Work of MPMI Members Featured in Science

In a recent Special Section in Science (pp. 234-236; April 9, 2004), research on the molecular genetics of rhizobial symbioses was prominently featured. The article nicely summarized the tremendous progress that has been made in this area since the earlier identification of nod genes and nod factors. It should be particularly gratifying to members of MPMI to note that many of the genes involved in establishment of the nitrogen fixation symbiosis are also involved in the establishment of fungal mycorrhizal associations, because the MPMI Congresses are one of the few venues that bring together researchers interested in both types of symbionts. Current MPMI members who were quoted or whose work was discussed include Sharon Long, Jens Stougaard, Martin Parniske, Peter Gresshoff, and Maria Harrison. Other colleagues mentioned in the piece included: Fred Ausubel, Doug Cook, Jean Denarie, Gyorgy Kiss, Ton Bisseling, R. Varma Pemetsa, and Masayoshi Kawaguchi. Much of this work was first presented at MPMI Congresses in Amsterdam, Madison, and St. Petersburg.

MPMI Installs New Editorial Board

In January 2004, the new editorial board of MPMI began its 3-year term. Jens Stougaard replaces Herman Spink as editor-in-chief and is joined by 11 new senior editors. To acquaint IS-PMPI members with the new board, brief biographies are presented.

Jens Stougaard was a senior editor of MPMI from 2000 to 2003 in the area of plant-bacterial symbioses. In 2003, he was elected to the board of directors of IS-PMPI and, as a function of his position as editor-in-chief of MPMI, he is also a member of the Publications Board of The American Phytopathological Society. Jens received his Ph.D. degree in 1983 from the University of Sussex, Brighton, U.K., and did postdoctoral research in the Department of Molecular Biology at the University of Aarhus, Denmark, and at the Max-Planck Institut für Züchtungsforschung, Cologne, Germany. He has been a visiting scientist in the Sainsbury Laboratory at the John Innes Centre for Plant Science Research, Norwich, U.K., and is currently a professor in the Department of Molecular Biology, University of Aarhus. His primary research is on genes regulating development of nitrogen-fixing root nodules and mycorrhiza in legumes. He is currently focusing on the mechanisms of Nod factor perception, the function of receptors involved and the downstream signal transduction cascade. The plant model system used for this research is Lotus japonicus, which is also used for investigating the long-range signaling integrating root nodule development into the general developmental program of the plant. Genetics, genomics, and biochemical methods are used to identify and characterize components of regulatory circuits. State-of-the-art microscopy and bioimaging are used for phenotypic description and studies at the cellular level.

Guido Bloemberg obtained his Ph.D. degree at Leiden University, Leiden, The Netherlands, in 1995, focusing on the analysis of host-specific lipochitin oligosaccharide signal molecules and the biochemical function of the host-specific nodulation gene products of Rhizobium spp. under the guidance of Herman Spink and Ben Lugtenberg. He then worked as a postdoctoral fellow in the laboratories of Roberto Kolter (Harvard Medical School) and Frans de Bruijn (Michigan State University). During these periods, he began working on the visualization of rhizosphere organisms and the regul
In 2003, the global area of transgenic crops continued to grow for the seventh consecutive year at a sustained double-digit growth rate of 15% compared with 12% in 2002. The estimated global area of transgenic or genetically modified (GM) crops for 2003 was 67.7 million hectares; this includes a provisional conservative estimate of 3 million hectares of GM soybean in Brazil (the final hectarage could be significantly higher), officially approved for planting for the first time in 2003. It is noteworthy that a double-digit rate of 10% growth in GM crops was sustained in 2003, even excluding the Brazilian hectarage. The 67.7 million hectares of GM crops in 2003, equivalent to 167 million acres was grown by 7 million farmers in 18 countries, an increase from 6 million farmers in 16 countries in 2002. The increase in area between 2002 and 2003 of 15% is equivalent to 9 million hectares or 22 million acres. During the eight-year period 1996 to 2003, global area of transgenic crops increased 40 fold, from 1.7 million hectares in 1996 to 67.7 million hectares in 2003, with an increasing proportion grown by developing countries. Almost one-third (30%) of the global transgenic crop area of 67.7 million hectares in 2003, equivalent to over 20 million hectares, was grown in developing countries where growth continued to be strong. It is noteworthy that the absolute growth in GM crop area between 2002 and 2003 was almost the same in developing countries (4.4 million hectares) and industrial countries (4.6 million hectares), with the percentage growth more than twice as high (28%) in the developing countries of the South compared with the industrial countries of the North (11%).

**GM Crop Area, by Country, Crop and Trait**

In 2003, six principal countries, compared with four in 2002, grew 99% of the global transgenic crop area; this reflects the broadening participation of the lead GM countries with ten countries now growing 50,000 hectares or more, of GM crops. The U.S.A. grew 42.8 million hectares (63% of global total), followed by Argentina with 13.9 million hectares (21%), Canada 4.4 million hectares (6%), Brazil 3 million hectares (4%), China 2.8 million hectares (4%) and South Africa 0.4 million hectares (1%). Of the six leading GM crop countries, China and South Africa had the highest year-on-year increase with a 33% growth rate. China increased its Bacillus thuringiensis (Bt) cotton area for the fifth consecutive year from 2.1 million hectares in 2002 to 2.8 million hectares in 2003, equivalent to 58% of the total cotton area of 4.8 million hectares in 2003. South Africa increased its combined area of GM maize, soybean and cotton to 0.4 million hectares in 2003 with particularly strong growth in white maize used for food, which has increased rapidly from 6,000 hectares in 2001 to 84,000 hectares in 2003. Canada’s GM crop area grew at a significant 26% between 2002 and 2003 to reach 4.4 million hectares in the three crops, canola, maize, and soybean. Despite the continuing economic constraints in Argentina, and soybean adoption rates already close to 100% in 2002, its GM crop area grew at 3% with strong growth in Bt maize. A growth rate of 10% was achieved in the U.S.A. (3.8 million hectares) reflecting strong growth in both Bt and herbicide tolerant maize, and continued growth in herbicide tolerant soybean. GM crop hectarage in Australia decreased slightly because of the continued severe drought, which is the worst in centuries, with total area planted to cotton at approximately one third of normal plantings. India increased its Bt cotton area by 100%; Spain also increased its Bt maize area by one third to reach over 6% of the national maize crop in 2003. Uruguay and Romania also reported significant growth, exceeding 50,000 hectares of GM crops for the first time, whilst countries that introduced GM crops for the first time in 2002, such as Colombia and Honduras reported modest growth.

Two countries, Brazil and the Philippines approved planting of GM crops for the first time in 2003. Brazil officially approved herbicide tolerant soybean in late September 2003, immediately before the start of the planting season. This late approval has exacerbated the difficulties in projecting provisional estimates of GM soybean hectarage in Brazil for the 2003/2004 season. At the time when this publication went to press, in late 2003, only 50% of soybeans had been planted in Brazil. A provisional conservative estimate of 3 million hectares of GM soybean has been projected for Brazil in 2003, in the knowledge that the final planted hectarage of GM soybean in Brazil in 2003 could be significantly higher. The Philippines grew approximately 20,000 hectares of Bt maize for the first time in 2003. Brazil and the Philippines joined 16 countries that already grew GM crops in 2002 for a total of 18 GM crop countries in 2003; notably, 11 are developing countries compared with seven industrial countries. Thus, the number of countries growing GM crops has increased steadily from six in 1996, to nine in 1998, to 13 in 2001, and 18 in 2003.

Globally, in 2003, growth continued in all four commercialized GM crops: GM soybean occupied 41.4 million hectares (61% of global GM area), up from 36.5 million hectares in 2002; GM maize was planted on 15.5 million hectares (23% of global GM area), up substantially from 12.4 million hectares in 2002, with the highest growth rate for all crops at 25% - this follows a 27% growth rate in GM maize in 2002; transgenic cotton was grown on 7.2 million hectares (11% of global GM area) compared with 6.8 million hectares in 2002; and GM canola occupied 3.6 million hectares (5% of global GM area), up from 3.0 million hectares in 2002.

During the eight-year period 1996 to 2003, herbicide tolerance has consistently been the dominant trait followed by
insect resistance. In 2003, herbicide tolerance, deployed in soybean, maize, canola, and cotton occupied 73% or 49.7 million hectares of the global GM 67.7 million hectares, with 12.2 million hectares (18%) planted to Bt crops. Stacked genes for herbicide tolerance and insect resistance deployed in both cotton and maize continued to grow and occupied 8% or 5.8 million hectares, up from 4.4 million hectares in 2002. The two dominant GM crop/trait combinations in 2003 were: herbicide tolerant soybean occupying 41.4 million hectares or 61% of the global total and grown in seven countries; and Bt maize, occupying 9.1 million hectares, equivalent to 13% of global transgenic area and grown in nine countries. Whereas the largest increase in Bt maize was in the U.S., growth was witnessed in all seven countries growing Bt maize. Notably, South Africa grew 84,000 hectares of Bt white maize for food in 2003, a substantial 14 fold increase from when it was first introduced in 2001. Bt/herbicide tolerant maize and cotton both increased substantially, reflecting a continuing trend for stacked genes to occupy an increasing percentage of the area planted to GM crops on a global basis.

A useful way to provide a global perspective of the adoption of GM crops is to express the global adoption rates for the four principal GM crops as a percentage of their respective global areas. In 2003, 55% of the 76 million hectares of soybean planted globally were transgenic - up from 51% in 2002. Twenty-one percent of the 34 million hectares of cotton were GM, up from 20% last year. The area planted to transgenic canola in 2003 was 16%, up from 12% in 2002. Finally, of the 140 million hectares of maize grown globally, 11% was GM in 2003 equivalent to 15.5 million hectares, up substantially from 9% or 12.4 million hectares in 2002. If the global areas (conventional and transgenic) of these four principal GM crops are aggregated, the total area is 272 million hectares of which 25%, up from 22% in 2002, was transgenic in 2003. Thus, for the first time one quarter of the aggregate area of the four crops, totaling over one quarter billion hectares is GM. The biggest increase in 2003 was a 4.9 million hectares increase in GM soybean equivalent to a 13% year-on-year growth, followed by a 3.1 million hectare increase in GM maize equivalent to a substantial 25% year-on-year growth, which follows a 27% year-on-year growth in 2002.

**The Potential Contribution of GM Crops**

The World Food Program recently reported that the number of people suffering from malnutrition increased by 25 million from 815 to 840 million. The most compelling case for biotechnology, and more specifically GM crops, is their capability to contribute to:

- increasing crop productivity, and thus contribute to global food, feed, and fiber security;
- conserving biodiversity, as a land-saving technology capable of higher productivity;
- more efficient use of external inputs, for a more sustainable agriculture and environment;

- increasing stability of production to lessen suffering during famines due to abiotic and biotic stresses;
- and, to the improvement of economic and social benefits and the alleviation of abject poverty in developing countries.

The experience of the first eight years, 1996 to 2003, during which a cumulative total of over 300 million hectares (approximately 750 million acres, equivalent to almost one-third of the total land area of the U.S. or China) of GM crops were planted globally in 21 countries, has met the expectations of millions of large and small farmers in both industrial and developing countries.

In 2003, coincidental with evidential confirmation that commercialized GM crops continue to deliver significant economic, environmental, and social benefits to both small and large farmers in developing and industrial countries, the global area of transgenic crops continued to grow at an annual sustained double-digit growth rate of more than 10%. The number of farmers that benefited from GM crops continued to grow and reached 7 million in 2003, up from 6 million in 2002. Notably, more than 85% of these 7 million farmers benefiting from GM crops in 2003, were resource-poor farmers planting Bt cotton, mainly in nine provinces in China and also in the Makhathini Flats in KwaZulu Natal province in South Africa.

**The Global Value of GM Crops**

In 2003, the global market value of GM crops is estimated to be $4.50 to $4.75 billion, having increased from $4.0 billion in 2002 when it represented 15% of the $31 billion global crop protection market and 13% of the $30 billion global commercial seed market. The market value of the global transgenic crop market is based on the sale price of transgenic seed plus any technology fees that apply. The global value of the GM crop market is projected at $5 billion or more, for 2005.

**Concluding Comments and Future Prospectives**

Despite the on-going debate in the European Union, there is cause for cautious optimism that the global area and the number of farmers planting GM crops will continue to grow in 2004 and beyond. Taking all factors into account, the outlook for the next five years points to continued growth in the global hectareage of GM crops to approximately 100 million hectares, with up to 10 million farmers growing GM crops in 25, or more, countries. The global number and proportion of small farmers from developing countries growing GM crops is expected to increase significantly. Established GM country markets are continuing to grow in GM area, with a more diversified portfolio of GM crop products available. New GM countries from the South, like India and Brazil, have increased their hectareage of Bt cotton and herbicide tolerant soybean respectively, and some like Uruguay have also approved new products such as GM maize, already deployed in other countries. New input trait products from industry that will contribute to sustained growth include the dual Bt gene

Global Status of Commercialized Transgenic Crops continued on page 7
IS-MPMI's diverse membership spans the globe and includes professionals who have been in their field for decades as well as those who are just starting out. To help members learn more about their colleagues, each issue of the *IS-MPMI* Reporter profiles three members chosen randomly in different career stages.

**Student**

**Andrea Chini**  
University of Edinburgh, Institute of Cell & Molecular Biology  
Edinburgh, Scotland

After receiving my degree in plant molecular biology from the University of Pavia, Italy, I started my Ph.D. in plant-pathogen interaction at Edinburgh University, Loake’s lab, in 2000. I became a member of IS-MPMI at the beginning of my Ph.D. course and have gained several benefits from my membership.

As a student, I received particular support to participate in the IS-MPMI meeting in 2001 (Madison) and in 2003 (St. Petersburg). In 2001, attending the international conference gave me the opportunity to discuss my project, learn new technologies, and acquire a broader scientific view.

In 2003, I presented my Ph.D. results at the St. Petersburg conference and, to my great surprise, my poster presentation received an award during the closing dinner. In addition, the MPMI journal is of fundamental importance in keeping my plant-pathogen interaction knowledge always up-to-date; hence I hope that IS-MPMI members can soon access PDF versions of all articles published in MPMI. This is my final year as a Ph.D. student, but thanks to several benefits offered by IS-MPMI, I will remain an IS-MPMI member for many years to come.

**Postdoctoral/Early Career**

**Dennis Halterman**  
USDA/ARS, Iowa State University  
Ames, IA, U.S.A.

My interest in the study of plant defense responses began at Cornell College in Mt. Vernon, Iowa, where I received a B.A. in biology and biochemistry in 1994. My undergraduate research project, under the supervision of Craig Tepper, involved the study of pathogenesis-related gene regulation in bean cotyledons after exposure to salicylic acid. My experiences at Cornell influenced my decision to begin a graduate career at Purdue University, where I joined the Purdue Genetics Program and studied with Greg Martin. The focus of my Ph.D. project involved the study of the tomato *Fen* gene, which confers a hypersensitive response-like phenotype after exposure to the insecticide fenithion. Specifically, my research involved the comparison of signal transduction pathways leading to the fenithion response with the bacterial resistance response mediated by a closely related gene, *Pto*. Upon the completion of my Ph.D., I joined the lab of Roger Wise as a USDA postdoctoral fellow in the Department of Plant Pathology at Iowa State University. In his lab, I began studying the interactions between barley and the biotrophic fungal pathogen *Blumeria graminis* f. sp. *bordei* (powdery mildew). I have been successful in cloning and beginning characterization of the *Mla6*, *Mla7*, *Mla10*, and *Mla13* genes, which are responsible for race-specific resistance to powdery mildew. Recently, my research has involved the study of transcriptional and translational control of *Mla* and the unique mechanisms involved in expression of this family of resistance genes.

I have recently accepted a position within the U.S. Department of Agriculture/Agricultural Research Service Vegetable Crops Research Unit in Madison, Wisconsin. This is a joint appointment within the Department of Plant Pathology at the University of Wisconsin, so I will be working with a strong and diverse group of researchers in Russell Labs. My research project will return me to the world of the *Solanaceae* and will focus on the molecular aspects of disease resistance in potato. Initially, I plan to concentrate on the study of late blight (caused by *Phytophthora infestans*) and other diseases important to Wisconsin potato growers. I look forward to the challenges that lie ahead.

I joined IS-MPMI three years ago in May 2001. I have found that attending IS-MPMI symposia and reading about the accomplishments of other researchers in *Molecular Plant-Microbe Interactions* is a great way to stay informed of current research ideas. Through interactions with other IS-MPMI members, I have formed valuable collaborations that have assisted me throughout my career. I encourage those of you who are not IS-MPMI members to consider joining this dynamic group of people.

**Distinguished member**

**Ann G. Matthysse**  
University of North Carolina  
Chapel Hill, NC

I did my undergraduate work at Radcliffe in biochemical sciences, working on diphtheria with A. M. Pappenheimer, Jr. (Pap as he liked to be called). This was my initial introduction to working with bacteria and I loved it. I have continued to enjoy working with bacteria to this day. Pap was very supportive of my desire to go on to graduate work. These were the days when the first question I was asked in interviews for graduate school admission was “Why should we admit you rather than a man?” (the implication being that a man would do more and better science).
I began my graduate work at Rockefeller University in the laboratory of Ed Tatum. While there, I got married and moved with my husband back to Boston and completed my graduate work in the laboratory of John Torrey, studying the control of cell division in pea root explants. I was very impressed with the new field of molecular biology and did postdoctoral work with James Bonner, in order to gain experience in plant molecular biology. I then returned to bacteria and Harvard, where I worked with Bernie Davis and taught undergraduate microbiology. It was at this time that I began to study the interactions between bacteria, particularly Agrobacterium, and plants. My first job as an assistant professor was at the medical school of Indiana University in Indianapolis, teaching infectious disease. Ned Shrigley was the chair of the microbiology department at that time; he believed that all infectious disease had elements in common and hired me, although I worked on plant bacterial interactions. I moved to the Botany Department at University of North Carolina in 1975, after Ned retired from the chair position at Indiana. I have been in Chapel Hill since that time, although the department has changed from botany into biology.

My research has been focused on the initial interactions between bacteria and plants, particularly attachment of bacteria to plant surfaces. We discovered that Agrobacterium tumefaciens makes cellulose during the course of binding to plants. This observation has led me to study the genetics and mechanism of cellulose synthesis in bacteria. Recently, my lab has been involved in collaborative studies with William Smith of the University of California at Santa Barbara of an apparent case of gene transfer from bacteria to the tunicate, Ciona, of the gene for cellulose synthase.

IS-MPMI has provided a meeting and a journal in which the focus is on the type of studies that interest me, which is the molecular biology and genetics of the interactions between plants and microbes. From the first one I attended in Ithaca, the meetings have provided a pleasant and useful interaction with colleagues.

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Plan Now to Attend the 12th International Congress on Molecular Plant-Microbe Interactions

The International Society for Molecular Plant-Microbe Interactions (IS-MPMI) and the Mexican Organizing Committee are pleased to announce that the 12th International Congress on Molecular Plant-Microbe Interactions will take place July 17-22, 2005 in Cancún, México.

The scientific program will consist of plenary lectures, plenary symposia, concurrent presentations (invited or selected from abstracts), and poster sessions.

The Congress will last for five working days. Mornings will be devoted to plenary lectures and plenary symposia, while in the afternoons, parallel symposia, and in the evenings, poster sessions will be held. In total, we plan to have 11 plenary lectures, 11 plenary symposia, 20 concurrent presentations and poster sessions. The cultural program of the Congress will include archeological sightseeing, scuba-diving and other aquatic activities, cultural performance(s), as well as pre- and post-Congress tours.

We cordially welcome you to participate in the Congress and recommend monitoring the web site that soon will be announced through the IS-MPMI.

Federico Sanchez
Congress Organizer

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Ph.D. Fellowships Offered

The International Max Planck Research School (IMPRS) on “The Exploration of Ecological Interactions with Molecular and Chemical Techniques” offers five Ph.D. fellowships for graduate students in molecular biology, ecology, entomology, or chemistry. The application deadline is July 31, 2004. The Ph.D. program starts in January 2005, but earlier arrangements are possible.

The Research School in Jena will be the first graduate school worldwide where modern chemical and molecular techniques will be used to study ecological systems. For detailed information on the school, application, and admission procedures please see our homepage at www.ice.mpg.de/imprs.

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Phytophthora Molecular Genetics Workshop

The NSF Research Network “Phytophthora Molecular Genetics” will meet in New Orleans, May 21-23, 2004. The annual workshop is preceding the 104th general meeting of the American Society of Microbiology (ASM) that is held from May 23-27, 2003 in New Orleans. If you are active in the field of molecular genetics and genomics of Phytophthora or related Oomycetes you are welcome to participate. For further information on program, costs and accommodation visit www.dpw.wau.nl/fyto/NSFworkshop/. For registration and submission of abstracts contact the meeting coordinators Francine Govers (Laboratory of Phytopathology, Wageningen University, Francine.Govers@wur.nl) or Paul Morris (Biological Sciences, Bowling Green State University, Ohio, pmorris@bgsu.edu).
EMPLOYMENT

Wheat Leaf Rust Molecular Genetics and Genomics Postdoctoral Fellow Position
A postdoctoral fellowship position at Agriculture & Agri-Food Canada, the Pacific Agri-Food Research Centre in Summerland, B.C., administered through the NSERC Visiting Fellowship in Government Laboratories Program (www.nserc.ca), is available for work on the wheat leaf rust (Puccinia triticina)/wheat (Triticum aestivum) pathosystem. We are looking for candidates who can perform independent research but work well in a larger collaborative setting and have received their Ph.D. within the last five years. The stipend is $40,800 (Canadian) per annum and is for two years, depending on performance and renewable for up to three years. Candidates must hold a degree in microbiology, biochemistry, plant pathology, or similar field and must have demonstrable experience in cDNA and genomic (preferably BAC) library construction, DNA and RNA blot, PCR, and protein techniques, as well as in the use of a wide variety of computer programs for DNA/RNA-genome analysis and manipulation, phylogeny, and database searches, preferably bioinformatics based on a Linux platform. Previous work on fungi, microarray profiling, or both would be advantageous. We have recently generated a large, 14,500 EST-containing database from this rust fungus, which is to be expanded to 30,000 reads from different life-cycle stages. A genomic library and physical contig map are needed. Collaboration with the Michael Smith Genome Sciences Centre in Vancouver, B.C. is in place. Integration with a genetic map (being constructed at the AAFC-Cereal Research Centre in Winnipeg) is envisaged. The focus will be on the isolation of several avirulence genes. However, several candidate pathogenicity and virulence genes need functional testing in an available heterologous expression system. Fungal expression profiling of the many different life-cycle stages during the infection process, using recently constructed microarrays, will be performed. Similarly, wheat and nonhost responses on barley will be assayed using microarrays. Many aspects of the program are in collaboration with other AAFC centers and USDA laboratories. For details on the program, visit http://res2.agr.ca/parc-crapac/summerland/progs/biotech/bakkeren_e.htm. Send a letter detailing how your experience would further the project, CV, and list of references to: Guus Bakkeren, Ph.D. Research Scientist, Agriculture & Agri-Food Canada, PARC, Summerland, Highway 97, BC, Canada V0H 1Z0; Phone: +1.250.494.6368; Fax: +1.250.494.0755; E-mail: BakkerenG@agr.gc.ca; Adjunct Professor, Dept. of Botany, University of British Columbia, Vancouver, B.C., Canada.

Postdoctoral Position - University of Maryland
A postdoctoral position to study host transcriptional responses to hypovirus infection using cDNA microarrays is available at the Center for Biosystems Research, at University of Maryland’s Biotechnology Institute. Cytoplasmically transmitted RNA viruses of the genus Hypovirus cause reduced virulence (hypovirulence) in the chestnut blight fungus Cryphonectria parasitica. The hypovirus-C. parasitica system is uniquely suited to take advantage of advances in DNA microarray technology for gaining deeper insight into virus-host interactions (Eukaryotic Cell 2:1253-1265, 2003). Hypovirus infection is persistent, with stable phenotypic changes. A C. parasitica EST library/database consisting of over 4,200 sequences has been used to construct a spotted DNA array representing approximately 2,200 unique genes. The hypovirus-C. parasitica system is one of the very few examples for which both a Eukaryotic virus and its host can be genetically modified with ease. Differentially expressed genes identified in the microarray hybridizations can be disrupted, silenced, or overexpressed for follow-up functional studies. The contribution of specific viral determinants to altered host gene expression can be examined with available infectious cDNA clones of chimeric hypoviruses and deletion mutants or by transformation into uninfected C. parasitica for expression in the absence of virus infection. Finally, a collection of mutant C. parasitica strains containing deletions of genes encoding signal transduction components are available for verifying the role of specific signaling pathways in regulation of specific gene families. The combined capabilities of the hypovirus-C. parasitica system provide the means for utilizing DNA microarray analysis as much more than a tool for simply identifying differentially expressed genes. Applicants should send curriculum vitae to Postdoctoral Position #R3-0033, Center for Biosystems Research, University of Maryland Biotechnology Institute, Plant Sciences Building, Rm 5115C, College Park, MD 20742-4450. The University System of Maryland is an equal opportunity/affirmative action employer.

Faculty Position - Plant Molecular Virologist
The Department of Plant Pathology at Ohio State University, Ohio Agricultural Research and Development Center, Wooster, Ohio, invites applicants for a tenure-track 90% research/10% teaching position at the assistant professor level in molecular plant virology. The successful candidate will develop a research program on the molecular characterization of viral gene function and replication, the basis of virus pathogenicity and resistance, or both and will have interactions with existing interdisciplinary teams. He/she will have access to state-of-the-art laboratory, phytotron, and greenhouse facilities. Teaching responsibilities include instruction in plant virology and advising graduate students. A curriculum vitae, copies of academic transcripts and selected publications, a statement of research interests, and three letters of recommendation should be sent to: Dr. S. Kamoun, Dept. of Plant Pathology, OSU-OARDC, Wooster, OH 44691-4096. The Ohio State University is an Equal Opportunity, Affirmative Action Employer. Women, minorities, Vietnam-era veterans, disabled veterans, and individuals with disabilities are encouraged to apply. A full description of the position and related information can be found at http://plantpath.osu.edu/whatsnew.php.

Two Bioorganic/Biological Chemistry Postdoctoral Positions
A new research project to investigate secondary metabolic pathways of cruciferous biotrophic fungal pathogens requires two postdoctoral fellows. This project is part of a
research program directed at understanding and controlling plant fungal diseases. The overall program has significant technological infrastructure integrated in a challenging multidisciplinary research environment. Positions require a recent Ph.D. in bioorganic or biological chemistry or related field with a strong background in plant/fungal metabolite analysis and isolation. Extensive experience with HPLC analysis using both diode array and mass detectors to detect and quantify a broad range of metabolites is essential. Additional expertise in spectroscopic techniques necessary for chemical structure elucidation, particularly modern high-field NMR spectroscopy, is highly relevant. Additionally, both positions require experience in developing biological assays to determine bioactivity (antifungal, antibacterial, phytotoxic) of secondary metabolites. Experience with microbiological techniques, protein and enzyme isolation, and plant cell culturing is considered an important asset. A strong publication record in the field should demonstrate the required qualifications. Positions are available immediately, however applications will be considered until positions are filled. Electronic applications are preferred. Candidates should send letter of application and resume and provide names, E-mail addresses, and telephone numbers of three references to the address below. Candidates whose first language is not English may be required to provide a certificate of English proficiency. Contact: Dr. M.S.C. Pedras, University of Saskatchewan, Department of Chemistry, 110 Science Place, Saskatoon, SK, S7N 5C9, CANADA; E-mail: s.pedras@usask.ca; Websites: www.usask.ca/chemistry/pedras.html; www.usask.ca/chemistry/groups/pedras.

In 2003, the three most populous countries in Asia – China, India, and Indonesia (total population 2.5 billion and a combined GDP of over $1.5 trillion), the three major economies of Latin America – Argentina, Brazil, and Mexico (population 300 million and a GDP of $1.5 trillion) and the largest economy on the continent of Africa - South Africa (population 45 million and GDP of $130 billion) are all officially growing GM crops. Their combined populations of 2.85 billion with a total GDP of over $3 trillion are recipients of the significant benefits that GM crops offer. The top 10 GM crop countries, each of which grew 50,000 hectares or more of GM crops in 2003, had a combined population of approximately 3 billion, close to half the world’s population, with a combined GDP of $13 trillion, almost half of the global GDP of $30 trillion. In 2003, GM crops were grown in 18 countries with a combined population of 3.4 billion, living on six continents in the North and the South: Asia, Africa, Latin America, North America, Europe, and Oceania. Thus, despite the continuing controversy about GM crops, the hectarage and number of farmers growing GM crops have continued to grow at a double digit rate or more, every year since their introduction in 1996, with 7 million farmers benefiting from the technology in 2003.

May 2004, Volume 17, Issue 5


The Disruption of a G Subunit Sheds New Light on the Pathogenicity of Stagonospora nodorum on Wheat. P. S. Solomon, K.-C. Tan, P. Sanchez, R. M. Cooper, and R. P. Oliver.


The Barley Apoptosis Suppressor Homologue Bax Inhibitor-1 Compromises Nonhost Penetration Resistance of Barley to the Inappropriate Pathogen Blumeria graminis f. sp. tritici. R. Eichmann, H. Schultheiss, K.-H. Kogel, and R. Hückelhoven.


Potyviral 6K2 Protein Long-Distance Movement and Symptom-Induction Functions Are Independent and Host-Specific. C. Spetz, and J. P. T. Valkonen.


Developmental Regulation of \( Mi \)-Mediated Aphid Resistance Is Independent of \( Mi-1.2 \) Transcript Levels. F. L. Goggin, G. Shah, V. M. Williamson, and D. E. Ullman.


Two PAK Kinase Genes, CHM1 and MST20, Have Distinct Functions in Magnaporthe grisea. L. Li, C. Xue, K. Bruno, M. Nishimura, and J.-R. Xu.


April 2004, Volume 17, Issue 4


The Avr1b Locus of Phytophthora sojae Encodes an Elicitor and a Regulator Required for Avirulence on Soybean Plants Carrying Resistance Gene Rps1b. W. Shan, M. Cao, D. Leung, and B. M. Tyler.


March 2004, Volume 17, Issue 3

The typeA Gene is Required for Stress Adaptation As Well as for Symbiosis of Sinorhizobium meliloti 1021 with Certain Medicago truncatula Lines. E. Kiss, T. Huguet, V. Poinso, and J. Batut.


Satellite Panicum Mosaic Virus Capsid Protein Elicits Symptoms on a Nonhost Plant and Interferes with a Suppressor of Virus-Induced Gene Silencing. W. Qiu and K.-B. G. Scholthof.


Multiple Pathways Regulate the Induction of Genes During Zoosporogenesis in Phytophthora infestans. S. Tani, E. Yatzkan, and H. S. Judelson.

February 2004, Volume 17, Issue 2


Importance of opgHXcv of Xanthomonas campestris pv. vesicatoria in Host-Parasite Interactions. G. V. Minsavage, M. B. Mudgett, R. E. Stull, and J. B. Jones.


Host-Specific Generation and Maintenance of Tomato bushy stunt virus Defective Interfering RNAs. R. T. Omarow, J. A. M. Rezende, and H. B. Scholthof.


loration of secondary metabolism in *Pseudomonas* spp. used in biocontrol. Since 2001, he has been an assistant professor in molecular microbiology at Leiden University. His research focuses on the interactions between biocontrol agents and phytopathogenic fungi, antifungal metabolite production by biocontrol strains, and bacterial biofilms, specifically the role of lipopeptide compounds in biofilm formation and degradation.

Otto Geiger received his Ph.D. degree in 1987 from the University of Hohenheim, Stuttgart, Germany. After postdoctoral work at Harvard Medical School, Boston, Massachusetts, U.S.A., with Eugene Kennedy and at Leiden University, The Netherlands, with Ben Lugtenberg and Herman Spank, he took a position at the Technical University of Berlin, Germany. In 1999, he moved to his current position as associate professor at the Research Center for Nitrogen Fixation at the National Autonomous University of Mexico in Guanavaca. His research focuses on the formation of bacterial membranes and other cell surface components as well as on the functions of these molecules in the interaction with eukaryotic hosts.

Godelieve Gheysen received an M.S. degree in zoology and a Ph.D. degree in plant molecular biology at Ghent University, Belgium. Her thesis work in the laboratory of Marc Van Montagu concerned the mechanism of plant transformation by *Agrobacterium tumefaciens*. In 1991, she started her own research group to study the molecular analysis of plant-nematode interactions. This research focused on i) the plant response in the compatible interaction at the molecular and cytological level, ii) characterization of the parasitism genes of nematodes, iii) unraveling the signal transduction pathway in the formation of nematode feeding sites, and iv) using this knowledge to engineer nematode resistance in plants. From 1996 to 2000, she coordinated a European project involving 12 labs that used *Arabidopsis thaliana* as a model system to study the compatible plant-nematode interaction. She is currently a professor in molecular genetics at Ghent University and teaches molecular biology and plant biotechnology.

Francine Govers is an associate professor of phytopathology in the Department of Plant Sciences of Wageningen University, The Netherlands, and a staff member at the Graduate School of Experimental Plant Sciences. She has an M.S. degree in plant pathology and a Ph.D. degree in plant molecular biology. Her thesis work in the laboratory of Ton Bisseling involved studies on nodulin gene expression in developing pea root nodules. She joined the Laboratory of Phytopathology in 1990. Her research interest is the biology and pathology of the oomycete *Phytophthora infestans*, the causal agent of potato late blight. Her research group focuses on i) characterizing pathogenicity factors and elicitors of defense responses, ii) unraveling signal transduction pathways underlying pathogenicity, iii) developing a molecular toolbox, iv) mapping the *P. infestans* genome, and v) genomics and functional genomics of *Phytophthora*. Results from these areas of research are directed toward designing rational control strategies for late blight and other diseases caused by oomycete pathogens. She teaches introductory plant pathology and advanced plant-microbe interaction courses to undergraduates and more specialized, thematic courses to graduate students.

Murray Grant is a senior lecturer in plant molecular biology at the Imperial College London, Wye Campus, Wye, Ashford, Kent, U.K. He received his Ph.D. degree in 1988 from Otago University, New Zealand, investigating the regulation of glutamine synthetase following infection of *Lupinus* spp. by *Rhizobium lupini*. He continued to study the host response to *Rhizobium* infection, with particular focus on regulation of asparaginase, initially at the former Department of Scientific and Industrial Research in New Zealand and later at the Cambridge Laboratory, John Innes Centre, U.K. Moving into plant-pathogen interactions, he studied *Arabidopsis*, cloning *RPM1* in Jeff Dangl’s laboratory at the Max Planck Institut in Köln, Germany. He later moved into academia and ended up at the Wye Campus in 1998. His research utilizes a combination of transcriptomic, proteomic, and real-time imaging approaches and focuses upon innate immune responses to *Pseudomonas syringae*, establishment of systemic immunity by avirulent *P. syringae* isolates, and dissection of signal transduction pathways recruited following *RPM1* elicitation.

Martin Parniske has been studying the plant genetics of symbiosis at the Sainsbury Laboratory, Norwich, U.K., since 1999, focusing on the functional and evolutionary aspects of plant genes required for fungal arbuscular mycorrhiza and bacterial nitrogen-fixing root nodule symbiosis. To enable this research, the lab built a TILLING-based reverse genetics tool that allows the isolation of plants carrying point mutations in any gene of interest in the legume *Lotus japonicus*. More details about this work can be found on the lab webpage: http://www.jic.bbsrc.ac.uk/sainsbury-lab/martin-parniske/homepage.htm. In his Ph.D. studies with Dietrich Werner in Marburg, Germany, he investigated the role of legume flavonoids as symbiotic signals and defense components in the nitrogen-fixing root nodule symbiosis. He received his Ph.D. degree in 1991 and continued to work in the same lab, generating and testing the
symbiotic performance of exopolysaccharide mutants of *Bradyrhizobium japonicum*. He received a postdoctoral fellowship from the Deutsche Forschungsgemeinschaft and from 1992 to 1994 studied transcription factors involved in the regulation of plant defense genes with Klaus Hahlbrock at the Max Planck Institut für Züchtungsforschung, Cologne. From 1994 to 1998, he studied the evolution of the Cf-4/9 resistance gene clusters in tomato as an EMBO and EU postdoctoral fellow with Jonathan Jones at the Sainsbury Laboratory, Norwich.

Pam Ronald is a professor in the Department of Plant Pathology, University of California, Davis. She joined the faculty in 1992. Pam received her B.A. degree in biology from Reed College, Portland, Oregon; her M.A. degree in biology in 1984 from Stanford University, California; and her M.S. degree in plant physiology in 1985 from the University of Uppsala, Uppsala, Sweden; and her Ph.D. degree in molecular and physiological plant biology in 1990 from the University of California, Berkeley. Research in her group is aimed at elucidating the signal transduction network controlling the rice defense responses after pathogen attack. Current projects in her lab include identification of the bacterial-produced signal molecule that interacts with the disease resistance gene product XA21, analysis of XA21-interacting proteins, analysis of genes expressed during the rice defense response, and characterization of the rice kinase. A more detailed overview of her research interests can be found at http://indica.ucdavis.edu/

Herman B. Scholthof is an associate professor of plant pathology and microbiology, specializing in the molecular biology of plant-virus interactions. He received B.S. and M.S. degrees from Wageningen University in The Netherlands and a Ph.D. degree from the University of Kentucky. After postdoctoral work at the University of California at Berkeley, he joined the faculty of the Department of Plant Pathology and Microbiology at Texas A&M University, College Station, in December 1994. His teaching responsibilities include graduate courses in plant virology, methods in the molecular biology of plant-microbe interactions, and a journal club on contemporary issues in biological sciences. Scholthof's research emphasizes the interactions of tomato bushy stunt virus with its various hosts to understand the molecular basis for susceptibility and resistance. He has been a visiting scientist at Harvard Medical School to conduct research in protein structural biology and to use cell-permeable dyes and liposomes for studying virus entry. He most recently was a senior editor for *Phytopathology*, is currently on the editorial board of *Virology*, and has been the coordinator for molecular and cellular biology symposia for annual meetings of The American Phytopathological Society. Scholthof is a founding executive member of the Intercollegiate Faculty for Virology at Texas A&M University.

Jim Sweigard is a principal investigator in the disease-resistance group of the Crop Genetics Research Division of Pioneer, a DuPont company. His interest in fungi began as an undergraduate at Goshen College, where he worked on hyphal tip growth under Stan Grove. His graduate work at Cornell University with Hans VanEtten concerned an oomycete pathogen of peas. Additional work at Cornell involved the epidemiology of late blight of potato with Bill Fry. He joined Barbara Valent's rice blast research group at DuPont in 1986. This research focused on the mechanisms of host specificity and on the general mechanisms of pathogenicity of *Magnaporthe grisea*. More recent research has focused on the corn pathogens *Fusarium verticillioides* and *Colletotrichum graminicola*. Jim previously served as an associate editor of *MPMI*.

Michael Udvardi received his Ph.D. degree in 1989 from the Australian National University (ANU), where he studied symbiotic nitrogen fixation. After postdoctoral work at Washington State University in the United States and then at the CSIRO Division of Plant Industry in Australia, he took a faculty position back at the ANU in 1994. From 1994 to 1998, he worked on both symbiotic nitrogen fixation and the acquisition of inorganic mineral nitrogen (nitrate and ammonium) in plants. In 1998, he moved to his current position as an associate professor at the Max Planck Institute of Molecular Plant Physiology in Germany, where his group continues to work on nitrogen acquisition in plants. As an extension of this work, they are also investigating macronutrient signaling in plants. Their work on symbiotic nitrogen fixation now focuses on the *Lotus japonicus-Mesorhizobium loti* symbiosis, and Udvardi coordinates a European functional genomics project involving nine labs that uses *L. japonicus* as a model to study mutualistic symbioses.

Frank White is a full professor in the Department of Plant Pathology at Kansas State University, Manhattan. He was appointed to this position in 1985 after both attaining his Ph.D. degree in microbiology (1981) and completing postdoctoral work at the University of Washington-Seattle. His research in Seattle involved the genetics of *Agrobacterium rhizogenes* under the direction of Eugene Nester and Milton Gordon. His undergraduate B.S. degree in molecular biology is from the University of Wisconsin-Madison. White’s present studies involve the mechanisms of virulence and avirulence in *Xanthomonas* species.
Biology of Plant-Microbe Interactions, Volume 3
Edited by Sally A. Leong, Caitilynn Allen, and Eric W. Triplett

Biology of Plant-Microbe Interactions, Volume 3 provides groundbreaking reports on the new studies related to the science of plant-microbe interactions as presented at the 10th International Congress on Molecular Plant-Microbe Interactions. Major themes include: recognition of pathogens by plants, defense signal nematode interactions, secretion of Avr and Vir factors, ecology and population biology of plant-associated microbes, cell biology of plant-microbe interactions, plant-rhizobium interactions, and functional genomics and biotechnology. Forty-nine figures, a subject/author index, and bibliography further enhance this title's emphasis on new research on the molecular basis of disease resistance.

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