

IN THIS ISSUE

XVI Congress Preliminary Details Now Available.....	1
A Letter from the President.....	2
Member Spotlights.....	3
Oomycete Community Meets.....	4
IS-MPMI Supports San Francisco Declaration.....	4
Coming Events.....	4
Hernán Burbano Interview.....	5
MPMI Journal Articles.....	6
Welcome New Members.....	7



Recent Tweets

- RT @TSL @KamounLab "Assessments based primarily on impact may also be contributing to an apparent epidemic of irreproducible results" <http://bit.ly/19Ob9dB>
- RT @MimiTanimoto Leafy Murder Mystery days are a big hit! - Read about @BS_PP's #PlantDay2013 event on the @UKPSF blog <http://ow.ly/1Rgun> #plantscience
- RT @BTIScience Arabidopsis syncytium development induced by a parasitic nematode is dependent on an ATPase gene <http://ow.ly/1LQHa>
- Happy 161st birthday Julius Petri! Check out Google search page. <http://bit.ly/1388Pjf>
- RT @TSL @KamounLab "The bug behind the potato blight." Interview with @NakedScientists <http://tumblr.co/Z9vs-xljYCzt>
- Oomycete bioinformatics workshop! <http://pmgn.vbi.vt.edu/workshops.php>
- Scientists Reveal The Cause Of The Irish Potato Famine <http://bit.ly/165PVHH>
- RT @microbiology Fungal isolation from soil... but which colonies can you see here? :) #microbiology pic.twitter.com/0NBZ0vY69
- Plant proteins may expand global agriculture <http://bit.ly/12VuZ59> via @farmpress

Check out

Twitter.com/ISMPMI

for the latest updates!

The Preliminary Details Are Now Available on the XVI International Congress Website!

Dear Colleagues and Friends,



Eris Tjamos



On behalf of the Local Organizing and Scientific Committee (LOSC) and the International Scientific Committee (ISC) we announce the current update of the initial website of the IS-MPMI Congress and inform you that the organization is moving according to the schedule.

The current update of the website includes among others:

- A preliminary plan of the program
- Recently revised program of the proposed topics
- The members of the International Scientific Committee
- Registration deadlines and fees
- Accommodation arrangements
- Details for exhibitors and sponsorships

Both scientific committees are currently collaborating to formalize the program and initially arrange the plenary and concurrent sessions. At a later stage the LOSC will communicate with potential speakers selected according to the rules of the IS-MPMI.

The LOSC promises once again to do its utmost to create a very positive environment for the presentation of your recent scientific achievements on Plant Microbe Interactions, to broaden the areas of related sciences, to promote fertile dialogue and personal interactions.

Exhibitors and sponsors are welcome to raise their visibility among the conference participants and to support the conference.

We will welcome you in Rhodes and will try to make your stay really memorable both scientifically and recreationally.

See you in Rhodes Island, Greece in July 6–10, 2014!

Eris Tjamos
Chairman of the XVI IS-MPMI Congress

Visit www.mpmi2014rhodes-hellas.gr for all recent congress information. ■



A view of Rhodes, Greece. (Courtesy of XVI International Congress website)

IS-MPMI Reporter

Editor-in-Chief: Brad Day
Managing Editor: Michelle Bjerkness
Editor: Lauren Bennett
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.

IS-MPMI Board of Directors

President
SOPHIEN KAMOUN

President-Elect
SHENG YANG HE

Immediate Past President, ex officio
FELICE CERVONE

Treasurer
PETER DODDS

Immediate Past Treasurer
MATTEO LORITO

Editor-in-Chief, Molecular Plant-Microbe Interactions
JANE GLAZEBROOK

Editor-in-Chief, IS-MPMI Reporter
BRAD DAY

Director
MARIA J. HARRISON

Director
ROGER W. INNES

Director
REGINE R. KAHMANN

Director
EVA KONDOROSI

Director
MARY BETH MUDGETT

Director
CORNE M. J. PIETERSE

Director
KEN SHIRASU

Executive Vice President, ex officio
AMY HOPE

IS-MPMI REPORTER DEADLINE

The deadline for submitting items for the next issue is August 20, 2013.

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 Brad Day
Michigan State University
Phone: +1.517.353.7991
Fax: +1.517.375.1781
E-mail: bday@msu.edu



Sophien Kamoun,
President

A Letter from the President

Science on The Med

Sophien Kamoun, *The Sainsbury Laboratory*
sophien.kamoun@tsl.ac.uk

I am pleased to report that preparations for the XVI International Congress, to be held July 6–10, 2014, on the Greek island of Rhodes, are proceeding according to plan. Congress Chief Organizer **Eris Tjamos** and his Local Organizing Committee have been working diligently toward an exciting high-quality program. They have been consulting closely with the Board of Directors (BOD), which forms the bulk of the International Scientific Committee.

In recent years, the International Society for Molecular Plant-Microbe Interactions (IS-MPMI) has received much feedback from its members about improving the scientific program of the international congresses. We listened. Our main action is the approval by the BOD in January 2013 of a document entitled “Guidelines for organizing the scientific program of IC-MPMI.” The objective of this framework is to streamline the organization of the congress to ensure a consistent scientific program that matches the expectations of the BOD and the society membership.

The key feature of the “Guidelines” document is that the program is developed through a collaboration between the local organizers and the BOD. Specific rules have been set. To encourage interactions between members of different communities, overly specialized concurrent session topics, particularly taxon-specific ones, will be avoided. For example, a session on “pathogenesis” is preferable to one on “bacterial pathogenesis.” Similarly, talks on “nematodes” are better spread throughout the program than grouped together in a single specialized session, which runs the risk of being attended mainly by specialists.

Another excellent decision that has broad support from the BOD is based on the positive experience of the 2007 Sorrento Congress. Concurrent session topics may be revised following abstract submission to ensure that the program reflects the interests of the participants and to bring about a balanced program. We also plan to offer abstract authors the option to choose an “OTHER” option, in addition to the preliminary list of topics, to capture the interests of all the participants. More than half of the congress speakers will be selected from the abstracts, so those who submit their best work will be rewarded.

A related decision is to mix speakers presenting different topics in the plenary sessions. This worked well at the 2012 Kyoto Congress. It should ensure better attendance throughout the conference. For instance, in the past, participants working on pathogens may have skipped the “Symbiosis” Plenary Session (I sheepishly admit to doing just that), and vice versa. Therefore, plenary sessions will not be labeled with specific themes but rather arbitrarily numbered to encourage broad and consistent attendance.

Finally, IS-MPMI must ensure that its congress truly reflects the diversity of the society membership. The speaker lineup must guarantee balance in gender, career stage, and geography. The BOD decided that gender balance should be at worst 35–65%. Also, at least 50% of the plenary speakers should be different from those who spoke at the preceding congress.

Many of us wait in anticipation for the biennial IC-MPMI. I am personally thrilled about the prospect of discovering historic Rhodes and experiencing again the legendary Greek hospitality. Our Greek hosts are fully dedicated to delivering an exceptional congress in the beautiful setting of the Mediterranean Sea. We hope that the “Guidelines” will contribute to the success of the next congress and beyond. You can be the judge and arbiter. ■

Member Spotlights

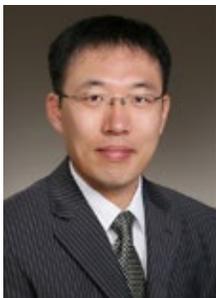
At IS-MPMI, we are very proud of the interactions, friendships, and accomplishments among our more than 650 members. We are especially proud of the achievements and successes of our young members, post-docs and students, as they move through the scientific and professional ranks. IS-MPMI has a long and proud tradition of training the next generation of scientists to be at the leading edge of plant biology. On that note, we are pleased to introduce our Member Spotlights, highlighting the recent successes of our colleagues. Please join us in welcoming the first class of many in our newest feature.



Marc Libault

Marc Libault is an assistant professor in the Department of Microbiology and Plant Biology at The University of Oklahoma (OU). Since 2005, as a post-doctoral researcher with **Gary Stacey** at the University of Missouri, he has been working on the molecular response of a single soybean root cell type, the root hair cell, to its infection by a mutualistic symbiotic bacterium, *Bradyrhizobium japonicum*. This plant-microbe symbiosis leads to the fixation and assimilation of

atmospheric nitrogen by the symbiont for the plant. Based on his work, the soybean root hair cell is now considered an attractive single cell-type model to investigate plant response to bacterial infection. As a new faculty member at OU, Libault is using the soybean root hair cell to characterize the molecular function of transcription factors controlling the early stages of nodulation and to evaluate the impact of the root hair epigenome on gene expression in response to rhizobia infection.



Woo-Suk Chang

Woo-Suk Chang recently joined the faculty at the University of Texas (Arlington) as an assistant professor in the Department of Biology. As a microbiologist interested in microbial genomics and environmental microbiology, Chang's interests are in symbiotic interactions between rhizobia and legume plants, nitrogen fixation, and microbial biofilms. Chang has been employing a culture-independent metagenomic approach to increase our understanding of how rhizobial communities, rather than a species, interact with soybean. In addition to metagenomics, microarray technology and RNA-seq have been used to reveal global gene expression patterns regarding the response of *Bradyrhizobium japonicum*, a soybean symbiont,

to several environmental factors, including desiccation, oxidative stress, heat stress, and low pH. Microbial biofilm (specifically unsaturated biofilm) in several soil bacteria is his other area of interest. Chang is interested in understanding how the molecular mechanism is involved in unsaturated biofilm formation and development.



Kee Hoon Sohn

Kee Hoon Sohn started his research career as an M.Sc. student in **Byung-Kook Hwang's** group at Korea University in 2001. His research there focused on the identification of pepper (*Capsicum annuum*) genes that are induced by *Xanthomonas campestris* pv. *vesicatoria* infection. This experience greatly motivated Sohn to study further plant-microbe interactions. After completing his M.Sc. degree, Sohn briefly worked as a research assistant with **Young-Jin**

Kim and **Kyung-Hee Paek** to identify the genes required for cell death pathways in *Nicotiana benthamiana*. He was very lucky to meet Kim, who taught him what a scientist should be. In 2004, Sohn joined **Jonathan Jones'** group at the Sainsbury Laboratory as a Ph.D. student to study the functions of the *Pseudomonas syringae* type III effector, AvrRps4. He continued working with Jones as a post-doc from 2009 until earlier this year. He hugely enjoyed his experience there (except the weather!) and learned to become a scientist (Thanks JJ!). Since March 2013, Sohn has been a research fellow working at the Institute of Agriculture and Environment at Massey University in New Zealand as a principal investigator, supported by Bioprotection CORE (New Zealand) and the Rural Development Administration (Korea). His lab will continue to investigate the fundamental mechanisms of plant disease resistance and contribute in developing durable resistance to *Pseudomonas syringae* pv. *actinidiae*, a causal agent of bacterial canker disease in kiwifruit. ■

Simple. Targeted. Relevant. IS-MPMI Job Center



Tired of searching through hundreds of random job postings to find your next opportunity? Looking through too many online resumes that don't meet your basic criteria?

Your search is about to become a whole lot easier...

The new IS-MPMI Job Center is the best targeted tool available for bringing job seekers and employers in the field together. This searchable, international database of jobs and candidates is designed specifically for those in the field of molecular plant-microbe interactions. The service is open to members and nonmembers alike, ensuring the broadest potential audience.

Job Seekers

- Find targeted opportunities by searching our current listings or by using the keyword search to find jobs in your area of expertise.
- Post your resume anonymously.
- Create job alerts.

Employers

- Easily post your jobs.
- Search the resume bank.
- Receive a \$49 discount if you are an IS-MPMI member. Enter the coupon code "IS-MPMIMember" to receive your discount.

Check out this simple, targeted, and relevant tool first-hand at www.ismpminet.org/career/ and start your search today!

Oomycete Community Meets by the Sea

Brett M. Tyler, Center for Genome Research and Biocomputing, Oregon State University, and coordinator of the Oomycete Molecular Genetics Research Collaboration Network, Brett.Tyler@oregonstate.edu



Oomycetes are devastating pathogens of plants of importance to agriculture, horticulture, forests, and natural ecosystems. Some oomycetes are also destructive pathogens of aquatic animals and are increasingly damaging to aquaculture and aquatic ecosystems. Genomic and molecular genetic approaches have propelled oomycetes to the forefront of plant–microbe interaction research over the last 10 years. On March 10–12, the oomycete molecular genetics community (Oomycete Molecular Genetics Research Collaboration Network (OMGN); pmgn.vbi.vt.edu) held its annual meeting in Asilomar, California, organized by **Mark Gijzen**, **John McDowell**, **Paul Morris**, and **Joel Shuman**. With support from the U.S. National Science Foundation, a record 122 researchers attended from 14 countries. Major topics were effectors, genomics, evolution and population genetics, and oomycete biology. Highlights included keynote addresses from

Jeff Dangl and **Sarah Grant** on the interaction of effectors with *Arabidopsis* hub proteins; five talks on the ongoing issue of effector entry mechanisms from the **Pieter Van West**, **Brett Tyler**, and **Shiv Kale** labs; a report from **Wenbo Ma** on *Phytophthora sojae* effectors that suppress RNA silencing; talks from **Richard Michelmore** and **Kurt Lamour** suggesting that the pan genomes of *Bremia lactucae* and *Phytophthora capsici* may contain thousands of different RxLR effector genes; and identification of a long-sought gene responsible for mefenoxam resistance in *Phytophthora infestans* by **Steven Whisson**. The OMGN meeting has a tradition of open dissemination via social media, especially Twitter, and this meeting generated a record 754 tweets from 10 attendees and 12 nonattendees (summarized at storify.com/KamounLab#stories). The 2014 OMGN meeting will be in Norwich, England, on July 3–5. ■

IS-MPMI Signs on to Support the San Francisco Declaration on Research Assessment

In December 2012, the American Society for Cell Biology (ASCB), along with a group of scholarly journal editors and publishers, met in San Francisco to develop a set of recommendations to address the pressing need to improve the ways in which the output of scientific research is evaluated by funding agencies, academic institutions, and other parties. As a result of this effort, a worldwide initiative, covering all scholarly disciplines, is now under way to build support for the developed guidelines referred to as the *San Francisco Declaration on Research Assessment* (DORA). More than 150 individuals and 80 organizations originally signed on to the declaration. During the recent IS-MPMI Board Meeting, the board approved including IS-MPMI as a supporting organization, agreeing to the adoption of the practices in research assessment as published at <http://am.ascb.org/dora>. If you have any additional feedback or interest in this initiative, please contact IS-MPMI President Sophien Kamoun (Sophien.kamoun@tsl.ac.uk). ■



COMING EVENTS

July 23–26, 2013

5th European Plant Science Retreat (for Ph.D. students)

Ghent University, Belgium
www.psb.ugent.be/~madub/EPSR5

August 10–14, 2013

APS-MSA Joint Meeting Austin, Texas, U.S.A. • www.apsnet.org/meet

August 25–30, 2013

10th International Congress of Plant Pathology (ICPP 2013)

Beijing, China • www.icppbj2013.org

October 14–18, 2013

18th International Congress on Nitrogen Fixation

Miyazaki, Japan • icnf18.brc.miyazaki-u.ac.jp

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

Discovering the Roots of the Cause of the Great Potato Famine

Brad Day, *IS-MPMI Reporter* editor-in-chief, recently interviewed **Hernán Burbano**, Max Planck Institute for Developmental Biology, about the recent discover of HERB-1, a strain of potato blight that triggered the Irish potato famine in the nineteenth century. Burbano, along with IS-MPMI President Sophien Kamoun, were part of an international team of scientists to make this incredible discovery using dried plants more than 120 years old. Burbano discusses the process and what this means for the MPMI community.

Q: First, congratulations on your recent discovery and manuscript. This is particularly exciting for many reasons, but in my mind, it solidifies the application of genomics as a means to travel back in time to understand agriculture practices, pressures, and culture. Can you speak a bit about the foundation this work lays for future similar studies?

A: The retrieval of sequences from historic samples opens a window to the past. Instead of inferences based on extant genetic variation, ancient DNA (aDNA) sequencing permits traveling back to the past to inspect directly DNA sequences that are hundreds and thousands of years old. The field of aDNA has experienced a blossoming in the last 7 years thanks to the advent of high-throughput sequencing. Traditionally, the DNA sources have been fossilized tissue such as teeth and bone. The completion of the Neanderthal genome and of the genome of the bacteria that caused the Black Death in the fourteenth century has radically change our views on human origins and disease emergence and re-emergence. Inspired by these studies, we used as a DNA source dried plants stored in herbaria and carried out the first whole-genome analysis of a plant pathogen and its host. We have shown that it is possible to do genomics using herbaria samples, which opens up a big road given the vast amount of samples stored in herbaria all around the world. Our study is perhaps a proof-of-principle experiment of a new field that we can call herbarium (meta) genomics.

Q: What is the next big question this type of analysis might address?

A: There are many questions in evolutionary biology that can be illuminated using aDNA: identification and timing of the key changes that allowed the domestication of crops, characterization of the diversity in historic crop material, understanding the colonization of new ecological niches by invasive or introduced species, studying the dynamics of past epidemics and the co-evolution of plant–pathogen interactions.

Q: From a molecular-assisted breeding approach, are we moving toward a point where we might understand—or elucidate—the breeding practice(s) of a particular crop or agricultural region from a historical standpoint?

A: It is possible to retrieve DNA not only from herbaria samples but also from archeological material, e.g., seeds and cobs. One can, for example, study the key genomic changes in crop domestication through time. It will also be possible to characterize the genetic diversity of crops prior to the advent of modern agriculture.

Q: Is it possible we might be able to understand at a molecular-genetic level which breeding practices worked, or did not work, and from that, identify the point in time when a trait or combination of traits that were not overtly visible might have led to the introduction of a weakness?

A: We will be able to study genetic changes in domesticated crops through time. Given the vast amount of genetic resources available in some crops, e.g., corn, it would possible to predict complex traits, such as flowering time, based on genome-wide genotyping of old (ancient) crops.

Q: What other complex traits or variables (e.g., environment) might be overlaid with a study of this type? How much further would you like to see future studies of this type take us?

A: One of the great advantages of working with herbaria samples is that the date of collection of the samples is known. This information helps to calculate accurately mutation rates and, therefore, divergence times between different species or lineages within the same species. One can then correlate these changes with historical events. For example, in our study we have found that a great increase in genetic diversity in *Phytophthora infestans* falls into the time window of the first contact between Americans and Europeans during the Spanish conquest.

Q: In the paper, the list of authors represent a diversity of expertise in the plant sciences. How will future studies learn from this and leverage broad expertise to deduce complex problems for the betterment of agriculture? What can we learn about the migration of pathogens from a study of this nature? What is the influence of man versus nature on agriculture diseases?

A: Collaboration between experts of different fields is the way to approach biological problems. All biological fields gain in freshness and novelty with the outsider view from experts of a different research area. This project has shown how the consequences of a plant disease vary depending on socioeconomic and political factors. Even though in the nineteenth century, the same *P. infestans* strain triggered the outbreaks everywhere, its effects were stronger in Ireland than in continental Europe. It has also shown us how the spread of pathogens is strongly associated with human activity. As I mentioned above, the burst of diversity in *P. infestans* coincides with the Spanish conquest, which starts a big movement of people, animals, and aliments in the New World and between the New World and Europe. We have observed also how the introduction of resistance in potato through breeding has been a major selective force for *P. infestans*. ■

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>.

March 2013, Volume 26, Number 3

CURRENT REVIEW—Nitric Oxide as a Mediator for Defense Responses.

Evidence for Functional Diversification Within a Fungal NEP1-Like Protein Family.

Cytokinins Act Synergistically with Salicylic Acid to Activate Defense Gene Expression in Rice.

Genetic Determinants of *Potato virus Y* Required to Overcome or Trigger Hypersensitive Resistance to PVY Strain Group O Controlled by the Gene *Ny* in Potato.

Citrus tristeza virus p23: Determinants for Nucleolar Localization and Their Influence on Suppression of RNA Silencing and Pathogenesis.

Conditional Requirement for Exopolysaccharide in the *Mesorhizobium*–*Lotus* Symbiosis.

Structural Basis for Interactions of the *Phytophthora sojae* RxLR Effector Avh5 with Phosphatidylinositol 3-Phosphate and for Host Cell Entry.

Differential Activation of Ammonium Transporters During the Accumulation of Ammonia by *Colletotrichum gloeosporioides* and Its Effect on Appressoria Formation and Pathogenicity.

A Metabolic Regulator Modulates Virulence and Quorum Sensing Signal Production in *Pectobacterium atrosepticum*.

The AAA+ ATPases and H₉B/FtsH Proteases of ‘*Candidatus* *Phytoplasma mali*’: Phylogenetic Diversity, Membrane Topology, and Relationship to Strain Virulence.

April 2013, Volume 26, Number 4

Phytoplasma-Triggered Ca²⁺ Influx Is Involved in Sieve-Tube Blockage.

Nonhost Resistance of Tomato to the Bean Pathogen *Pseudomonas syringae* pv. *syringae* B728a Is Due to a Defective E3 Ubiquitin Ligase Domain in AvrPtoB_{B728a}.

Gene-for-Gene Tolerance to Bacterial Wilt in *Arabidopsis*.

The *rpg4*-Mediated Resistance to Wheat Stem Rust (*Puccinia graminis*) in Barley (*Hordeum vulgare*) Requires *Rpg5*, a Second NBS-LRR Gene, and an Actin Depolymerization Factor.

The AvrB_AvrC Domain of AvrXccC of *Xanthomonas campestris* pv. *campestris* Is Required to Elicit Plant Defense Responses and Manipulate ABA Homeostasis.

Random T-DNA Mutagenesis Identifies a Cu/Zn Superoxide Dismutase Gene as a Virulence Factor of *Sclerotinia sclerotiorum*.

Identification of Functional Genic Components of Major *Fusarium* Head Blight Resistance Quantitative Trait Loci in Wheat Cultivar Sumai 3.

High NaCl Concentrations Induce the *nod* Genes of *Rhizobium tropici* CIAT899 in the Absence of Flavonoid Inducers.

The Absence of Eukaryotic Initiation Factor eIF(iso)4E Affects the Systemic Spread of a *Tobacco etch virus* Isolate in *Arabidopsis thaliana*.

May 2013, Volume 26, Number 5

CURRENT REVIEW—Glutamate Metabolism in Plant Disease and Defense: Friend or Foe?

CURRENT REVIEW—Biological Nitrogen Fixation in the Context of Global Change.

Unexpected Phytostimulatory Behavior for *Escherichia coli* and *Agrobacterium tumefaciens* Model Strains.

Modification of *Tobacco rattle virus* RNA1 to Serve as a VIGS Vector Reveals That the 29K Movement Protein Is an RNA Silencing Suppressor of the Virus.

Genomic Segments RNA1 and RNA2 of *Prunus necrotic ringspot virus* Codetermine Viral Pathogenicity to Adapt to Alternating Natural *Prunus* Hosts.

In Vitro Translocation Experiments with RxLR-Reporter Fusion Proteins of Avr1b from *Phytophthora sojae* and AVR3a from *Phytophthora infestans* Fail to Demonstrate Specific Autonomous Uptake in Plant and Animal Cells.

Host Cell Ploidy Underlying the Fungal Feeding Site Is a Determinant of Powdery Mildew Growth and Reproduction.

Quorum Sensing and Indole-3-Acetic Acid Degradation Play a Role in Colonization and Plant Growth Promotion of *Arabidopsis thaliana* by *Burkholderia phytofirmans* PsJN.

The *dar* Genes of *Pseudomonas chlororaphis* PCL1606 Are Crucial for Biocontrol Activity via Production of the Antifungal Compound 2-Hexyl, 5-Propyl Resorcinol.

Effect of Clay Mineralogy on Iron Bioavailability and Rhizosphere Transcription of 2,4-Diacetylphloroglucinol Biosynthetic Genes in Biocontrol *Pseudomonas protegens*.

Trans-Specific Gene Silencing of Acetyl-CoA Carboxylase in a Root-Parasitic Plant.

New Linear Lipopeptides Produced by *Pseudomonas cichorii* SF1-54 Are Involved in Virulence, Swarming Motility, and Biofilm Formation.

The Mutualistic Fungus *Piriformospora indica* Protects Barley Roots from a Loss of Antioxidant Capacity Caused by the Necrotrophic Pathogen *Fusarium culmorum*.

June 2013, Volume 26, Number 6

LETTER TO THE EDITOR—Microbe-Independent Entry of Oomycete RxLR Effectors and Fungal RxLR-Like Effectors Into Plant and Animal Cells Is Specific and Reproducible.

CURRENT REVIEW—Contribution of Small RNA Pathway Components in Plant Immunity.

CURRENT REVIEW—Guarding the Green: Pathways to Stomatal Immunity.

Host-Induced Gene Silencing in Barley Powdery Mildew Reveals a Class of Ribonuclease-Like Effectors.

Water Deficit Modulates the Response of *Vitis vinifera* to the Pierce's Disease Pathogen *Xylella fastidiosa*.

A Simple Method for Comparing Fungal Biomass in Infected Plant Tissues.

Tobacco MAP Kinase Phosphatase (NtMKP1) Negatively Regulates Wound Response and Induced Resistance Against Necrotrophic Pathogens and Lepidopteran Herbivores.

A Rhamnose-Rich O-Antigen Mediates Adhesion, Virulence, and Host Colonization for the Xylem-Limited Phytopathogen *Xylella fastidiosa*.

Functional Interplay Between *Arabidopsis* NADPH Oxidases and Heterotrimeric G Protein.

Infection Structure-Specific Reductive Iron Assimilation Is Required for Cell Wall Integrity and Full Virulence of the Maize Pathogen *Colletotrichum graminicola*. ■

Welcome New Members

We have had 17 people join IS-MPMI between February 1 and May 31, 2013.
Please join us in welcoming them to the society!

Maik Boehmer
Westfaelische Wilhelms-
University
Muenster, Germany

Gulin Boztas
University of Worcester
Worcester, United Kingdom

Woo-Suk Chang
University of Texas at Arlington
Arlington, TX, U.S.A.

Ravendra P. Chauhan
Oklahoma State University
Stillwater, OK, U.S.A.

Elena Fantozzi
University of Worcester
Worcester, United Kingdom

Manjula Govindarajulu
University of California
Davis, CA, U.S.A.

Benjamin Kent Hall
John Innes Centre
Norwich, United Kingdom

Seogchan Kang
Penn State University
University Park, PA, U.S.A.

Eric Kemen
Max Planck Institute for Plant
Breeding Research
Cologne, Germany

Inju Ko
Los Angeles, CA, U.S.A.

Marc Libault
University of Oklahoma
Norman, OK, U.S.A.

Ana Lopez Sanchez
University of Sheffield
Sheffield, United Kingdom

Estrella Luna Diez
University of Sheffield
Sheffield, United Kingdom

Rofina Y. Othman
University of Malaya
Kuala Lumpur, Malaysia

Kee Sohn
Massey University
Palmerston North, New Zealand

Bethany L. Van Hameren
Centre for Integrative Legume Research
(CILR)
Brisbane, QLD, Australia

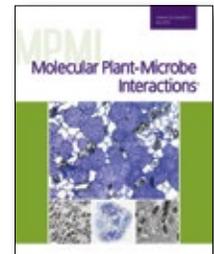
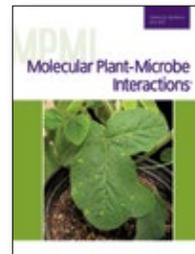
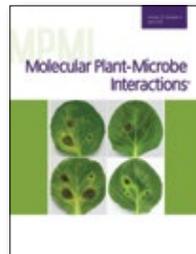
Christie E. Williams
USDA ARS at Purdue University
West Lafayette, IN, U.S.A.



Ground-Breaking Research

Top 10 MPMI Articles

May 2012–April 2013*



- Modulation of Host Immunity by Beneficial Microbes
- A Draft Genome Sequence of *Nicotiana benthamiana* to Enhance Molecular Plant-Microbe Biology Research
- Callose Deposition: A Multifaceted Plant Defense Response
- Bacterial Endophytes and Their Interactions with Hosts
- Oxalic Acid Is an Elicitor of Plant Programmed Cell Death during *Sclerotinia sclerotiorum* Disease Development
- Functional Characteristics of an Endophyte Community Colonizing Rice Roots as Revealed by Metagenomic Analysis
- The Type VI Secretion System: A Multipurpose Delivery System with a Phage-Like Machinery
- *Nicotiana benthamiana*: Its History and Future as a Model for Plant-Pathogen Interactions
- Activation of the *Arabidopsis thaliana* Mitogen-Activated Protein Kinase MPK11 by the Flagellin-Derived Elicitor Peptide, flg22
- Understanding the Plant Immune System

*COUNTER 3-compliant statistical report.

Publish in MPMI: Be Included in the Translational Research MPMI Focus Issue

This special issue of *Molecular Plant-Microbe Interactions* (MPMI) will bring extra attention to scientists who are making advancements in this critically important area.

“We expect this issue to be highly cited, and the single-topic format gives researchers a place to present their work alongside the related work of their peers to show the collective progress being made in translational research. If you are doing work in this area, you will want to take advantage of this opportunity to be part of something special.”

—Jane Glazebrook, MPMI Editor-in-Chief

Submit today at www.ismpminet.org/journal/MPMIFocus13_TranslationalResearch.htm