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Mark Your Calendar for the XV International Congress in Japan

Mark your calendar for the XV International Congress on Molecular Plant-Microbe Interactions! The congress will take place August 2–6, 2011, in Kyoto, Japan. Kyoto, which includes 17 UNESCO World Heritage Monuments, is rich with history, beautiful gardens, and cultural attractions. The congress draws world-renowned speakers and attendees from around the globe to discuss the latest technological advancements and industry achievements. More information will be available soon on IS-MPMI.net. ■

Conquering Conker Canker

David Studholme, Senior Lecturer, School of Biosciences, University of Exeter, United Kingdom, D. J. Studholme@exeter.ac.uk



David Studholme

Despite safety concerns ranging from eye injuries to anaphylactic shock in nut allergy sufferers, the game of conkers is thriving and the next World Conker Championship is scheduled for October 2010 in the picturesque English village of Ashton. For those readers outside of Britain, Ireland, and the former British colonies who are not familiar with the game, it is played with the seed (conker) of the horse chestnut tree (*Aesculus hippocastanum*) threaded onto a string. Basically, the objective is to smash the opponent's conker. Aside from the children's game, the purported uses of conkers have included prevention of piles and rheumatism and deterring spiders and moths. The latter is particularly ironic, given that the tree is currently suffering from an epidemic of horse chestnut leafminer (*Cameraria ohridella*) that has spread out from the London area since 2000. The horse chestnut is an iconic tree in the British landscape, commonly planted in public spaces and lining avenues. In the last few years, it has come under attack not just from the leafminer moths but also from fungal infection (*Guignardia aesculi*). Both the insect and the fungus cause very obvious symptoms on the foliage and have evoked concern in the general public, but the damage they cause to the tree is relatively superficial. Much more serious is a newly emerging bleeding canker disease, caused by the bacterium *Pseudomonas syringae* pv. *aesculi*, which may infect at least one in three British horse chestnut trees and is potentially fatal. *P. syringae* pv. *aesculi* has only ever previously been reported in Himachal Pradesh in northern India, where the type strain was isolated in 1969.

The Sainsbury Laboratory (led by **Sophien Kamoun**) recently used so-called “next-generation” sequencing technology to generate complete genome sequences for three geographically distinct isolates of *P. syringae* pv. *aesculi* (kindly supplied by **Richard Thwaites** at the Food and Environment Research Agency [FERA]): the original Indian isolate, a recent isolate from Scotland, and a recent isolate from southern England. By comparing our data with previously published genomes from other pathovars of *P. syringae*, I was able to identify regions of the genome that were apparently pathovar-specific to *P. syringae* pv. *aesculi*. These contain genes implicated in catabolism of aromatics, nitric oxide metabolism, secondary metabolism, and iron acquisition.



The University of Exeter.

The two British strains shared almost identical genome sequences and probably originated from a single introduction, even though they were isolated from very different geographical locations. Previous studies used real-time polymerase chain reaction amplification of a single gene (*gyrB*) to detect and quantify *P. syringae* pv. *aesculi* in diseased trees. British strains were indistinguishable from the Indian type strain on this basis; they all shared identical *gyrB* gene sequences, reflecting a very close evolutionary relationship. However, our genome-wide sequence data revealed a surprisingly

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IS-MPMI Reporter

Editor-in-Chief: Jean-Pierre Metraux
Managing Editor: Michelle Bjerkness
Editor: Amanda Aranowski
Design: Joel Berg

The *IS-MPMI Reporter* is published three times per year by the International Society of Molecular Plant-Microbe Interactions at 3340 Pilot Knob Road, St. Paul, MN 55121 U.S.A. Phone: +1.651.454.7250, Fax: +1.651.454.0766, E-mail: ismpmi@scisoc.org, Web: www.ismpminet.org. The *IS-MPMI Reporter* is distributed to all members.

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IS-MPMI REPORTER DEADLINE

The deadline for submitting items for the next issue is August 27, 2010.

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).

Send items to:

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



Felice Cervone, President

A Letter from the President

Basic Knowledge of Molecular Plant-Microbe Interactions Provides Technology for Improving Durable Resistance Against Pests

Members of IS-MPMI, recent, exciting news shows that our society is actively engaged not only in tackling important basic questions in the field of plant-microbe interactions but also in providing useful technologies for improving plant productivity and durable resistance against pests.

A recent paper by Lacombe et al. (*Nature Biotechnology* 28:365-369) reports the important evidence that the expression in *Nicotiana benthamiana* and tomato of the *Arabidopsis* pattern recognition receptor (PRR) EFR provides a broad-spectrum resistance against agriculturally relevant bacterial pathogens of different genera (*Agrobacterium*, *Pseudomonas*, *Ralstonia*, *Xanthomonas*). EFR is an LRR (leucine-rich repeat) receptor kinase and recognizes the elongation factor Tu (EF-Tu), a pathogen-associated molecular pattern (PAMP) widely conserved among bacteria. Upon binding to elf18, a peptide deriving from EF-Tu, EFR initiates kinase signaling cascades that activate many downstream immune responses and lead to disease resistance. Solanaceae members do not respond to elf18 because EFR-like receptors may be absent or not expressed in these plants. The paper of Lacombe et al. opens the possibility of protecting Solanaceae members from bacteria through transformation with EFR.

Another report adds possible developments to the use of EFR. Brutus et al. (*PNAS* 107:9452-9457) demonstrate how structurally diverse PRRs can be engineered to form chimeric receptors that are functional not only in *Arabidopsis* but also in tobacco, i.e., an agricultural species belonging to the Solanaceae family. The chimera formed by the kinase domain of EFR and the extracellular domain of FLS2, the other well-known *Arabidopsis* PRR, was able to activate immune responses upon binding to the elicitor flg22, another PAMP deriving from flagellin and conserved among pathogenic bacteria. The possibility of constructing functional chimeric receptors by using EFR and FLS2 has also been reported by Albert et al. (*JBC* 285:19035-19042). Moreover, Brutus et al. have shown that the kinase domain of EFR is amenable to the construction of functional and resistance-conferring chimeric receptors not only when coupled to an LRR domain, such as that of FLS2, but also when combined with the extracellular domain of a structurally unrelated PRR, such as the wall-associated kinase 1 (WAK1). WAK1 displays an ectodomain containing several EGF-like repeats and is capable of sensing oligogalacturonides (OGs), i.e., pectic fragments released from the plant cell wall that are active as damage-associated molecular patterns (DAMPs) for the activation of the plant immune responses. WAK1/EFR chimeric receptors work in both directions: upon stimulation with OGs, the WAK1 ectodomain is capable of activating the EFR kinase domain and, correspondingly, upon binding to elf18, EFR ectodomain activates the WAK1 kinase, mirroring defense responses normally activated by OGs.

These studies open the possibility of extending the protective action of EFR to many plants and enlarging its spectrum against diverse pathogens. They clearly indicate that the distance between laboratory research and field application is decreasing and that we are rapidly approaching the possible tailoring of new PR-based chimeric receptors controlled by a variety of signals (PAMPs, DAMPs, and others). These may be used to confer durable resistance to a variety of agriculturally relevant plant species against a variety of diseases caused either by bacteria or fungi. The domain swap technology among PRRs may also turn out to be a powerful tool to engineer not only disease resistance but also other traits that are useful for plant productivity. ■

Meet IS-MPMI Reporter Editor-in-Chief Jean-Pierre Metraux



Jean-Pierre Metraux,
Editor-in-Chief

Q: Tell us about yourself and your work.

A: My interest in plant-pathogen interactions started during my post-doctoral work at the Michigan State University Department of Energy Plant Research Laboratory from 1980 to 1981, when I had a chance to follow lectures given by the late **Bob Scheffer** and **Ray Hammerschmidt**. I was then hired by CIBA Corporation in Basel to carry out research on a very practical and standing problem: developing a novel type of protectant based on the stimulation of the plant defenses. This led to the development of a series of compounds, the best known of which was BION, also referred to as ACTIGARD. Fortunately, I was also able to initiate basic research projects; for example, our search for a systemic signal for induced resistance led to salicylic acid, a compound that opened the door to molecular investigations on the regulation of defense responses. In 1991, I was offered a full professorship at the University of Fribourg, and it was a welcome opportunity to give a free run to my passion for directing research and teaching students. My work in Fribourg has dealt with various aspects of plant defense responses (biosynthesis of salicylic acid; signaling and defense). Recently, we have become interested in the cuticle and the role of its permeability as a potential barrier to elicitors. How virulent fungal pathogens deviate the physiology of their host to their own advantage is another topic we are working on, using the interaction between *Botrytis cinerea* and *Arabidopsis*.

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

A: In the 1990s; the society is a dynamic structure in a dynamic field and is well organized.

Q: Which IS-MPMI Congress did you first attend?

A: In 1990, I attended the meeting in Interlaken, where I was invited to present our work on 2,6-dichloroisonicotinic acid. It was a great gathering where I finally met many people I knew from the literature.

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

A: I discovered a fascinating area for basic research in the general framework of very important practical problems.

Q: Who have some of your role models been (alive or a historical figure)? Why?

A: As a high school kid, I was attracted to science and read many biographies of figures such as **[Louis] Pasteur**, **[Robert] Koch**, **[Frederick] Banting**, and **Marie Curie**. *Microbe Hunters* by **Paul de Kruif** also left its mark. I had a formidable chance to meet almost on a daily basis many of the fine plant biologists that were active while I was a graduate student, and figures such as **Kenneth Thimann**, **Harry Beevers**, and **Paul Green** have greatly impressed me. Not to forget my former mentors, **Lincoln Taiz**, **Russell Jones**, and **Hans Kende**, who contributed to my education and challenged my mind. Integrity, enthusiasm, kindness, and a sense of humor are the common denominators that characterize them all.

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

A: The paper by S. Lacombe et al. (*Nature Biotechnology* 28:365, 2010) relates great findings that open a potential for improving crop protection by transferring pattern recognition receptors.

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

A: The interface between roots and soil and soilborne pathogens has not been studied intensely. A single root cell might be confronted with symbionts or pathogens at the same time. How are decisions taken, how are defenses coordinated? Obviously, we are likely to witness an increased impact of system biology on our field; many tools are being developed in that direction.

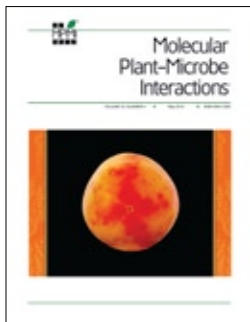
Q: What book are you reading right now?

A: I am always reading several books; this time I am into **Vidiadhar Naipaul** (*Among the Believers*; a great eye-opener), **Francisco Coloane** (*Tierra del Fuego* and other novels; makes me dream), and **Alejo Carpentier** (*Music in Cuba*; amazing what happened there).

Q: What's something people may not know about you?

A: Besides science, I have a passion for music and play the sax. I share this with friends and we often play gigs with our Latin-jazz group "Cocinando." ■

MPMI Current Review: Emerging Viral Diseases of Tomato Crops



Viral diseases are an important limiting factor in many crop production systems. Because antiviral products are not available, control strategies rely on genetic resistance or hygienic measures to prevent viral diseases or on eradication of diseased crops to control such diseases. Tomato is economically the most important vegetable crop worldwide and many

viruses infecting tomato have been described, while new viral diseases keep emerging. Read the Current Review in *MPMI*'s May 2010 print issue or online at <http://apsjournals.apsnet.org/doi/abs/10.1094/MPMI-23-5-0539>.

Authors interested in submitting Current Reviews for publication are encouraged to contact an *MPMI* senior editor. ■

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An Update on *PLoS Pathogens*

PLoS Pathogens (www.plospathogens.org) has broadened its focus. This peer-reviewed, open-access journal, run by and for the community of pathogens researchers, aims to publish outstanding original research articles. Since its inception four years ago, the journal has presented original research in six well-defined areas, including prions, parasites, bacteria, viruses, fungi, and evolutionary biology. The Editorial Board has been expanded to accommodate the growing number of plant pathogen submissions. The editorial focus is on mechanistic studies with clearly defined hypothesis testing using all available tools, from genomics to cell biology and ecology. A presubmission inquiry is recommended for a rapid response as to whether your proposed work adheres to the journal's scope. Please send any general questions to the staff at plospathogens@plos.org. ■

22nd New Phytologist Symposium: Effectors in Plant-Microbe Interactions

The 22nd New Phytologist Symposium, held September 2009 at the INRA Versailles Research Centre, Paris, France, included more than 20 talks spanning four days, providing a lively forum for exchanging ideas and discussing new approaches. There was also a poster session, reception, and conference dinner. The study of effectors is a rapidly expanding research field that benefits from recent advances in microbial and plant genomics. The symposium aimed to support this research field by bringing together scientists from around the world working on various aspects of plant-microbe interactions, covering a wide range of pathosystems (i.e., viruses, bacteria, fungi, oomycetes, nematodes, and insects). The symposium occurred shortly after the XIV International Congress on Molecular Plant-Microbe Interactions in Quebec. The symposium translated this mainstream research on microbial effectors into lively discussion sessions. The symposium was also covered with a live Twitter feed (#NPS09 tag, at <http://tinyurl.com/y877xoy>). Poster prize winners included **Silke Klopffholz**, University of Karlsruhe, Germany—first place; and **Philippe Remigi**, INRA-CNRS, Castanet Tolosan, and **Franco** and **Johana Misas**, Villamil Max Planck Institute for Plant Breeding Research, Cologne, Germany—runners up. A complete summary article on the meeting has been posted online (http://web.mac.com/sophien/KamounLab/pdfs/NewPhytol_2010.pdf). ■

2010 APS Annual Meeting Relocates to Charlotte, NC

The Gaylord Opryland Resort & Convention Center in Nashville, TN, the original site of The American Phytopathological Society's 2010 Annual Meeting, recently sustained severe flood damage due to unprecedented rain in the area. As a result, the 2010 Annual Meeting can no longer be held in Nashville and has been relocated to Charlotte, NC, over the same dates, August 7–11.

The world's top plant pathologists will be in Charlotte this summer to present their latest research in a variety of formats, including 28 special sessions, four workshops, hundreds of posters, and dozens of networking events and socials. Registration and housing are open. Register by July 8, 2010, to avoid late/onsite fees. Visit <http://meeting.apsnet.org> for the full preliminary program and schedule. ■



Horse chestnut tree seeds (conkers).

of genomic sequences that were found in either British or Indian isolates, but not shared in both, as well as 1,600 single-nucleotide polymorphisms. These differences included genes encoding type III secretion system effectors, filamentous hemagglutinins, fatty acid metabolism, type VI secretion, and microcin biosynthesis, among others. Jackson's laboratory has followed up some of the sequence-based predictions with functional work. These genetic differences presumably contribute to the phenotypic differences between British and Indian strains. The Indian strain causes only a mild leaf spot disease, while the British strains are much more aggressive and attack woody parts of the tree.



Conquering conker canker.

isolate shared an almost identical genome sequence with those of the two British strains that we had sequenced, further suggesting that the British epidemic of *P. syringae* pv. *aesculi* may have originated from a single inoculum. We exchanged data with the Forest Research team and recently cowrote and published a paper describing all four genomes in *PLoS One*. Due to the iconic status of the horse chestnut tree, this attracted the attention of the British media, with coverage by the BBC as well as by several national and local newspapers. My favorite headline was "Norwich boffins save our conkers."

Whole-genome sequencing of multiple isolates has become an almost routine weapon in the fight against emerging diseases of humans and animals. With recent advances in sequencing technology, meaning dramatic reductions in costs and increases in throughput, such an approach is now within the grasp of many plant pathology labs. Our main motivation for the horse chestnut disease study was to draw attention to this approach. The complete genome sequences of *P. syringae* pv. *aesculi*

large degree of intrapathovar variability between the Indian and British strains. Working closely with **Rob Jackson** of the University of Reading, I identified several hundred kilobases

While we were analyzing our data, we learned that a team led by **Sarah Green** at the Forest Research Northern Research Station had also sequenced a strain of *P. syringae* pv. *aesculi* recently isolated in Scotland. This

have revealed important genetic similarities and differences among strains that would not have been discovered by relying solely on more traditional methods of plant pathology. This opens up new avenues for studying the molecular basis of the disease and possible interactions with insect vectors in addition to providing sequence information that can be used for further diagnostics and epidemiology. A consortium in Spain recently published the complete genome of *P. savastanoi* pv. *savastanoi*, which infects olive trees. We have sequenced *P. syringae* pv. *syringae* strain FF5, which infects pear trees. By comparing the genomes of these with those of *P. syringae* pv. *aesculi*, we may begin to understand common themes in adaptation of phytopathogenic *Pseudomonas* to woody hosts.

In November 2009, I moved from the Sainsbury Laboratory (www.tsl.ac.uk), where I was leading the bioinformatics team, to take up a faculty position at the University of Exeter (www.exeter.ac.uk). I plan to use bioinformatics, comparative genomics, and metagenomics to study the evolution of emerging diseases of crops and other plants. For example, in collaboration with FERA and others, we are trying to elucidate the genetic basis for the emergence of banana Xanthomonas wilt, which threatens to devastate the staple food crop in East Africa. I continue to have very enjoyable and productive collaborations on *Pseudomonas* genomics with **Gail Preston** at Oxford University, Jackson at the University of Reading, **Boris Vinatzer** at Virginia Tech, and **Dawn Arnold** at the University of the West of England.

Also based at the University of Exeter are several other research groups in the field of molecular plant-microbe interactions (MPMI). **Murray Grant**'s laboratory adopts an integrative approach to molecular plant pathology using genome-based technologies (transcriptomics, interaction and expression proteomics, metabolic profiling, and real-time imaging) to understand the dynamics of four fundamental and interrelated aspects of *Arabidopsis*-*Pseudomonas* interactions. **Nick Talbot** studies the mechanisms by which fungal pathogens can infect living host plants, invade their tissues, and cause disease. His laboratory uses interaction between the rice blast fungus *Magnaporthe oryzae* and cultivated rice, *Oryza sativa*, as the model system. **Nick Smirnov** studies transcriptomic metabolomic responses in plants to pathogens and other stresses. The University of Exeter also offers a master's program in food security and sustainable agriculture, directed by **Chris Thornton**, who studies rhizosphere fungi. All of the MPMI research groups at Exeter benefit from access to in-house facilities, such as an Illumina GA2 sequencing instrument, bio-imaging suite, and mass spectrometry for metabolomics and proteomics. Having just joined IS-MPMI at the end of 2009, I am looking forward to interacting and collaborating with fellow members for many years to come. ■

People



Hemanth K. N. Vasanthaiah

Hemanth K. N. Vasanthaiah, Center for Viticulture and Small Fruit Research, Florida A&M University, in Tallahassee, FL, was invited to present on his research work at the prestigious Plant and Animal Genome Conference in San Diego, CA, January 9–13, 2010. He presented on the transcriptome and proteome approach to unveil

Pierce's disease tolerance genes in grape and on the identification of molecular markers associated with low chill/heat tolerance in raspberry.

In 2009, the following 13 students associated with the Netherlands Graduate School Experimental Plant Sciences (EPS) and participating in research on interactions between plants and biotic agents, defended their Ph.D. theses. The EPS Graduate School is a collaborative research and teaching institution of Wageningen University (WU), Radboud University in Nijmegen (RU), Free University in Amsterdam (VU), Leiden University (LU), University of Amsterdam (UvA), and Utrecht University (UU). **P. M. J. A. van Poppel**, "The *Phytophthora infestans* avirulence gene *PiAvr4* and its counterpart *R4* in potato," F. Govers and P. J. G. M. de Wit (promoters), WU, Wageningen, February 4, 2009. **U. Ellendorff**, "Genome-wide investigation into roles of *Arabidopsis* receptor-like proteins in pathogen defense," P. J. G. M. de Wit (promoter) and B. P. H. J. Thomma (copromoter), WU, Wageningen, March 11, 2009. **I. de Bruijn**, "Biosynthesis and regulation of cyclic lipopeptides in *Pseudomonas fluorescens*," P. J. G. M. de Wit (promoter) and J. M. Raaijmakers (copromoter), WU, Wageningen, March 31, 2009. **M. H. A. van Hulst**, "Priming *Arabidopsis* for defense: Molecular and

ecological aspects," C. M. J. Pieterse (promoter) and J. Ton and S. C. M. van Wees (copromoters), UU, Utrecht, April 8, 2009. **T. A. L. Snoeren**, "Herbivore-induced indirect defense of *Arabidopsis*: Ecogenomic approach to the role of infochemicals in parasitoid attraction," M. Dicke (promoter), WU, Wageningen, May 11, 2009. **G. Wang**, "The role of receptor-like proteins in *Arabidopsis* development," G. C. Angenent and P. J. G. M. de Wit (promoters) and B. P. H. J. Thomma (copromoter), WU, Wageningen, May 13, 2009. **R. Aghnoum**, "Basal resistance of barley to adapted and non-adapted forms of *Blumeria graminis*," R. G. F. Visser (promoter) and R. E. Niks (copromoter), WU, Wageningen, June 16, 2009. **H. A. Leon-Reyes**, "Making sense out of signaling during plant defense," C. M. J. Pieterse (promoter) and T. Ritsema (copromoter), UU, Utrecht, July 8, 2009. **A. Kavalenka**, "Modeling membrane protein structure through site-directed ESR spectroscopy," H. van Amerongen (promoter) and M. A. Hemminga and J. Strancar (copromoters), WU, Wageningen, September 30, 2009. **W. Jonkers**, "The role of the F-box protein Frp1 in pathogenicity of *Fusarium oxysporum* f. sp. *lycopersici*," B. J. C. Cornelissen (promoter) and M. Rep (copromoter), UvA, Amsterdam, October 6, 2009. **E. J. Sloopweg**, "Structure, function and subcellular localization of the potato resistance protein Rx1," J. Bakker (promoter) and A. Schots and A. Goverse (copromoters), WU, Wageningen, October 23, 2009. **A. C. M. E. Agbicodo**, "Genetic analysis of abiotic and biotic resistance in cowpea," R. G. F. Visser (promoter) and G. C. van der Linden and C. Fatokun (copromoters), WU, Wageningen, October 27, 2009. **R. F. Doorbos**, "Analysis of rhizosphere bacterial communities in *Arabidopsis*: Impact of plant defense signaling," L. C. van Loon (promoter) and P. A. H. M. Bakker (copromoter), UU, Utrecht, November 23, 2009. ■

IS-MPMI Members Elected into the National Academy of Sciences



Eva Kondorosi

IS-MPMI members **Eva Kondorosi** and **Paul Schulze-Lefert** have been elected into the National Academy of Sciences in recognition of their distinguished and continuing achievements in original research.

The election was held during the business session of the 147th Annual Meeting of the academy, held April 24–27, 2009. Established

in 1863, the academy is a private organization of scientists



Paul Schulze-Lefert

and engineers dedicated to furthering science and its use for the general welfare. Kondorosi is the founder and director of the Institute for Plant Genomics, Human Biotechnology, and Bioenergy in Szeged, Hungary and Institut des Sciences ju Végétal, France. Schulze-Lefert is the director of the Department of Plant Microbe Interactions at the Max Planck Institute for Plant Breeding

Research in Cologne, Germany. ■

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.



Ksenia V. Krasileva

Student Member

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

I grew up in Saint Petersburg, Russia, moved to the United States as a teenager, and received my undergraduate degree from the University of California, Berkeley (UCB). As an undergraduate, I worked for two and a half years with **Steven Lindow**, studying mechanisms of bacterial interference of quorum sensing in *Pseudomonas syringae*. This research stimulated my interests in both microbiology and plant pathology. Thus, in 2005, as I received a B.S. degree in plant genetics and microbiology, I was eager to enter graduate school.

For the past four years, I have been working toward a Ph.D. degree in **Brian Staskawicz's** lab in the Department of Plant and Microbial Biology at UCB. The goal of my graduate work is to broaden our understanding of the molecular mechanisms that define plant-pathogen interactions. Specifically, I have been working with the RPP1 resistance protein from *Arabidopsis thaliana* and its cognate effector ATR1 from an obligate biotrophic oomycete pathogen *Hyaloperonospora arabidopsidis* (originally known as *Peronospora parasitica*). We have shown that RPP1 physically associates in a protein complex with ATR1 in the plant in a recognition-specific manner. I am currently interested in studying the immediate molecular events that happen downstream of effector recognition that result in the activation of RPP1. Additionally, I am investigating localization of RPP1 and its importance for eliciting different types of resistance responses. Since both RPP1 and ATR1 are encoded by rapidly evolving gene loci, I want to obtain further insight into the coevolution of these genes by characterizing the natural variation in RPP1-mediated responses among different accession lines of *Arabidopsis*.

I am also interested in the application of the next-generation high-throughput sequencing technologies toward the characterization of plant-pathogen interactions on genomic and transcriptional levels. In collaboration with **Sophien Kamoun's** laboratory, we have been able to computationally predict a set of effectors from *H. arabidopsidis*. We are currently sequencing and assembling the genome of *H. arabidopsidis* strain Emwa1, which should complement the current genome project of *H. arabidopsidis* strain Emoy2. I am also interested in exploring the RNA-seq technology to characterize the transcriptional profiles of *A. thaliana*-*H. arabidopsidis* interactions under different conditions.

I joined IS-MPMI in 2009. The first IS-MPMI congress that I attended was the XIV International Congress in Quebec, Canada. I was honored with an opportunity to present my research in Quebec and was simply thrilled to be there. This congress provided me with an outstanding opportunity to meet a variety of scientists from around the world; to talk to my peer students, post-docs, and professors; to learn about their work; and to get feedback about my research. I am looking forward to the next IS-MPMI meeting in Japan.



Maud Bernoux

Post-Doctoral Member

Maud Bernoux
CSIRO Plant Industry
ACT, Australia

I first started to work in the field of molecular plant-microbe interactions as a Ph.D. student in **Laurent Deslandes'** and **Yves Marco's** group at INRA in Toulouse, France. Their research focused on the molecular resistance mechanisms of *Arabidopsis* to the phytopathogenic bacteria *Ralstonia solanacearum*. In this pathosystem, RRS1-R is an atypical TIR-NB-LRR resistance protein fused to a WRKY transcription factor in its C-terminal end. PopP2 is an *R. solanacearum* type III effector that triggers RRS1-R-mediated resistance. During my Ph.D. work, I identified the vacuolar *Arabidopsis* cysteine protease RD19 as a PopP2-interacting protein. I showed that RD19 is required for RRS1-R-mediated resistance and that it is relocalized in the presence of PopP2 to the plant nucleus, where both proteins physically interact.

I attended my first IS-MPMI Congress in 2007 in Sorrento, Italy. While there, I presented a poster on my Ph.D. work. I found it really interesting to exchange ideas and hear about the latest breakthroughs in the field. That is where I also met my current post-doctoral supervisor, **Peter Dodds**, and have been working in his group for two years at CSIRO in Canberra, Australia. Using the powerful model interaction between flax and flax rust, I work on the structure-function analysis of TIR-NB-LRR flax rust resistance proteins. More specifically, I am interested in deciphering the role of the TIR domain in defense signaling.

On Dodds' advice, I joined IS-MPMI in 2008 and enjoy receiving the latest news through the newsletter. I also participated in the last IS-MPMI Congress, July 2009, in Quebec City, Canada, and I'm looking forward to attending the next one. ■

Recently published research in *Molecular Plant-Microbe Interactions*

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March 2010, Volume 23, Number 3

A Fungal Parasite Regulates a Putative Female-Suppressor Gene Homologous to Maize *Tasselseed2* and Causes Induced Hermaphroditism in Male Buffalograss.

Genome-Wide Identification of a Large Repertoire of *Ralstonia solanacearum* Type III Effector Proteins by a New Functional Screen.

The Intra- and Intercellular Movement of *Melon necrotic spot virus* (MNSV) Depends on an Active Secretory Pathway.

Salmonella SdiA Recognizes *N*-acyl Homoserine Lactone Signals from *Pectobacterium carotovorum* In Vitro, but Not in a Bacterial Soft Rot.

Viral-Induced Systemic Necrosis in Plants Involves Both Programmed Cell Death and the Inhibition of Viral Multiplication, Which Are Regulated by Independent Pathways.

Cucumber Mosaic Virus 2b Protein Subcellular Targets and Interactions: Their Significance to RNA Silencing Suppressor Activity.

pH Regulation of Ammonia Secretion by *Colletotrichum gloeosporioides* and Its Effect on Appressorium Formation and Pathogenicity.

MoRlc8 Is a Novel Component of G-Protein Signaling During Plant Infection by the Rice Blast Fungus *Magnaporthe oryzae*.

A Progeny Virus from a *Cucumovirus* Pseudorecombinant Evolved to Gain the Ability to Accumulate Its RNA-Silencing Suppressor Leading to Systemic Infection in Tobacco.

Ascorbic Acid Deficiency in *Arabidopsis* Induces Constitutive Priming That is Dependent on Hydrogen Peroxide, Salicylic Acid, and the *NPR1* Gene.

April 2010, Volume 23, Number 4

Role of the *Sinorhizobium meliloti* Global Regulator Hfq in Gene Regulation and Symbiosis.

A Homeobox Gene Is Essential for Conidiogenesis of the Rice Blast Fungus *Magnaporthe oryzae*.

Multiple Coat Protein Mutations Abolish Recognition of *Pepino mosaic potexvirus* (PepMV) by the Potato Rx Resistance Gene in Transgenic Tomatoes.



Complete Genome Sequence of the Fire Blight Pathogen *Erwinia amylovora* CFBP 1430 and Comparison to Other *Erwinia* spp.

Salicylic Acid Is Involved in the *Nb*-Mediated Defense Responses to *Potato virus X* in *Solanum tuberosum*.

ACTTS3 Encoding a Polyketide Synthase Is Essential for the Biosynthesis of ACT-Toxin and Pathogenicity in the Tangerine Pathotype of *Alternaria alternata*.

Molecular and Evolutionary Analyses of *Pseudomonas syringae* pv. *tomato* Race 1.

Different Domains of *Phytophthora sojae* Effector Avr4/6 Are Recognized by Soybean Resistance Genes *Rps4* and *Rps6*.

Peroxisome Biogenesis Factor PEX13 Is Required for Appressorium-Mediated Plant Infection by the Anthracnose Fungus *Colletotrichum orbiculare*.

Expression of *BuGLP-1* Encoding a Germin-Like Protein from Sugar Beet in *Arabidopsis thaliana* Leads to Resistance Against Phytopathogenic Fungi.

Six New Genes Required for Production of T-Toxin, a Polyketide Determinant of High Virulence of *Cochliobolus heterostrophus* to Maize.

Maize Leaf Epiphytic Bacteria Diversity Patterns Are Genetically Correlated with Resistance to Fungal Pathogen Infection.

Armillaria mellea Induces a Set of Defense Genes in Grapevine Roots and One of Them Codifies a Protein with Antifungal Activity.

Diversity at the *Mla* Powdery Mildew Resistance Locus from Cultivated Barley Reveals Sites of Positive Selection.

Evolution and Regulation of the *Lotus japonicus* *LysM Receptor* Gene Family.

The cAMP Signaling Pathway in *Fusarium verticillioides* Is Important for Conidiation, Plant Infection, and Stress Responses but Not Fumonisin Production.

May 2010, Volume 23, Number 5

CURRENT REVIEW—Emerging Viral Diseases of Tomato Crops.

The Role of Callose Deposition Along Plasmodesmata in Nematode Feeding Sites.

Wounding-Induced WRKY8 Is Involved in Basal Defense in *Arabidopsis*.

A Role for Topoisomerase I in *Fusarium graminearum* and *F. culmorum* Pathogenesis and Sporulation.

Synergistic Activation of Defense Responses in *Arabidopsis* by Simultaneous Loss of the GSL5 Callose Synthase and the EDR1 Protein Kinase.

DL- β -Aminobutyric Acid-Induced Resistance of Potato Against *Phytophthora infestans* Requires Salicylic Acid but Not Oxylipins.

The *Frankia alni* Symbiotic Transcriptome.

The *Rvi15* (*Vr2*) Apple Scab Resistance Locus Contains Three TIR-NBS-LRR Genes.

PAD4-Dependent Antibiosis Contributes to the *ssi2*-Conferred Hyper-Resistance to the Green Peach Aphid.

Temperature-Dependent Expression of Type III Secretion System Genes and Its Regulation in *Bradyrhizobium japonicum*.

Atypical Transcriptional Regulation and Role of a New Toxin-Antitoxin-Like Module and Its Effect on the Lipid Composition of *Bradyrhizobium japonicum*.

Variations in the Mycorrhization Characteristics in Roots of Wild-Type and ABA-Deficient Tomato Are Accompanied by Specific Transcriptomic Alterations.

Positive Regulation of the Hrp Type III Secretion System in *Pseudomonas syringae* pv. *phaseolicola*.

Negative Regulation of the Hrp Type III Secretion System in *Pseudomonas syringae* pv. *phaseolicola*.

Production of Nitric Oxide and Nitrosylhemoglobin Complexes in Soybean Nodules in Response to Flooding.

June 2010, Volume 23, Number 6

Identification of *Nicotiana benthamiana* Genes Involved in Pathogen-Associated Molecular Pattern-Triggered Immunity.

Components of the *Pseudomonas syringae* Type III Secretion System Can Suppress and May Elicit Plant Innate Immunity.

Infection-Specific Activation of the *Medicago truncatula* Enod11 Early Nodulin Gene Promoter During Actinorhizal Root Nodulation.

The Response to Nitric Oxide of the Nitrogen-Fixing Symbiont *Sinorhizobium meliloti*.

Large-Scale Transposon Mutagenesis of Photosynthetic *Bradyrhizobium* sp. Strain ORS278 Reveals New Genetic Loci Putatively Important for Nod-Independent Symbiosis with *Aeschynomene indica*.

Evolution of the *Eleusine* Subgroup of *Pyricularia oryzae* Inferred from Rearrangement at the *Pwl1* Locus.

Rhizobial Adaptation to Hosts, a New Facet in the Legume Root-Nodule Symbiosis.

Abscisic Acid Interacts Antagonistically with Salicylic Acid Signaling Pathway in Rice-*Magnaporthe grisea* Interaction.

Phloem Protein Partners of *Cucurbit aphid borne yellows virus*: Possible Involvement of Phloem Proteins in Virus Transmission by Aphids.

Host Selection of Symbiotic Cyanobacteria in 31 Species of the Australian Cycad Genus: *Macrozamia* (Zamiaceae).

A Point Mutation in the Polymerase of *Potato virus Y* Confers Virulence Toward the *Pvr4* Resistance of Pepper and a High Competitiveness Cost in Susceptible Cultivar. ■



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www.geyseco.es/fespb

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www.ced.osu.edu/pvb2010conference

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www.brc.miyazaki-u.ac.jp/apmnf

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