doige Memorial lecture was presented by **David Geiser** from the Fusarium Research Center, Pennsylvania State University, USA. His lecture was entitled "Using multilocus phylogenetics to figure out Fusarium species". Dr. **Jeremy Burdon**, CSIRO-Plant Industry, Australia addressed the topic "Disease in space and time – coevolutionary patterns in natural plant-pathogen associations". Dr. D. **Shtienberg**, Volcani Center, Israel, gave examples of plant disease management case histories based on an epidemiological understanding of the disease triangle (host-pathogen-environment). Prof. **Walter Gams** from the Centraalbureau voor Schimmelcultures, The Netherlands, made a presentation entitled "A revolution in *Verticillium* systematics". **Aaron Maxwell** from Murdoch University, Western Australia, spoke on "*Mycosphaerella nubilosa*: a recent incursion into Western Australia".

The SASPP maintains great respect for the history of the discipline in the region and takes trouble to remember eminent scientists from the past. Tributes to these so-called "Pillars of Plant Pathology" can be found on the website (http://www.saspp.org/historic_figures.php). **J.E. Vanderplank**, whose books on the epidemiology of plant diseases continue to line the shelves of plant pathologists world wide, is a son of South African soil. In recognition of the great impact Vanderplank's ideas had on the discipline, an eminent local plant pathologist is invited to present the Vanderplank lecture at each congress. This year, Prof. **Zakkie Pretorius**, Department of Plant Pathology, UOFS spoke on "Challenges in breeding for durable resistance in plants".

Oral presentation sessions included disease control and management, disease detection and losses, ecology and epidemiology, post harvest pathology, disease resistance and two sessions of pathogen identification and characterization. In addition, 67 posters were displayed. There is increasing interest in Molecular Plant Pathology in laboratories of the region, which has been initiated over the years by the adoption of molecular tools for pathogen characterization. Molecular phylogenetic studies of fungal pathogens is a major focus of the Tree Pathology Co-operative Programme of FABI (more about this in a future issue of *IS-MPMI Reporter*), which was represented by a large contingent of students at this meeting, necessitating two sessions on this topic. All abstracts of SASPP presentations of the past few years are published in the South African Journal of Science.

Interesting new disease reports were the invasion of soybean rust (*Phakopsora pachyrhizi*) into commercial plantings of soybean, the characterization of a complex of fungal pathogens (*Phaeomoniella chlamydospora* and *Phaeoacremonium sp.*) causing black goo decline (Petri disease) on grapevine, and the identification of nutritional factors in *Protea magnifica* that are linked to the conversion of *Botryospharea sp.* from an endophytic to pathogenic existence, causing stem cankers in commercial stands.

Over 100 delegates attended from throughout the region. Participants came from six Universities in South Africa, the University of Botswana and the University of Mauritius. Agricultural research organizations were well represented, including the Savannah Agricultural Research Institute, Ghana, and there was participation from local industry including a business producing biological control agents. Local companies provided sponsorship support for the meeting.

The importance of agriculture in Southern Africa will always ensure that a large element of plant pathology research is field-based with an applied focus. However, this local knowledge of both pathogen and host biology provides excellent opportunities for collaborations with scientists interested in molecular mechanisms.

Research into the molecular mechanisms of host response to pathogens was covered in the disease resistance session at this year's congress. Laboratories in South Africa have been slow to explore the new tools of molecular genetics and genomics. For example, there were only two talks on *Arabidopsis thaliana*, and these are most likely the first presentations on this model plant at a congress of the SASPP. However, molecular biology training is strong at several universities in South Africa and it is likely that more laboratories will recognize the utility of basic plant science research, and find ways to apply concepts of

plant defense from model plants to locally important crops. Promising developments in the post-genomic era are the DNA Microarray initiatives at the University of Pretoria and University of Cape Town.

Development of transgenic crops or the use of transformation in studies of plant disease are also in their infancy in South Africa. However several collaborative projects are underway especially between the Botany Department, University of Pretoria, ARC-Roodeplaat and CSIR-Bio/Chemtek (http://www.up.ac.za/academic/botany/index.html). There is also a local interest in the role of polygalacturonase inhibiting proteins in defense against fungi. Currently, there are seven laboratories throughout the country conducting research on PGIPs from different plants.

There are many opportunities for international collaboration with South African researchers through bi-lateral agreements administered through the National Research Foundation (http://www.nrf.co.za) (more about this in future edition of *IS-MPMI Reporter*).

The strength of the Society is the emphasis on young scientists (the committee is very youthful!) and student participation. For example, the sessions this year were all chaired by postgraduate students. They prepared well and gained valuable experience in this important scientific activity. All carried off the task with aplomb and were not reticent to keep faculty members to their allotted time. The society awards twenty travel grants to students on merit, and prizes sponsored by industry for the best oral presentation and poster presentation are keenly contested. When possible, there are no parallel sessions, which gives a broad perspective of plant health issues in the region. Furthermore, congress venues are chosen so that all participants are "trapped" at a single venue far from city distractions, which leads to maximum networking at social events. Next year's congress will be at an exciting venue next to the Orange river in the Free State Province.

## Meeting Report: 3rd IBWS Combines Molecular and Applied Research

**Caitilyn Allen** and **Dave Berger**
Associate Professor, Dept of Plant Pathology, University of Wisconsin-Madison (http://www.plantpath.wisc.edu/fac/cza.htm)
Associate Professor, Botany Department, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria (http://www.up.ac.za/academic/botany/berger.html)

The 3rd International Bacterial Wilt Symposium was held in White River, South Africa February 4-8, 2002. The particular interest of these meetings, which are held once every five years, is that they bring together basic and applied researchers from all over the world. Participants gain a broad perspective on the disease, both geographically and in terms of scientific approaches (which ranged from nitty-gritty low-tech management strategies developed for use by subsistence farmers to genomic analysis of both host and pathogen). It was especially appropriate that this IBWS took place in Africa, because bacterial wilt has a large social and economic impact on the African continent.

Bacterial wilt (BW), caused by *Ralstonia solanacearum*, is widely considered the single most destructive plant pathogenic bacterium because of its unusually broad host range. The disease affects plants in over 200 families all over the tropical and sub-tropical world. Hosts include key carbohydrate crops like plantains, bananas, and potatoes as well as such diverse cash crops as tomato, tobacco, pepper, peanut, eggplant, ginger, cloves, eucalyptus, and mulberry. In addition, a cold-tolerant subgroup of the pathogen has recently broken out on potatoes in western Europe, resulting in economic damage and quarantine problems. Losses caused by this disease are known to be enormous but cannot be accurately estimated because of its large but undocumentable impact on subsistence agriculture, and because planting of wilt-susceptible crops has been abandoned altogether in many parts of the world. The disease has become a steadily larger problem for growers, with a serious epidemic currently raging on bananas in the Philippines and Indonesia and losses consistently over 50% on potatoes in central African and South American highlands.

Despite its importance, bacterial wilt has not received a great deal of attention from researchers in the developed world, although this is changing as the disease has emerged in Europe and the bacterium has gained credence as a model pathogen. The field thus consists of a curious mixture of fundamental researchers studying the molecular basis of wilt disease in sterile laboratories and a much larger number of applied researchers in the tropics who study the ecology, population biology, epidemiology, and management of *R. solanacearum*, often working in the field with minimal resources. The IBWS presentations reflected this fascinating diversity.

**Studies of the pathogen**

Applied and basic researchers alike were dazzled by images of the infection and colonization process illuminated by bacteria expressing the lacZ and GFP reporter genes. **Jaques Vasse** (INRA-Toulouse) and **Tim Denny** (U. Georgia-Athens) presented histopathological studies comparing behavior of marked wildtype and mutant bacteria during bacterial wilt pathogenesis.

**3rd IBWS** *continued on page12*

Interestingly, the infection process was quite different when hydroponically-grown tomatoes infected by lacZ-expressing bacteria were observed after fixing compared to live microscopy of GFP strains that infected tomato roots grown in soil. The challenge in future will be to determine if these differences are due to different inoculation methods, bacterial strains, or microscopy techniques. Using the soil inoculation method, Denny found that one or more xylem vessels were colonized throughout the plant by four days, well before the first wilt symptoms appear. These tools are likely to be invaluable for understanding mechanisms of pathogenesis and unravelling the host response in resistant cultivars.

The microscopy results and several other studies with defined mutants reinforced the emerging paradigm that this bacterium causes disease with a wide array of quantitative virulence factors that have additive effects. Apart from genes with pleiotropic effects such as those controlling regulatory or secretory functions, no single trait appears to be absolutely required for wilting. However, many factors contribute quantitatively to virulence; these include EPS, extracellular plant cell wall-degrading enzymes, effectors secreted by the Type III secretory system, and presented at this meeting, bacterial swimming and twitching motility. Thus, this broad host-range pathogen represents a strikingly different model from the well-studied gene-for-gene pathosystems.

**Alison Robertson**, working with **Bruce Fortnum** at Clemson University, presented an elegant combination of molecular and population biology working with one of *R. solanacearum*'s few avirulence genes, *avrA*. Robertson and co-workers found that populations of the pathogen in North and South Carolina have insertions in *avrA*, apparently allowing them to avoid recognition by tobacco; in contrast, most strains in Georgia and Florida still carry the intact gene and are thus unable to cause disease on tobacco.

An EU consortium lead by **Dick Van Elsas** of Wagenigen, the Netherlands presented the interesting and epidemiologically significant discovery that *R. solanacearum* can become viable but nonculturable (VBNC). Some evidence suggests that VBNC cells are revived in the presence of host plants. This finding explains the many instances in which susceptible crops planted in field soils apparently free from *R. solanacearum* subsequently experienced rapid high levels of bacterial wilt. The mechanisms controlling the switch from culturable to non-culturable phenotype remain to be elucidated.

Of particular interest to IS-MPMI members, we now have complete genome sequence of both a model host (Arabidopsis) and one strain of the bacterium (M. Salanoubat et al. 2002. Genome sequence of the plant pathogen *Ralstonia solanacearum*. Nature 415:497-502). The group of Christian Boucher in Toulouse France, which sequenced the bacterium, has identified several hundred potential genes involved in virulence based on regulatory evidence and homology to known virulence factor genes. In complementary studies, **John Elphinstone** and co-workers in York UK, are using microarrays to identify novel bacterial genes expressed during pathogenesis. Similarly, an IVET (in vitro expression technology) system for *R. solanacearum* has been developed in the group of **Caitilyn Allen** in Madison, Wisconsin. It is to be hoped that these diverse approaches will yield substantial new insights into the molecular mechanisms underlying bacterial wilt.

**Breeding for resistance to *Ralstonia***

The only truly effective control for bacterial wilt is resistant crop varieties; as a result, bacterial wilt resistance is the focus of active breeding programs all over the tropical world. The several successes in this area lay the foundation for research into both marker development for marker-assisted selection, as well as more basic studies into the molecular basis of resistance, which could lead to genetic engineering strategies.

In China, BW is an important constraint to groundnut (peanut) production; 10% of the annual crop is threatened. Breeding carried out at the Oil Crops Research Institute of Chinese Academy of Agricultural Sciences, Wuhan over the past ten years has resulted in the release of seven BW-resistant cultivars with improved yield potential. Several breeding lines have been developed with BW resistance transferred from a diploid species, *Arachis chacoense*. Through the International Groundnut Bacterial Wilt Working Group coordinated by **Liao Boshou**, collaborative efforts in the region are aimed at genotyping mapping populations.

In Brazil, where tomato, pepper, banana, and potato crops are threatened, partial disease control has been achieved after adoption of cultural measures, especially by planting potato largely in cooler highland areas, where disease pressure is reduced. However, a very wilt-susceptible potato cultivar from Europe has recently replaced a partially resistant cultivar, resulting in increased losses. Resistance breeding efforts by **Carlos Lopez** at EMBRAPA in collaboration with **Sylvie Priou** and co-workers at the International Potato Center (CIP) over the last 15 years have resulted in several resistant clones. Interestingly, one of the resistant clones had genetic material derived from *Solanum phureja-S. tuberosum* lines developed by **Luis Sequeira** years ago at Wisconsin. Reports of catastrophic losses from several countries in sub-Saharan Africa made it clear that resistant potato varieties suitable for use in the tropics are urgently needed.

Progress was also reported on resistant lines of eggplant (Kerala Agricultural University, India), tomato (U. Philippines-Los Banos), pepper (EMBRAPA, Brazil).

Long term tomato breeding for BW resistance is complicated by the extraordinary heterogenity of the

pathogen populations, such that tomatoes that are highly resistant in Taiwan may be fully susceptible in Thailand, to the great frustration of researchers and growers. Multilocation field trials coordinated by the Asian Vegetable Research and Development Center in Taiwan suggest that a 30-year-old tomato cultivar called Hawaii 7996 remains the best source of quantitative resistance. Mapping of resistance QTLs in this cultivar and others is ongoing at the University of the Philippines Los Baños, but in general, there is not enough effort on tomato breeding for BW resistance; molecular breeders are urgently needed.

**Plant Host Response to *Ralstonia***

A novel pathosystem between the model plant *Arabidopsis thaliana* and the bacterium *Ralstonia solanacearum* has been developed at CNRS-INRA, Toulouse. Work over the last several years has culminated in the cloning of a novel resistance gene, RRS1, from *Arabidopsis thaliana* (Deslandes et al., 2002 Resistance to *Ralstonia solanacearum* in *Arabidopsis thaliana* is conferred by the recessive RRS1-R gene, a member of a novel family of resistance genes. Proc Natl. Acad. Sci USA. 2002 99:2404-9). The pathosystem has turned out to be a powerful tool for studying the molecular basis of the plant host response to this pathogen, since a representative genome sequence for both the host and pathogen are now available. Research into the host response and signalling pathways involved in resistance are now well advanced through transcriptome analysis using microarrays of Arabidopsis genes. This work is being extended in collaboration between the Toulouse group and the University of Pretoria in South Africa, with the aim of identifying varying plant host responses to different *Ralstonia* isolates.

Surprisingly, there were no presentations at IBWS on attempts at genetic engineering solutions to bacterial wilt. This may reflect the fact that the disease is mainly a problem of developing countries and therefore it has not attracted the attention of multinationals focussed on lucrative commercial markets. It's also possible that research efforts are underway but not reported until products are ready for general release either due to secrecy agreements with multinationals or due to current public perceptions. Alternatively, public funding on this topic may have suffered because of the controversy surrounding GMOs. Notwithstanding these issues, it is likely that with the emerging interest in plant genomics, future IBWS will feature an increasing interest in molecular breeding approaches.

For more information (including all abstracts) on the congress and Bacterial Wilt research please visit http://ibws.nexenservices.com/. APS Press will publish this fall the full proceedings of the 3rd IBWS, which will be edited by Allen, Hayward, & Prior.

## Welcome New Members

The following members joined IS-MPMI between December 2001 through February 2002.
Please join us in welcoming them to the Society!

**W. Allen Miller**
Iowa State Univ, Ames, IA,

**Hirofumi Yoshioka**
Nagoya Univ, Nagoya, Aichi, , JAPAN

**David O. Nino-Liu**
Pennsylvania State Univ, University Park, PA,

**Andrzej Mazur**
Univ of Maria Curie

**Lublin Sklodowska**
POLAND

**Philipp Franken**
Max Planck Inst for Terrestrial Microbiology, Marburg, GERMANY

**Qingli Liu**
Univ of California, Davis, CA,

**Jorgelina Ottado**
Natl Univ of Rosario, Rosario, SE, ARGENTINA

**Benjamin F. Matthews**
USDA ARS SGIL, Beltsville, MD

**Yeon-Ki Kim**
Myongji Univ, Yongin-City, Kyongi-do, KOREA

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**Postdoc Position in Functional Genomics**
The Disease Resistance Group at Pioneer Hi-Bred, International, Inc. (A DuPont Company) is seeking to hire a postdoc to develop and implement functional genomics assays for maize. We are looking for a highly motivated molecular biologist with superior laboratory skills and an interest in uncovering gene function in plants, especially with regard to pathways involved in response to infection by pathogens. A position description and instructions for submitting an application can be found at: http://www.pioneer.com/employment/general/pp26_functional_genomics.htm

**Two Post-Doctoral Positions in Enzyme/Protein Chemistry**
Research PROJECTS to investigate metabolism of biologically active secondary metabolites require two postdoctoral fellows with a Ph.D. in enzyme/protein Chemistry or related field, a strong background in fungal and plant protein/enzyme isolation/characterization, extensive experience with HPLC analysis (diode array and radio detectors), and radioisotope use. The required qualifications should be evidenced by a strong publication record in the field. Positions are available immediately. Candidates should send letter of application and resume, and provide names, e-mail addresses, and telephone numbers of three referees. Electronic applications to: Dr. M.S.C. Pedras, University of Saskatchewan, Department of Chemistry, 110 Science Place, SASKATOON SK, S7N 5C9, CANADA, E-mail: soledade.pedras@usask.ca
http://www.usask.ca/chemistry/pedras.html

**Postdoctoral Position**
A postdoctoral position is available to study the molecular basis for infection of conifer trees by the root rot fungus-*Heterobasidion annosum*. Candidates for this position should have a strong background in molecular biology. Experience in the construction of Bacterial Artificial Chromosome (BAC) libraries is an added advantage. To apply, please send a full CV together with the names of two referees to Dr. Fred Asiegbu, Department of Forest Mycology & Pathology, Swedish University of Agricultural Sciences, Box 7026, SE-750 07 Uppsala, Sweden. E-mail: Fred.Asiegbu@mykopat.slu.se

**Post Doctoral Research Assistant**
Division of Microbiology School of AMS University of Reading. A 3-year position is available funded by the BBSRC to work with Dr. Philip Poole on the development of environmental biosensors based on green fluorescent fusions to all ABC transporter-binding proteins identified in the Sinorhizobium meliloti genome. These will enable the spatial and temporal monitoring of the root and rhizosphere environment for ion and metabolite levels. The aim is to identify factors that are crucial to microbial competition and plant infection by S. meliloti. Further details of this project can be found at http://www.ams.rdg.ac.uk/microbiology/position.htm. Candidates should have a Ph.D. in a relevant subject, which include, molecular biology, microbiology and biochemistry. Starting salary £19,681. For further information contact Dr. Philip Poole Tel:0118 9318895 Fax:01189316671
E-mail p.s.poole@reading.ac.uk

**Postdoctoral Research Associate and Doctoral Student**
Two positions available to study the molecular basis of non race-specific disease resistance in the model plant, Arabidopsis thaliana, the Institute of Plant Biochemistry Halle invites applications for a Postdoctoral Research Associate (BAT-O IIa) and a Doctoral Student (BAT-OIIa/2) who will identify and characterize leucine-rich repeat receptor-like kinases (LRR-RLK) implicated in plant disease resistance against various microbial pathogens. This project is part of a 10-year German "Arabidopsis Functional Genomics Network" (AFGN). Positions are available immediately and will be for 2 years with a renewal option for one year. Candidates should have a strong background in plant molecular biology/genetics and phytopathology. Knowledge on bioinformatics and protein biochemistry will surely be an asset. Interested individuals may submit their curriculum vitae and names of three references to: Dr. Thorsten Nürnberger, Institute of Plant Biochemistry, Weinberg 3, D-06120 Halle/Saale, Germany. Fax: +49-345-55821409. E-mail: TNUERNBE@IPB-HALLE.DE. For more information please refer to: http://www.ipb-halle.de/english/institute/research/nuernberger/introduction.

**Postdoctoral Research Associate**
Postdoctoral Research Associate (BAT-O IIa) will identify and characterize Arabidopsis mutants impaired in the recognition of Phytophthora spp.-derived protein elicitors. This project is part of the BMBF-funded project "GABI-NONHOST – A consortium-based functional genomics initiative on plant non-host disease resistance". The position will be available on April 1, 2002, and will be for 3 years. Candidates should have a strong background in plant molecular biology/genetics, biochemistry, and phytopathology. Interested individuals may submit their curriculum vitae and names of three references to: Dr. Thorsten Nürnberger, Institute of Plant Biochemistry, Weinberg 3,D-06120 Halle/Saale, Germany. Fax: +49-345-55821409, E-mail: TNUERNBE@IPB-HALLE.DE. For more information please refer to: http://www.ipb-halle.de/english/institute/research/nuernberger/introduction.

**Postdoctoral Associate and Doctoral Student**
Two positions available to identify and characterize Arabidopsis mutants impaired in the non-host resistance to the oomycete, Phytophthora infestans. This project is part of the BMBF-funded project "GABI-NONHOST – A consortium-based functional genomics initiative on plant non-host disease resistance". Positions will be available on April 1, 2002, and will be for 3 years. Candidates should have a strong background in plant molecular biology/genetics and phytopathology. Interested individuals may submit their curriculum vitae and names of three references to: Prof. Dierk Scheel, Institute of Plant Biochemistry, Weinberg 3, D-06120 Halle/Saale, Germany. FAX : +49-345-55821409.
E-mail: DSCHEEL@IPB-HALLE.DE. For more information please refer to: http://www.ipb-halle.de/english/institute/research/scheel/introduction.htm

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