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A Letter from the President **Cheers to 20 Years of Success!**



I am very proud to be president of the International Society for Molecular Plant-Microbe Interactions (IS-MPMI), a society with a relatively short life but strong vitality, which, during the last few years, has promoted a tremendous number of successful scientific activities and meetings. This was the result of the excellent leadership of the previous presidents and of my immediate predecessor Federico Sanchez. I hope I can do as well as they did. Although, the biannual symposium series began in 1982, IS-MPMI was formally inaugurated on September 7, 1990, making this year its official 20th anniversary. Much has happened in 20 years and the society has grown from its charter membership in 1990 to more than 1,000 members in 2009. In addition, our journal, MPMI, continues to grow in reputation.

The success of the society is evident if we consider the number of outstanding biologists who became members during the past 20 years. Thomas Boller and Jeff Dangl, who received the first and the second IS-MPMI Awards, are two examples of those eminent colleagues who have significantly contributed to better understanding of molecular plant-microbe interactions. The award ceremonies and other events of our last congresses in Sorrento and Québec City confirmed the tradition that the best science in the field of the interactions between plants and microbes, either beneficial or pathogenic, finds an important forum and a privileged auditorium in the society. Despite the economic difficulties resulting from the global crisis, the last congress in Québec City gathered nearly 1,000 people, with a large number of young scientists (almost 50%

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Interview with Gary Stacey New Editor-in-Chief of MPMI



Gary Stacey, MPMI Editor-in-Chief

In January 2010, the new Editorial Board for MPMI began its three-year term. Gary Stacey replaces Jonathan D. Walton as editor-in-chief.

Q: Tell us about yourself and your work.

A: I currently hold the title of endowed professor in the Division of Plant Sciences at the University of Missouri. I am also affiliated with the C. S. Bond Life Sciences Center, Division of Biochemistry and the Department of Molecular Microbiology and Immunology. I serve as director of the University of Missouri Center for Sustainable Energy and as associate director of the National Center for Soybean Biotechnology.

My Ph.D. degree is in microbiology but, through our work on plant-microbe interactions, the research has evolved over the years from largely microbial to its present heavy focus on plant molecular biology. The lab has worked for many years to try to understand the molecular mechanism of legume root infection by the nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum. However, more recently, our research has taken on new dimensions to focus more on plant-pathogen interactions with a specific interest in pathogen-associated molecular patterns (PAMPs) signaling. We also have a new

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IS-MPMI Reporter

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Share your news, accomplishments, and upcoming meeting details with your colleagues. Submit articles, announcements, and any ideas you may have for the next issue. You can send an e-mail (ismpmireportereditor@scisoc. org) or submit your item online (www.ismpminet.org/newsletter/ submissionform.asp).

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Editor-in-Chief Jean-Pierre Métraux University of Fribourg Biology Dept. Rue Du Musee 10 Fribourg, 1700 Switzerland Phone: + 41 26 300 8811 E-mail: jean-pierre.metraux@unifr.ch

Jean-Pierre Métraux Named Editor-in-Chief of IS-MPMI Reporter



Jean-Pierre Métraux, a chair in biology at the University of Fribourg, Switzerland, has been named editor-in-chief of the IS-MPMI Reporter. Métraux obtained his Ph.D. degree in plant biology at the University of California-Santa Cruz in 1979 with Lincoln Taiz as his thesis advisor. In 1979, he was awarded a Miller Fellowship at the University of California-Berkeley, where he worked with R. L. Jones. He joined the group of the late Hans Kende at the Plant Research Laboratory in East Lansing, MI, from 1981 to 1983. During this period, he became fascinated by plant pathology, while following lectures by Bob Scheffer

and Ray Hammerschmidt. He moved to the Agricultural Department of CIBA in Basel, Switzerland, in 1983 and headed a team working on the resistance of plants to pathogens. During this period, his group discovered systemic induction of chitinase and a few years later the involvement of salicylic acid as a signal for induced resistance. The same team identified dichloroisonicotinic acid and soon after benzothiadiazole as synthetic inducers of resistance. Fruitful collaborations also took place during this period with John Ryals and Eric Ward of the overseas branch of CIBA in North Carolina. In the beginning, such actions were unwanted by the company for obscure corporate reasons. But researchers are difficult to control and eventually the company realized the power of this transatlantic network. Benzothidiazole was later commercialized under the name BION. In 1991, Métraux joined the faculty of the Natural Sciences Department at the University of Fribourg as a full professor. Since then, he has continued to study various aspects of induced resistance in plants with an international group of graduate students and post-doctoral fellows. Current research focuses on signaling for disease resistance in response to biotic and abiotic stress. Finally, Métraux was elected as research council into the Swiss National Science Foundation in 2007.

MPMI Review Article Recognized as a Fast-Breaking Paper by ScienceWatch













Sophien Kamoun

"Emerging concepts in effector biology of plant-associated organisms," by Saskia Hogenhout, Renier Van der Hoorn, Ryohei Terauchi, and Sophien Kamoun, has been identified as a "Fast-Breaking Paper" in the category of Plant & Animal Science by ScienceWatch, a citation-ranking service of Thomson Reuters that tracks trends and performance in basic research. This distinction comes because it is one of the most-cited papers in its discipline published during the past two years. Read "Emerging concepts in effector biology of plant-associated organisms" in February 2009's MPMI print issue or online at http://apsjournals.apsnet.org/doi/abs/10.1094/MPMI-22-2-0115.

Unraveling a 20-Year Enigma

Sebastian Schornack¹ and Jens Boch²

Studying plant-pathogen interactions enables us to elucidate intricate mechanisms deployed by pathogens to manipulate the host. *Xanthomonas* bacteria, the causal agents of diseases in pepper, tomato, rice, cabbage, and other plants, employ a set of specific proteins for that purpose. Transcription activator-like (TAL) effector family proteins are translocated via a type III secretion system into the cytoplasm of host cells and subsequently imported into the nucleus. TAL effectors are modular, containing a central DNA-binding domain and a C-terminal transcription activation domain to bind to and activate host gene promoters.

In 2007, the groups of **Ulla Bonas** and **Thomas Lahaye** succeeded in demonstrating that AvrBs3, a TAL effector of *Xanthomonas campestris* pv. *vesicatoria*, directly binds to promoters of the pepper target genes *UPA20* and *Bs3* via a novel domain that consists of nearly perfect amino acid repeats (2,4). Recently, after 20 years of research on AvrBs3, it was revealed that DNA-target specificity of TAL effectors is encoded in the order and composition of these repeats in a very unique fashion (1,3).

Sebastian: I started working with Thomas and Ulla as a diploma student and contributed to the characterization of an R protein (Bs4) that recognizes the TAL effector AvrBs4. My biggest leap forward occurred on an evening while watching a boring TV show with the notebook on my lap when I spotted the conservation between type and order of repeats of AvrBs3 and AvrHah1, two different TAL effectors. Although different in their repeats, both activate the *Bs3* gene.

Jens: Sebastian came back from a lab meeting (a Thursday) and was in discussion-mode. He puzzled about the similarities between AvrBs3 and AvrHah1 repeats and the fact that they both induce expression of the resistance gene *Bs3*. I was happy to discuss science and challenged him with the idea that one repeat corresponds to one base on the DNA. Sebastian immediately jumped onto the idea and said we should check to see if it's true.

Sebastian: Of course, it was long known that amino acids 12 and 13 in a repeat play a special role because they are the most variable amino acids. A few other positions vary, too, but for the sake of simplicity, we focused on amino acid 12 and 13 to group the repeats into different types.

Jens: Sebastian had the AvrBs3-repeat types at hand and we knew that the *UPA20* promoter and the *Bs3* promoter were two sequences to look for target boxes. A few facts that had recently been solved by Ulla Bonas's and Thomas Lahaye's groups were essential for our search: (1) the differences between the *Bs3* and *Bs3-E* promoters

	-
HONGINSHANI HI NI HOHO NG NSNS HOHE, MO L 3 4 3 111 22 3 44 222 3 Upato HAAACCA ACCCC B83 AAACCTAACCAT Upazo AAACCTGACCCT	NI = 1 A $HO = 2 C$ $NG = 3 WA/T$ $NS = 4 H C/A$ $NN = 5 R G/A$ $HG =$
алабы сроке A/C ротолиз АБА Х 6 А А Б А С СС АТА ал Xa27 15 * 34555 15 1 * 22133 А V NHK V V А N А М ССАНЫ	$NI = 1 \qquad A$ $HD = 2 \qquad G'$ $NG = 3 \qquad T/A$ $NS = 4 \qquad A/G$ $NN = 5 \qquad A/G$
Bry16 11122323(23) AAACCTKITCT Greenog 111223443 AAACCTKITCT AAACCTKITCT AAACCTKITCT	

First notes taken at code-breaking.

are confined to one insertion and this should be close to the AvrBs3-target site (*Bs3* is induced by AvrBs3, but *Bs3-E* is not). In addition, a 36-bp fragment from the *UPA20* promoter was known to be bound by AvrBs3 and a fragment of 15–17 bp (*UPA* box) was proposed to be correlated with AvrBs3 responsiveness (2,4).

Sebastian: Finding a pattern with no idea what specificities to look for is futile. Luckily we had patterns: AvrBs3 contains three NI-type repeats in a row and further downstream several HD repeats. Amazingly, we could identify three adenines (A) in the predicted target DNA sequence and further downstream also several cytosines (C) that matched the NI and HD repeats nicely. We were flabbergasted. Could the specificity of TAL effectors be so simple? Why on earth has no one else seen this, so far? Quickly, we found a third repeat specificity: NG=T.

Jens: We looked for other boxes: AvrBs3 Δ rep16 (an AvrBs3 derivative lacking four repeats) induces the *Bs3-E* allele but not *Bs3*; AvrXa27 induces *Xa27* but not *xa27*; and PthXo1 induces *Xa13* but not *xa13*. We went to the computer to extract the promoter sequences and determine where the differences were (those are expected to be the target sites). This was not easy, especially because we could expect to (and did) see "mismatches" where a nonoptimal base was present. This strongly interferes with "pattern search by hand" as we did it. Nevertheless, after a while, we identified possible sites for these effectors.

¹Sainsbury Laboratory, John Innes Centre, Norwich, Norfolk NR4 7UH, U.K., Sebastian.Schornack@sainsbury-laboratory.ac.uk. ²Department of Genetics, Institute of Biology, Martin-Luther-University Halle-Wittenberg, Weinbergweg 10, D-06120 Halle (Saale), Germany, jens.boch@genetik.uni-balle.de.

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Unraveling a 20-Year Enigma continued from page 3

I don't remember how much time passed when we sat next to each other on the computers that day, but I was electrified. The significance of our finding became immediately clear to me. The mechanism behind the TAL-DNA recognition had strong potential for applications. The simple recognition code implies that one can change the repeat order and thereby easily build TAL effectors with novel DNA-binding specificities. One could build TAL proteins to specifically induce possibly any gene of interest.

Sebastian: We designed several experiments to prove our initial model. I suggested using the *Bs4* promoter as minimal promoter to see if the addition of target boxes renders these promoters inducible by a given TAL. We chose to use GUS as reporter to enable quantification and Jens suggested to test our code predictions on three TAL effectors of *Xanthomonas campestris* pv. *armoraciae* (Hax2, 3, 4), which Ulla and he had been working with in the past.

Jens: Unfortunately, I was going on vacation to hike in the Dolomite Alps two days after our finding and Sebastian was also busy, so we had to delay experiments. I couldn't sleep for the next two nights, thinking about the possibility of our model being true and possible ways to proceed experimentally.

Sebastian: Back from his vacation, Jens puzzled over the problem of how to construct a TAL effector with artificial repeat composition to prove that we can design novel DNA-binding specificities. This was a key to show people that this technique can be used to target novel sites. The problem was that PCR cloning is impossible, because any repeat-specific primer would have multiple binding positions within the near-identical repeats. I suggested having the repeats synthesized, but Jens was afraid to waste a lot of money if we made a mistake.

Jens: There had to be a more elegant way. Luckily, restriction sites for *Esp*3I, a type II restriction enzyme are present once in every repeat. These enzymes have separate recognition and cut sites and generated nonpalindromic overhangs which made it possible that *Esp*3I restriction fragments are ligated in one "sense" orientation. Technically, we had a few hurdles to solve,

but the expert technician **Angelika Landgraf** helped with many of the experiments that came along during the next months. Holding up the first leaf disks stained for GUS activity, we were excited to see that our expectations were matched. Looking back, those experiments were far from perfect, but the take-home message was clear.

Sebastian: To finally assemble the data for the *Science* publication involved so much more work than we initially anticipated and I was on my move to Norwich. Luckily, **Heidi Scholze** joined the group as a Ph.D. student.

Jens: In total, Angelika generated and analyzed literally thousands of constructs and Heidi did more than 3,000 leaf infiltrations for GUS assays. It is still unbelievable for me that all of this resulted in only four printed pages (and supplemental data; 1). Finally, the first presentation of the TAL effector code by Ulla Bonas at the MPMI meeting 2009 in Quebec City was exciting. The impact on the audience was impressive and the people were electrified. Ulla indicated that **Adam Bogdanove**'s group came up with similar conclusions (3), which was well appreciated.

Sebastian & Jens: We believe that "Breaking the Code" was a unique situation in a scientific career. It's rare that one simple model has such immediate and broad implications and even rarer that this model emerges directly from one intense discussion. The importance to always be open to discuss science and to contribute with ideas to projects is the main take-home message for both of us.

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MPMI Announces New Editorial Board Members

The new Editorial Board of *Molecular Plant-Microbe Interactions* will begin its three-year term in January 2010. **Gary Stacey** replaces **Jonathan Walton** as editor-in-chief and has chosen an impressive group of senior editors to work with him. To acquaint IS-MPMI members with the new board members, brief biographies are presented.



Gary Stacey is an endowed professor of plant sciences, director of the Center for Sustainable Energy, and associate director of the National Center for Soybean Biotechnology at the University of Missouri-Columbia. He also holds joint appointments in the Division of Biochemistry and Department of Molecular Microbiology and Immunology. He has received in excess of \$12 million in competitive research funding

Gary Stacey

as principal investigator or coprincipal investigator, has mentored 34 post-doctoral fellows, and has chaired 17 Ph.D. and six M.S. graduate programs. He has authored or coauthored 160 peer-reviewed research articles, 72 book chapters, and nine patents. Two of his patents support the product Optimize, sold by EMD Biosciences, Inc. to enhance rhizobial inoculant performance on soybean. He has also edited or coedited 14 books, six of which were part of the Biology of Plant-Microbe Interactions series that he cofounded. He is a past senior editor of MPMI and *Plant Physiology*. He serves on various advisory boards and currently serves on the Editorial Board of Journal of Crop Science and Biotechnology. In 2005, he was elected by the soybean community to a three-year term on the National Soybean Genetics Executive Committee. He is current chair of the Public Affairs Committee of the American Society of Plant Biologists. He is also currently the chair of the Department of Energy, Biological and Environmental Research Advisory Committee. In 2008, he founded a not-for-profit corporation, Missouri Energy Initiative, a resource network for building partnerships to move Missouri forward in terms of energy information and solutions, and currently serves as its acting executive director. In 1988, he was awarded a research fellowship by the Alexander Von Humboldt Stiftung and in 1990 was awarded the title of van der Klaauw Chair of Molecular Biology at the University of Leiden, the Netherlands. In 1992, he was given the Chancellor's Award for Research and Creative Achievement at the University of Tennessee. In 2007, he received the Distinguished Research Award in the College of Agriculture, Food and Natural Resources at the University of Missouri. In 2008, he was elected a fellow of the American Association for the Advancement of Science.



James R. Alfano

James R. Alfano grew up in southern California. He attended Moorpark Junior College for 2 years before transferring to San Diego State University, where he received a B.S. degree in microbiology in 1986. Alfano worked with **Michael Kahn** at Washington State University, studying the symbiotic nitrogenfixing relationship occurring between legume plants and *Sinorhizobium* and receiving his Ph.D. degree in

microbiology in 1993. His post-doctoral research was with Alan Collmer at Cornell University, studying bacterial pathogens and their protein secretion systems. In 1997, Alfano joined the Department of Biological Sciences at the University of Nevada-Las Vegas as an assistant professor. He moved to the Plant Science Initiative and the Department of Plant Pathology at the University of Nebraska in 2000 and was promoted to associate professor in 2002. Alfano's research has focused mainly on the bacterial pathogen Pseudomonas syringae and the type III protein secretion system that it uses to inject bacterial effector proteins into plant cells. Past research focused on how effectors were being delivered into plant cells by P. syringae's type III system. Another focus of his research group is the secretion signals of type III effectors and type III chaperones, accessory proteins required by many type III-secreted proteins. His research group has identified many type III-secreted proteins from P. syringae and determined that many type III effectors suppress plant innate immunity. Currently, several projects are focused on the plant targets of specific type III effectors.



Gwyn Beattie is an associate professor in the Department of Plant Pathology at Iowa State University (ISU). After obtaining her B.A. degree in chemistry at Carleton College in Northfield, Minnesota, she received her Ph.D. degree in cellular and molecular biology from the University of Wisconsin-Madison, where she worked with **Jo Handelsman** on nodulation competitiveness among *Rhizobium*

Gwyn Beattie

etli strains. Her post-doctoral research with **Steven Lindow** at the University of California-Berkeley focused on the epiphytic fitness of *Pseudomonas syringae*. Since joining the faculty at ISU in 1995, she has explored the biology of leaf-associated bacteria. Her studies have included examining the effect of leaf surface waxes on epiphytic bacterial colonization, the molecular basis of osmotolerance in pseudomonads and the osmoadaptation strategies employed during bacterial growth on leaves, and the role of water limitation in host resistance to *P. syringae*. She has also explored the ecological functions of

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phyllosphere communities, recently demonstrating a role for leaf surface bacteria in degrading airborne pollutants. She currently holds the position of the Robert Earle Buchanan Distinguished Professor of Bacteriology for Research and Nomenclature at ISU.



John Carr

John Carr is a senior lecturer in molecular plant pathology in the Department of Plant Sciences at the University of Cambridge. He conducted his Ph.D. research on pathogenesis-related (PR) proteins at Rothamsted Experimental Station (supervisors John Antoniw and Ray White) and the Biochemistry Department of Liverpool University (supervisor Mike Wilson). He carried out post-doctoral work with

Dan Klessig at the University of Utah Medical School in Salt Lake City and subsequently at the Waksman Institute (Rutgers University) on light-regulated gene expression, PR proteins, and the role of salicylic acid in the induction of resistance to plant viruses. He then worked as a research associate in **Milt Zaitlin**'s laboratory in the Plant Pathology Department at Cornell, working on transgenic resistance to viruses. He started his own research group in Cambridge in 1993. The group works on the mechanisms underlying salicylic acid-induced resistance and on viral evasion of induced resistance. Further details on the work of the group can be found at www.plantsci.cam.ac.uk/ research/johncarr.html.



Biao Ding

Biao Ding grew up in Yunnan Province, China. He obtained his B.S. degree in forestry from Beijing Forestry College (now Beijing Forestry University) in Beijing. Following his undergraduate studies, he went to Cornell University for graduate studies, where he obtained an M.S. degree in plant anatomy and then a Ph.D. degree in plant cell biology with work on the structure of phloem, plasmodesmata, and

the cytoskeleton under the supervision of Mandayam V. Parthasarathy. From there, he went on to pursue postdoctoral research with William J. Lucas at the University of California-Davis, working on viral cell-to-cell movement, the structure of plasmodesmata, and protein trafficking. He then started his faculty position as an assistant professor in the Department of Botany at Oklahoma State University-Stillwater in 1994. He initiated research programs to study viroid systemic trafficking and plant developmental regulation of protein trafficking. In 1999, he was promoted to associate professor. A year later, he moved to The Ohio State University-Columbus as an associate professor in the Department of Plant Biology (now the Department of Plant Cellular and Molecular Biology) and was promoted to full professor in 2005. His current research focuses on viroid-host interactions, addressing fundamental questions in RNA replication and systemic trafficking for the

establishment of pathogen infection and for systemic gene regulation in plant growth and development.



Barbara Kunkel earned her B.S. degree in genetics from the University of California-Davis in 1985. She carried out her Ph.D. research on gene expression in *Bacillus thuringensis* under the guidance of **Richard Losick** at Harvard University and completed her Ph.D. dissertation in 1990. She joined the laboratory of **Brian Staskawicz** at the University of California-Berkeley for her post-

Barbara Kunkel

doctoral studies and worked as a member of one of the first teams of researchers studying the interactions between Pseudomonas syringae and Arabidopsis thaliana. In 1994, she joined the faculty of the Department of Biology at Washington University in St. Louis, Missouri, where she has since been teaching and running her own research group. A primary objective of Kunkel's research is to elucidate the strategies used by plant pathogens to colonize and cause disease on their hosts. Specifically, this involves identifying and characterizing P. syringae virulence factors and studying their mode of action in A. thaliana and tomato. Her research group is currently focusing on mechanisms used by *P. syringae* to modulate the hormone physiology of its hosts and understanding why P. syringae appears to specifically target the plant hormones jasmonate and auxin. She is spending the 2009/2010 academic year on sabbatical in France, studying auxin signaling in the laboratory of Catherine Perrot-Rechenmann at the Centre National de la Recherche Scientifique (CNRS) in Gif-sur-Yvette. Additional information about research in the Kunkel lab can be found at www.biology.wustl.edu/faculty/kunkel/index.html.



Matteo Lorito is presently a full professor of plant pathology and biotechnology in the Department of Arboriculture, Botany and Plant Pathology at the University of Naples "Federico II" and an affiliated professor of the National Research Council (CNR), Institute for Plant Protection, at Portici, Naples, Italy. His major interest has been focused on various aspects of biological control and in particular on the

Matteo Lorito

use of the fungal agents *Trichoderma* spp., on which he has become an internationally recognized authority. His ongoing research aims to understand the relationships that these antagonists establish with the plant and pathogens and the mechanisms involved in producing beneficial effects to the plant. Important findings include the discovery of molecular factors that regulate these interactions and antimicrobial genes useful for increasing plant disease resistance. His research has contributed to the development of new biopesticide and biofertilizer products that utilize natural antimicrobial compounds

produced by diverse antagonists. Lorito is a fellow of the Organization for Economic Co-operation and Development and a Fulbright Research Fellow, and he was recently made a fellow of The American Phytopathological Society (APS). He has served as an associate editor of MPMI, the European associate editor of IS-MPMI Reporter, chair of the XIII International Congress of IS-MPMI, and a member of the Board of Directors of the Italian Society of Plant Pathology. He has also been a member of the APS Phytopathology News Advisory Committee, the APS Biological Control Committee, the International Commission of the Taxonomy of Fungi of the International Union of Microbiological Societies, and the Scientific Committee of the National Biotechnology Center in Tripoli, Libya. Presently, he is an elected member of the IS-MPMI Board of Directors and serves as the treasurer of IS-MPMI.



John McDowell is an associate professor in the Department of Plant Pathology, Physiology, and Weed Science at Virginia Tech, Blacksburg. He received his Ph.D. degree in 1995 from the University of Georgia under the guidance of **Rich Meagher**. His dissertation was on the structure, expression, and evolution of actin genes in *Arabidopsis*. He then entered the field of molecular plantmicrobe interactions through post-

John McDowell

doctoral research in **Jeff Dangl**'s lab at the University of North Carolina-Chapel Hill. There, he studied the structure, evolution, and signaling of disease resistance (*R*) genes in *Arabidopsis*, with emphasis on genes against the oomycete pathogen *Hyaloperonospora arabidopsidis* (cause of downy mildew). In 2000, he started his own group at Virginia Tech to continue investigating plantoomycete interactions. His group is investigating the role of recombination in *R* gene cluster evolution and the mechanisms through which plant cells succumb to manipulation by oomycete pathogens. His group is part of a collaboration to sequence and analyze the *H. arabidopsidis* genome. Another area of emphasis is secreted effector proteins and their targets inside plant cells.



head of the Department of Plant Biochemistry, Center for Plant Molecular Biology, at the University of Tübingen, Tübingen, Germany. In 1991, he received his Ph.D. degree in biochemistry from the University of Halle-Wittenberg and, from 1991 to 1994, did postdoctoral research at the Max-Planck-Institute of Plant Breeding, Cologne, Germany, with **K. Hahlbrock**. In

Thorsten Nürnberger is the

Thorsten Nürnberger

1995, he continued his research at the Centre National de la Recherche Scientifique, Gif-sur-Yvette, France, with **J. Guern**. From 1996 to 2003, he was a scientific

group leader at the Institute of Plant Biochemistry, Halle, Germany. In 2003, he became a full professor at the University of Tübingen, Center for Plant Molecular Biology, Faculty of Chemistry and Pharmacy. Nürnberger's research interests include the identification/characterization of pathogen-associated patterns and their cognate pattern recognition receptors in plants, the functional analysis of bacterial and oomycete virulence factors, and the characterization of immunity-associated plant cell death. He has served as an associate editor of *MPMI*, *Planta*, and *The Plant Journal* and as a senior editor of *Molecular Plant Pathology*.



Uta Paszkowski is an assistant professor in the Department of Plant Molecular Biology at the University of Lausanne, Lausanne, Switzerland. From the beginning of her scientific career, her research interest has revolved around plant interactions. She worked as a master's student with **Jeff Dangl** on the regulation of defense genes and received her Ph.D. degree from the ETH-Zurich, researching the use of viral

Uta Paszkowski

vectors for gene targeting in plants in the group of Ingo Potrykus. During her post-doctoral time, she started researching root interactions, in particular arbuscular mycorrhizal (AM) symbiosis. Using a fellowship from the Swiss National Science Foundation, she employed molecular genetics tools to investigate AM symbiosis in maize in the group of **Thomas Boller** at the University of Basel and later included rice for genomics approaches when employed as a staff scientist with Steve Briggs at the Torrey Mesa Research Institute in San Diego, California. At the University of Geneva, she established a research group to study the symbiotic root interactions of rice and maize and received the prestigious Swiss National Science Foundation assistant professor award to move to the University of Lausanne. She runs one of the very few labs that use cereal crops for the study of AM symbiosis. The present focus of her research team is the identification and characterization of plant factors essential for the development and functioning of AM symbiosis.



Silke Robatzek

senescence. She then moved to Basel, Switzerland, and did her post-doctoral research at the Friedrich Miescher Institute for Biomedical Research (Novartis Foundation) on flagellin sensing and FLS2. She

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Silke Robatzek studied biology in

initially worked on plant physiology

biosynthesis. For her Ph.D. research,

Institut für Züchtungsforschung in

Cologne, Germany, and addressed

the role of WRKY transcription

factors during plant defense and

Göttingen, Germany, where she

with a focus on gibberellin

she joined the Department of Phytopathology at the Max-Planck-

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continued her research on FLS2 at the Botanical Institute, University of Basel, where she discovered flagellinmediated endocytosis of FLS2. Robatzek rejoined the Max-Planck Institute in 2005 and she set up her own research group focusing on microbe-induced signaling and endocytosis in *Arabidopsis*. Her research is also supported by the SFB670 Cell-Autonomous Immunity, SPP1212 Plant-Micro, and ERA-PG PROSIG initiatives. In 2009, she took a group leader position at the Sainsbury Laboratory in Norwich, United Kingdom, and is studying the dynamics of membrane trafficking in plant immunity. "If we are to understand plant-microbe interactions, we need to investigate the associated subcellular adaptations at the molecular level."



Dominique Roby

Dominique Roby is a principal researcher at the Plant-Microbe Interaction Laboratory (LIPM, INRA-CNRS) in Toulouse, France, and the director of the Federative Research Institute (IFR40) "Agrobiosciences, Interactions, Biodiversity," which associates the principal research strengths in Toulouse in the fields of plant biology and molecular ecology. She obtained her Ph.D. degree in plant pathology at the University

Paul Sabatier of Toulouse in 1982, working on plant defense responses to fungal pathogens. She moved to the Department of Biological Sciences at Rutgers University, where she investigated the transcriptional regulation of defense genes in bean in response to different pathogens. She continued this work as a visiting scientist at the experimental station of DuPont de Nemours in the Department of Agricultural Products in Wilmington, DE, in the lab of **Rich Broglie**. She is currently heading a team at the LIPM, working on resistance of plants to pathogens and more specifically on the transcriptional control of the hypersensitive response in *Arabidopsis* and the genetic basis of quantitative resistance to bacterial pathogens. She has recently been on the Editorial Board of *Molecular Plant Pathology*.



Michael J. Sadowsky is the director of the BioTechnology Institute and Distinguished McKnight University Professor, Department of Soil, Water and Climate at the University of Minnesota, St. Paul. Sadowsky studied at the Department of Bacteriology at the University of Wisconsin-Madison and received his Ph.D. degree in microbiology from the University of Hawaii in 1983. Between 1983 and 1985, he did post-

doctoral research at the McGill University in the plantmicrobe interactions group of the Plant Molecular Biology Laboratory. He worked shortly for Allied Corporation as a molecular biologist and then worked for four years with the U.S. Department of Agriculture in Beltsville, Maryland, in the Nitrogen Fixation and Soybean Genetics Laboratory. In 1989, he joined the faculty at the University of Minnesota, where he is currently a professor in two departments and a member of seven graduate faculties. In addition to his teaching and research efforts, Sadowsky is the director of graduate studies for the microbial ecology program. He was an editor of the journal Applied and Environmental Microbiology (where he has served on the Editorial Board for 17 years) and is also an Editorial Board member of the journals Symbiosis and Microbes and Environments. He has authored or coauthored more than 145 articles in scientific journals and books and was elected fellow of the American Academy of Microbiology in 1999. His research efforts are directed toward the identification and examination of bacterial genes involved in the early periods of legume-microbe symbioses. His laboratory has been using genome sequencing and transcriptomic approaches to study Rhizobium and Bradyrbizobium genes that play a prominent role in host/ microbe recognition, stress survival, and the establishment of symbiotic, nitrogen-fixing nodules. His laboratory also uses metagenomic approaches to study microbial diversity in soils, water, and human intestinal systems and is involved in the identification and characterization of bacterial genes and metabolic pathways involved in the biodegradation of chlorinated herbicides, such as atrazine, using recombinant DNA methodologies. He and his collaborators have cloned all the genes involved in the atrazine biodegradation pathway and have sequenced whole catabolic plasmids and genomes of atrazinedegrading bacteria. His laboratory uses PCR, microarrays, combinatorial DNA methodologies, genomics, and other recombinant DNA techniques to investigate the ecology of atrazine-degrading microorganisms in soil, the regulation of gene expression, and the evolution of atrazine-degradation genes. He has explored the use of purified enzymes, as well as transgenic bacteria and plants, to bioremediate atrazine-contaminated soils and water. Lastly, research in his laboratory is directed toward the development and evaluation of technologies to determine sources of fecal pollution in waterways. He is using DNA fingerprinting, QPCR, and DNA hybridization techniques to examine large populations of Escherichia coli to determine which animal sources are contributing to the fecal loading of critical rural and urban streams, lakes, and rivers. He has also developed high-throughput, robotassisted methods to determine virulence gene profiles of E. coli from water and beach sand. He has been examining alternate sources and sinks of E. coli and waterborne pathogens in the environment and microbial ecological factors leading to the establishment and persistence of these populations in soils and sands and in birds and coldblooded animals.



Ken Shirasu

Norwich, United Kingdom, as a researcher and in 2000 became group leader of the laboratory. He joined the RIKEN Plant Science Center, Yokohama City, Kanagawa, Japan, as group director in 2005 and, since 2008, has also held the position of visiting professor of the Department of Biological Sciences at the University of Tokyo. He is interested in understanding the molecular mechanisms of plant immunity.

Ken Shirasu graduated from

the Department of Agricultural

of California-Davis in 1993. He

then served as a Salk-Noble post-

of the late **Chris Lamb** at the Salk

Institute, La Jolla, California, where

he studied plant immunity. In 1996,

he joined the Sainsbury Laboratory,

Geert Smant obtained an M.Sc.

degree in plant pathology in 1994

and a Ph.D. degree in agricultural

sciences in 1998 from Wageningen

University in the Netherlands. In

2000, he received a prestigious

Vidi grant from the Netherlands

to start his own group at the

Laboratory of Nematology at

Organization for Scientific Research

doctoral fellow in the laboratory

Chemistry of the University of Tokyo

in 1988 and was awarded his Ph.D.

degree in genetics at the University



Wageningen University. His group Geert Smant has focused on the molecular aspects of cyst and root-knot nematode interactions on solanaceous host plants with a particular emphasis on the role of nematode secretions in host invasion and feeding site formation. Smant discovered the first endosymbiontindependent production of cell wall-degrading enzymes in animals. Cyst and root-knot nematodes use cell walldegrading enzymes to invade the host. The unexpectedly high similarity of these cell wall-degrading enzymes with homologous genes in soilborne and plant-pathogenic bacteria could point to a role for horizontal gene transfer in the evolution of parasitism in nematodes, which is now one of the focal points of the group. Following host invasion, cyst and root-knot nematodes transform host

cells into an elaborate multinucleate feeding site on which they can feed for several weeks without eliciting a massive immune response in the plant. Smant's group is also studying how nematodes use their effectors to modulate innate immunity in plants, including possible parallels with animal-nematode interactions. Smant is currently one of the coordinators of the European Community's integrated project BIOEXPLOIT on molecular breeding disease resistance in potato and wheat involving 68 research labs from all over Europe. In addition to his research projects, Smant teaches several courses in plant pathology and animal parasitology at Wageningen University.



Krzysztof Szczyglowski received his Ph.D. degree in 1989 from the Institute of Bioorganic Chemistry, Polish Academy of Sciences, where he studied nitrogen-fixing root symbiosis with Andrzej Legocki. In 1990, he was the recipient of a long-term Max-Planck Fellowship in Jeff Schell's department at the Max-Planck Institute for Plant Genetics in Cologne, Germany. In 1991, Szczyglowski assumed a position

Krzysztof Szczyglowski

as senior post-doctoral research associate in Frans **deBruijn**'s laboratory in the Department of Energy-Plant Research Laboratory at Michigan State University and, in 1996, as research assistant professor position (nontenure) in the same department. In 2000, he moved to his current position as a research scientist at Agriculture and Agri-Food Canada, where his work focuses on understanding how plant regulatory pathways are modified in response to Rhizobium signaling in order to house the bacteria and establish a functional root symbiosis. Using Lotus *japonicus* as an experimental organism, his group has been studying the genetic determinants of nitrogen-fixing symbiosis by performing functional analyses of the host plant genome. Complementary work on selected aspects of root development in Szczyglowski's laboratory aims at contributing to basic knowledge of the regulatory circuits that govern root plasticity, an important agronomic trait. Szczyglowski is also an adjunct professor in the Department of Biology at the University of Western Ontario.

SAVE THE DATE!

XV International Congress on Molecular Plant-Microbe Interactions

August 2-6, 2011 Kyoto, Japan www.ismpminet.org/meetings





IS-MPMI Social Media Survey Results

Thank you to all IS-MPMI members who recently took the survey regarding social media. It was interesting to gauge the various opinions regarding these new communications tools. Through the survey, we learned that the majority of IS-MPMI members are aware of social media and have used one or more online social media outlets. Many members see promise in the use of social media and its use by the society; while others expressed concern regarding these tools. There was an excellent response to the survey, with a diverse range of members responding to the survey.

Fifty percent of respondents said they were somewhat familiar or familiar with the tools; 8.5% of respondents said they were very familiar with social media. Almost 40% of respondents claimed they were not at all familiar with social media.

Of those tools members were aware of, Facebook, MySpace, Twitter, and YouTube were the best known. Forty-three percent of respondents said they are active on Facebook.

And while 60% of respondents said they were aware of Twitter, only 22% have tried it. Almost half of respondents were not aware that IS-MPMI had a Facebook group, and 63% were not aware IS-MPMI had a Twitter page. Less than 3% of respondents were participating in either. The majority of members responding felt they would like to see association information delivered via Facebook. Only 11% of respondents felt that social media would not become a key communications activity, and only 17% felt that social media would not allow IS-MPMI to add value to member interactions. Forty percent felt that social media give members the opportunity to converse with their society and people in their industry.

Suggestions from members included the addition of more outlets such as LinkedIn. Members also noted their appreciation for the society's use of social media,

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http://twitter.com/ismpmi

as it provides another opportunity for members to connect with their colleagues. A few members suggested posting job opportunities via social media. As a direct result, you will now find the latest job postings sent via IS-MPMI's Twitter page. Members also expressed concerns such as privacy, not being able to access such sites at work, and how social media will only add to the bombardment of information members already experience.

www.facebook.com/group.php?gid=185915680283 Members responding to the survey ranged widely in age and location, with 33% of respondents ages 25-34 and the rest equally distributed among other age ranges. Forty-six percent of respondents were from Europe, with 37% from the United States/Canada. Asia was the next highest represented area, with 11%, and the remaining 6% were from Africa, Oceania, and South America/Caribbean. The majority of respondents were from academia, with government and students the next highest groups represented.

> Given the anticipated growth and use of these tools by membership.

IS-MPMI will continue to utilize social media outlets but will keep in mind the concerns brought forward, as well the suggestions for additional activity. It is difficult to ignore the popularity of these tools and how they have reached into professional and academic lives. In addition, a small society like IS-MPMI should be prudent when deciding on additional opportunities to reach members; the no-cost aspect of these tools is an important consideration. Finally, social media is an excellent extension of the international aspect of IS-MPMImembers from around the world can share and receive notices instantly for free.

To view the IS-MPMI Facebook Group, visit www.facebook.com/group.php?gid=185915680283. To view the IS-MPMI Twitter page, visit http://twitter.com/ismpmi.



Do You Twitter?

If so, we'd like to follow you! Please send your twitter name to **kdeuschle@scisoc.org** so we can add you to our list. Then check out our follow list to get connected with others tweeting about molecular plant-microbe interactions!

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Meet IS-MPMI Members

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, the *IS-MPMI Reporter* includes profiles of randomly chosen members at different career stages.



Student Member

Wanessa Wight

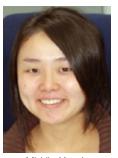
Department of Energy Plant Research Laboratory Michigan State University East Lansing, MI, U.S.A.

I am currently in my fourth year as a Ph.D. student in the Cell and Molecular Biology Program at Michigan State University (MSU). I

must admit that I was a bit of a late-comer to science. The first degree that I earned was a B.S. degree in psychology from MSU in 1999. After working in the "real" world for a couple of years, I decided that I was unsatisfied with my career choice and chose to return to school in 2002 in order to pursue a degree in a vastly different fieldhorticulture. I earned my second degree, a B.S. degree in horticulture, from MSU in 2004. While working on my horticulture degree, I interned for the Wheat Breeding Program in the Crops and Soil Sciences Department under the supervision of Richard Ward. I assisted in scoring plants for disease, harvesting, and data entry. It was at that time that I was first exposed to and became interested in plant diseases and their importance on agricultural crops. After completing that internship, I worked on an independent undergraduate project in Andreas Weber's lab in the Plant Biology Department, researching the limiting factors of nitrate reduction. This was my first real experience in a lab setting and I loved it! I immediately realized that I wanted to combine my interests in plant pathogens and molecular biology to pursue a third degree.

In 2005, I joined the U.S. Department of Energy Plant Research Laboratory (DOE-PRL) through the Cell and Molecular Biology Ph.D. Program at MSU. I joined **Jonathan Walton**'s lab in the spring of 2006. The Walton group has a number of interests, ranging from cellulosic ethanol to poisonous mushrooms to microbial secondary metabolites. I am currently researching the role of histone deacetylase inhibitors as virulence factors. More specifically, I am investigating the role and biosynthesis of depudecin, a polyketide with histone deacetylase inhibition activity, from the necrotrophic fungal plant pathogen *Alternaria brassicicola*.

I joined IS-MPMI in 2007 as a way to get to know others in the field and to keep up-to-date with the most recent progress that is applicable to my research and interests. I am looking forward to attending the next meeting and to meeting many new people with similar research interests.



Post-Doctoral/Early Career Member

Michiko Yasuda Saitama University Saitama, Japan

I completed my Ph.D. degree at Saitama University, Saitama, Japan, in the laboratory of **Shigeo Yoshida**, who had a laboratory in the RIKEN Wako campus

Michiko Yasuda

and worked on signal perception and biosynthetic mechanism of brassinosteroids. I have been interested in induced resistance of plants because it is a very smart system to survive surrounded by various pathogens. The fact that plant activators have been used in Japanese rice paddy fields for 30 years to induce systemic acquired resistance is another reason why I began research in this field.

First, I have characterized the mode of action of several plant activators. Then, the exciting progress in brassinosteroid research gave me a chance to study its function in disease resistance mechanisms. A specific inhibitor of brassinosteroid biosynthesis, newly developed by **Tadao Asami**, was a useful tool for chemical biology research, which I applied to confirm the requirement of brassinosteroid in the disease resistance. I enjoyed the research atmosphere at the RIKEN Wako campus that contains various departments from physics to chemistry to biology, with equipment from a cycrotoron to brain research to greenhouses.

After completing my Ph.D. degree, I started postdoctoral research in the laboratory of Hideo Nakashita at RIKEN. I started the research project focused on the regulation mechanisms of systemic acquired resistance. In the practical fields, plant activators sometimes fail to protect crops from pathogens under some specific environmental conditions. I applied chemical biology techniques to analyze relationships between salicylic acid-mediated signal transduction and other hormonal signaling pathways. Using different types of plant activators and specific inhibitors for plant hormone-mediated signal transduction, I contributed to clarifying the antagonistic interaction between systemic acquired resistance and abscisic acid-mediated abiotic stress response. There are multiple crosstalk points between salicylic acid- and abscisic acid-mediated signaling pathways, which are in biosynthesis and signal perception of plant hormones. Considering the interaction with jasmonic acid-mediated signaling pathway, three-sided antagonistic interactions among

Meet IS-MPMI Members continued on page 12

Meet IS-MPMI Members continued from page 11

plant hormone-mediated signaling appear to function in the regulation of responses to exogenous biotic and abiotic stresses. As a result of this work, I became interested in the network of plant hormone signaling, controlling plant physiological systems ability to survive in the environment that continuously changes.

I am currently working as a post-doctoral researcher in the laboratory of **Satoshi Shinozaki** and Nakashita at RIKEN. The laboratory focuses on the mechanism of induced resistance and the development of the practically effective control method of induced resistance. This is for the establishment of recently expected disease-control schemes, with less impact on environment and for safer food. I am continuing to study the detailed mechanism of the plant hormone network in the regulation of induced resistance. In the research group, I also enjoy the colleagueship with researchers working for practical projects.

I joined IS-MPMI in March 2007. The first international IS-MPMI Congress I attended was in Sorrento, Italy, where I presented a poster of my research concerning the antagonistic interaction between salicylic acidand abscisic acid-signaling pathways. It was a very nice experience to talk with researchers from various countries and to meet people of such excellent studies. I also enjoy the *MPMI* journal that broadens my knowledge in the field of plant-microbe interactions.



Early Career Member

Sen Subramanian Plant Science Department South Dakota State University Brookings, SD, U.S.A.

"They can live without us; but, we can't live without them" was a memorable quote I heard regarding microbes. Each day, more and more is discovered

Sen Subramanian

about the fascinating world of microbes, including their interactions with plants. My first major involvement in plant-microbe interaction research was at **Oliver Yu**'s lab at the Donald Danforth Plant Science Center in St. Louis, MO, where I began my post-doctoral research in 2002 to study the biosynthesis and role of flavonoids in plant-microbe interactions in soybean.

I began by examining the expression patterns of isoflavone synthase (IFS), a key enzyme responsible for the biosynthesis of isoflavones (a group of flavonoids mostly present in legumes). I was intrigued by the distinct, tissue-specific expression of this gene in response to symbiotic signals by *Bradyrhizobium japonicum* (a nitrogen-fixing rhizobium that colonizes and nodulates soybean roots) and pathogenic signals from *Phytophthora sojae* (an oomycete that causes soybean root rot). I proceeded to generate IFSsilenced roots to study the functional significance of isoflavones in these plant-microbe interactions. Loss of isoflavones in the roots resulted in what I call "double jeopardy." Not only did the IFS-silenced soybean roots became susceptible to P. sojae, but they also lost their ability to produce nodules when colonized by *B. jabonicum*. I was involved in two really valuable collaborations during this period: one with Gary Stacey at the University of Missouri, Columbia, to study the role of isoflavones in soybean nodulation and the other with Terry Graham at The Ohio State University, Columbus, to study the role of isoflavones in *P. sojae* interaction. Through these collaborations and other studies in the Yu lab, we discovered that different flavonoids play distinct critical roles in legume nodulation. In determinate nodule-producing legumes (such as soybean, peanut), they play an essential role as inducers of rhizobial nod gene expression inside the plant roots, and in indeterminate nodule-producing legumes (such as alfalfa, pea), they play an additional essential role as regulators of auxin transport. The more I learned about the intricacies of signal exchange, temporal and spatial control of gene expression, and cellular responses during legume nodulation, the more interested I became in studying and understanding them. In addition, due to the potential of legume nodulation in alleviating the use of chemical fertilizers, research on this fascinating plant-microbe interaction clearly has economic and environmental benefits. As a side note, I used transgenic hairy root composite plants and cotyledon hairy roots generated by yet another plant-microbe interaction (Agrobacterium rhizogenes capable of infecting a number of plants, mostly dicots). This rapid and efficient technique to produce transgenic roots was really handy to study root-microbe interactions.

Wanting to study the role of auxin transport inhibition and to identify additional components involved in signal transduction during legume nodule development, I proceeded to explore the role of microRNAs in this process. In collaboration with Jian-Kang Zhu (University of California, Riverside) and Brad Barbazuk (University of Florida, Gainesville), I identified a number of novel and nodulation-regulated microRNAs from soybean roots by high-throughput sequencing and analysis of a small RNA library. In April 2009, I joined the Plant Science Department of South Dakota State University (SDU), Brookings, as an assistant professor. My lab's primary research focuses on the "Silenceomics' of nodule development in legumes." My lab is studying the functional role of miRNAs involved in auxin signaling during legume nodule development. I am also responsible for team-teaching molecular plant physiology and plant-microbe interactions.

I decided to join IS-MPMI when I read several issues of *MPMI* to learn more about legume-rhizobia interactions during my post-doctoral work. In my mind, being a

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member of the society is the best way to interact and meet with a number of scientists with similar interests. Additionally, the society represents scientists from more than 30 countries and therefore makes you part of a large family of plant-microbe interaction scientists. The society also publishes *MPMI*, which is a great journal with a wide and interested readership. I am really proud of my membership in this valuable professional society.

My early introduction to plants was from our family farm managed by my grandfather. The significance of plant-microbe interactions was introduced to me by some enthusiastic undergraduate microbiology and plant pathology teachers in India in the early 1990s. During my master's studies under the supervision of M. Jayapragasam, my research was to study phenolic acid biosynthesis in a rice variety, Purple Puttu, that was used as a breeding source for pathogen resistance, presumably due to its highly inducible flavonoid biosynthesis pathway. It was a great experience since it taught me both the hardships, as well as the value, of scientific research. During my brief stint as a research assistant at University Putra Malaysia, I studied plantassociated microbes that provided protection against food pathogens in native fermented foods of Malaysia

in the labs of **Gulam Rusul** and **Son Radu**. This was when I learned about and got training in hands-on microbial isolation and culture. I moved to **Chris Rock**'s lab (then at Hong Kong University of Science and Technology) in 1998 to study ABA-signaling in *Arabidopsis* due to my interest in plant hormones. My Ph.D. training helped to hone my skills in experimental design, develop skills to interpret and troubleshoot, and most of all, present research results correctly and with clarity.

In the little free time I get while establishing a new lab, recruiting students, and managing a family, I have taken to golfing and tennis in the short but beautiful summer that we have here in South Dakota. I also enjoy camping and canoeing and like to watch baseball and cricket (an English sport popular in commowealth nations). I take great pleasure in educating the general public about plant science and biotechnology, an interest cultivated in me through my participation in outreach activities by the Danforth Center and the American Society of Plant Biologists. I founded and maintain a website, www.knowplants.org, which has links to plant science resources and games for kids, including one that was developed by me and my friends.

Celebrating a Milestone

For 20 years, IS-MPMI has been bringing people together through the sharing of research and new ideas. As our community continues to grow, please invite your colleagues to become part of IS-MPMI and experience the premier science and connections to scientists worldwide. Tell your colleagues to visit www.ismpminet.org/members/ join.asp to learn more about the benefits of membership and download an application.

1990-2010

Here's to another successful 20 years and more! Thank you for your continued support.

Interview with Gary Stacey continued from page 1

interest in understanding the role of extracellular ATP in plants, which we believe is an underexplored but critical signal in plant growth and development.

Q: When and why did you first join the society?

A: I joined the society in 1991 when it was still a very young organization. I believe that the society formed due to a growing realization that the various plant-microbe interactions had similarities. There was a feeling that a new organization would speed the development of our scientific understanding of plant-microbe interactions. I shared this view and, therefore, it was natural to become a member. I also saw value in the biennial symposia; the society was a clear mechanism to support their continuation.

Q: Do you think it is important that Ph.D. and post-doc students in your lab are IS-MPMI members? What can/ should IS-MPMI offer young scientists in our field?

A: Scientific societies provide a number of services to the scientific community, including those relevant to young scientists. Of course, it is important to support the society's journal, MPMI, which has grown through the years to be a premier journal for research in our area. Given the rising costs of publishing and the rapidly changing industry of publishing, it is more important than ever to maintain society journals that are, on average, significantly less expensive. I think all of our Ph.D. students and post-doctoral associates realize the difficult current job market. Hence, networking with your colleagues is now more important than ever. The biennial meetings and interactions through the society are excellent ways to build the networks and friendships that will last a lifetime. Clearly, in my case, I have greatly benefited from the friendships, collaborations, and casual interactions that have occurred through IS-MPMI activities through the years. The society should continue to expand its activities to reach out to young scientists, support their professional development, and aid them as they move from student to post-doc to professional scientist.

Q: What first attracted you to the field of plant-microbe interactions?

A: I was attracted to the field through my interest in symbiotic nitrogen fixation. This research system has now held my interest for more than three decades. I must admit, on occasion, I have thought it wise to move away from this area but the research results always pulled me back. There is still so much to learn. Perhaps the biggest development of this time period has been the realization that so many of the basic mechanisms of plant-microbe interactions are shared by the various biological systems. Hence, the impacts of earlier research using Agrobacterium and Rhizobium can easily be seen in current research on plant bacterial and fungal pathogens. What started as distinctly separate research fields has now clearly evolved into a more cohesive plant-microbe interactions discipline. IS-MPMI deserves some of the credit for this evolution.

Q: What/who has inspired you most in your career?

A: This is a difficult question for me to answer. With regard to "who," I certainly was inspired by my Ph.D. advisors, Bob Tabita and Chase Van Baalen; my postdoctoral advisor, Winston Brill; during my sabbatical, Jeff Schell; and many others through the years. I have been and continue to be blessed by having wonderful young scientists in my lab, as well as supportive colleagues. I am not sure I can answer the "what." I certainly have always enjoyed the personal interaction aspect of science. There is nothing I enjoy more than a good, heated scientific discussion. I will say that what excites me most about academic science is how it tests you at so many levels. To be successful, you need to be innovative and creative, a good writer and communicator, a good teacher and mentor, and also, a bit of a salesman. The challenge of responding to these kinds of pressures is what continues to drive me.

Q: What's the most exciting paper you read recently?

A: Schmutz,et al.'s paper (2010) that is now in press in *Nature*. This paper describes the sequencing of the complete soybean genome. It is the result of a community effort in which I was very active and took some years to accomplish. There were a variety of frustrations along the way with the funding agencies and efforts to build the community coalition. However, this all proved successful. Access to the complete soybean genome has already revolutionized our own research and is having a broad impact on plant science. We fully expect that it will also have a real impact on soybean as a crop.

Q: What is the next "big thing" in plant-microbe interactions?

A: There are always major "breakthroughs" on the horizon and I am likely not the best person to predict them. Therefore, I will be a bit "self-serving" here to bring up again the subject of the role of extracellular ATP (eATP) in plants. The role of eATP in signaling in animal cells is well established where eATP has been implicated in muscle contraction, inflammation, nerve function, and a variety of other situations. In contrast, research on the role of eATP in plants is just beginning. However, our data and that now being published by other labs suggest that eATP is essential for normal plant growth and development. It clearly plays a role in plant wounding and in plant-microbe interactions. I believe that the community will grow to realize the importance of eATP over the next few years.

Q: What's your favorite gene?

A: My favorite gene is always the one that I am currently trying to understand. For example, at present, I could say it is the Arabidopsis *LYK1* (*CERK1*) gene, which we cloned recently and encoded the plant receptor for chitin, a PAMP that induces resistance to fungal pathogens. However, there are other genes we are currently investigating in the lab that we hope will be equally interesting.

Q: What are your favorite activities outside of the lab?

A: I most enjoy being with family and friends. When I find the time, I enjoy fishing, as well as quiet time spent reading, etc. I also enjoy traveling, especially when my wife can come along.

A Letter from the President continued from page 1

of the attendees were students and post-docs) and many participants from developing countries. The presence of excellent, established scientists and young, motivated students from all over the world in IS-MPMI guarantees a bright future for the society.

The scientific content of our meetings has always been intense, reflecting the quality of the science performed by our people who continually produce a high number of publications in top journals. There is an expanding interest by the entire scientific community for our discipline, which is capable of not only tackling basic biological questions but also providing answers to solve emerging problems of crop productivity. It is vital that we continue to learn about the mechanisms governing plant interactions with beneficial microbes, as well as the mechanisms of pathogen recognition and plant responses to invading microorganisms. Our challenge is improving plant productivity and resistance and contributing to sustainable agriculture by developing an effective, durable, and environmentally sound control of crop diseases. Many members of this society are prefiguring possible roads to these goals and are developing sophisticated strategies for engineering broad-spectrum and durable, diseaseresistant crops. Among the many important contributions heard at the recent meetings, I would like to mention those aiming at deciphering the mechanisms of PAMPtriggered immunity, as well as those aiming at elucidating the activities of virulence effectors in important pathogens, such as Phytophthora infestans. I also want to mention the efforts of our colleagues working on genetically dissecting the pathways required for Rhizobium-plant symbiosis.

Q: What book are you reading these days?

A: Although I enjoy biographies and history, most of my reading lately has been fiction. I just completed *The Confessor*, the last in the *Sword of Truth* book series by Terry Goodkind.

Thus far, the tradition of the society has been to alternate the biannual meetings between North America and Europe, because the main group of IS-MPMI founders was mainly located on these two continents. Recently, our congresses have seen an increasing and qualified participation of colleagues from Asian countries, including Japan, China, Korea, and India. This participation is expected to grow in the future due to the new economic scenarios of the world. The scientific strength and the growing impact of the contributions of our colleagues from Asia clearly emerged during the Québec meeting. There, the Japanese delegation offered to organize the next congress of 2011 in Kyoto; the Board of Directors was very pleased to accept the proposal. I am sure that the Kyoto meeting will be another milestone in the successful life of the society in terms of scientific output and participation of delegates. New possibilities of interactions between our scientists will open and the development of new technologies that are necessary in our field and are a key of its success will be promoted. By doing so, we hope to contribute to an accelerated exit from the economic/ food crisis. By the measure of other scientific societies, IS-MPMI is still quite young. However, like the science studied by its members, it is evolving. Members are invited to help develop the society and position it for the future through contributing to the *IS-MPMI Reporter*, becoming a board member, or publishing with MPMI. We celebrate this milestone together and hope for another successful 20 vears!

Asian Conference on Plant-Microbe Symbiosis and Nitrogen Fixation

The 1st Asian Conference on Plant-Microbe Symbiosis and Nitrogen Fixation will be held in Miyazaki, Japan, September 20–24, 2010. In Asian countries, many works have been developed on plant-microbe symbiosis, including excellent basic research and its applications. Thus, this conference is organized so that attendees can enjoy their science and friendly communication with microbiologists, plant molecular biologists, and agronomists. In particular, young Asian scientists should be encouraged to attend the conference. The conference is open for scientists not only from Asian countries but from all over the world. Topics will include plant-microbe signaling, bioresource and genomics, nonleguminous associations, nitrogen fixation and nitrogen cycles, legume-*Rhizobium* symbiosis, and applications for sustainable agriculture and environments. The conference will be held at the Aoshima Palm Beach Hotel, which is located on the center of Miyazaki Aoshima resort and close to the seashore. Registration will open soon. For more information, please visit www.brc.miyazaki-u.ac.jp/apmnf or contact apmnf@cc.miyazaki-u.ac.jp.

Recently published research in Molecular Plant-Microbe Interactions

Find complete abstracts online with links to full-text articles at http://apsjournals.apsnet.org/loi/mpmi

November 2009, Volume 22, Number 11

A Comprehensive Transcriptomic Analysis of the Effect of Silicon on Wheat Plants Under Control and Pathogen Stress Conditions.

AGB1 and PMR5 Contribute to PEN2-Mediated Preinvasion Resistance to *Magnaporthe oryzae* in *Arabidopsis thaliana*.

Pseudomonas syringae pv. *tomato* DC3000 Type III Effector HopAA1-1 Functions Redundantly with Chlorosis-Promoting Factor PSPTO4723 to Produce Bacterial Speck Lesions in Host Tomato.

Agrobacterium-Mediated T-DNA Transfer and Integration by Minimal VirD2 Consisting of the Relaxase Domain and a Type IV Secretion System Translocation Signal.

Transcriptome Analysis of a Wheat Near-Isogenic Line Pair Carrying Fusarium Head Blight–Resistant and –Susceptible Alleles.

The Two Conserved Cysteine Residues of the Triple Gene Block Protein 2 Are Critical for Both Cell-to-Cell and Systemic Movement of *Bamboo mosaic virus*.

The Pepper Calmodulin Gene *CaCaM1* Is Involved in Reactive Oxygen Species and Nitric Oxide Generation Required for Cell Death and the Defense Response.

Identification of Six Type III Effector Genes with the PIP Box in *Xanthomonas campestris* pv. *campestris* and Five of Them Contribute Individually to Full Pathogenicity.

SOD1-Targeted Gene Disruption in the Ericoid Mycorrhizal Fungus *Oidiodendron maius* Reduces Conidiation and the Capacity for Mycorrhization.

Genetic Analysis of the *rkp-3* Gene Region in *Sinorhizobium meliloti* 41: *rkpY* Directs Capsular Polysaccharide Synthesis to K_p5 Antigen Production.

Transcriptional Changes and Oxidative Stress Associated with the Synergistic Interaction Between *Potato virus X* and *Potato virus Y* and Their Relationship with Symptom Expression.

The Absence of Nops Secretion in *Sinorhizobium fredii* HH103 Increases *GmPR1* Expression in Williams Soybean.

Hexanoic Acid-Induced Resistance Against *Botrytis cinerea* in Tomato Plants.

RNA Interference Highlights the Role of CCaMK in Dissemination of Endosymbionts in the Aeschynomeneae Legume *Arachis*.



December 2009, Volume 22, Number 12

MEETING REVIEW—Effectors, Effectors *et encore des* Effectors: The XIV International Congress on Molecular-Plant Microbe Interactions, Quebec.

Ammonium Secretion by *Colletotrichum coccodes* Activates Host NADPH Oxidase Activity Enhancing Host Cell Death and Fungal Virulence in Tomato Fruits.

Triacylglyceride Metabolism by *Fusarium graminearum* During Colonization and Sexual Development on Wheat.

Comparative Analysis of Expression Profiles in Shoots and Roots of Tomato Systemically Infected by *Tomato spotted wilt virus* Reveals Organ-Specific Transcriptional Responses.

The Transcriptional Activator *rfiA* Is Quorum-Sensing Regulated by Cotranscription with the *luxI* Homolog *pcoI* and Is Essential for Plant Virulence in *Pseudomonas corrugata*.

Plastocyanin Transit Peptide Interacts with *Potato virus X* Coat Protein, While Silencing of Plastocyanin Reduces Coat Protein Accumulation in Chloroplasts and Symptom Severity in Host Plants.

Phytophthora infestans Isolates Lacking Class I *ipiO* Variants Are Virulent on *Rpi-blb1* Potato.

Nodulation Gene Mutants of *Mesorhizobium loti* R7A *nodZ* and *nolL* Mutants Have Host-Specific Phenotypes on *Lotus* spp.

Integration of Ethylene and Jasmonic Acid Signaling Pathways in the Expression of Maize Defense Protein Mir1-CP.

Carbon Metabolism and Bacteroid Functioning Are Involved in the Regulation of Nitrogen Fixation in *Medicago truncatula* Under Drought and Recovery.

The *Medicago truncatula N5* Gene Encoding a Root-Specific Lipid Transfer Protein Is Required for the Symbiotic Interaction with *Sinorbizobium meliloti*.

Novel Genes of *Fusarium graminearum* That Negatively Regulate Deoxynivalenol Production and Virulence.

Analysis of a *Blumeria graminis*-Secreted Lipase Reveals the Importance of Host Epicuticular Wax Components for Fungal Adhesion and Development.

Effect of Wheat Roots Infected with the Pathogenic Fungus *Gaeumannomyces graminis* var. *tritici* on Gene Expression of the Biocontrol Bacterium *Pseudomonas fluorescens* Pf29Arp. Confirmation of the Sequence of '*Candidatus* Liberibacter asiaticus' and Assessment of Microbial Diversity in Huanglongbing-Infected Citrus Phloem Using a Metagenomic Approach.

Overexpression of Rice (*Oryza sativa* L.) *OscDR1* Leads to Constitutive Activation of Defense Responses in Rice and *Arabidopsis*.

The *RAP1* Gene Confers Effective, Race-Specific Resistance to the Pea Aphid in *Medicago truncatula* Independent of the Hypersensitive Reaction.

Production of Succinoglycan Polymer in *Sinorhizobium meliloti* Is Affected by SMb21506 and Requires the N-terminal Domain of ExoP.

January 2010, Volume 23, Number 1

SPOTLIGHT—Biology of Maize Kernel Infection by *Fusarium verticillioides*.

Discriminating Mutations of HC-Pro of *Zucchini yellow mosaic virus* with Differential Effects on Small RNA Pathways Involved in Viral Pathogenicity and Symptom Development.

Single Nucleotide Polymorphisms in a Gene for Translation Initiation Factor (eIF4G) of Rice (*Oryza sativa*) Associated with Resistance to *Rice tungro spherical virus*.

Systemic Induction and Role of Mitochondrial Alternative Oxidase and Nitric Oxide in a Compatible Tomato– *Tobacco mosaic virus* Interaction.

The AvrM Effector from Flax Rust Has a Structured C-Terminal Domain and Interacts Directly with the M Resistance Protein.

Improved Characterization of Nod Factors and Genetically Based Variation in LysM Receptor Domains Identify Amino Acids Expendable for Nod Factor Recognition in *Lotus* spp.

Erl1, a Novel Era-Like GTPase from *Magnaporthe oryzae*, Is Required for Full Root Virulence and Is Conserved in the Mutualistic Symbiont *Glomus intraradices*.

Altering Expression of *Benzoic Acid/Salicylic Acid Carboxyl Methyltransferase 1* Compromises Systemic Acquired Resistance and PAMP-Triggered Immunity in *Arabidopsis*. Basal Host Resistance of Barley to Powdery Mildew: Connecting Quantitative Trait Loci and Candidate Genes.

A Kelch Repeat Protein, Cokel1p, Associates with Microtubules and Is Involved in Appressorium Development in *Colletotrichum orbiculare*.

A Novel Protein Com1 Is Required for Normal Conidium Morphology and Full Virulence in *Magnaporthe oryzae*.

The Type III–Secreted Protein NopE1 Affects Symbiosis and Exhibits a Calcium-Dependent Autocleavage Activity.

February 2010, Volume 23, Number 2

TECHNICAL ADVANCE—*Arabidopsis thaliana* Cells: A Model to Evaluate the Virulence of *Pectobacterium carotovorum*.

The P3 Protein of *Turnip mosaic virus* Can Alone Induce Hypersensitive Response-Like Cell Death in *Arabidopsis thaliana* Carrying *TuNI*.

Sinorbizobium meliloti 1021 Loss-of-Function Deletion Mutation in *chvI* and Its Phenotypic Characteristics.

Streptomyces scabies 87-22 Contains a Coronafacic Acid-Like Biosynthetic Cluster That Contributes to Plant– Microbe Interactions.

Overexpression of a Redox-Regulated Cutinase Gene, *MfCUT1*, Increases Virulence of the Brown Rot Pathogen *Monilinia fructicola* on *Prunus* spp.

Ethylene Signaling Renders the Jasmonate Response of *Arabidopsis* Insensitive to Future Suppression by Salicylic Acid.

Pseudomonas syringae Strains Naturally Lacking the Classical *P. syringae brp/brc* Locus Are Common Leaf Colonizers Equipped with an Atypical Type III Secretion System.

Regulation of *Ustilago maydis* Dimorphism, Sporulation, and Pathogenic Development by a Transcription Factor with a Highly Conserved APSES Domain.

Identification and Functional Analysis of Type III Effector Proteins in *Mesorbizobium loti*.

Employment

Post-Doctoral Position Available in Fungal Genomics A position is available for a highly motivated and skilled post-doctoral fellow to take a lead role in work that involves genome resequencing, genome annotation, and gene mapping for the ascomycete fungus Grosmannia clavigera and related species. The work will include characterizing and comparing transcriptomes. G. clavigera is a bark beetle-associated fungus that is responsible for tree mortality in the large mountain pine beetle epidemic that has recently destroyed more than 14 M hectares of pine forests in western Canada. In a collaboration between the University of British Columbia Michael Smith Laboratories (www.michaelsmith.ubc.ca), the Faculty of Forestry (www.forestry.ubc.ca), and the BC Cancer Agency Genome Sciences Centre (www.bcgsc.ca), we have used an approach that combines Sanger, 454, and Illumina sequencing to generate a draft reference genome sequence and transcriptome sequences for G. clavigera (DiGuistini et al., 2009. De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. Genome Biol. 2009-10-9-r94). The position requires demonstrated experience with sequencing technology (Sanger/Illumina), sequence annotation, computational gene expression analysis with Illumina reads, basic programming, and molecular biochemistry. In addition, the candidate should have excellent written and oral communication skills in English. The project is funded in part by Genome Canada and Genomes British Columbia/Alberta (www.genomebc.ca). The position is available immediately and is initially for one year, with possibilities of renewal for subsequent years. Please send a letter of application with a CV and provide two to three reference letters to Kyeema Burns, project director (www. thetriaproject.ca). Contact: Kyeema Burns, Michael Smith Laboratories, University of British Columbia, 301-2185 East Mall, Vancouver, BC V6T 1Z4, Canada. E-mail: kyeema@ interchange.ubc.ca.

Research Molecular Biologist/Research Plant Pathologist (Research Associate)

The USDA, Agricultural Research Service, Hard Winter Wheat Genetics Research Laboratory in Manhattan, Kansas, seeks a post-doctoral research associate for a two-year appointment. A Ph.D. degree in plant pathology, plant molecular biology, fungal genetics, or a closely related scientific discipline is required. The incumbent will use next generation sequencing to identify polymorphisms in secreted peptides of the wheat leaf rust pathogen, Puccinia triticina Eriks., as a method to identify avirulence factors. Using an association mapping type approach, the incumbent will develop a panel of PCR primers and screen rust races that differ in virulence. Candidate factors will be evaluated using transient expression in leaves of wheat isolines that contain different leaf rust resistance genes. Knowledge of bioinformatics, DNA isolation and cloning, PCR, microbial culture, and genetics is desirable. A comprehensive benefits package includes paid sick leave and annual leave, life and health

insurance, a savings and investment plan (401K type), and a federal retirement plan. Refer to www.afm.ars. usda.gov/divisions/hrd/hrdhomepage/vacancy/pd962. html for further information on post-doctoral research associate jobs, complete application instructions, and the full announcement (RA-10-035-H). Send application materials and references to John Fellers. Applications must be marked RA-10-035-H and postmarked by 11:59 p.m. on February 28, 2010. Citizen restrictions apply. USDA/ ARS is an equal opportunity employer and provider. Salary: \$56,411-67,613 per annum. Contact: John Fellers, USDA/ARS, Hard Winter Wheat Genetics Research Unit, 4006 Throckmorton Hall, Department of Plant Pathology, Manhattan, KS 66506, U.S.A. E-mail: John.Fellers@ars. usda.gov; Web: www.afm.ars.usda.gov/divisions/hrd/ hrdhomepage/vacancy/pd962.html.

Excellence in Plant Molecular Biology/Biotechnology Graduate Fellowship Program at OSU

The Plant Molecular Biology/Biotechnology (PMBB) program at The Ohio State University (OSU)is being dramatically expanded as a Targeted Investment for Excellence initiative by OSU. PMBB is an interdisciplinary group that includes faculty members from the Colleges of Biological Sciences and Food, Agriculture and Environmental Sciences. PMBB research programs conduct molecular studies on the cutting edge of plant science, including plant development, plant signaling, plant metabolic engineering, photosynthesis biochemistry, and plant-pathogen interactions. For the fourth straight year, PMBB invites outstanding students seeking to earn a Ph.D. degree in plant science from any of the participating graduate programs at OSU to apply for Excellence in Plant Molecular Biology/Biotechnology Graduate Fellowships. The fellowships provide up to four years of support, including stipend (\$25K/year), full benefits, tuition and fee waivers, and travel opportunities. Application instructions and detailed information, including a directory of PMBB faculty and participating graduate programs, is available at www.ag.ohio-state.edu/~pmbb. Ohio encourages applications from individuals with disabilities, minorities, veterans, and women, EEO/AA. Closing Date: February 21, 2010.

Research Scientist Position at OSU

The Kottman Hall Translational Plant Sciences (KH-TPS) laboratory is a core research facility of The Ohio State University (OSU) and seeks applicants for a research scientist with strong expertise in bioinformatics. The successful candidate will supervise and coordinate all core laboratory activities, including the use and maintenance of a range of analytical and molecular biology equipment, and user training and assistance. Main duties will include providing bioinformatics support and implementing new computational tools for genomics, proteomics, and metabolomics research. The scientist will be responsible for maintaining the laboratory operating budget and for facilitating the acquisition of extramural funds for new

equipment, facility maintenance, and improvement. He/she will conduct collaborative research in the bioinformatics area, advise faculty, and train students in data analysis and interpretation and will contribute to project development with faculty, including grant proposal preparation. Requirements: Ph.D. degree in plant biology, bioinformatics, biochemistry, molecular biology, or related discipline and demonstrated expertise in bioinformatics, genomics, biochemistry, or molecular biology, including knowledge of computational tools required for genetic database searches, genome annotations, whole genome comparisons, and large data set analyses. Must be familiar with Linux, with at least one of the scripting languages, such as Perl, C, C++, Java, or Python, and with MySQL databases. Post-doctoral experience is highly desirable. Contact: Tea Meulia. E-mail: meulia.1@osu.edu; Web: http://jobs.osu.edu.

COMING EVENTS 2010

March 14-19 Receptors and Signaling in Plant Development and Biotic Interactions Tahoe City, California, U.S.A. www.keystonesymposia. org/meetings

March 21-26 **Plasmodesmata 2010—Seventh International Conference** Sydney, Australia www.bio.usyd.edu.au/ pd2010/index.html

April 18-22 Fifth EPSO Conference Olos (Lapland), Finland www.epsoweb.org

June 6-8 Oomycete Molecular Genetics Network Meeting Toulouse, France www.polebio.scsv.ups-tlse. fr/OMGN2010/index.htm

July 4-9 XVII Congress of the Federation of the

Federation of the European Societies of Plant Biology (FESB) Valencia, Spain www.geyseco.es/fespb

July 24-28 International Conference on Plant Vascular Biology 2010 Columbus, OH, U.S.A. www.ced.osu.edu/

pvb2010conference

August 7-11 **The American Phytopathological Society Annual Meeting** Nashville,TN, U.S.A. http://meeting.apsnet.org



Include your meeting in IS-MPMI's printed and online event calendar. Submit online at www.ismpminet.org/meetings/calsubmit.asp

Effectome—A French Network Aimed at the Study of Plant Pathogen Effectors



Left to right, (inset) Sebastien Duplessis, Nemo Peeters, Thomas Kroj, Boris Szurek, and Marie-Noelle Rosso.

The Effectome Network held its second meeting in Montpellier, France, November 3–5, 2009. The Effectome Network (www.effectome.org) was initiated one year ago with the aim of sharing resources and forging collaborations in the field of pathogen effector research. The network comprises more than 80 researchers from approximately 20 French research groups studying the molecular bases of microbial pathogenicity and plant disease in fungal, bacterial, oomycete, and nematode pathosystems. These pathogens use different means to translocate so-called effector molecules into host tissues and cells. There, effectors may lead to the suppression of host defenses and the maintenance of feeding structures that allow the withdrawal of nutrients. Alternatively, effectors might be recognized by the plant as nonself molecules and trigger host defenses. The fine tuning of the host-pathogen interplay and the adaptations of pathogens and plants in the evolutive arms race determine the success or failure of infection. The Effectome Network was created from the observation that understanding a given pathosystem at the molecular level generally leads to the study of the pathogen's effectors and their plant targets. Research groups studying diverse pathosystems end up using very similar approaches to understand the contribution of a given effector to pathogenicity and to assess the durability of new sustainable control methods.

This year's meeting took place in the charming Mediterranean atmosphere of southern France, where around 50 people gathered to share and discuss new findings concerning their favorite effectors. The Plant Health and the Environment Division of the French National Institute for Agricultural Research (INRA) and the French Society of Phytopathology made financial contributions, which enabled us to invite renowned speakers who presented their latest updates on effectors of mammalian pathogens, new high-throughput approaches in Arabidopsis and yeast, and the impact of structural biology and next-generation sequencing technologies on effector research.

The organizers and attendees are looking forward to next year's meeting. \blacksquare

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International Society for Molecular Plant-Microbe Interactions 3340 Pilot Knob Road St. Paul, MN 55121 United States of America

Welcome New Members

The following members joined IS-MPMI between September 1 and December 31, 2009. Please join us in welcoming them to the society!

Martine Batoux John Innes Centre Norwich, United Kingdom

Pier-Anne Belanger Univ de Sherbrooke Sherbrooke, QC, Canada

Leila M. Blackman Australian Natl Univ Canberra, ACT, Australia

Natacha Bodenhausen Univ of Chicago Chicago, IL, U.S.A.

Marie-Andree Chaine Univ de Sherbrooke Sherbrooke, QC, Canada

Emerson P. Crabill Univ of Nebraska Lincoln, NE, U.S.A.

Abdelaleim Elsayed Bayreuth Univ Bayreuth, Germany

Abdollah Fardin AB Ghobakhlou Univ Laval Quebec, QC, Canada

Ellen H. James Imperial College London London, United Kingdom **Brent N. Kaiser** Univ of Adelaide Glen Osmond, SA, Australia

Hong Gu Kang Boyce Thompson Inst for Plant Research Ithaca, NY, U.S.A.

Ki-Jeong Kim NIER Incheon, South Korea

Ksenia V. Krasileva Univ of California Berkeley, CA, U.S.A.

Jing Li Univ of Helsinki Helsinki, Finland

Alberto P. Macho Escribano Univ of Malaga Malaga, Spain

Cristina Micali Max-Planck Inst for Plant Breeding Res Cologne, Germany

Karolina Pajerowska-Mukhtar Duke Univ Durham, NC, U.S.A. **Vijayapalani Paramasivan** Iowa State Univ Ames, IA, U.S.A.

Mathieu Pel Wageningen Univ Wageningen, Netherlands

Andreja Preradov Univ Laval Quebec, QC, Canada

Feng Qu Ohio State Univ Wooster, OH, U.S.A.

Cecile Ribot UMR BGPI Montpellier, France

Dominique Roby CNRS/INRA Castanet Tolosan, France

Sebastian Schornack John Innes Centre Norwich, United Kingdom

Aswathy Sreedharan Univ of Florida Lake Alfred, FL, U.S.A.

David J. Studholme University of Exeter Exeter, United Kingdom Krzysztof Szczyglowski Agric & Agri-Food Canada London, ON, Canada

Nicholas J. Talbot Univ of Exeter Exeter, Devon, United Kingdom

Armin Toller Max-Planck-Inst for Plant Breeding Res Cologne, Germany

Corina Vlot Helmholtz Ctr for Env Res (Munich) Neuherberg, Germany

David Wendehenne Univ De Bourgogne INRA Dijon, France

Lirong Zeng Univ of Arkansas Little Rock, AR, U.S.A.