

Biology of Plant-Microbe Interactions, Volume 6

Edited by

Matteo Lorito
Sheridan Lois Woo
Felice Scala

Università Degli Studi Di Napoli
Portici, Italy

Proceedings of the 13th International Congress
on Molecular Plant-Microbe Interactions
Sorrento (Naples), Italy
July 21–27, 2007

Published by the
International Society for Molecular Plant-Microbe Interactions
St. Paul, Minnesota, USA

Articles may be referenced as follows:

[Authors' names]. 2008. [Paper title]. Paper [number] in: *Biology of Plant-Microbe Interactions*, Volume 6. M. Lorito, S. L. Woo, and F. Scala, eds. International Society for Molecular Plant-Microbe Interactions, St. Paul, MN.

Cover photo by Gianfranco Capodilupo; logo design by Antonino Balsamo

This CD-Rom has been reproduced directly from edited, computer-generated copy submitted by the authors to the editors of this volume. The editors have verified text formatting, references, and quality of text and figures. No editing or proofreading has been done by the publisher.

Reference in this publication to a trademark, proprietary product, or company name by personnel of the U.S. Department of Agriculture or anyone else is intended for explicit description only and does not imply approval or recommendation to the exclusion of others that may be suitable.

ISBN: 978-0-9654625-5-6

© 2008 by the International Society for Molecular Plant-Microbe Interactions

All rights reserved.

No part of this book may be reproduced in any form, including photocopy, microfilm, information storage and retrieval system, computer database or software, or by any other means, including electronic or mechanical, without written permission from the publisher.

Copyright is not claimed in any portion of this work written by U.S. government employees as part of their official duties.

International Society for Molecular Plant-Microbe Interactions
3340 Pilot Knob Road
St. Paul, Minnesota 55121 U.S.A.

Preface

The XIII International Congress of the IS-MPMI began in Sorrento, Italy, on July 21, lasted for five full days packed with an abundance of scientific, social, cultural, and gastronomic activity, and then ended in a flurry on July 27 with the bustle of people, luggage, and buses. Approximately 1,250 participants registered, originating from about 60 countries worldwide! This turnout reflects a good response from the MPMI scientific community to this event, even though only 1.5 years had passed since the last congress in Mexico. Furthermore, the policy for meeting registration elicited an increase of about 45% in the number of IS-MPMI memberships versus the December 2006 count.

The scientific program proved to be comprehensive, covering a wide range of topics. The opening lecture by James C. Carrington gave us a novel insight into the role of small RNAs in plants, an exciting, topical, growing field of research. The IS-MPMI Award Lecture by Thomas Boller presented an inside view into the development of his exceptionally innovative research career. The regular congress day started every morning with talks in the plenary sessions, followed by informal lunch discussions. The afternoon activities included concurrent sessions and poster sessions, which immediately rolled into the evening special-interest workshops that, in some cases, proceeded until after 23:00. Then, if 15 hours of listening to the organized presentations weren't enough, nightcap sessions continued into the wee hours for those who were not yet satiated and wanted to discuss more science and organize collaboration! A heartfelt thank you is extended to all the speakers. Their participation formed a strong scientific foundation for the congress. Hearing about their "hot" findings was exciting, and their interpretations of the subject were stimulating and thought-provoking.

The visual impact of the about 1,000 posters throughout the congress venue was impressive. These scientific presentations were equally attractive and instigated much discussion thanks to the availability of the authors during the two sessions. Needless to say, the poster committees had a daunting task in selecting the award recipients.

The congress venue was put to a rigorous test in hosting so many congress delegates! Its strategic location overlooking the sea of the sirens was indeed

brehtaking. We had the fortune of having the Congress Centre renovated for the start of the congress – the paint was still wet the day before the opening! Every possible conference space was utilized and optimized! Every problem was dealt with and resolved. The organization of the community lunches together worked well! All participants must agree that it was indeed an extraordinary sight to see, not to mention notable to hear, about 1,200 delegates seated all together for lunch! The lunches, normally consisting of several courses, were served efficiently in order to accommodate the schedule of the scientific program. The little cakes, tarts, or cookies served during the coffee breaks were delicious and so colourful and beautifully arranged.

The social program began with the welcome reception, which was held outdoors in the refreshing lemon orchard against the backdrop of the Gulf of Naples and the background music and dance of the classic Neapolitan “tarantella”. The full attendance made it difficult to move about and locate old acquaintances in the crowd, but with patience, circulation was possible and encounters were successful. The week of the congress was substantially sunny and hot, hot, hot. Many participants, corresponding to about 20 busloads, braved the climate to participate in the congress tour to the Pompeii excavation site! It was striking to see so many bright yellow congress hats moving around the extensive archaeological complex. Fortunately, no PAMP (Pompei-Associated Missing People) were registered. In spite of the heat, seeing the ancient town of Pompeii below the shadow of the volcano Vesuvius provided a thrill and merited the visit, no matter what meteorological conditions prevailed.

In the closing ceremony, the presidency of the IS-MPMI was passed from Pierre de Wit to the new elected president, Federico Sanchez, who addressed the crowd, presented the poster awards, and introduced the site for the XIV IS-MPMI Congress in 2009.

The congress dinner was also hosted in the lemon orchard. A sumptuous meal was served, accompanied by an interactive Neapolitan music spectacle that was capable of drawing in all attendees. A highlight to the evening of entertainment involved the participation of the past and present presidents of IS-MPMI and the congress chair at centre stage.

The ultimate goals for these IS-MPMI congresses are to reinforce and expand the community, to share new and exciting scientific findings, as well to initiate and sustain personal contacts during these biennial encounters. Consensus is that these objectives have been achieved.

Thank you for joining us in Sorrento and see you in Quebec City !

Matteo Lorito and the Local Organizers

Plant carbohydrate scavenging through TonB-dependent receptors by the phytopathogenic bacterium *Xanthomonas campestris* pv. *campestris*

Servane Blanvillain^{1#}, Damien Meyer¹, Guillaume Déjean¹, Alice Boulanger¹, Martine Lautier^{1,2}, Catherine Guynet¹, Nicolas Denancé¹, Jacques Vasse¹, Emmanuelle Lauber^{1#}, and Matthieu Arlat^{1,2#}

¹ Laboratoire des Interactions Plantes-Microorganismes, CNRS/INRA UMR2594/441, Chemin de Borde Rouge BP52627, 31326 Castanet-Tolosan, France ; ² Université Paul Sabatier, Toulouse III, 118 Route de Narbonne, 31062 Toulouse, France ;

These authors contributed equally to this work.

arlat@toulouse.inra.fr

Phytopathogenic bacteria have in general a dual life: they are able to infect and colonize their host plants but they also have the ability to survive outside their hosts in various environments. This remarkable feature likely reflects a high degree of adaptability and the presence of specific genetic programs devoted to the exploitation of nutrients present in these diverse habitats. With the aim to study molecular mechanisms controlling adaptation of phytopathogenic bacteria to their host-plants, we undertook a global analysis of receptors and regulators of *Xanthomonas campestris* pv. *campestris* (*Xcc*), the causal agent of black rot of crucifers. This pathogen infects a wide range of *Brassicaceae* plants of economic interest, including cabbage, cauliflower and radish as well as the model plant *Arabidopsis thaliana* (Meyer et al. 2005).

Our analysis of the *Xcc* (ATCC33913) genome revealed an overrepresentation of a particular family of receptors, named TonB-dependent receptors (TBDRs) (Blanvillain et al. 2007). These proteins are located in the outer membrane of Gram-negative bacteria and are mainly known to transport iron-siderophore complexes and vitamin B12 into the periplasm (Postle and Kadner 2003). In most cases, the expression of genes encoding these receptors is under the control of the Fur repressor (ferric

uptake regulator) and activated under conditions of iron starvation (Bagg and Neilands 1987). In *Xcc*, we showed that only 9 TBDRs out of 72 are directly associated with iron uptake: these nine genes are indeed regulated by the iron status, have a Fur-Box in their promoter region, and are repressed by the Fur protein.

The sucrose utilization locus

A systematic study of *Xcc* TBDRs, based on mutagenesis and pathogenicity tests, identified one *Xcc* TBDR (XCC3358) controlling pathogenicity on *A. thaliana*. In the genome, this TBDR gene, named *suxA* (sucrose utilization in *Xanthomonas*), is associated with genes related to sucrose metabolism: XCC3359 (*suxB*) encodes an amylosucrase, XCC3356 (*suxR*) encodes a transcriptional repressor of the LacI family and XCC3357 (*suxC*) encodes a sugar transporter of the inner membrane (Fig. 1).

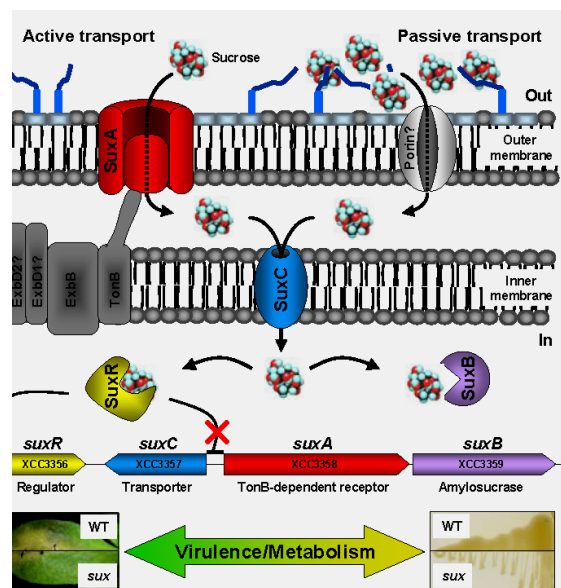


Fig. 1. Model of the *Xanthomonas campestris* pv. *campestris* *sux* locus functioning (reprinted by permission, from Blanvillain et al. 2007). This scheme shows sucrose outer membrane active transport *via* the SuxA TBDR or by passive diffusion through a putative porin. After crossing the inner membrane through the SuxC transporter, sucrose is proposed to interact with the SuxR repressor (thus allowing *sux* gene induction) and also to serve as a substrate for the SuxB amylosucrase. The large double headed arrow below the *sux* locus represents the balance between metabolic adaptation and virulence control putatively mediated by the *sux* locus.

Expression studies showed that *suxC*, *suxA* and *suxB* are specifically induced by sucrose, and that these three genes are repressed by the upstream regulator *suxR* in the absence of sucrose. Moreover, *suxC* and *suxB* mutants are affected in growth on sucrose and in pathogenicity on *Arabidopsis*, showing, like the *suxA* mutant, a clear delay in symptom development as compared to the wild-type strain.

The role of the *sux* locus in sucrose transport was confirmed by time course uptake experiments using radioactively labelled sucrose. We showed that *suxA* and *suxC* are necessary for sucrose entry into *Xcc*. However, even if SuxA is the predominant pathway for sucrose transport through the outer membrane, a second slower pathway exists, probably by passive diffusion through porins (Fig. 1). This hypothesis is reinforced by *suxA* expression studies which showed that this gene is required for its own induction only at low sucrose concentrations. Indeed, in the presence of 100 μM sucrose, *suxA* induction by sucrose was clearly slower in the mutant than in the wild-type background, whereas no significant difference was observed in the presence of 20 mM sucrose.

Concentration-dependent sucrose transport experiments showed a biphasic kinetic similar to those observed for vitamin B12 transport through the BtuB TBDR in *E. coli* and more recently for maltose transport through the MalA TBDR in *Caulobacter crescentus* (Neugebauer et al. 2005). As proposed for these two systems, we presume that the low K_d value (0.033 μM) mainly reflects binding to the SuxA TBDR whereas the higher K_d value (0.59 μM) reflects binding to the inner membrane transporter SuxC. Interestingly, the K_d value of sucrose binding to SuxA is 1500- to 3000-fold lower than that of the *E. coli* ScrY sucrose porin (Schulein et al. 1991; Van Gelder et al. 2001). Similar results were obtained for the *C. crescentus* MalA TBDR suggesting that both SuxA and MalA represent a new class of outer membrane carbohydrate transporters showing a much higher affinity for their substrate than porins.

The importance of the *sux* locus in *Xcc* is highlighted by its requirement for full virulence on *A. thaliana*. Thus, it appears that the ability to scavenge sucrose with a very high affinity plays a key role during the interaction with host plants. This study is the first one showing the functionality of a carbohydrate utilization locus containing a TBDR, or “CUT locus”, which can be defined by high affinity uptake systems involved in the scavenging of plant molecules.

A CUT system involved in xylan utilization

The exploration of the *Xcc* genome revealed the existence of other putative CUT loci involved in carbohydrate utilization. Among these, the *XCC4115-XCC4122* locus was proposed to be involved in xylan degradation and uptake, as this locus contains genes coding for xylan degradation enzymes as well as inner membrane and outer membrane transporters. Interestingly, the *XCC4120* TBDR gene was found to be specifically induced by xylose and xylan. A similar pattern was also obtained for the *XCC2828* TBDR gene. *In silico* analyses revealed the presence of a perfectly conserved palindromic motif (X-box) in their promoter region, as well as upstream two other genes: *XCC4100* and *XCC4119*. Experiments based on mutagenesis and expression assays suggest that the X-box is recognized by *XCC4101*, a transcriptional repressor of the LacI family (Fig. 2).

These data suggest that the *XCC4101* regulon encompasses 3 operons, one containing the major xylanase (*XCC4118*) detectable *in vitro*. Furthermore, direct and indirect transport assays suggest that inner membrane and outer membrane transporters of the studied CUT system are involved in xylo-oligosaccharides uptake rather than in xylose uptake. Thus, this *Xcc* CUT system defines a new pathway for the utilisation of xylan by bacteria.

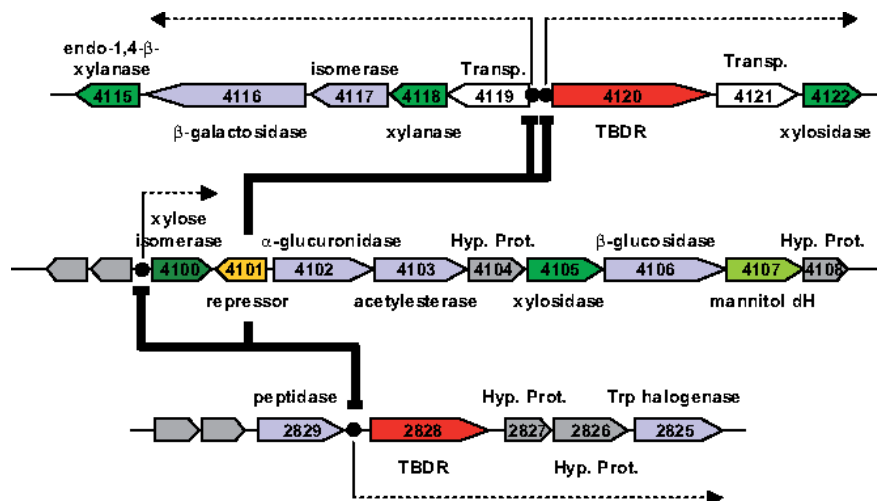


Fig. 2. Schematic representation of the *Xanthomonas campestris* pv. *campestris* CUT system involved in xylan utilization and its regulation by *XCC4101* repressor. Dashed arrows indicate putative operons. Repression by *XCC4101* is illustrated by bolded lines. Filled circles represent palindromic X-box motifs. Gene function description are from *Xcc* ATCC33913 genome annotation (da Silva et al. 2002).

CUT loci and carbohydrate scavenging in Gram negative bacteria

A survey of TBDR was performed in 226 eubacterial completely sequenced genomes (Blanvillain et al. 2007). Most bacteria have less than 20 TBDRs per proteome, but some possess more than 40 TBDRs, thus forming a particular class in which TBDRs seem to be over represented. Very interestingly, in addition to *Xanthomonas* species, this class contains several aquatic bacteria, that are either oligotrophic or well known for their ability to degrade complex carbohydrates from algae, mollusc or arthropods. This class also contains *Bacteroides thetaiotaomicron*, which is a prominent mutualist in the distal intestine of human adults that has the ability to scavenge complex plant carbohydrates (Backhed et al. 2005; Sonnenburg et al. 2005; Xu and Gordon 2003). Furthermore, phytopathogenic bacteria, such as *Pseudomonas syringae* pathovars and *Erwinia carotovora* subsp. *atroseptica*, belong to an intermediary class comprising bacteria having between 21 and 39 TBDRs. Therefore, it is likely that TBDR overrepresentation might be related to the ability to utilize or even to scavenge complex carbohydrates in various environments and in particular from plant origin. This hypothesis is strengthened by the observation that several *Xcc* putative CUT loci are partially conserved in some of the bacteria displaying TBDR overrepresentation. TBDR might allow these bacteria to scavenge complex carbohydrates, too large to pass through porins, even if they are present at very low concentrations in their environment. Thus CUT loci, which seem to participate to the adaptation of phytopathogenic bacteria to their host plants, might also play a very important role in human health as well as in the biogeochemical cycling of organic carbon in the environment. Our work on *Xcc* TBDRs which opens a new research area in plant-microbe interactions might also have a broader impact in the study of bacterial adaptation and evolution.

Literature cited

- Backhed, F., Ley, R.E., Sonnenburg, J.L., Peterson, D.A., and Gordon, J.I. 2005. Host-bacterial mutualism in the human intestine. *Science* 307:1915-1920.
- Bagg, A., and Neilands, J.B. 1987. Ferric uptake regulation protein acts as a repressor, employing iron (II) as a cofactor to bind the operator of an iron transport operon in *Escherichia coli*. *Biochemistry* 26:5471-5477.
- Blanvillain, S., Meyer, D., Boulanger, A., Lautier, M., Guynet, C., Denance, N., Vasse, J., Lauber, E., and Arlat, M. 2007. Plant Carbohydrate Scavenging through TonB-Dependent Receptors: A Feature Shared by Phytopathogenic and Aquatic Bacteria. *PLoS ONE* 2:e224.

- da Silva, A.C.R., Ferro, J.A., Reinach, F.C., et al. 2002. Comparison of the genomes of two *Xanthomonas* pathogens with differing host specificities. *Nature* 417:459-463.
- Meyer, D., Lauber, E., Roby, D., Arlat, M., and Kroj, T. 2005. Optimization of pathogenicity assays to study the *Arabidopsis thaliana*-*Xanthomonas campestris* pv. *campestris* pathosystem. *Mol. Plant Pathol.* 6:327-333.
- Neugebauer, H., Herrmann, C., Kammer, W., Schwarz, G., Nordheim, A., and Braun, V. 2005. ExbBD-dependent transport of maltodextrins through the novel MalA protein across the outer membrane of *Caulobacter crescentus*. *J. Bacteriol.* 187:8300-8311.
- Postle, K., and Kadner, R.J. 2003. Touch and go: tying TonB to transport. *Mol. Microbiol.* 49:869-882.
- Schulein, K., Schmid, K., and Benzl, R. 1991. The sugar-specific outer membrane channel ScrY contains functional characteristics of general diffusion pores and substrate-specific porins. *Mol. Microbiol.* 5:2233-2241.
- Sonnenburg, J.L., Xu, J., Leip, D.D., Chen, C.H., Westover, B.P., Weatherford, J., Buhler, J.D., and Gordon, J.I. 2005. Glycan foraging in vivo by an intestine-adapted bacterial symbiont. *Science* 307:1955-1959.
- Van Gelder, P., Dutzler, R., Dumas, F., Koebnik, R., and Schirmer, T. 2001. Sucrose transport through maltoporin mutants of *Escherichia coli*. *Protein Eng* 14:943-948.
- Xu, J., and Gordon, J.I. 2003. Inaugural Article: Honor thy symbionts. *Proc. Natl. Acad. Sci. U S A* 100:10452-10459.

CONTENTS

Preface

OPENING LECTURE

Diversification of RNA silencing mechanisms
James C. Carrington

CHAPTER 1. Pathogenic and symbiotic plant-bacterium interactions

1. Recognition of pathogen effectors and activation of disease resistance signaling pathways in *Arabidopsis thaliana*
Brian Staskawicz
2. Suppression of host defense by *Pseudomonas syringae* in *Arabidopsis*
S. Y. He, E. Bray-Speth, Wei-Ning Huang, L. Imboden, Young Nam Lee, Christy Mecey, M. Melotto, K. Nomura, W. Underwood, Francisco Uribe, Jian Yao, and Weiqing Zeng
3. A *Pseudomonas syringae* effector ADP-ribosylates plant RNA binding proteins and suppresses innate immunity
James R. Alfano, Zheng Qing Fu, Ming Guo, Byeong-ryool Jeong, Fang Tian, Thomas E. Elthon, Ronald L. Cerny, and Dorothee Staiger
4. Coordinated expression of type III secretion system-dependent effectors, small diffusible molecules and phytohormone analogues in the bacterial wilt pathogen *Ralstonia solanacearum*
S. Genin, N. Peeters, M. Poueymiro, A. Angot, F. Delaspre, C. Nieto-Peñalver, O. Saurel, A. Milon, M. Valls, P. Barberis, J. Vorholt, and C. Boucher
5. Functional genomic analysis of the *Pseudomonas syringae* pv. *tomato* DC3000 type III effector repertoire
Alan Collmer, Marshall L. Hayes, Brian H. Kvitko, Joanne E. Morello, Hye-Sook Oh, and Chia-Fong Wei
6. Plant carbohydrate scavenging through TonB-dependent receptors by the phytopathogenic bacterium *Xanthomonas campestris* pv. *campestris*
Servane Blanvillain, Damien Meyer, Guillaume Déjean, Alice Boulanger, Martine Lautier, Catherine Guynet, Nicolas Denancé, Jacques Vasse, Emmanuelle Lauber, and Matthieu Arlat
7. Bacterial extracellular polysaccharides promote pathogenicity by suppressing plant basal defences
Shazia N. Aslam, Robert W. Jackson, Kate L. Morrissey, Marc R. Knight, Delphine Chinchilla, Thomas Boller, Gitte Erbs, Tina Tandrup Jensen, Mari-Anne Newman, and Richard M. Cooper
8. Regulation and function of anti-eukaryote factors in *Pseudomonas fluorescens* NZ17
Peter Burlinson, Joanna Knaggs, Jonathan Hodgkin, and Gail Preston
9. Composite plants, a tool to study functional genomics of Npv30, a gene family highly expressed in *Phaseolus vulgaris* root nodules
Olivares, J. E., Estrada, G., Guillén, G., Campos, F., Alvarado-Affantranger, X., Díaz-Camino, C., Quinto, C., Zavala, G., and Sanchez, F.
10. *Lotus japonicus* NSP2 functions as activator of nodule and lateral root initiation
Y. Murakami, S. Tomisawa, S. Kawasaki, and M. Kawaguchi
11. Terminal bacteroid differentiation in nodules of IRLC legumes is linked to the evolution of high diversity of secreted, nodule-specific peptides in the host plant
Eva Kondorosi, Benoît Alunni, Zoltan Kevei, Nicolas Maunoury, Willem Van de Velde, Agnes Szatmari, Adam Kondorosi, and Peter Mergaert
12. Biofilm formation in *Sinorhizobium meliloti*
Nancy A. Fujishige, Kat Jankaew, and Ann M. Hirsch
13. The nucleus as a central player in symbiotic signaling
Brendan K. Riely, Elsa Messinese, Jeong-Hwan Mun, Edgar Peiter, Jongho Sun, Li Huey Yeun, Muthusubramanian Venkateshwaran, Dhileepkumar Jayaraman, Anne B. Heckmann, , Géraldine Lougnon, Anne Edwards, Pierre Rougé, Annick Barre, Dale Sanders, J. Allan Downie, Giles E. D. Oldroyd, Jean-Jacques Bono, Douglas R. Cook, and Jean-Michel Ané

CHAPTER 2. Pathogenic and symbiotic plant-fungus and plant-oomycete interactions

14. Investigating the biology of plant infection by the rice blast fungus *Magnaporthe grisea*
Nicholas J. Talbot, Diane O. C. Saunders, Darren M. Soanes, Richard A. Wilson, Claire Veneault-Fourrey, Thomas A. Richards, Michael J. Kershaw, Romain Huguet, Martin J. Egan, Han-Min Wong, Elise Lambeth, and Zaira Caracuel-Rios
15. Trichothecene diversity and evolution of *Fusarium graminearum*
H. Corby Kistler and Liane R. Gale
16. *Botrytis cinerea*: Special aspects of a necrotrophic life-style
Paul Tudzynski
17. Cost of virulence: Case of *Puccinia striiformis* f.sp. *tritici*
B. Bahri, M. Leconte, C. de Vallavieille-Pope, and J. Enjalbert
18. A gene cluster on a conditionally dispensable chromosome controlling AAL-toxin biosynthesis and pathogenicity in the tomato pathotype of *Alternaria alternata*
Motoichiro Kodama, Yasunori Akagi, Hajime Akamatsu, Hiroshi Otani, Mikihiro Yamamoto, and Takashi Tsuge
19. Function and evolution of avirulence genes in cereal powdery mildew
Christopher J. Ridout, Soledad Sacristán, Marielle Vigouroux, and James K. M. Brown
20. Dissecting cellular and molecular responses of host plants during early arbuscular mycorrhizal interactions
Paola Bonfante, Andrea Genre, Valeria Siciliano, Mike Guether, Jorge Gomez Ariza, Antonella Faccio, Mara Novero, Lorella Navazio, Raffaella Balestrini, Luisa Lanfranco
21. Genetics and genomics of the arbuscular mycorrhizal symbiosis in cereals
Uta Paszkowski, Ruairidh Sawers, Caroline Gutjahr, Sylvain Marcel, and Leonardo Casieri
22. Mastering mycorrhizal symbiosis: Sugar as nutrient and signal in ectomycorrhizas
Uwe Nehls, Mónica Fajardo López, Marlis Reich, Margret Ecke, and Andrea Bock
23. Lipid signals in the arbuscular mycorrhizal symbiosis
Genot Kunze, David Drissner, Thomas Boller, Nikolaus Amrhein, and Marcel Bucher
24. Arthur Schüßler: The *Geosiphon-Nostoc* symbiosis as a tool to characterize symbiotic nutrient transporters in the arbuscular mycorrhiza symbiosis
Arthur Schüßler, Holger Martin, David Cohen, and Daniel Wipf
25. Medicago truncatula plants with reduced levels of the sucrose synthase MtSucS1 are handicapped in nodulation and mycorrhization
Natalija Hohnjec, Markus C. Baier, and Helge Küster
26. Groovy times: Structure, evolution, and function of filamentous pathogen effectors
Sophien Kamoun
27. Lectin receptor kinase 79, a putative target of the *Phytophthora infestans* effector IPI-O
Klaas Bouwmeester, Sofieke Klammer, Anne Gouget, Nathalie Haget, Hervé Canut, and Francine Govers
28. Loss of downy mildew susceptibility in Arabidopsis through mutation in genes encoding metabolic enzymes
Mireille Van Damme, Robin Huibers, Tieme Zeilmaker, Annemieke Andel, Joyce Elberse, and Guido Van den Ackerveken

CHAPTER 3. Multitrophic interactions (pathogens, insects, nematodes, endophytes, parasitic plants)

29. Cross-talk between signaling pathways leading to defense against pathogens and insects
Corné M. J. Pieterse, Annemart Koornneef, Antonio Leon Reyes, Tita Ritsema, Adriaan Verhage, Ruth Joosten, Martin De Vos, Vivian Van Oosten, and Marcel Dicke
30. Early stages in parasitism of roots by root-knot nematodes
Valerie M. Williamson, Qingli Liu, Congli Wang, and Varghese Thomas
31. Towards a global view of the root-knot nematode genome
Pierre Abad, Marie-Noëlle Rosso, Géraldine Dubreuil, Emeline Deleury, Jérôme Gouzy, Laetitia Zurletto, Bruno Favery, and Philippe Castagnone-Sereno
32. A look through the stylet: Deciphering the mechanisms of nematode parasitism
Tarek Hewezi, Anoop Sindhu, Peter Howe, Axel A. Elling, Melissa G. Mitchum, Eric L. Davis, Richard S. Hussey, and Thomas J. Baum

33. Chorismate mutases of *Globodera pallida*: Genetic and functional characterisation
Vivian Blok, Mark Phillips, Liliya Pylypenko, Juan Manuel Rodriguez, Rujuta Shaw, Allan Booth, Ailsa Smith, Anne Holt, Eleanor Gilroy, Casey Plain, and John Jones
34. Functional analysis of a host microtubule-associated protein acting in nematode feeding cell formation
Marie-Cécile Caillaud, Michaël Quentin, Philippe Lecomte, Janice De Almeida-Engler, Pierre Abad, and Bruno Favery
35. Structural and functional analysis of Gpa2-mediated resistance against the potato cyst nematode *Globodera pallida*
Kamila Koropacka, Erik Sloomweg, Jan Roosien, Robert Dees, Melanie Ann Sacco, Peter Moffett, Geert Smant, Jaap Bakker, Aska Goverse
36. Reactive oxygen species signalling is critical for maintaining a mutualistic symbiotic interaction between *Epichloë festucae* and perennial ryegrass
Aiko Tanaka, Daigo Takemoto, and Barry Scott
37. Interactions of *Piriformospora indica* with *Arabidopsis thaliana*: early plant signaling events involved in a beneficial symbiosis with a growth- and seed yield-promoting endophytic fungus
Ralf Oelmüller
38. Non-culturable Rhizobia and diverse endophytic bacteria co-inhabiting wild legume nodules
Rosella Muresu, Elisa Polone, Leonardo Sulas, Barbara Baldan, Alessandra Tondello, Giuseppe Delogu, Piero Cappuccinelli, Sara Alberghini, Yacine Benhizia, Hayet Benhizia, Ammar Benguedouar, Bruno Mori, Roberto Calamassi, Frank B. Dazzo, and Andrea Squartini
39. Recent findings and new perspectives on volatile signaling between plants and insects and among plants
Mark C. Mescher, Christopher J. Frost, Justin Runyon, and Consuelo M. De Moraes
40. Molecular genetics and transcriptomics of *Striga*-rice interactions
Krittika Kaewchumngong and Adam Price

CHAPTER 4. Recognition and signalling

41. Signal integration in the plant immune system
Qian-Hua Shen, Yusuke Saijo, Stefan Mauch, Nico Tintor, Christoph Biskup, Bekir Ülker, Imre E. Somssich, Ralph Panstruga, Silke Robatzek, and Paul Schulze-Lefert
42. Oligogalacturonide signalling: sensing a breach in the wall
Simone Ferrari, Roberta Galletti, Vincenzo Lionetti, Benedetta Mattei, Manuela Casasoli, Daniela Pontiggia, Felice Cervone, and Giulia De Lorenzo
43. Chitin signaling in *Arabidopsis*
Jinrong Wan, Katrina Ramonell, Xuecheng Zhang, Steve Clough, Ren Zhang, Marc Libault, Geon H. Son, Minviluz G. Stacey, Jong C. Hong, and Gary Stacey
44. The roles of salicylic acid-binding protein 2 and methyl salicylate in systemic acquired resistance in tobacco and *Arabidopsis*
Sang-Wook Park, Dharendra Kumar, Evans Kaimoyo, Anna Corina Vlot, and Daniel F. Klessig
45. The downy mildew effector proteins ATR1 and ATR13 promote disease susceptibility in *Arabidopsis thaliana*
Keehoon Sohn, Rita Lei, Adnane Nemri, and Jonathan D. G. Jones
46. The role of BAK1/SERK3 in innate immunity in *Arabidopsis*
Delphine Chinchilla, Cyril Zipfel, Georg Felix, and Thomas Boller
47. Genetic analysis of PAMP-triggered immunity in *Arabidopsis*
Cyril Zipfel, Ben Schwessinger, Milena Roux, and Jonathan Dg Jones
48. High through-put genetics separates many plant signaling pathways towards programmed cell death
Hans Thordal-Christensen, Ziguo Zhang, Andrea Lenk, Angela Feechan, Carsten Pedersen, Mads Eggert Nielsen, Mats X. Andersson, Dale Godfrey, and Sara Melhedegård Mørch
49. Natural variation of the FLS2 mediated flagellin response
Susanne Salomon and Silke Robatzek
50. Jasmonate-insensitive 3 is a nuclear target of SCF^{COI1} negatively regulating JA signalling
A. Chini, S. Fonseca, G. Fernández, B. Adie, J. M. Chico, O. Lorenzo, G. García-Casado, I. López-Vidriero, F. M. Lozano, M. R. Ponce, J. L. Micol, and R. Solano
51. Effectors, their targets and host responses in the pathosystem *Cladosporium fulvum*-tomato
Pierre J. G. M. de Wit, Ioannis I. Stergiopoulos, John W. van 't Klooster, H. Peter van Esse, Emilie F. Fradin, Ursula

Ellendorff, Susan H. E. J. Gabriëls, Iris J. E. Stulemeijer, Melvin D. Bolton, Orlando Borrás-Hidalgo, Wladimir I. L. Tameling, Ahmed M. Abd-El-Halim, Grady C. M. van den Berg-Velthuis, Jacques Vervoort, Sjeff Boeren, Matthieu H. A. J. Joosten, and Bart P. H. J. Thomma

52. *Pseudomonas syringae* type III effector AvrPtoB uses multiple mechanisms to suppress plant immunity
Tracy R. Rosebrock, Fangming Xiao, and Gregory B. Martin

CHAPTER 5. Molecular dialogues, and plant- virus/viroid/phytoplasma interactions

53. Gene expression in *Medicago truncatula* associated with appressoria formation by *Glomus versiforme*
S. Karen Gomez, Melina Lopez-Meyer, and Maria J. Harrison
54. The role of cell to cell signaling in the *Sinorhizobium meliloti*–alfalfa symbiosis
Audry C. Almengor, Sarah Glenn, Nataliya Gurich, Hanh H. Hoang, Jennifer Morris, Konrad Mueller, Arati Patankar, Luciana Rinaudi, and Juan E. González
55. The role of secreted proteins during establishment of biotrophy in the *Ustilago maydis*/maize pathosystem
Thomas Brefort, Lazaro Molina, Gunther Doehlemann, Kerstin Schipper, Artemio-Mendoza-Mendoza, Olaf Mueller, Jan Schirawski, and Regine Kahmann
56. Reverse genetic analysis of pathogenicity in *Stagonospora nodorum*
Simon V. S. Ipcho, Peter S. Solomon, and Richard P. Oliver
57. PAMP signals and their perception by receptor kinases in plants
Markus Albert, Pascal Bittel, Thomas Boller, Delphine Chinchilla, Martin Lipschis, Katharina Müller, and Georg Felix
58. Viroid-host interactions: A molecular dialogue between two uneven partners
Ricardo Flores, Alberto Carbonell, Selma Gago, Angel-Emilio Martínez de Alba, Sonia Delgado, María-Elena Rodio, and Francesco Di Serio
59. Iron-dependent quorum sensing controls epiphytic fitness and virulence in *Pseudomonas syringae*
Glenn Dulla and Steven E. Lindow
60. Dual role of quorum sensing molecules in swarming
Kristien Braeken, Ruth Daniels, Eleonora Capozzi, Natalie Verstraeten, Jan Fransaer, Jan Vermant, and Jan Michiels
61. Quorum sensing regulation in the biocontrol strain *Pseudomonas fluorescens* CHA0
Karine Lapouge, Christophe Dubuis, and Dieter Haas
62. Quorum sensing control of Stewartan exopolysaccharide production, biofilm formation and virulence in the plant pathogenic bacterium, *Pantoea stewartii* subsp. *stewartii*
Susanne B. von Bodman, Aurelien Carlier, and Carmen M. Herrera
63. Oxylipins act as quorum sensing molecules and mediate the *Aspergillus*-seed dialogue
Dimitrios I. Tsiatsigiannis, Marion Brodhagen, and Nancy P. Keller
64. Interactions between replicase proteins and host cell membranes in positive-strand RNA plant virus replication
Luisa Rubino and Marcello Russo
65. The suppressor of gene silencing P0 is a viral F-box protein that targets ARGONAUTE1
Diane Bortolamiol, Maghsoud Pazhouhandeh, Katia Marrocco, Pascal Genschik, and Véronique Ziegler-Graff
66. Cauliflower mosaic virus P6 protein suppresses SA-dependent defense responses in *Arabidopsis*
Andrew J. Love, Chiara Geri, Janet Laird, Byung W. Yun, Gary J. Loake, Ari Sadanandom, and Joel J. Milner
67. Molecular and developmental alterations elicited by a chloroplastic viroid
Francesco Di Serio, Maria-Elena Rodio, Sonia Delgado, Angelo De Stradis, Maria-Dolores Gómez, and Ricardo Flores

CHAPTER 6. Dynamics of plant responses to microbes, and evolution of susceptibility and resistance

68. Dynamic host responses in plant powdery-mildew interactions
Chian Kwon, Riyaz Bhat, Stephane Bieri, Natascha Clemens, Chiara Consonni, Matt Humphry, Mark Kwaaitaal, Volker Lipka, Dorit Meyer, Simone Pajonk, Anja Reinstädler, Paul Schulze-Lefert, Nana Zappel, and Ralph Panstruga
69. Driving innate immunity: ‘R’ we there yet?
Tessa M. Burch-Smith and Savithamma P. Dinesh-Kumar
70. Molecular mechanisms underlying the activation of NBS-LRR proteins
Roger Innes, Jules Ade, Thomas Ashfield, Brody DeYoung, and Laura Ong

71. MLO-mediated resistance: How to prevent undesirable early senescence and callose deposition without affecting the resistance to powdery mildew fungi
Chiara Consonni, Matt Humphry, Pawel Bednarek, and Ralph Panstruga
72. Functional studies of a ternary chaperone complex in plant immunity
Ken Shirasu, Marta Boter, Beatrice Amigues, Yasuhiro Kadota, Jack Peart, Christian Breuer, Catarina Casais, Françoise Ochsenein, and Raphael Guerois
73. Responses of plants to secreted effectors from the pathogenic bacteria *Pseudomonas syringae*
Jose Castillo, Min Woo Lee, Joanna Jelenska, Ho Won Jung, Gail Teitzel, Boris A. Vinatzer, and Jean T. Greenberg
74. Recognition and activation by the NB-LRR proteins Rx and Gpa2; involvement of a Ran GTPase-activating protein
Melanie Sacco, Greg Rairdan, Sarah Collier, Teresa Boettrich, Thomas T. Baldwin, and Peter Moffett
75. Methods for LRR functional site identification and manipulation: The FLS2 example
Andrew Bent, Wenxian Sun, F. Mark Dunning, Laura Helft, Kristin Jansen, and James Murphy
76. Evolution and function of the *Pseudomonas syringae* HopZ type III effector family
Wenbo Ma, Jennifer D. Lewis, Darrell Desveaux, and David S. Guttman
77. Processes in plant resistance to invasive pathogens and probing insects
J. Parker, S. Rietz, L. Wirthmüller, M. Bartsch, J. Bautor, V. Pegadaraju, J. Louis, V. Singh, J. Reese, and J. Shah
78. Regulation of cell death in plants: A role for plant metacaspases?
Petra Epple, Nuria Sanchez Coll, Charles Clover, and Jeffery L. Dangl
79. Members of the Iid subfamily WRKY transcription factors act as negative regulators of resistance in *Arabidopsis*
Noëllie Journot-Catalino, Imre E. Somssich, Dominique Roby, and Thomas Kroj
80. A MYB transcription factor regulates fatty acid biosynthesis for the activation of the hypersensitive cell death in *Arabidopsis*
Sylvain Raffaele, Fabienne Vaillau, Amandine Léger, Jérôme Joubes, Elisabeth Blée, Frédéric Domergue, Sébastien Mongrand, and Dominique Roby
81. New insights into the molecular events underlying systemic acquired resistance
T. E. Mishina, T. Griebel, M. Geuecke, E. Attaran, and J. Zeier
82. Functional constraints and evolutionary dynamics of the Rx1/Gpa2 cluster in potato
Patrick Butterbach, Erik Sloopweg, Kamila Koropacka, Pjotr Prins, Jan Roosien, Laurentiu Spiridon, Andrei Petrescu, Geert Smant, Erin Bakker, Jaap Bakker, and Aska Goverse
83. Rac GTPase regulates reactive oxygen production by binding to the N-terminal extension of NADPH oxidase in rice
Hann Ling Wong, Reinhard Pinontoan, Kokoro Hayashi, Ryo Tabata, Takashi Yaeno, Kana Hasegawa, Chojiro Kojima, Hirofumi Yoshioka, Koh Iba, Tsutomu Kawasaki, and Ko Shimamoto
84. Integrating molecular evolution and desolvation energy analyses to dissect protein-protein recognition: The PG-PGIP interaction
Manuela Casasoli, Luca Federici, Nicoletta Vella, Juan Fernandez-Recio, Adele Di Matteo, Benedetta Mattei, Felice Cervone, and Giulia De Lorenzo

CHAPTER 7. Common host mechanisms, plant hormones and non-host resistance

85. Genetic and genomic studies of plant defense signaling pathways
Xinnian Dong, Wendy Durrant, Rebecca Mosher, Junqi Song, Dong Wang, and Shui Wang
86. Signaling specificity and complexity of MAPK cascades in plant innate immunity
Jen Sheen, Ping He, Libo Shan, Yan Xiong, Guillaume Tena, Sangdong Yoo, Younghee Cho, Marie Boudsocq, and Horim Lee
87. Characterization of *Arabidopsis* MAMP response pathways
Carine Denoux, Roberta Galletti, Simone Ferrari, Wisuwat Songnuan, Cristian Danna, Yves Millet, Nicole K. Clay, Suresh Gopalan, Giulia De Lorenzo, Julia Dewdney, and Frederick M. Ausubel
88. A seedling assay for MAMP signaling and infection studies
Wisuwat Songnuan, Yves Millet, Carine Denoux, Nicole K. Clay, Cristian Danna, and Frederick M. Ausubel
89. Basal defence in *Arabidopsis* against *Pseudomonas syringae* pv. *phaseolicola*: Beyond FLS2?
Alec Forsyth, Nina Grabov, Marta De Torres, and John Mansfield
90. A novel function for indole glucosinolate degradation products in *Arabidopsis* non-host immunity
Pawel Bednarek, Mariola Piślewska-Bednarek, Ales Svatos, Bernd Schneider, and Paul Schulze-Lefert

91. The *Arabidopsis* BRI1-associated receptor kinase 1 (BAK1) controls infection-induced cell death and immunity to necrotrophic fungal infection
Birgit Kemmerling, Anne Schwedt, Patricia Rodriguez, Sara Mazzotta, and Thorsten Nürnberger
92. A gain-of-function mutation in a LysM-RLK affects *Arabidopsis* non-host resistance to fungal pathogens
Ulrike S. Lipka, Elena Petutschnig, and Volker Lipka
93. Roles of DELLA proteins in plant defence and susceptibility
Rajendra Bari, Lionel Navarro, and Jonathan D. G. Jones
94. Arbuscular mycorrhiza mutants in *Lotus japonicus*
Kristina Haage, Martin Groth, Sonja Kosuta, and Martin Parniske
95. Phytohormones in disease and defence – the role of ABA
Marta de Torres Zabala, Bill Truman, Mark Bennett, Silvia Forcat, Gail Preston, John Mansfield, and Murray Grant
96. Susceptibility and resistance during necrotrophic interactions are influenced by the plant's hormone balance
Victor Flors, Jurriaan Ton, and Brigitte Mauch-Mani
97. Roles of brassinosteroid in disease resistance in plants
Hideo Nakashita, Michiko Yasuda, Miyuki Kusajima, Hideki Takahashi, Tadao Asami, and Shigeo Yoshida
98. The transcription factor AtMYC2 shapes plant defense responses in *Arabidopsis* upon *Pieris rapae* herbivory
Adriaan Verhage, Martin De Vos, Marcel Dicke, and Corné M. J. Pieterse

CHAPTER 8. Biocontrol interactions and biotechnology

99. Selection, monitoring, and enhancement of bacterial biocontrol agents
Linda S. Thomashow, Stacey B. Bankhead, Kurtis L. Schroeder, Dmitri V. Mavrodi, and David M. Weller
100. Biological control of avocado Dematophora root rot and tomato foot and root rot
Francisco M. Cazorla, Diego Romero, Alejandro Pérez-García, Antonio Vicente, Simon B. Duckett, Ed T. Bergström, Sadaf Noreen, Roeland Odijk, Ben J. J. Lugtenberg, Jane E. Thomas-Oates, and Guido V. Bloemberg
101. Genomic analysis of secondary metabolite production by *Pseudomonas fluorescens* Pf-5
Joyce E. Loper, Denny Bruck, Maria Pechy-Tarr, Monika Maurhofer, Christoph Keel, and Harald Gross
102. Is biofilm formation a requirement for rhizosphere colonization?
Emma Barahona, Ana Navazo, Miguel Redondo-Nieto, Francisco Martínez-Granero, Daniel Aguirre De Cárcer, Marta Martín, and Rafael Rivilla
103. Dynamic communication between plants and rhizobacteria via volatile signals
Choong-Min Ryu, Hwe-Su Yi, Yeo-Rim Ahn, Won-il Kim, Huiming Zhang, Seung-Hwan Park, Chang Seuk Park, Mohamed A. Farag, Paul W. Paré, and Joseph W. Kloepper
104. Quorum sensing as a target for novel biocontrol strategies directed at *Pectobacterium*
Yves Dessaux, Amélie Cirou, Stéphane Uroz, Emilie Chapelle, Xavier Latour, and Denis Faure
105. Listening to the molecular cross-talk between plants, pathogens and biocontrol fungi
Sheridan Lois Woo, Michelina Ruocco, Francesco Vinale, Roberta Marra, Stefania Lanzuise, Felice Scala, and Matteo Lorito
106. Possible role of *Trichoderma* peptaibols in plant induced resistance
Yariv Brotman, Eden Briff, Ada Viterbo, and Ilan Chet
107. Interactions of *Trichoderma* spp. with plants
Gary E. Harman and Michel Shoshitashvili
108. Oxalate-degrading bacteria can protect *Arabidopsis thaliana* and crop plants against *Botrytis cinerea*
Henk-jan Schoonbeek, Sibylle Ackermann, Francine Balet, Francesca Stefanato, and Jean-Pierre Métraux
109. Unholy trinity of crop, attached parasitic weed, and transgenic biocontrol agents
Sagit Meir, Yoav Herschkovitz, Clemence Larroche, Hani Al-Ahmad, Ziva Amsellem, and Jonathan Gressel
110. Virus-resistant transgenic crops: Insights into their environmental impact after the first decade of release
Marc Fuchs

CHAPTER 9. The impact of ‘omics’

111. The effector repertoire of *Phytophthora sojae*: structure, function and evolution
Brett M. Tyler, Daolong Dou, Shiv D. Kale, Rays H. Y. Jiang, Yubo Chen, Qunqing Wang, Xia Wang, Felipe D. Arredondo, and Yuanchao Wang
112. Genome evolution of fungal plant pathogens
Christina Cuomo, Manfred Grabherr, Chinnappa Kodira, Li-Jun Ma, Evan Mauceli, Matthew Pearson, James Galagan, Jacquie Schein, Les Szabo, Corby Kistler, and Bruce Birren
113. Construction of coexpression networks to explore barley-powdery mildew interactions
M. J. Moscou, R. A. Caldo, N. Lauter, and R. P. Wise
114. A multi-faceted genomics approach toward understanding *Magnaporthe*-rice interactions
Ryohei Terauchi, Joe Win, Sophien Kamoun, Hideo Matsumura, Hiromasa Saitoh, Kentaro Yoshida, Shizuko Fujisawa, Matt Shenton, Thomas Berberich, Akiko Ito, Yoshitaka Takano, and Yukio Tosa