Issue No. 3, 2011

IS-MPMI Reporter

International Society for Molecular Plant-Microbe Interactions

IN THIS ISSUE

XV International Congress in 2012 — Present Your Innovative Plant-Microbe Research in Japan

The fourth meeting of the Local Organization Committee (not all organizers were able to participate). View a listing of the committee members at http://mpmi2011.umin.jp/about.html.

The XV International Congress on Molecular Plant-Microbe Interactions (MPMI) will be held in Kyoto, Japan, from July 29 to August 2, 2012. The venue is the Kyoto International Conference Center, which is situated on a hillside in the northern area of Kyoto. Kyoto is the old capital of Japan with beautiful temples, shrines, and palaces throughout the city. The Kyoto International Conference Center is located approximately 5 km north of the downtown area. In downtown, there are a number of restaurants that serve traditional Japanese foods as well as Asian, Indian, and western cuisines.

We sincerely hope you will be able to participate. With the XV International Congress moving to 2012, we have had more time to provide you with the best program possible. The website now has updated program information at http://mpmi2011.umin.jp/program.html. The XV International Congress on Molecular Plant-Microbe Interactions is recognized as the most important international meeting for plant-microbe interactions to discuss research and network with colleagues from around the world. This meeting is the global venue for presenting and discussing new research and developments in molecular plant-microbe interactions. Through plenary lectures, concurrent sessions, special workshops, and various events, attendees will experience innovative plant-microbe interactions research. The meeting will feature hundreds of abstracts and provide multiple networking and professional development opportunities.

Prepare your abstracts today, and plan to present your findings to your MPMI colleagues. Make sure to check out the important information regarding the call for abstracts. Submission opens December 7, 2011, and closes on April 17, 2012. Registration for the event opens December 7, 2011, with the deadline for early registration on May 15, 2012. Accommodation information is also available at http://mpmi2011.umin.jp/regist.html.

I apologize to you for the postponement of the congress due to the Great East Japan Earthquake on March 11, 2011. I have received messages of sympathy and encouragement from around the world. I would like to express our heartfelt thanks for your warm messages of concern and comfort. All the members of the Organizing Committee feel that we should cheer up Japan by having a successful IS-MPMI Congress in Kyoto in 2012. Therefore, I would like to ask you to give a talk or poster that will include the most exciting new results from your group. This is your chance to be a part of a staple in the MPMI community. Tell your colleagues today, and sign up to join us.

I look forward to seeing you all in Kyoto next year!

Ko Shimamoto
Chair, Organizing Committee for the 2012 IS-MPMI Congress in Kyoto
mpmikyoto2012@bs.naist.jp ■

Important Dates for the XV International Congress on MPMI

Call for Abstracts
- Opens **December 7, 2011**
- Closes **April 17, 2012**

Registration
- Opens **December 7, 2011**

Early registration deadline
- **May 15, 2012**

IX International Congress
- **July 29–August 2, 2012**

http://mpmi2011.umin.jp/

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***IS-MPMI REPORTER* DEADLINE**

The deadline for submitting items for the next issue is January 16, 2012.

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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Felice Cervone, President

A Letter from the President

The message that appeared in the *Reporter* last June was announced to be my last message as a president of IS-MPMI. Soon after, given the cancellation of the Kyoto meeting and considering that my regular presidency (2010–2011) would not allow me to open our biennial congress, which was postponed to 2012, the Board of Directors asked me to remain in charge for one year longer. I accepted with great pleasure because, as I said in previous messages, it is a great honor to represent the vibrant IS-MPMI scientific community. It is also a pleasure for me to see how our colleagues in Japan, in spite of the adversities suffered for the earthquake and tsunami, are enthusiastically working to organize an exciting XV IS-MPMI Congress for next year. I look forward to meeting them and all of you next year in Kyoto. I am sure that young researchers and prestigious scientists will come from all over the world and contribute to make the Kyoto meeting another step of the successful life of our society. ■

Welcome New Members

The following members joined IS-MPMI between May 1 and November 30, 2011.
Please join us in welcoming them to the society!

Xiaoli Chang
Botanical Institute 1
Karlsruhe, Germany

Jigang Han
Shanghai Botanical Garden
Shanghai, Peoples Rep of China

Yuichiro Iida
Natl Inst of Vegetable & Tea Science
Tsu, Japan

James M. Kremer
Michigan State University
East Lansing, MI, U.S.A.

Yi Li
Peking University
Beijing, Peoples Rep of China

Vanessa J. Melino
Murdoch University
Coolbellup, WA, Australia

Junji Miyazaki
CSIRO Plant Industry
Narrabri, NSW, Australia

Jose F. Moran
Public University of Navarre
Pamplona, Spain

David Munch
Copenhagen University
Copenhagen, Denmark

Catalina I. Pislariu
The Samuel Roberts Noble Foundation
Ardmore, OK, U.S.A.

Daniel Tome
University of Warwick
Warwick, United Kingdom

Mireille Van Damme
Wageningen University
Wageningen, Netherlands

Martin J. Wubben
USDA ARS
Starkville, MS, U.S.A.

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.

Wladimir Tameling

Post-Doctoral/Early Career Member

Wladimir Tameling
Laboratory of Phytopathology
Wageningen University
Wageningen, The Netherlands

Nibblers, that has been my main topic since 1999. So, by now I have gained quite some knowledge on these interesting proteins. Nibblers, you probably have heard about them before, it's an acronym used for nucleotide-binding, leucine-rich repeat proteins (NB-LRRs) that compose the biggest class of immune receptors from plants.

During my Ph.D. project I started working on a nibbler from tomato, called I-2, that confers resistance to *Fusarium oxysporum*. This was at the Plant Pathology Department of the University of Amsterdam, The Netherlands, under the supervision of **Frank Takken** and **Ben Cornelissen**. In the early nineties of the last century, the first nibblers were cloned and in the last month of that century I started my Ph.D. project. Since the cloning of the first nibblers, it was noted that they contain highly conserved sequence motifs that were also detected in P-loop-containing ATP/GTP-binding proteins. The nibbler domain that carries these motifs was later called the NB-ARC domain. My goal was to study whether this domain could indeed function as an ATPase/GTPase. By performing experiments with recombinant I-2 purified from *E. coli*, I could show for the first time that the NB-ARC domain indeed binds ATP and is able to hydrolyze it to ADP. The later discovery of constitutively active I-2 mutants that were locked in the ATP-bound state led to our model that the NB-ARC domain functions as a molecular switch. This switch most likely regulates the signaling activity of these immune receptors after recognition of the matching pathogen-derived effector. In 2009, Frank and I updated the molecular switch model on the basis of new research in the nibbler field and published this in *Science*. It was a great pioneering project that was quite successful.

After obtaining my Ph.D. degree, I met **David Baulcombe** at a conference and I asked him whether he had a post-doc position available. Luckily, this was the case, so at the beginning of 2004, I joined his group at the Sainsbury Laboratory, Norwich, United Kingdom. I started to work on another nibbler called Rx, which confers resistance to *Potato virus X* (PVX) in potato, but also in other solanaceous plants. As we wanted to know how immune receptors initiate the signal transduction cascade upon pathogen-recognition leading to defense, I affinity-purified a tagged version of Rx from *Nicotiana benthamiana*. Ran GTPase-activating protein 2 (RanGAP2) was copurified as an interacting protein and identified by mass spectrometry. Silencing of the encoding gene revealed that it is required for resistance against PVX. As David's group has its main focus on elucidating the molecular mechanism of the RNA silencing machinery, I also had the opportunity to learn about this topic. However, because of this strong focus we were only with a few scientists that studied nibblers. As scientists of other groups in the Sainsbury Laboratory (the Rathjen lab, the Shirasu lab, and the Jones lab) also worked on this topic, I decided to set up the NB-LRR forum that we held once a month. I enjoyed this forum a lot and in this way we could all learn from each other's results and ideas. I enjoyed working at the Sainsbury Laboratory a lot.

By the end of 2006, I moved for a senior post-doc position to the SOL-group of **Matthieu Joosten** in the Laboratory of Phytopathology of Wageningen University, The Netherlands. As part of the EU-funded integrated project Bioexploit, I was able to bring the nibbler research (on Rx) from Norwich to Wageningen. In collaboration with **Erik Slootweg**, working in the group of **Aska Goverse** at the Laboratory of Nematology from our university, we focused on the subcellular localization of Rx. We discovered that it did not only localize to the cytoplasm, as was hypothesized for a long time, but also in the nucleus. In 2008, I received a personal Veni grant from the Netherlands Organization for Scientific Research (NWO) with which I could proceed my research on this nibbler. We discovered that for proper immune signal-initiation a pool of Rx needs to be present in both the cytoplasm as well as in the nucleus. Shifting the equilibrium to either side compromised the resistance to PVX. Furthermore, we found that Rx binding to RanGAP2 is important for its stability and that the latter serves as a cytoplasmic retention factor that balances the ratio between the pool of Rx in the cytoplasm and the nucleus. This work has recently been published as a back-to-back publication with the Laboratory of Nematology in *The Plant Cell*, which resulted in 39 pages of Rx research in one issue!

Within the SOL-group of Joosten, I am leading the NB-LRR subgroup. In addition to Rx, we also study a nibbler from tomato called NRC1, which functions as a signal transduction protein downstream of both extracellular as well as intracellular immune receptors, rather than serving as an immune receptor itself. Our aim is to unravel the mechanism by which it can integrate the signaling events from different types of immune receptors. **Daniela Sueldo**

Meet IS-MPMI Members *continued on page 4*

Meet IS-MPMI Members *continued from page 3*

(Ph.D. student) and **Patrick Smit** (post-doc) are trying to shed light on this, for example by identifying NRC1-interactors. With nibblers being my subject, I now would like to start my own lab, which might be in Wageningen, but could also be somewhere else. This will depend on the opportunities that will come on my path in the near future.

Being a member of IS-MPMI is very nice. You get to know easily about what other scientists are doing in your field, not only at the IS-MPMI congres, but you can also read it in the *Molecular Plant-Microbe Interactions* journal or the *IS-MPMI Reporter*. Two months before I started my Ph.D. project, I had the opportunity to join the IS-MPMI conference in Amsterdam, The Netherlands. I could use the conference as a crash course on plant-microbe interactions, which was quite useful, although also a little bit intimidating for a Ph.D. student that had not even started. Since then I have attended all IS-MPMI conferences, except one, which was very valuable to gain a lot of knowledge in this field. ■

Daniel F. Klessig Named 2011 Noel T. Keen Awardee

Daniel F. Klessig

This year, the recipient of The American Phytopathological Society's Noel T. Keen Award for Research Excellence in Molecular Plant Pathology is IS-MPMI member **Daniel F. Klessig**, Boyce Thompson Institute. This award recognizes those who have made outstanding contributions and demonstrated sustained excellence and leadership in research that significantly advances the understanding of molecular aspects of host-pathogen interactions, plant pathogens or plant-associated microbes, or molecular biology of disease development or defense mechanisms.

Klessig, in an interview with IS-MPMI, provided the following perspectives on his research and mentors who have supported him during his career. When notified he was this year's recipient of the award, he indicated, "I felt honored to receive the Noel T. Keen Award, which is named for a friend and colleague who was a pioneer in molecular plant pathology."

Q: What would you consider your contributions to the field of molecular plant-microbe interactions?

A: In 31 years of research, I worked on both plant and animals. I made contributions in the field of plant-microbe interactions and have worked with a group to establish that salicylic acid and nitric oxide act as critical endogenous signaling molecules for the activation of plant defenses. Recently we showed that methyl salicylic acid acts as the mobile signal for the induction of systemic acquired resistance, a phenomenon that was discovered over 100 years ago.

Q: Who have been your mentors? Are there any scientists who have guided you along the way or carved a path for you (historical or real life)?

A: I have had several excellent mentors—the most famous being **Jim Watson**, my Ph.D. advisor. But equally important was **Barbara McClintock**, who befriended and encouraged me as a young Harvard graduate student in a highly competitive Cold Spring Harbor Laboratory (CSHL). She admonished me to "think outside the box", to let nature reveal it secrets through careful observation, and to not be confined or restricted in one's thinking by the current scientific dogma. This advice was extremely important when I was trying to understand the confusing data that **Rich Gelinas**, **Rich Roberts**, and I had obtained concerning transcription of human adenovirus in the mid-1970s. The data did not fit the established dogma, which was based largely on results from studies on prokaryotes, that a gene was encoded as a contiguous unit on the genome. Most of our colleagues at CSHL, including my mentor, thought we were "chasing" experimental artifacts since the data was totally inconsistent with this established dogma. As I struggled for almost two years to make sense of our conflicting results, Barbara's admonishment to think outside the dogma box probably acted as a catalyst, leading to my proposal that genes in eukaryotes are noncontiguous/split, with the encoded primary transcripts corresponding to the then-mysterious large heterogeneous nuclear (hn)RNA, which was processed by RNA splicing (intramolecular ligation) into mRNA. To relax and reflect, I frequently walk a few blocks from my lab to Cornell University's Plantation. The Plantation grounds includes Barbara's former corn plots, where she conducted some of her pioneering work on maize genetics that lead to her discovery of transposable elements (jumping genes). Those breaks occasionally have lead to insight into our current research, so one might say that I'm still being inspired by Barbara.

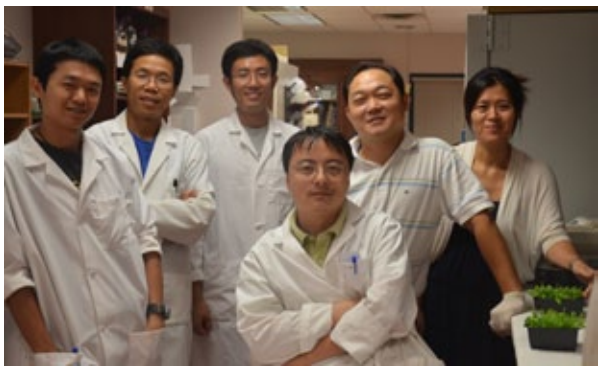
Q: What's next for you?

A: I will continue, for the next few years, our studies on plant immunity with a focus on i) further characterization of SA signal transduction and its mechanisms of action, and ii) determining the mechanism of action CRT1, which is involved in four distinct levels of immunity. Obviously, there is more than enough to do until retirement. ■

Toward an Understanding of Early Signaling Events in Plant Innate Immunity

Below is an interview with **Libo Shan** and colleagues from the Molecular & Environmental Plant Sciences, Institute for Plant Genomics and Biotechnology at Texas A&M University on their article "Direct Ubiquitination of Pattern Recognition Receptor FLS2 Attenuates Plant Innate Immunity" recently published in *Science* (Lu et. al, 2011, *Science* 332 (6036): 1439-1442)

Q: How did the study start (was it all completely planned from the beginning, did some unexpected findings play a role, where did ideas come from)?



Key members of the collaborative team working on this research include those pictured here (from left to right) Wenwei Lin, Xiquan Gao, Cheng Cheng, Dongping Lu, Ping He, and Libo Shan.

A: Our long-term research goal is to understand early signaling events in plant innate immunity. We, along with several groups, have demonstrated the importance of BAK1 in multiple microbe-associated molecular pattern (MAMP)-mediated responses. This provoked us to use BAK1 as bait to look for additional components involved in innate immune signaling. We initiated an unbiased yeast two-hybrid screen using BAK1 kinase domain as bait against bacteria-treated Arabidopsis cDNA library. One of the interactors isolated from the screen encoded an E3 ubiquitin ligase PUB13, which later turned out to be the central player of our story. We confirmed the interaction with in vivo and in vitro assays. However, like most of screening projects, the progress was rather slow at the beginning, as we were not very sure which BAK1 interactors were biological significant. The project took off at the moment when the leading author of the paper, Dr. **Dongping Lu**, demonstrated that PUB13 associated with flagellin receptor FLS2 in a ligand-dependent manner, which is distinct from the constitutive association of BAK1 and PUB13. We were also excited to see ligand-induced FLS2-PUB13 interaction depended on BAK1. We were confident that PUB13 must play certain roles in flagellin-mediated signaling.

Q: What is the composition of the group involved (Ph.D. students, post-docs, other collaborators, nationalities, atmosphere during the work)?

A: The project was led mainly by a group of extremely motivated and hard-working post-doc and students. They formed a very collaborative team and shared the results and experience freely. At the beginning, we failed to detect the ubiquitination of PUB13 on FLS2 or BAK1 with commercial ubiquitination system. On a joint-group meeting with Dr. **Timothy Devarenne**'s lab, we were fascinated by their "home-made" Arabidopsis ubiquitination system. In collaboration with Devarenne's lab, we were able to detect PUB13 ubiquitination on FLS2 but not BAK1, which was another excitement along the story development. When we attempted to examine the endogenous FLS2 protein level, we got great help from Dr. **Antje Heese** at the University of Missouri–Columbia. The collaborative atmosphere among different groups was absolutely essential for our discovery in various perspectives.

Q: What were the big stumbling blocks? How did you manage to get them out of the way (if any)?

A: We have had many stumbling blocks along the way, just like many other scientific discoveries. But the persistence and critical thinking are the keys to move the science forward. For instance, at the beginning, we were unable to amplify PUB12 cDNA despite multiple trials. Later, Dr. Lu figured out a mis-annotation in the TAIR database. Although in vitro ubiquitination assay has been routinely used in plant research, the system to examine in vivo ubiquitination status for plant proteins is limited. We spent quite some time to develop a protoplast transient transfection-based in vivo system to study FLS2 ubiquitination. Unlike in vitro ubiquitination, this system could reveal the dynamics of protein ubiquitination upon ligand perception. We believe this is a great tool for plant research.

Q: What's next?

A: Many interesting and obvious questions await us to explore. For example, we are examining the detailed biochemical mechanisms of how FLS2 is ubiquitinated and testing whether other pattern recognition receptors are regulated in a similar way. We know way too little about how the immune signaling is regulated and we believe that evolution must have shaped elegant yet complex signaling networks to fine-tune the immune responses upon infection. We are continuing our exploratory journey with the development of innovative genetic and biochemical tools and strategies. ■

XV International Congress on Molecular Plant-Microbe Interactions

Date:
July 29 (Sun.)–
August 2 (Thu.), 2012

Abstract submission:
December 7 (Wed.), 2011–
April 17(Tue.), 2012

Venue:
Kyoto International Conference Center
(Kyoto, Japan)

Chair:
Ko Shimamoto
(Nara Institute of Science and Technology)

Confirmed speakers

- Jeff Dangl (USA)
- Jean Dénarié (France)
- Maria Harrison (USA)
- Sheng Yang He (USA)
- Jonathan Jones (UK)
- Sophien Kamoun (UK)
- Paul Schulze-Lefert (Germany)
- Jen Sheen (USA)
- Brian J Staskawicz (USA)
- Jens Stougaard (Denmark)
- Jian-min Zhou (China)
- Cyril Zipfel (UK)

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IS-MPMI Kyoto 2012

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Employment

R&D Group Leader—BioAg
We are seeking an energetic, results- and action-oriented individual to lead our BioAg R&D team. As a key member of management, you will drive project execution by properly anchoring and monitoring many technically complex R&D projects in the organization. If you're looking for a leadership opportunity in a growing business, you may be the leader we're looking for to lead and develop a team of scientists; establish and drive project execution within a research program that leads to new technologies, products, and meaningful intellectual property; foster an atmosphere of continuous improvement and champion the implementation of solutions that impact the department or overall business; interact effectively cross-functionally providing technical and resource insight; and build and maintain a network of external collaborations that cultivate project success as well as provide access to new technologies and intellectual property. Requirements: Ph.D. degree with 8+ years of industry experience or M.S. degree with significant industrial experience, applicable disciplines include microbiology, plant pathology, plant physiology, or mycology (Ph.D. degree is strongly preferred); strong research experience in areas of plant-microbe interactions, insect-microbe interactions, environmental microbiology, microbial physiology, microbial ecology, or fungal biology preferred; 8+ years of agricultural industry experience a plus; demonstrated leadership skills; experience in the development or validation of agricultural products; experience with microbial or microbial-derived products for the agriculture industry preferred; ability to work independently and effectively manage multiple projects; ability and willingness to travel domestically and internationally (20–25%); and ability to work in the United States without sponsorship. Step up for the challenge and apply online at www15.i-grasp.com/fe/tpl_Novozymes01.asp?newms=jj&id=42468 or www15.i-grasp.com/fe/tpl_Novozymes01.asp?newms=jj&id=38011. Novozymes is an equal opportunity/affirmative action employer M/F/D/V.

Post-Doctoral Position
A post-doctoral research position in molecular nematology is available in the laboratory of Martin Wubben (USDA-ARS) through the Department of Plant and Soil Sciences at Mississippi State University, Starkville, MS. Plant-parasitic nematodes secrete effector proteins into host root cells in order to initiate feeding site formation. These effector proteins are transcribed from parasitism genes located within the nematode esophageal gland cells. Feeding site formation requires significant changes in root cell morphology, signal transduction, and gene expression. The successful candidate will work to identify and characterize candidate parasitism genes of the reniform nematode, *Rotylenchulus reniformis*, using a combination of targeted next-generation sequencing, bioinformatics, and molecular tools including RNA interference. It is expected that discoveries made during this project will lead to the development of novel control measures of plant-parasitic nematodes in soybean and cotton. The position will have a duration of three years and will be renewable annually dependent upon satisfactory performance and continuation of funding. To be considered, applicants must possess a Ph.D. degree in genetics, plant pathology, biochemistry, or related field with demonstrated expertise in molecular biological methods and bioinformatics. Previous experience in plant-microbe interactions or nematology is a plus but not required. The successful candidate must also possess excellent written skills and be able to communicate effectively with other members of the research group. Send curriculum vita, including names of three referees, to Martin Wubben, Crop Science Research Lab, 810 Highway 12 East, Mississippi State, MS 39762 U.S.A., or by e-mail to Martin.Wubben@ars.usda.gov.

Post-Doctoral Position in Jeff Dangl's Lab, University of North Carolina, Chapel Hill
My lab will have space and resources for several new post-docs starting now and over the next 18 months. Successful candidates will have expertise and success in the relevant areas noted below, as demonstrated by *first author* papers in highly ranked international journals. Priority will be given to candidates who have identified independent funding sources for which they are eligible and to which they are prepared to apply. Send CV and the names and contact information of three references to dangl@email.unc.edu. See www.bio.unc.edu/faculty/dangl. **Dissection of functionally relevant signaling nodes in the Arabidopsis immune system network.** We defined 105 proteins in the Arabidopsis proteome that are direct targets of ~100 pathogen virulence factors isolated from a bacterial and a eukaryotic pathogen. These virulence factors have independently evolved for ~3 billion years and are deployed by organisms that use completely different protein delivery systems to perturb host cell immune function. Nevertheless, and amazingly, the virulence factors from these two diverse pathogens converge onto a set of 105 interconnected host cellular nodes. Using reverse genetics, we established that 15 of the first 17 host proteins assayed, those that are targeted by both pathogens, are required for wild-type immune responses. We have shown that mutations in a total of 58/80 of the 105 host proteins tested to date also suppress immune system output. The goal of this project is to dissect further selected cellular machines that are repeatedly target by pathogen virulence factors. Skills required: This project requires a fascination with genetics, plant pathology, and systems biology/genomics. (*Arabidopsis* Interactome Mapping Consortium. 2011. Evidence for network evolution in an *Arabidopsis* interactome map. Science 333:602-607.) (Mukhtar, M. S., Carvunis, A.-R., Dreze, M., Epple, P., Steinbrenner, J., Moore, J., Tasan, M., Galli, M., Hao, T., Nishimura, M. T., Pevzner, S. J., Donovan, S. E., Ghamsari, L., Santhanam, B., Romero, V., Poulin, M. M., Gebreab, F., Gutierrez, B. J., Tam, S., Monachello, D., Boxem, M., Harbort, C. J., McDonald, N., Gai, L., Chen, H., He, Y., EU Effectoromics Consortium, Vandenhaute, J., Roth, F. P., Hill, D. E., Ecker, J. R., Vidal, M., Beynon, J.,

Employment *continued on page 8*

Employment *continued from page 7*

Braun, P., and Dangl, J. L. 2011. Independently evolved virulence effectors converge onto hubs in a plant immune system network. Science 333:596-601.)

Post-Doctoral Positions in Microbiomes and Innate Immune Receptors

Jeff Dangl's lab will have space and resources for several new post-docs starting now and over the next 18 months. Successful candidates will have expertise and success in the relevant areas noted below, as demonstrated by *first author* papers in highly ranked international journals. Priority will be given to candidates who have identified independent funding sources for which they are eligible and to which they are prepared to apply. Send CV and the names and contact information of three references to dangl@email.unc.edu. See www.bio.unc.edu/faculty/dangl. **Plant associated microbiomes.** Essentially all land plants grow in intimate association with complex microbial communities both above the ground (phyllosphere) and below the ground on roots and the immediately surrounding area (rhizosphere). The relationships between a microbiota (the community of microbes intimately associated with a plant) and its host can vary from pathogenic to mutualistic or commensal. The microbiome (the set of genes encoded by any particular microbiota) can perform ecosystem services, such as providing the host plant with one or more critical nutrients, protecting a plant from pathogens, producing functional plant hormones, and providing tolerance to abiotic stress. In this project, we use next-gen DNA sequencing technologies to define root-associated microbiomes and then we will use plant genetics to define the host loci that control assembly of specific microbial consortia. Skills required: This project requires a fascination with, and demonstrated expertise in, some combination of large-scale genomics and HT DNA sequencing technologies, computational biology, population genetics, and/or root biology, as well as an appreciation for the large-scale organization skills that define success in this arena. **Function of plant innate immune receptors.** Plants, like animals, deploy a specific kind of intracellular receptor to recognize intracellular microbial molecules of "damaged" host proteins that are the targets of pathogen virulence factors. We study these in several contexts in the plant immune system using the highly developed Arabidopsis model system and various bacterial and fungal pathogens. Skills required: This project will focus on techniques to understand protein localization and function and requires a fascination with cell biology, immunology, plant-microbe interactions, and protein structure. (Chung, E. H., da Cunha, L., Wu, A.-J., Gao, Z., Cherkis, K., Afzal, A. J., Mackey, D., and Dangl, J. L. 2011. Specific threonine phosphorylation of a host target by two unrelated type III effectors activates a host innate immune receptor in plants. Cell Host Microbe 9:125-136. doi:10.1016/j.chom.2011.01.009.) (Gao, Z., Chung, E.-H., Eitas, T. K., and Dangl, J. L. 2011. The plant intracellular innate immune receptor RPM1 is activated at, and functions on, the plasma membrane. Proc. Natl. Acad. Sci. USA 108:7619-7624. doi:10.1073/pnas.1104410108.)

Post-Doctoral Position in Genetic and Biochemical Processes

A post-doctoral position is available in the laboratory of Brad Day at Michigan State University to study the genetic and biochemical processes involved in disease resistance of plant-pathogen interactions mediated by the actin cytoskeleton. Research in our laboratory focuses on the model host-pathogen system *Arabidopsis thaliana-Pseudomonas syringae*, with an interest in host defenses required for resistance to bacterial infection. The current position will work in the area of biochemistry and genetics, specifically in the area of elucidating the role of the actin skeleton in plants and its role in defense signaling. Recent work can be found in Tian et al. (2009) in *Plant Physiology* and Day et al. (2011) in *Annual Review of Phytopathology*. The incumbent should posses a Ph.D. degree in molecular biology, plant biology, or biochemistry and have working knowledge of bacterial or fungal pathogenesis, as well as plant biochemistry and molecular biology. A recent Ph.D. degree is preferred. Interested applicants should send a CV, a copy of at least one recent paper, and the names and contact information of three persons who can provide a letter of reference. Please send information by e-mail to bday@msu.edu.

Post-Doctoral Positions in Biology of Soybean Root Hair Cell and Chitin

Two post-doctoral positions are available immediately in the laboratory of Gary Stacey at the University of Missouri, Columbia, MO, U.S.A. The first position relates to our continuing studies of the systems biology of the soybean root hair cell (see *Trends in Plant Science* 15:641). The second position relates to our studies on the role of chitin as an elicitor of plant disease resistance (see *Plant Cell* 20:471). The laboratory is highly productive and the successful candidate will be joining excellent teams working on these projects. The successful candidates should have excellent training in genetics, molecular biology, and/or biochemistry with clear evidence of past research productivity. With regard to the chitin project, applicants should demonstrate a strong background in plant pathology or related area. Further information about the laboratory can be obtained at www.staceylab.missouri.edu. Candidates should submit a cover letter indicating their interest in one of the two positions and detailing experience and past research success. Include a copy of your curriculum vitae and submit three reference letters attesting to your suitability for this position. Send all information via e-mail to staceyg@missouri.edu.

Assistant Professor in Molecular Plant-Virus Interactions

The Department of Plant Pathology, Physiology & Weed Science, College of Agriculture & Life Sciences, at Virginia Polytechnic Institute and State University (Virginia Tech) in Blacksburg, Virginia, seeks applicants for a tenure-track position at the assistant professor level. We seek a creative individual who will employ cellular, molecular, and/or genomic approaches to understand interactions between plants and viruses. We are interested in scientists who will focus on understanding molecular aspects of plant-virus interactions in crop and/or model systems, with preference given to research that relates directly to important viral disease problems. Research areas could include mechanisms of viral infection or movement,

reprogramming of host gene expression by gene silencing or other mechanisms, host resistance, and/or interaction with arthropod vectors. These questions will be addressed through advanced molecular, cellular, or genomic methodologies. It is essential that the candidate possess the background and expertise to teach virology modules in graduate-level courses. The successful candidate will develop an extramurally funded, internationally recognized research program; contribute to graduate-level courses in plant-microbe interactions; and mentor students. The candidate will participate in a strong interdepartmental molecular plant science graduate program. Additional information can be found at www.ppws.vt.edu and www.molplantsci.org.vt.edu. Applicants are to submit an online application for position #0111067 at https://listings.jobs.vt.edu. A complete application must include a cover letter, curriculum vitae, a research and teaching statement, and names and complete contact information of three references. Review of applications will begin on December 5, 2011, and will continue until the position is filled or the search is closed. Virginia Tech has a strong commitment to the principles of diversity, inclusion, and maintaining a work and learning environment that is free of all forms of discrimination. As a result, this institution does not tolerate discrimination or harassment on the basis of age, color, disability, gender, national origin, political affiliation, race, religion, sexual orientation, or veteran status. Anyone having questions concerning discrimination should contact the office of equal opportunity. Responsibilities: Develop and maintain a productive, internationally recognized research program through extramural funding; contribute to graduate courses in molecular plant-microbe interactions and plant pathology; advise and mentor undergraduate and graduate students, as well as post-doctoral fellows; participate in department, college, university, and professional service and outreach activities; adhere to the responsibilities of the faculty as described by the Faculty Handbook (www.provost.vt.edu/fhb.html); and commitment and sensitivity to issues of diversity in the campus community. Qualification/Requirements: An earned doctorate in the life sciences with demonstrated experience in molecular and/or cellular aspects of plant-virus interactions; a record of publication indicative of the potential to establish and maintain a productive research program; ability to articulate a coherent agenda of research or scholarship and to identify potential funding sources to support such research; and effective communication skills and ability to work within a team environment. Preferred Qualifications: Post-doctoral experience; success in attracting extramural research funding; shared interests with other scientists studying plant biology and infectious disease across the university; ability and willingness to work collaboratively with faculty from a variety of disciplines; teaching expertise in plant virology; and ability to work with a student body from diverse backgrounds. ■

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

July 2011, Volume 24, Number 7

CURRENT REVIEW—The Type VI Secretion System: A Multipurpose Delivery System with a Phage-Like Machinery.

Transcript Profiles in Sugar Beet Genotypes Uncover Timing and Strength of Defense Reactions to *Cercospora beticola* Infection.

Pectobacterium carotovorum Elicits Plant Cell Death with DspE/F but the *P. carotovorum* DspE Does Not Suppress Callose or Induce Expression of Plant Genes Early in Plant–Microbe Interactions.

The Helper Component Proteinase Cistron of *Potato virus Y* Induces Hypersensitivity and Resistance in Potato Genotypes Carrying Dominant Resistance Genes on Chromosome IV.

Development of Functional Symbiotic White Clover Root Hairs and Nodules Requires Tightly Regulated Production of Rhizobial Cellulase CelC2.

Melampsora larici-populina Transcript Profiling During Germination and Timecourse Infection of Poplar Leaves Reveals Dynamic Expression Patterns Associated with Virulence and Biotrophy.

PvRACK1 Loss-of-Function Impairs Cell Expansion and Morphogenesis in *Phaseolus vulgaris* L. Root Nodules.

Molecular Cloning of ATR5^{Emoy2} from *Hyaloperonospora arabidopsidis*, an Avirulence Determinant That Triggers RPP5-Mediated Defense in *Arabidopsis*.

Expression of an Oxalate Decarboxylase Impairs the Necrotic Effect Induced by Nep1-like Protein (NLP) of *Moniliophthora perniciosa* in Transgenic Tobacco.

Resistance to *Tomato yellow leaf curl virus* Accumulation in the Tomato Wild Relative *Solanum habrochaites* Associated with the C4 Viral Protein.

August 2011, Volume 24, Number 8

CURRENT REVIEW—Lipo-chitooligosaccharide Signaling in Endosymbiotic Plant-Microbe Interactions.

CURRENT REVIEW—Horizontal Gene Transfer in Nematodes: A Catalyst for Plant Parasitism?

The Sesquiterpene Botrydial Produced by *Botrytis cinerea* Induces the Hypersensitive Response on Plant Tissues and Its Action Is Modulated by Salicylic Acid and Jasmonic Acid Signaling.

An Autoactive Mutant of the M Flax Rust Resistance Protein Has a Preference for Binding ATP, Whereas Wild-Type M Protein Binds ADP.

Phytobacterial Type III Effectors HopX1, HopAB1 and HopF2 Enhance Sense-Post-Transcriptional Gene Silencing Independently of Plant R Gene-Effector Recognition.

Cell Death Mediated by the N-Terminal Domains of a Unique and Highly Conserved Class of NB-LRR Protein.

Phosphoproteome Analysis of *Lotus japonicus* Roots Reveals Shared and Distinct Components of Symbiosis and Defense.

Protein Kinase C Is Likely to be Involved in Zoosporogenesis and Maintenance of Flagellar Motility in the Peronosporomycete Zoospores.

Xanthomonas campestris Diffusible Factor Is 3-Hydroxybenzoic Acid and Is Associated with Xanthomonadin Biosynthesis, Cell Viability, Antioxidant Activity, and Systemic Invasion.

Transcriptional Analysis of Soybean Root Response to *Fusarium virguliforme*, the Causal Agent of Sudden Death Syndrome.

Suppressors of RNA Silencing Encoded by the Components of the Cotton Leaf Curl Begomovirus-BetaSatellite Complex.

High Levels of a Fungal Superoxide Dismutase and Increased Concentration of a PR-10 Plant Protein in Associations Between the Endophytic Fungus *Neotyphodium lolii* and Ryegrass.

September 2011, Volume 24, Number 9

The Transcriptome of *Fusarium graminearum* During the Infection of Wheat.

Role of Type IV Pili in Virulence of *Pseudomonas syringae* pv. *tabaci* 6605: Correlation of Motility, Multidrug Resistance, and HR-Inducing Activity on a Nonhost Plant.

The Ectopic Expression of a Pectin Methyl Esterase Inhibitor Increases Pectin Methyl Esterification and Limits Fungal Diseases in Wheat.

Role of Hydroxycinnamic Acids in the Infection of Maize Silks by *Fusarium graminearum* Schwabe.

Systematic Mutagenesis of All Predicted *gntR* Genes in *Xanthomonas campestris* pv. *campestris* Reveals a GntR Family Transcriptional Regulator Controlling Hypersensitive Response and Virulence.

The Cucurbit Pathogenic Bacterium *Acidovorax citrulli* Requires a Polar Flagellum for Full Virulence Before and After Host-Tissue Penetration.

A Dual-Targeted Soybean Protein Is Involved in *Bradyrhizobium japonicum* Infection of Soybean Root Hair and Cortical Cells.

Changes in Carbohydrate Metabolism in *Plasmopara viticola*-Infected Grapevine Leaves.

The *Botrytis cinerea* Reg1 Protein, a Putative Transcriptional Regulator, Is Required for Pathogenicity, Conidiogenesis, and the Production of Secondary Metabolites.

A Novel Regulatory Role of HrpD6 in Regulating *hrp-hrc-hpa* Genes in *Xanthomonas oryzae* pv. *oryzicola*.

Colonization of Rice Leaf Blades by an African Strain of *Xanthomonas oryzae* pv. *oryzae* Depends on a New TAL Effector That Induces the Rice Nodulin-3 *Os11N3* Gene.

October 2011, Volume 24, Number 10

Agroinoculation of *Citrus tristeza virus* Causes Systemic Infection and Symptoms in the Presumed Nonhost *Nicotiana benthamiana*.

Cloning and Characterization of *R3b*; Members of the *R3* Superfamily of Late Blight Resistance Genes Show Sequence and Functional Divergence.

Nonhost Resistance of Rice to Rust Pathogens.

A Novel Multidomain Polyketide Synthase Is Essential for Zeamine Production and the Virulence of *Dickeya zeae*.

Microbial Volatile-Induced Accumulation of Exceptionally High Levels of Starch in *Arabidopsis* Leaves Is a Process Involving NTRC and Starch Synthase Classes III and IV.

The *Fusarium virguliforme* Toxin FvTox1 Causes Foliar Sudden Death Syndrome-Like Symptoms in Soybean.

Enhanced Viral Intergenic Region–Specific Short Interfering RNA Accumulation and DNA Methylation Correlates with Resistance Against a Geminivirus.

Identification of an Operon, Pil-Chp, That Controls Twitching Motility and Virulence in *Xylella fastidiosa*.

Induction of *Pseudomonas syringae* pv. *tomato* DC3000 MexAB-OprM Multidrug Efflux Pump by Flavonoids Is Mediated by the Repressor PmeR.

A High Level of Transgenic Viral Small RNA Is Associated with Broad Potyvirus Resistance in Cucurbits.

Protein Elicitor PemG1 from *Magnaporthe grisea* Induces Systemic Acquired Resistance (SAR) in Plants.

Expression and Localization of a *Rhizobium*-Derived Cambialistic Superoxide Dismutase in Pea (*Pisum sativum*) Nodules Subjected to Oxidative Stress.

HflB Gene-Based Phytopathogenic Classification of 'Candidatus Phytoplasma mali' Strains and Evidence that Strain Composition Determines Virulence in Multiply Infected Apple Trees. ■

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COMING EVENTS

February 5–8, 2012
Microbial Virulence Determinants & Plant Immunity
Tel-Aviv University, Tel-Aviv, Israel
www.tau.ac.il/lifesci/bard2012/home.html

May 21–25, 2012
4th International Workshop for Phyphthora, Pythium, and Phytopythium
University of Maryland, College Park, MD
www.psla.umd.edu/faculty/balci/workshop2011/index.cfm

July 29–August 2, 2012
XV International Congress on Molecular Plant-Microbe Interactions
Kyoto, Japan
www.ismpminet.org

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