

WHEN DEVELOPMENT MEETS STRESS:

UNDERSTANDING DEVELOPMENTAL
REPROGRAMMING UPON PATHOGENESIS IN PLANTS

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WHEN DEVELOPMENT MEETS STRESS:

UNDERSTANDING DEVELOPMENTAL REPROGRAMMING UPON PATHOGENESIS IN PLANTS

September 3 and 4, 2018

WELCOME

Dear Invited Speakers and Participants,

We are pleased to welcome you to Barcelona and to the meeting “**When development meets stress: Understanding developmental reprogramming upon pathogenesis in plants**”, co-organised by **B·DEBATE** International Center for Scientific Debate Barcelona, an initiative of Biocat and “la Caixa” Foundation, and the Centre for Research in Agricultural Genomics (CRAG).

Climate change and the current growth in the world’s population constitute unprecedented challenges for food security. In such a context, optimization of food security by increasing yield and decreasing losses is mandatory for a sustainable production and supply, and it is one of the central topics within most Governments’ agendas around the world. An effective way of achieving such sustainability relies on enhancing natural plant defenses in order to diminish pest-related losses. Unfortunately, strong immune responses are often detrimental to plant growth affecting yield production. Intense efforts have been devoted in the past to understand both plant growth and defense separately. However, very little is known about their interplay and the molecular and cellular basis underlying that trade-off.

Our main goal is to bring together renowned scientists working in plant development and defense, as well as experts on the incipient merging of both disciplines, which will provide new promising approaches to better understand stress-development trade-offs. This interdisciplinary meeting will cover, among others, the topics of plant-pathogen co-evolution and adaptation, hormone and signaling cascades, chromatin modifications and genome dynamics, cell biology and molecular single-cell approaches.

On behalf of **CRAG** and **B·Debate**, we thank you for joining us in this exciting debate. We are confident that it will foster the understanding of the trade-offs between plant defense and development, hopefully opening new avenues to promote a more intelligent, sustainable agriculture.

Sincerely yours,

Ignacio Rubio-Somoza, Paloma Más and Núria Sánchez Coll (CRAG) and B·Debate

PROGRAM

Monday, September 3, 2018

9:00	Registration
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9:30	Welcome Jordi Portabella , "la Caixa" Banking Foundation Núria Martí , Biocat Ignacio Rubio Somoza , Centre for Research in Agricultural Genomics (CRAG)
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10:00	SESSION 1: Pathogen perception and signalling Chairperson: Clara Sánchez-Rodríguez , ETH Zurich, Switzerland FERONIA and the regulation of receptor kinase-mediated signalling Cyril Zipfel , Institute of Plant and Microbial Biology, University of Zurich, Switzerland Organ-specific regulation of growth-defense trade-offs by a cognate receptor-peptide pair Youssef Belkadir , Gregor Mendel Institute, Austria How phytoplasma effectors induce dramatic changes in plant architecture and modulate plant defense to insect pests Saskia Hogenhout , John Innes Centre, UK
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11:30	Coffee break
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12:00	Plant hormones on the crossroads of plant growth and defense Cris Argueso , Colorado State University, USA Coordinating patterning and growth during early flower morphogenesis Teva Vernoux , RDP Laboratory, France Toward understanding "Disease-Climate-Microbiome" interactions in plants Sheng Yang He , DOE Plant Research Lab, USA
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13.30	Lunch and poster session
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15:00	SESSION 2: Cellular and nuclear basis of the interplay growth-defense Chairperson: Cris Argueso , Colorado State University, USA Precision in Plant Immune Expression: Not Lost in Translation Xinnian Dong , Duke University, USA Retinoblastoma - a jack of all trades in development and stress response Arp Schnittger , University of Hamburg, Germany
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16:00	Coffee break
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16:30 **Cell wall-dependent immunity-growth balance**

Clara Sánchez-Rodríguez, ETH Zurich, Switzerland

Symplastic regulation of immunity and infection

Christine Faulkner, John Innes Centre, UK

Modulation of autophagy during pathogen attack

Tolga Bozkurt, Imperial College London, UK

18:00 **Round table: “Future challenges for feeding the world”**

Chair: **Pere Puigdomenech** (Centre for Research in Agricultural Genomics, Spain)

Participants:

- **Carmen R. Beuzon** (University of Malaga, Spain)
 - **Hailing Jin** (University of California Riverside, USA)
 - **Rachil Koumproglou** (Semillas Fitó, Spain)
 - **Detlef Weigel** (MPI for Developmental Biology, Germany)
 - **José Luis Riechmann** (Centre for Research in Agricultural Genomics, Spain)
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19:00 **Adjourn**

Tuesday, September 4, 2018

9:30 **SESSION 3: Pathogen and host co-evolution and adaptation**

Chairperson: **Hernán A. Burbano**, Max Planck Institute for Developmental Biology, Germany

Arabidopsis and its pathogens - tales from the wild

Detlef Weigel, Max Planck Institute for Developmental Biology, Germany

Differences among *A. thaliana* ecotypes in response to infection drives patterns of virus adaptation

Santiago Elena, Institute for Plant Molecular and Cell Biology (IBMCP-CSIC), Spain

Cross-Kingdom RNAi and small RNA trafficking between plants and fungal pathogens

Hailing Jin, University of California, Riverside, USA

11:00 **Coffee break**

11:30 **Impact of plant immunity on a bacterial pathogen**

Kenichi Tsuda, Max Planck Institute for Plant Breeding Research, Germany

Bacterial adaptation to host environment during the onset of the infection

Emilia López-Solalla, Centre for Plant Biotechnology and Genomics (UPM-INIA), Spain

Novel defense and defense evasion mechanisms in *Pseudomonas syringae*-plant interactions

Carmen R. Beuzón, Institute for Mediterranean and Subtropical Horticulture "La Mayora" (UMA-CSIC), Spain

13:00 **Lunch and poster session**

SESSION 4: New approaches to understand growth-defense trade-off

Chairperson: **Kenichi Tsuda**, Max Planck Institute for Plant Breeding Research, Germany

Novel phenotypic approaches in quantitative analysis of biotic stress in plants

Klára Panzarová, Photon Systems Instruments, Czech Republic

Reinforcing plant evolutionary genomics using ancient DNA

Hernán A. Burbano, Max Planck Institute for Developmental Biology, Germany

Origin and evolution of the nuclear auxin response system

Dolf Weijers, Wageningen University, The Netherlands

16:00

Coffee break

16:30

Formation of root meristems

Idan Efroni, The Hebrew University, Israel

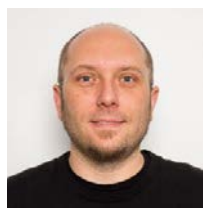
Root damage and immune responses at cellular resolution

Niko Geldner, University of Lausanne, Switzerland

17:30

Closing remarks and farewell

SCIENTIFIC COMMITTEE



Ignacio Rubio Somoza, Group Leader at **Centre for Research in Agricultural Genomics**, Barcelona, Spain

Ignacio Rubio Somoza studied Biology at the University of Santiago de Compostela (Spain) where he was firstly introduced to the exciting world of plant research working on somatic embryogenesis in *Vitis vinifera*. He moved to the Centre of Molecular Biology "Severo Ochoa" for carrying out a Master in Biotechnology (Madrid, Spain). Funded by a FPI fellowship he obtained his PhD working in the transcriptional regulation of antagonistic genetic programs orchestrating barley seed maturation and germination at the Polytechnic University of Madrid. After a short stay at the Roberto Solano's lab (CNB, Spain) as CSIC IP3 postdoctoral fellow, he moved to Tübingen (Germany). There, he joined Weigel Lab at the MPI for Developmental Biology funded by fellowships from the Spanish Government and EMBO to work on miRNA-mediated regulation of hormone pathways and Transcription factors. Since 2016, Ignacio is the group leader of the Molecular Reprogramming and Evolution (MoRE) lab at the CRAG (Barcelona, Spain). The main focus of the MoRE lab is to understand how organisms, more concretely plants, coordinate their genetic programs devoted to control development and immunity.



Núria Sánchez Coll, Ramón y Cajal researcher and Group Leader at **Centre for Research in Agricultural Genomics**, Barcelona, Spain

Núria Sánchez Coll obtained her PhD degree at the Swiss Federal Institute of Technology (ETH-Zürich) in 2006 under Dr. Klaus Apel direction. Her work focused on the signalling pathways leading to programmed cell death in response to reactive oxygen species. She then joined the lab of Dr. Jeff Dangl at the University of North Carolina with a Swiss National Research Foundation fellowship to study the mechanisms driving programmed cell death during plant immune reactions to pathogens. Since 2012 she is the co-group leader of the team "Bacterial plant diseases and cell death" at the Centre of Research in Agricultural Genomics (CRAG) in Barcelona. She has been awarded a Marie Curie Fellowship and Career Integration Grant, a Beatriu de Pinós fellowship and she is currently a Ramon y Cajal fellow. She has recently obtained research awards from the Spanish Association of Scientists and from the Catalan Society of Biology. Her team is currently investigating the multilayered plant defense mechanisms against against vascular pathogens and also the spatio-temporal regulation of pathogen-triggered immune cell death.



Paloma Mas, Research Professor at **Centre for Research in Agricultural Genomics - CSIC**, Barcelona, Spain

Paloma Mas is a CSIC Research Professor at CRAG (Centre for Research in Agricultural Genomics). Her research interest deals with understanding the circadian clock using *Arabidopsis thaliana* as a model system. The main research topics are based on identifying components and mechanisms of clock function exploiting multidisciplinary approaches. Recent research projects in the lab have specifically focused on the elucidation the circadian organization and hierarchical structure of the circadian system; on studies about the connection between the cell cycle and the circadian clock, and on the molecular mechanisms responsible for the generation of circadian rhythms in nascent RNAs.

P. Mas was elected EMBO YIP, and currently is an EMBO Member. She received the EURYI Award, the National Award from the Carmen and Severo Ochoa Foundation and the special mention for the Life Sciences Award of the City of Barcelona. She is currently the Deputy Director of CRAG; member of the Internal Scientific Advisory Board and was Head of the Department of Molecular Genetics (2011-2014).

DETAILED PROGRAM AND INVITED SPEAKERS

Monday, September 3, 2018

Session 1: Pathogen perception and signalling



Cyril Zipfel, Professor at **Institute of Plant and Microbial Biology, University of Zurich, Zurich, Switzerland**

Cyril Zipfel is the Chair of Molecular & Cellular Plant Physiology at the University of Zurich (Switzerland) (since June 2018). Before that, he was Senior Group Leader and Head of The Sainsbury Laboratory (TSL) in Norwich (UK) where he had his group since 2007. He performed his doctoral (2001-2005) and post-doctoral research (2005-2007) in the laboratories of Profs. Thomas Boller (Friedrich-Miescher Institute, Basel, Switzerland) and Jonathan Jones (TSL Norwich, UK) (supported by an EMBO Long-Term Post-Doctoral Fellowship), respectively. He is a pioneer and leader in the field of plant innate immunity and receptor kinases. His work is focused on understanding the molecular basis of plant innate immunity mediated by surface-localized immune receptors, as well as the application of this research to engineer disease resistance in crops. He was awarded competitive European Research Council grants in 2012 and 2018, is a Highly Cited Researcher (since 2014), and was awarded Charles Albert Shull Award from the American Society of Plant Biologists in 2015 and the 4th Tsuneko & Reiji Okazaki Award from Nagoya University in 2018. He was elected to the European Molecular Biology Organization in 2018.

FERONIA and the regulation of receptor kinase-mediated signaling

Plants genomes encode hundreds of cell surface-localized receptor kinases (RKs) that control almost all aspects of plant life, ranging from reproduction, growth to responses to the external environment. Using RKs that function as immune receptors by perceiving microbial elicitors, we are studying the molecular basis of plant immunity, but also more generally how plant RKs work at the mechanistic level. Using the leucine-rich repeat RKs FLS2 and EFR (which perceive bacterial flagellin and EF-Tu, respectively) as model systems, we are investigating how plant RKs function as part of multimeric protein complexes at the plasma membrane – often in complex with other RKs, which act as regulatory proteins. Our recent work uncovered the importance of these regulatory RKs and RK-associated proteins in controlling the activity, as well as the assembly of these heteromeric receptor complexes. These observations also raise the inherent question of how these dynamic receptor complexes get formed and organized at the plasma membrane. Notably, we have recently uncovered an important role of the *Catharantus roseus* RLK1-like (CrRLK1L) FERONIA (FER) as a regulatory RKs controlling immunity. Building on this recent published work, I will present our unpublished work that sheds light on ligand perception by FER function and on the more general role that FER may play in the regulation of multiple signaling pathways beyond immunity and reproduction.



Youssef Belkhadir, Group Leader at **Gregor Mendel Institute, Vienna, Austria**

PhD: Jeff Dangl, UNC-Chapel Hill 2003-2005

- Used plant molecular genetics to understand the signaling mechanisms that lead to the specific activation of plant defenses responses.
- Helped to establish and strengthen the tenets of the “Guard Hypothesis”
- Contributed to the discovery of a tripartite regulatory module required to maintain the competency of the plant immune system prior to infection.

Postdoc: Joanne Chory, SALK institute 2006-2010

- Departed from the field of plant immunity to study the signaling mechanisms by which a cell-surface steroid hormone receptor promotes cellular elongation and overall plant growth.

- Contributed to solve the atomic structure of the steroid binding domain of this receptor
- Helped to further our understanding of the molecular events happening downstream of ligand perception.
- Took advantage of my doctoral training to demonstrate that plants set endogenous steroid hormone levels and signaling to a particular range for optimal defenses.

Entrepreneur: 2011-2013

- Launch and co-found Atlas Genomics, (the first African biotech start-up).
- Act as the chief scientist officer and raise public and private funds to discover genes that code for novel enzymatic variants in collections of both endemic medicinal plants located in the Atlas mountains and microorganisms that leave in the Sahara desert.

Group Leader at Geger Mendel Institute since June 2014:

- Start a lab to understand why receptor signaling systems operate as unified regulatory networks to fine-tune plant growth and defense programs.

Organ-specific regulation of growth-defense trade-offs by a cognate receptor-peptide pair

Because defense and growth are both costly programs, a plant's success in colonizing resource-scarce environments requires tradeoffs between the two. Here, we will present efforts aimed at understanding how plants use iterative tradeoffs that modulates differential organ growth when defenses are elicited by a cognate peptide-receptor pair. The less well-characterized principles of root defense systems together with the inherent complexity of root growth makes it challenging to understand the regulation of growth-defense tradeoffs in this organ. Here, using large-scale quantitative genetic studies, cell biology and biochemistry we dive in the regulation of growth-defense trade-offs in the root, to show that the recognition of a peptide by its receptor at the cell surface is critical for the role of this organ in acquiring resources in an environment entrenched with microbes.



Saskia Hogenhout, Project Leader at **John Innes Centre**, Norwich, UK

Saskia Hogenhout obtained her MSc in Biology at de Vrije University, Amsterdam, The Netherlands in 1994. She conducted her PhD research on the molecular basis of luteovirus-aphid interactions at Wageningen University and Research Centre, The Netherlands, and graduated in 1999. In the same year she became an independent Project Leader (Assistant Professor) at The Ohio State University (OSU), USA. Her group at OSU investigated leafhopper and planthopper transmission of phytoplasmas and rhabdoviruses. Saskia obtained tenure as Associate Professor in 2005. She moved her research group to the John Innes Centre, UK, in June 2007, and became Honorary Professor at the University of East Anglia, Norwich, UK, in 2013. She is currently a member of the Department of Crop Genetics at the John Innes Centre. Her research focuses on the molecular basis of plant-microbe-insect interactions, and includes research on how phytoplasma effectors modulate plant architecture and development, and plant resistance to leafhopper vectors. More recently, her research program also includes aphid functional genomics, functional analyses of aphid effectors and plant defense responses to aphids.

How phytoplasma effectors induce dramatic changes in plant architecture and modulate plant defense to insect pests

One of the most spectacular phenomena in biology is the complete hijacking of hosts by parasites such that these hosts become 'zombies' destined to advance survival of the parasites often to the detriment of the hosts. Phytoplasmas are obligate intracellular bacterial parasites of plants that induce dramatic changes in plant development, including proliferation of stems (witches' brooms) and the reversion of flowers into leaf-like structures (phyllody). These bacterial parasites produce at least two virulence proteins (effectors), including SAP11 and SAP54, that promote the degradation of plant TCP and MADS-box transcription factors, respectively, thus altering leaf and flower development. Phytoplasmas are dependent on sap-feeding insects for transmission to plants. Interestingly, SAP11 and SAP54 also convert plants into more attractive hosts for egg laying and reproduction of the insect vectors. Thus, phytoplasma effectors interfere with key plant developmental processes. Moreover, these effectors increase the colonization of plants by insect vectors thereby promoting transmission of the obligate phytoplasmas to new plant hosts.



Cris Argueso, Assistant Professor at **Colorado State University**, Fort Collins, USA

Cris Argueso is an Assistant Professor at Colorado State University, In First Collins, CO. She has a Bachelors degree in Biology, and a Masters in Plant Genetics, from Campinas State University in Brazil. She obtained her PhD in Plant Pathology at Cornell University, which was followed by a postdoc at the University of North Carolina at Chapel Hill, on plant hormones and immunity. Her lab focuses on hormonal crosstalk, and how plant hormones regulate plant immunity and growth.

Plant hormones on the crossroads of plant growth and defense

Plants, like all other organisms, need to assess and adapt to constant environmental changes throughout their life cycle. Responding to biotic stress requires tightly controlled mechanisms to ensure activation of appropriate levels of defense responses. The molecular mechanisms that control metabolic reprogramming from cellular growth to activation of defense responses are not well understood. With advancements in high throughput molecular techniques and computation data analysis, tools are now available that allow us to gain a better understanding of how plant hormones shape the outcome of defense activation and its consequences to plant growth. We employed transcriptomics and targeted metabolomics profiling to monitor global gene expression and the levels of major plant hormones in Arabidopsis mutants with altered states of growth and defense. A hormonal interplay between two plant hormones, salicylic acid and cytokinins, was identified that may play a key regulatory role in the control of the growth as well as defense regulation. Results from this project will help understand how plant hormones regulate plant metabolic processes linked to growth and defense to pathogens.



Teva Vernoux, Director at **RDP Laboratory**, Lyon, France

Teva Vernoux is a group leader and the director of the RDP Laboratory, a joint institute of the CNRS/INRA/INRIA/ENS de Lyon/UCBL from the Université de Lyon. He conducts interdisciplinary research focusing on the role of hormonal signals in self-organization and morphogenesis at the shoot apical meristem.

Coordinating patterning and growth during early flower morphogenesis

In multicellular organisms, undifferentiated cells have the competence to respond to endogenous signals and switch identity, resulting in cell fate determination and morphological changes. How these two processes are coordinated is a key question in developmental biology. In plants, leaves and flowers are formed in the periphery of Shoot Apical Meristems (SAMs), from cells that have progressively lost their stem cell identity and acquired the competence to respond to the small signalling molecule auxin. We have used a genome-wide gene profiling meta-analysis to explore the gene network triggered by auxin during flower initiation. This approach allowed us to identify a tissue-specific set of genes involved in early flower development and we will show how this dataset inform us on mechanisms coordinating growth and patterning that shapes the young flower. We will notably discuss evidence for a balance between growth-promoting hormones and stress-related hormones during the early phases of flower morphogenesis as well as a novel regulatory module at the interface of growth and identity regulation.



Sheng Yang He, Professor at **DOE Plant Research Lab**, East Lansing, USA

Sheng Yang He is a University Distinguished Professor at Michigan State University and an Investigator at Howard Hughes Medical institute. Dr. He is best known for his study of plant-pathogen interactions. In the past two decades, Dr. He's lab uses the Arabidopsis thaliana-Pseudomonas syringae pathosystem to discover some of the basic principles that govern bacterial pathogenesis and disease susceptibility in plants. His lab also uses microbial pathogenesis as a probe to gain insights into important cellular processes in plant biology, including immunity, jasmonate signaling and stomatal defense. Recent research in his lab begins to shed light on how climate conditions and phyllosphere microbiota influence disease development. Dr. He received his Bachelor's and Master's degrees from Zhejiang (Agricultural) University, China, and a PhD degree from Cornell University, USA. He is a Thomson Reuters Highly Cited Researcher, a Past-President of the

International Society of Molecular Plant-Microbe Interactions, a fellow of the American Association for the Advancement of Science and a member of the United States National Academy of Sciences.

Toward understanding “Disease-Climate-Microbiome” Interactions In plants

One of the most significant challenges of the 21st century is to discover innovative ways of increasing global crop production to meet the demands for food from the growing human population. A major roadblock to global food sufficiency is persistent loss of staple crops to pathogen infections. Greater efforts are needed to accelerate the buildup of a comprehensive knowledge base that explains how plant diseases occur; how plants defend against microbial pathogens; and how dynamic climate conditions impact plants, microbes, and their interactions. In 1960, RB Stevens (Plant Pathology, an Advanced Treatise. Vol. 3, Academic Press, New York) formulated the famous “Disease Triangle” concept, proposing that plant disease outbreaks require not only a susceptible plant and a virulent pathogen, but also conducive environmental conditions. For practical reasons, however, most contemporary investigations into plant-pathogen interactions at the molecular level devote little effort to understanding why climatic conditions, such as humidity and temperature, have a profound effect on pathogen virulence and host susceptibility. Moreover, these studies often ignore the potentially pervasive effect a plant’s endogenous microbiome may have on basic plant health and host-pathogen interactions. In this talk, I will give an example of interplays between disease, humidity, temperature and microbiota during *Pseudomonas syringae* infection of *Arabidopsis thaliana* leaves. Future studies of plant-pathogen interactions should increasingly consider the multi-dimensional nature of “disease-environment-microbiome” interactions that are more reflective of what occur in crop fields and natural ecosystems.

Session 2: Cellular and nuclear basis of the interplay growth-defense



Xinnian Dong, HHMI Investigator, Arts & Sciences Professor of Biology at **Duke University**, Durham, USA

Xinnian Dong received her B.S. degree in microbiology from Wuhan University in China in 1982 and came to the US to pursue her graduate degree in the same year. Xinnian Dong was awarded Ph.D. degree in molecular biology by Northwestern University in Chicago in 1988. She became interested in using *Arabidopsis thaliana* as model organism to study plant immune mechanisms when she was a postdoctoral fellow with Dr. Fred Ausubel at Massachusetts General Hospital in Harvard Medical School. Xinnian Dong became an Assistant Professor at Duke University in 1992 and was promoted to Associate Professor in 1999 and Full Professor in 2004. She is currently an Arts & Sciences Distinguished Professor of Biology (since 2007). The Dong laboratory identified NPR1, a master regulator of immune regulator in plants, and made several important discoveries on how NPR1 transduces the immune signal salicylic acid in conferring broad-spectrum disease resistance. In recent years, the Dong lab discovered surprising connections between plant defense with the circadian clock and with the DNA damage repair machinery. Moreover, they found that translational regulation is a critical step of immune induction and controlling translation of master immune regulators, such as NPR1, in a pathogen inducible manner can render broad-spectrum disease resistance to rice without any significant yield penalty normally associated with enhanced immunity.

Xinnian Dong became a HHMI investigator in 2011, elected as an AAAS fellow in 2011, a member of the National Academy of Sciences in 2012 and an American Academy of Microbiology Fellow in 2013. She was also named as an outstanding alumna of Wuhan University in the same year.

Precision in Plant Immune Expression: Not Lost in Translation

A major consequence of pathogen infection is perturbation of host metabolism, including protein synthesis. However, little is known about how host cells may respond to such perturbations and selectively synthesize defense-proteins to mount immune responses. My lab showed that TBF1, a transcription factor controlling the growth-to-defense transition in plants, is tightly regulated at both transcriptional and translational levels. The TBF1 mRNA contains two upstream open reading frames (uORFs) besides the main ORF. Translation of TBF1 is normally inhibited by these uORFs, which presumably cause dissociation of the ribosome from the mRNA before it reaches the downstream TBF1 ORF. Upon induction of both pattern-triggered immunity (PTI) and effector-triggered immunity (ETI), the inhibitory effects of uORFs are rapidly and transiently alleviated, leading to TBF1 protein translation. To elucidate the regulatory mechanisms, we performed global translome profiling, using the recently developed ribosome footprinting technology,

and identified several trans-acting regulators, a highly conserved RNA sequence (“R-motif”), and many new uORFs. Moreover, we used the pathogen-responsive TBF1 cassette to drive the production of defense proteins and provided the proof of concept, in *Arabidopsis* and in rice, that adding translational control to defense protein production is an effective new strategy for minimizing fitness costs associated with broad-spectrum disease resistance and reducing the selective pressure for resistant pathogens.



Arp Schnittger, Professor at **University of Hamburg**, Hamburg, Germany

Academic education

- 2012: Directeur de recherche première classe (DR1), Centre national de la recherche scientifique (CNRS), Institut de Biologie Moléculaire des Plantes (IBMP), Strasbourg, France
- 2007: Directeur de recherche deuxième classe (DR2), IBMP-CNRS, Strasbourg, France
- 2007: Habilitation and *venia legendi* in Botany, University of Cologne, Germany
- 2001: Dissertation in Genetics, University of Tübingen, Germany
- 1991-1999: Study of Biology at the University of Tübingen, Germany and the University of Washington, Seattle, USA

Research experience & scientific training

- Since 2014: Professor of Developmental Biology (W3/full professor), University of Hamburg, Germany
- 2009 – 2013: Head of the department Molecular Mechanisms of Plant Plasticity (former Cell Biology) at the Institut de Biologie Moléculaire des Plantes (IBMP), Strasbourg, France
- 2007 – 2013: Research group leader, Centre national de la recherche scientifique (CNRS), Institut de Biologie Moléculaire des Plantes (IBMP), Strasbourg, France
- 2004 – 2006: Fellow of the Volkswagen Stiftung and independent research group leader, University of Cologne, Department of Botany III, Germany
- 2001 – 2007: Group leader at the Department of Botany III, University of Cologne, Germany
- 1997 – 2001: Doctorate thesis, Center of molecular plant biology, Department of developmental genetics, University of Tübingen, Germany

Retinoblastoma – a jack of all trades in development and stress response

Retinoblastoma (Rb) is a multifunctional regulator, which was likely present in the last common ancestor of all eukaryotes. The *Arabidopsis* Rb homolog RETINOBLASTOMA RELATED 1 (RBR1), similar to its animal counterparts, controls not only cell proliferation but is also implicated in developmental decisions, stress responses and maintenance of genome integrity. RBR1 largely exerts its function as a transcriptional repressor and in the case of cell cycle regulation, the up to now the best-studied function of Rb-type proteins, inhibits the expression of genes regulated by the E2F transcription factor family. To undercover the multi-faceted function of RBR1, we have characterized a weak-loss-function allele of RBR1 and combine these studies with the analysis of RBR1 target genes and RBR1 interactors. Here, we focus on the role of RBR1 during the plant response to DNA stress. This work not only shed light onto the mechanism of transcriptional repression by RBR1 but also led to the identification of novel DNA damage regulators in plants.



Clara Sánchez-Rodríguez, Assistant Professor at **ETH Zurich**, Zurich, Switzerland

Clara Sánchez-Rodríguez is Assistant Professor of Plant Cell Biology at ETH Zurich since April 2015, and co-chair of the Institute of Molecular Plant Biology (ETHZ) since February 2017. She has a Master in Agronomy from Polytechnic University of Madrid, where she also obtained her PhD on plant resistance to necrotrophic fungi (supervised by A. Molina). During a short visit to Sommerville’s labs, she was fascinated by plant cell walls. Thus, her postdoctoral research focused on the mechanisms of cellulose synthesis in plants (at S. Persson’s group), pioneering the fields of cellulose synthesis regulation by hormones and vesicle trafficking. She is one of the leader discoverers of the TPLATE complex, a clathrin-mediated endocytosis adaptor essential in plants, but not present in animals and yeast. This achievement was honoured by the Jeff Schell Award for Plant Scientists. Her independent research at ETHZ focuses on

the molecular basis of plant-pathogen communication at the plant apoplast (i.e, plant cell walls). Employing molecular and cell biology methods, her group studies the plant cell wall role in the intercellular growth of vascular fungi.

Cell wall-dependent Immunity-growth balance

The cell wall (CW) provides stability and protection to the plant and is the first layer of stimuli perception. Therefore, a controlled remodelling of this structure is essential for the plant to adapt its growth to environmental stresses. Regulation of perception and response to CW perturbations is a major driver towards balancing optimal plant development and stress response activation. To understand this equilibrium we use the pathosystem *Arabidopsis thaliana*-*Fusarium oxysporum*. This fungus advances intercellularly through the root layers towards the xylem, interacting with the plant cells and their CW in a very particular and interesting way. Among the plant CW components, cellulose is the most abundant and essential one, being synthesized by plasma membrane-localized cellulose synthases (CSCs) moving along cortical microtubule (MT) tracks. We are studying different aspects of the cellulose need for plant response and growth adaptation to *F. oxysporum*. Through in vivo imaging of CSC and MT, we show that the plant cell is able to modulate its growth by pausing the cellulose synthesis machinery immediately upon microbe contact by sensing apoplast pH changes. This observation explains the reduction of cell elongation monitored in response to microbes. We have identified a protein needed for growth inhibition upon those apoplastic pH changes, whose molecular function we are currently investigating. In addition, we have observed that deficiencies in cellulose lead to reduced xylem colonization of *F. oxysporum*. Combining genetic, biochemist and cell biological studies we aim to understand the molecular and mechanical aspects of the cellulose role in plant-microbe interaction.



Christine Faulkner, Project Leader at **John Innes Centre**, Norwich, UK

I'm a project leader at the John Innes Centre (UK) where my lab studies the regulation of plasmodesmata and cell-to-cell communication during plant defence. I did my PhD at the University of Sydney (Australia) on plasmodesmal proteomics and continued to study plasmodesmata in a variety of contexts during postdoctoral positions at the University of Edinburgh (UK), the John Innes Centre (UK) and the Sainsbury Laboratory (UK). I started my independent research programme at Oxford Brookes University (UK) in 2012 on plasmodesmal responses to pathogens, and I continue this research at the JIC. My lab employs cell and molecular biology approaches in determining how plant cells control symplastic communication during immunity, and how pathogens exploit the plant symplast to enhance infection.

Symplastic regulation of Immunity and Infection

The plant immune system is broadly characterised as a cell autonomous response system - generally all plant cells are capable of pathogen perception and response. However, the observation that plasmodesmata, plasma membrane-lined pores that connect neighbouring cells, are regulated during immune responses identifies that cell-to-cell connectivity and communication influences the establishment of immune responses. Plasmodesmata close in response to a range of microbe associated molecular patterns (MAMPs); for chitin and flagellin that this is mediated by specialised immune signalling components located at plasmodesmata. Chitin plasmodesmal responses are triggered by the plasmodesmata-located, LysM domain receptor protein LYM2 and two additional LysM domain receptor kinases. Plasmodesmal responses are executed via calcium and reactive oxygen species signalling that ultimately triggers callose deposition causes plasmodesmata to close. We have begun to identify defence responses that are associated with the regulation of cell-to-cell connectivity and communication. Further, preliminary data suggests that pathogens also manipulate and exploit plasmodesmata. These data build a complex picture of how both host and pathogen depend on cell-to-cell connectivity during defence and infection, illustrating that plant pathogen interactions are executed via multicellular orchestration.



Tolga Bozkurt, Senior Lecturer at Imperial College London, London, UK

I initiated my career working on filamentous plant pathogens and focused on yellow rust-wheat pathosystem during my PhD in Turkey. My postdoctoral studies centered around the functions of *Phytophthora infestans* secreted effector proteins in the Sainsbury Laboratory. Following this, I am appointed a Lecturer position at the Imperial College London and I recently got promoted to Senior Lecturer position. My group mainly focuses on dissecting the molecular mechanisms underlying plant cell autonomous immunity and the role of endomembrane traffic in this process. I had ground-breaking contributions to the biology of plant-parasite interactions, especially on how pathogen effectors modulate membrane trafficking at the host interface. I was first to report that a plant pathogen effector focally accumulates at the host-pathogen interface and neutralizes a secreted host defense protease as a novel counter defense strategy. More recently, my work on effector biology shed light on the poorly understood question of how plant pathogens manipulate autophagy to enable infection. This work highlighted the extensive remodeling of endomembrane compartments during plant-microbe interactions and opened up novel perspectives in understanding the role of autophagy in plant immunity.

Modulation of autophagy during pathogen attack

During plant invasion, the Irish potato famine pathogen *Phytophthora infestans* forms hyphal extensions that grow into host cells, which are enveloped by host-derived membranes whose functions and biogenesis are poorly understood. Through this interface, the pathogen secretes effector proteins to vigorously reprogram cellular trafficking. Our earlier work revealed that, one of these effectors, PexRD54 modulates host selective autophagy by antagonizing the antimicrobial-autophagy receptor NBR1/Joka2. PexRD54 specifically binds to a plant ATG8 isoform ATG8CL to stimulate autophagosome formation, whilst depleting NBR1/Joka2 from ATG8CL-autophagosomes.

Here I summarize our latest work on modulation of selective autophagy during *P. infestans* infection. We discovered that defense-related selective autophagy is targeted to host- pathogen interface to contribute to immunity. The pathogen counteracts this through secreting PexRD54, which remodels host-microbe interface by first disarming and then co-opting the host autophagy machinery. Furthermore, we found that PexRD54 stimulates starvation like responses in plant cells and triggers autophagosome formation by coupling host vesicle transport regulators to ATG8CL-coated autophagosomes. Consistently, our proteomics analysis of different ATG8 clade members revealed two diverse plant RabGAPs as novel autophagy adaptors that compete with PexRD54 for ATG8 binding, further highlighting the role of endomembrane trafficking in plant selective autophagy. Our results implicate selective autophagy in polarized immune responses of plants and provide insights into effector-mediated autophagosome biogenesis. These findings point to more complex functions for autophagy than the widely known degradative roles.

Tuesday, September 4, 2018

Session 3: Pathogen and host co-evolution and adaptation



Detlef Weigel, Director at **Max Planck Institute for Developmental Biology**, Tübingen, Germany

Detlef Weigel, a German-American scientist, is currently a director at the Max Planck Institute for Developmental Biology. He is a member of the US National Academy of Sciences, the German National Academy of Sciences Leopoldina and the Royal Society, and recipient of several scientific awards.

The first major finding from his lab was that an *Arabidopsis thaliana* gene could dramatically accelerate flowering of trees; this established a proof of concept for *Arabidopsis* genetics as a platform for biotechnological discoveries. His group later discovered the first plant microRNA mutant and identified the factor that we now know to be the long sought-after mobile flower-inducing signal. Detlef was one of the first to exploit natural genetic variation for understanding how the environment affects plant development. In recent years, his work in evolutionary genetics and genomics has focused on plant immunity and epigenetics. In addition to hypothesis-driven research, his group has a long history of providing new technologies and resources to the community. This has culminated in an effort to sequence the genomes of over 1000 natural *A. thaliana* strains (The 1001 Genomes Project).

Detlef has an extensive record of service to the scientific community, having served on a series of editorial and advisory boards. He is a forceful advocate of open access publishing, and founding Deputy Editor of eLife. He is a co-founder of three biotech startups, including the bioinformatics service provider Computomics.

Arabidopsis and its pathogens - tales from the wild

My group is addressing fundamental questions in evolutionary biology, using both genome-first and phenotype-first approaches. A major interest in the lab is the analysis of fitness tradeoffs in immunity. A few years ago, we developed *A. thaliana* as a model for the study of hybrid necrosis, a widespread syndrome of hybrid failure in plants, due to adverse autoimmune reactions that greatly inhibit growth and development. Several of the causal loci are immune receptor genes, and thus members of the most polymorphic gene family in plants. While most systems involve two loci, autoimmunity can also be caused by inter-allelic interactions at a single locus, ACD6, which is involved in a major fitness tradeoff between growth and pathogen resistance in inbred strains. The effects of ACD6 alleles are in turn modified by a series of extragenic suppressors segregating in natural populations of *A. thaliana*. One of these corresponds to the SNC1 NLR locus.

Our goal for the next decade is to understand the genomic and geographic patterns for immune system diversity. Together with collaborators Jeff Dangl, Jonathan Jones and Brian Staskawicz, we have been describing species-wide diversity of NLR immune receptor genes. In parallel, we have been describing with collaborator Eric Kemen the local diversity on *A. thaliana* plants of the microbial pathogen, *Pseudomonas*. This year, we initiated an ambitious new project, Pathodopsis (Patho[gen]s in Arabi[dopsis]), in which we aim to describe genetic diversity in the host and two important pathogens, the generalist *Pseudomonas* and specialist *Hyaloperonospora arabidopsidis*. The long-term vision is to produce maps of resistance alleles in the host, and of effector alleles in the pathogens, in order to learn whether local adaptation is more common for the host or for the pathogens.



Santiago Elena, Professor at **Institute for Plant Molecular and Cell Biology (IBMCP-CSIC)**, Valencia, Spain

Graduated in Biological Sciences (Biochemistry) by the Universitat de València in 1990 I received my PhD in Genetics from that same university in 1995 under the supervision of Profs. Andrés Moya and Esteban Domingo. During my thesis, I worked on the experimental evolution of RNA viruses, specifically in the effect of accumulation of deleterious mutations and dynamics of compensatory evolution. After a postdoctoral stay in the laboratory of Prof. Richard E. Lenski (Michigan State University) working on the experimental evolution of bacteria and on evaluating the impact of epistasis on the architecture of fitness, I joined the U. de València Department of Genetics as an Assistant Professor, where in 2001 I was promoted to Associate Professor of Population Genetics. In 2002 I changed the University for the CSIC and joined the Instituto de Biología Molecular y Celular

de Plantas as a Scientific Investigator. In 2005 I was promoted to CSIC full Professor. Since I joined the CSIC, I has been working on the experimental evolution of plant RNA viruses and the systems biology of virus-host interactions. Throughout my career, I have published more than 230 papers in journals in the areas of evolutionary biology, virology and systems biology, contributed more than 250 communications to congresses and gave more than 80 invited seminars in institutions around the world. I have directed 20 PhD theses and have been principal investigator for 18 national and international grants. Among other merits, I was elected EMBO Young Investigator in 2004, awarded as Young Virologist by the Spanish Society of Virology in 2006, elected external professor of the Santa Fe Institute (New Mexico, USA) in 2008, elected EMBO Member in 2011, and elected Professor of the Chinese Academy of Agricultural Sciences in 2018.

Differences among *A. thaliana* ecotypes in response to infection drives patterns of virus adaptation

It is generally assumed that genetic variability in host species for susceptibility to infection will necessarily condition the evolution of viral populations, either by driving them to the diversification of the virus into antigenically diverse strains that track the different host defense alleles, or by canalization of the virus to infect only the most susceptible genotypes. Associated to these processes, virulence may or may not increase concomitantly. In any case, the pathogen's fitness must be optimized.

To tackle these questions, we have been performing evolution experiments with tobacco etch (TEV) and turnip mosaic (TuMV) potyviruses in different genotypes of the experimental host *Arabidopsis thaliana*. In a first set of experiments, we explored the role of within-host species genetic variability for susceptibility to infection in the extent of TEV local adaptation and virulence. Results were always consistent with a pattern of local adaptation, characterized by a higher infectivity and virulence on the host ecotype(s) encountered during evolution. However, local adaptation not always paid a cost on the foreign host ecotypes: viral lineages evolved in more susceptible ecotypes evolved as specialists, whereas adaptation to the less susceptible ecotypes always resulted in more virulent generalist viruses. Therefore, the antagonistic pleiotropy cost of generalism depends on the characteristics of each particular pathosystem.

In a second set of experiments, we are exploring the effect that the amount of genetic diversity for susceptibility has on the rate of TuMV adaptation to different experimental host populations. In good agreement with theoretical expectations, we have found that viral lineages evolving in host populations composed by multiple ecotypes and with maximal genetic diversity evolved slower and were quickly dominated by mild generalist viruses. By contrast, genetically homogeneous host populations composed by a single plant ecotype rapidly selected for locally-adapted more virulent specialists.

Finally, in a third set of ongoing experiments, we are evolving TuMV lineages in mutant genotypes of the Col-0 ecotype. Each of these genotypes differ in mutations in genes involved in resistance pathways (e.g., RNAi-mediated, methylation-mediated and ethylene and salicylic acid pathways) and in genes whose products have been shown to be essential for TuMV or other potyviruses to complete its infection cycle (e.g., translation initiation factors or heat-shock proteins). Plant genotypes can be classified into three categories according to their response to infection: hypersusceptible, equal to the wildtype and hyposusceptible. TuMV is more infectious and induces severer symptoms in hypersusceptible plant genotypes than those observed in Col-0. By contrast, it is less infectious and induces weaker or no symptoms in hyposusceptible genotypes.



Hailing Jin, Professor at **University of California, Riverside**, Riverside, USA

Professional Experience

- 2016-Present: Professor and Cy Mouradick Endowed Chair
- 2015-2016: Professor and UC President's Chair
- 2014-2017: Director of Genetics, Genomics and Bioinformatics Graduate Program
- 2014-2015: Vice Chair of the Department of Plant Pathology and Microbiology
- 2013-Present: Professor, University of California, Riverside
- 2009-2013: Associate Professor, University of California, Riverside
- 2004-2009: Assistant Professor, University of California, Riverside
- 2000-2004: Research Specialist, Plant Gene Expression Center, University of California, Berkeley
- 1996-1999: Postdoctoral Fellow, John Innes Center, UK

Education

- Ph.D. 1996: Molecular Genetics, Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences
- B.Sc. 1991: Genetics, Wuhan University, China

Honors and Awards

- Ruth Allen Award, American Phytopathological Society, 2017
- Cy Mouradick Endowed Chair, 2016 - present
- Elected Fellow of American Association for the Advancement of Science (AAAS), 2015
- University of California, Endowed President's Chair Professor, 2015
- NSF Career Award 2007

Cross-Kingdom RNAi and small RNA trafficking between plants and fungal pathogens

Small RNAs (sRNAs) are a class of short non-coding RNAs that mediate gene silencing in a sequence-specific manner. We have demonstrated that some sRNAs from eukaryotic pathogens, such as *Botrytis cinerea*, the fungal pathogen that causes grey mold disease on more than 1000 plant species, can transfer into host plant cells and suppress host immunity genes for successful infection (Weiberg et al., Science 2013).

To examine whether host endogenous sRNAs are delivered into fungal cells, we developed a sequential protoplast preparation protocol to isolate pure fungal cells from the infected tissue, then profiled sRNA populations from the isolated *B. cinerea* cells. We also observed a drastic increase of extracellular vesicles (EVs) at the fungal infection sites, which led us to isolate EVs from the infection tissue and perform small RNA-profiling analysis. We identified a panel of plant endogenous sRNAs that are secreted by EVs and transferred into fungal cells. These sRNAs induce cross-kingdom RNAi of fungal genes involved in pathogenicity. Furthermore, we discovered two *Arabidopsis* exosome markers that are induced by *B. cinerea* inoculation. Mutation in these exosome marker genes leads to reduced sRNA transport and enhanced plant susceptibility. These data support that exosome-like extracellular vesicles are one of the major pathways to deliver host sRNAs into fungal cells and induce cross-kingdom RNAi of fungal virulent genes (Cai et al., Science 2018).

Furthermore, we also discovered that *B. cinerea* can take up double-stranded RNAs and sRNAs from the environment. Applying sRNAs or dsRNAs that target *Botrytis* Dicer genes on the surface of fruits, vegetables and flowers significantly inhibits grey mold disease (Wang et al., Nature Plants, 2016). Such pathogen gene-targeting RNAs represent a new generation of fungicides that are durable and environmentally-friendly.



Kenichi Tsuda, Group Leader at Max Planck Institute for Plant Breeding Research, Cologne, Germany

Kenichi Tsuda studied plant transcriptional mechanisms and obtained a PhD at Hokkaido University (Japan) in 2004. He did a postdoctoral research in the laboratory of Fumiaki Katagiri at University of Minnesota (US) with a focus on plant immune signaling networks from 2005 to 2011. Since 2011, he has been leading a research group as Group Leader at Max Planck Institute for Plant Breeding Research (Germany). His research interests include molecular mechanisms and (co)evolution of plant-microbe interactions in fluctuating environments.

Impact of plant immunity on a bacterial pathogen

Despite extensive studies into the molecular and genetic bases of plant immunity, the impact of plant immunity on pathogens to control their behavior and growth is poorly understood. We studied in planta bacterial transcriptome responses of the foliar pathogen *Pseudomonas syringae* and identified specific immune-responsive bacterial genes and processes, including those that are activated in susceptible plants and suppressed by plant immunity. Expression patterns of immune-responsive bacterial genes at an early time point explained later bacterial growth levels in different host genotypes. We also determined in planta bacterial proteome responses and found that specific bacterial proteins were suppressed or degraded by plant immune components. These results illuminate impacts of host immunity on bacterial metabolisms and provide clues for how plants control bacterial behavior and growth. We extend our analysis to members of the plant microbiota to understand the commonality and specificity of plant immunity on different bacterial species and principles of microbiota assembly govern by host immunity.



Emilia López-Solaila, Head of the research group Phytopathogenic Bacteria at **Centre for Plant Biotechnology and Genomics** (UPM-INIA), Madrid, Spain

BS degree in Biological Sciences (1994), from Complutense University and PhD in Biological Sciences (1998) from Polytechnic University of Madrid. Associate Professor of Biochemistry and Molecular Biology since 2010 at the Polytechnic University of Madrid. Principal investigator of the Plant Pathogenic Bacteria Group at the Centre for Biotechnology and Plant Genomics (UPM-INIA) established in 2008. Scientific expertise focused in the research area bacteria-plant interaction. During the first phase of her scientific carrier, her contribution was focused on the study of resistance mechanisms to plant defense in the plant pathogenic model *Dickeya dadantii*. During a postdoctoral stage (2001-2002) at Cornell University (Department of Plant Pathology, Dr. Collmer's lab), she was part of the initiative responsible for carrying out pioneering studies on bacterial functional genomics of plant pathogens, expanding her experience to the pathogen *Pseudomonas syringae* pv tomato. Since then, she has been involved in the study of the early stages of infection in both bacterial models. Likewise, and under collaborative projects with other groups she has participated in functional studies related to bacterial pathogenesis in other pathosystems (*Pseudomonas savastanoi*-olive, *Erwinia amylovora*-fruit trees and others) as well as in functional studies in soil bacteria. Her scientific interests currently focus on the study of the mechanisms of perception and response to plant and environmental factors in bacterial phytopathogens.

Bacterial adaptation to host environment during the onset of the infection

During part of their life cycle, prior to the onset of infection, phytopathogenic bacteria live, and spread on the phyllosphere environment. Bacteria have evolved to resist and adapt to this environment and to perceive entry points to the plant apoplast where nutrients are available. Light is pervasive in the leaf environment, creating opportunities for both plants and pathogens to cue into light as a signal to regulate plant-microbe interactions. Bacterial perception of light could determine the switch to a pathogenic program when conditions for motility and other virulence traits are more favorable. At the same time, motility is driven by chemotaxis processes in which perception of specific molecules could determine the success during the entry process.

Our group has been involved during the last years in the study of the entry and adaptation to the host during the first stages of the infection. We have initiated the analysis of the role of environmental and plant signals in these processes. In this talk some of the results that have allowed us to state the function of specific perception mechanisms will be presented.



Carmen R. Beuzón, Full Professor at **Institute for Mediterranean and Subtropical Horticulture "La Mayora"** (UMA-CSIC), Málaga, Spain

Carmen R. Beuzón obtained her Ph.D in Biological Sciences at the University of Seville in 1996, under the supervision of Prof. Josep Casadesús studying the regulation of transposition of IS200 in *Salmonella typhimurium*. She moved to Imperial College London in 1998 with a Long-Term EMBO Fellowship (1998-1999) and remained there with an MRC Contract until 2002, working throughout her entire stay as a Research Associate to Prof. David Holden studying type III secretion regulation and role in pathogenesis in *Salmonella typhimurium*. Afterwards, she joined the University of Malaga as a Ramón y Cajal Researcher (2003-2007), Associate Professor/ Profesor Contratado Doctor (2007-2010), Associate Professor/ Profesor Titular (2010-2017), and since 2017 as Full Professor of Genetics/ Catedrático.

Since joining University of Málaga, she leads a research team focused on the identification and characterization of molecular and cellular mechanisms of defense and defense evasion involved in the interaction between the pathogenic bacterium model *Pseudomonas syringae* and the plant.

Novel defence and defence evasion mechanisms in *Pseudomonas syringae*-plant interactions

Pseudomonas syringae is a remarkably adaptive pathogen and an important model for the study of plant-pathogen interactions. In plants, *P. syringae* can be found in the surface of leaves, entering the leaf through natural openings and wounds to reach the intercellular spaces of the leaf parenchyma, the apoplast, where it replicates causing disease. There, it encounters a two-tiered defence response, starting with the recognition by plant receptors on the cell membrane of conserved molecular patterns such as flagellin (pathogen-associated molecular patterns or PAMPs), which triggers the first line of defence against incoming microorganisms, known as basal resistance or PTI (PAMP-triggered immunity). *P. syringae*

uses a type III secretion system (T3SS) to directly deliver effector proteins (T3Es) inside the plant cell cytosol, many of which can suppress PTI. However, the activity of T3Es can trigger a second more intense response known as effector-triggered immunity (ETI), associated to a programmed cell death process known as the hypersensitive response (HR) that determines resistance against the pathogen.

During the infection process, plants recognize the presence of the pathogen and modulate the expression of a variety of genes involved in the defense response. In this process miRNAs have recently been shown to play a fundamental role in reprogramming for a successful defense response. Different analysis of the expression profiles of mutant plants in the biogenesis of small RNAs and plants infected with *P. syringae*, led us to identify a series of uncharacterized "R" genes (TIR-NBS-LRR) differentially expressed in both conditions. With the use of different bioinformatic tools, we identified a miRNA* of 22 as a potential regulator of these "R" genes directly and indirectly through the generation of small phased RNAs (phased-siRNAs) from one of the target genes. We will present our most recent findings on the subject.

Session 4: New approaches to understand growth-defense trade-off



Klára Panzarová, Chief Scientist at **Photon Systems Instruments**, Drásov, Czech Republic

Klára Panzarová (Šimková) obtained her PhD titel at ETH Zurich in Switzerland in group of Prof. Klaus Apel, where she focused on understanding regulatory mechanisms of retrograde signalling. She has strong background in plant physiology and molecular biology. Currently her professional interest is in understanding non-invasive multi-dimensional analysis of plant performance in

automated high-throughput manner and in investigation of novel technologies for image-based plant monitoring. She is appointed as chief scientist for technical support in PSI (Photon Systems Instruments, spol. s r.o.) where she is currently also head of the PSI Research Center.

During past few years she worked in the team that developed complete solutions for multi-dimensional image-based monitoring of plant growth and performance, PlantScreen™ Systems. These systems are using various techniques on small and large scale level for simultaneous quantification of plant photosynthetic capacity, plant growth and morphological characteristics, plant biochemical characteristics and plant surface temperature. PlantScreen™ Systems have implemented range of commercial and customized in-house developed sensors to ensure high precision, sensitivity and integration capacity into the phenotyping systems, which can be operated in fully automated manner including data acquisition, processing and management.

Very recently PSI Research Center was opened, which integrates all of the above mentioned sensors in automated phenotyping platforms designed either for phenotyping small-size plants such as Arabidopsis and young cereal seedlings in controlled environment or platform for phenotyping of large plants of adult corn type in greenhouse environment.

Novel phenotypic approaches in quantitative analysis of biotic stress in plants

Plant diseases, causing the losses of agriculture production, have become the acute problem nowadays, when the agriculture struggles to support the rapidly growing population. Not only disease symptoms affect the growth and development of the crops and thus decrease the overall yields, but the agricultural products might not be suitable for storage or even consumption due to the postharvest pathogens producing toxins causing serious health problems. Every year, millions of dollars are spent on disease management, often without adequate knowledge of the infection symptoms and disease mechanisms, resulting in poor disease control and food pollution.

Recently, an integrative plant phenotyping approach, based on implementation of Red Green Blue (RGB) imaging, kinetic chlorophyll fluorescence, hyperspectral and thermal imaging sensors, was successfully used to quantify drought stress induced dynamic changes in complex set of morpho-physiological traits (Awlia et al. 2016). Application of this approach to the biotic stress has potential to unravel the hidden link between the physiological mechanisms and disease symptoms development, allowing early and thorough infection detection and symptoms quantification. Here we propose that the integrative non-invasive phenotypical approach offers efficient tool for plant breeders to screen for and develop resistant crop cultivars.

The aim of the presentation is to summarize the current state of the art of the plant phenotyping approaches and to discuss the potential, pros and cons of individual imaging sensors application for various types of biotic stress factors.



Hernán A. Burbano, Group Leader at **Max Planck Institute for Developmental Biology**, Tübingen, Germany

Hernán A. Burbano studied veterinary medicine and biology (1996-2006) at the Universidad Nacional de Colombia in Bogotá. He moved afterwards to the Max Planck Institute (MPI) for Evolutionary Anthropology in Leipzig, Germany, where he worked on ancient genomics of humans and archaic hominins under the supervision of Svante Pääbo and Michael Lachmann. Burbano obtained a PhD in evolutionary genetics from the University of Leipzig (2012). In Leipzig he was part of the team that sequenced the first draft of the Neandertal Genome and established capture methods to enrich for Neandertal DNA in samples highly contaminated with microbial DNA. Burbano then relocated as a postdoctoral researcher (2012-2014) at the MPI for Developmental Biology in Tuebingen, Germany, under the supervision of Detlef Weigel. There, he integrated plant evolutionary genomics and ancient DNA. He studied the evolution of plant pathogens from historical epidemics of potato late blight during the 19th century. Since 2014 Burbano leads the research group for Ancient Genomics and Evolution at the MPI for Developmental Biology. He combines the use of both modern and historical samples and focuses on the co-evolution of plant and pathogens, the colonization of new ecological niches by plant species, and the characterization and timing of key steps of plant domestication.

In August 2019 Burbano will take a faculty position at the Department of Genetics, Evolution and Environment at the University College London, where he will be affiliated with the newly formed Centre for Life's Origin and Evolution (CLOE).

Reinforcing plant evolutionary genomics using ancient DNA

Abstract not available.



Dolf Weijers, Professor and Chair at **Wageningen University**, Wageningen, The Netherlands

Dolf Weijers is a professor and chair of Biochemistry at Wageningen University (the Netherlands), and leads a group focused on how cells acquire identity; the mechanisms that specify individual cells and how cells communicate to form an ordered pattern, especially in the Arabidopsis embryo. Given the central role of the signaling molecule auxin in cellular decisions, a key focus area is on understanding the mechanisms underlying auxin responses. Projects include identifying and investigating the functions of key proteins that regulate these processes, using a wide range of approaches in cell biology, molecular biology and biochemistry, structural biology, mathematics, and bioinformatics.

Prior to assuming his current position in 2017, Dolf was junior group leader (2006), assistant (2008), associate (2010) and full (2012) professor at the Laboratory of Biochemistry in Wageningen, post-doc with Gerd Jürgens at the University of Tübingen (Germany; 2002-2005) and PhD student in Leiden (the Netherlands; 1997-2002).

Origin and evolution of the nuclear auxin response system

The small signaling molecule auxin controls numerous developmental processes in land plants, acting mostly by regulating gene expression. Auxin response proteins are represented by large families of diverse functions, but neither their origin nor the evolution of diversity is understood. We have used a deep phylogenomics approach to reconstruct both the origin and the evolutionary trajectory of all nuclear auxin response protein families. We found that, while all subdomains found in auxin response proteins are ancient, a complete auxin response mechanism is limited to land plants. Functional phylogenomics predicts defined steps in the evolution of response system properties. We have performed a comparative transcriptome analysis across six ancient lineages of charophytic green algae, bryophytes and ferns and show how these innovations have shaped a sophisticated response mechanism. We discovered the existence of a mechanistically independent transcriptional auxin response system in green algae. Finally, genetic analysis in the liverwort *Marchantia polymorpha* revealed unexpected contributions of ancient non-canonical proteins in auxin response as well as auxin-unrelated function of core transcription factors. Our study provides a functional evolutionary framework for understanding diverse functions of the auxin signal. I will present our progress in dissecting the evolutionary, structural and functional basis of the mechanism mediating auxin-dependent gene regulation.



Idan Efroni, Principal Investigator at **The Hebrew University**, Rehovot, Israel

I have obtained my Ph.D. from the Weizmann Institute, in Israel, working on regulation of leaf development in the lab of Prof. Yuval Eshed. Supported by an EMBO long-term fellowship, I did my post-doc with Prof. Ken Birnbaum at NYU where we studied root regeneration and developed tools for single-cell transcriptomics in plants. In 2016, I started my lab at The Hebrew University working on root meristem initiation and regeneration. At 2017, I was selected as an HHMI International Research Scholar.

Formation of root meristems

Plants are able to generate root meristems in multiple developmental contexts. The most common and best described is the initiation of lateral roots which are produced from prepatterned regions of the specialized root pericycle. However, plants can also form root meristems de novo, in a process that is much less understood. This crucial ability for meristem initiation underlies plants remarkable capacity for regeneration.

To study de novo meristem initiation, we introduced the tomato as a new model system. Unlike the commonly used Arabidopsis, tomato naturally initiate root meristems on easily accessible stems, without the need for injury. A genetic screen for tomato plants defective in stem-borne root meristem initiation has identified several novel mutants and their role in the process is being investigated. To profile the very early stages of tomato de novo meristem initiation we employed high resolution and single-cell-level transcriptomics across multiple developmental stages. We utilize cross-species comparative transcriptomics and analysis of hormonal dynamics to identify components of an evolutionary-conserved common program for meristem formation.



Niko Geldner, Professor at **University of Lausanne**, Lausanne, Switzerland

Niko Geldner studied biology at the Universities of Mainz, Bordeaux 2 and Tübingen. In Tübingen, he did his PhD in the lab of Gerd Juergens, working on the role of GNOM in Arabidopsis embryogenesis and the polar localisation of the PIN1 auxin efflux carrier. In 2004 he went as an EMBO and HFSP fellow to the Salk Institute in La Jolla in the lab of Joanne Chory, working on the trafficking of the steroid receptor kinase BRI1 and the development of the WAVE sub-cellular membrane marker set. In 2007 he started as an Assistant Professor at the University of Lausanne, being promoted to Associate Professor in 2012 and Full Professor in 2018. He was awarded a Starting and Consolidator grant of the European Research Council (ERC) in 2007 and 2013, respectively. In 2011 he became an EMBO Young Investigator and was elected EMBO member in 2017.

Root damage and immune responses at cellular resolution

The study of the molecular mechanisms that underlie plant damage and immune responses is among the most active areas of plant research. Yet much of the paradigmatic models in this field have been developed working on aerial tissues and there is reason to assume that roots have significantly different ways of integrating and responding to cellular damage, perception of microbe-associated molecular patterns (MAMP) and other stresses. We have previously developed transcriptional, live-imaging reporters for stress and immune responses, covering ethylene (ET), jasmonic acid (JA), salicylic acid (SA) and MAMP responsive genes. Using single cell laser ablations, we show that such a restricted damage of root cells already leads to local surface depolarisation, ROS induction and Calcium increases, yet only causes a transcriptional response to ET, but not to JA, in contrast to laser-induced damage of leaf cells. Since roots are able to produce and respond to JA, this indicates that translation of cell damage into hormonal responses is very different from leaves. Using our MAMP-responsive markers, we confirmed previous reports that root responses to MAMPs are restricted to the elongation/late division zone. We could demonstrate that this is largely controlled by receptor presence, since expressing a MAMP receptor in non-responsive tissues installed responsiveness in those cell layers in many cases. Intriguingly, laser-induced cell ablation could “unlock” MAMP-responsiveness in neighboring cells, associated with an upregulation of the MAMP receptor. Neither damage nor PAMP treatment alone were able to induce a MAMP response, suggesting that root cells perceive and combine cellular damage and MAMPs as two distinct signals. A similar “unlocking” of PAMP responsiveness was observed in cortical cells surrounding an emerging lateral root, although root emergence is not consistently associated with cell death and thus MAMP-responsiveness in these cells might be due to other factors, such as lateral root-produced peptides, small molecule signals or mechanical/cell wall stresses.

POSTERS

1. Aditi Gupta, Norma Fabregas, Fidel Lozano-Elena, David Blasco-Escamez and Ana Cano-Delgado. **Role of BRL3 in source to sink movement of metabolite signals during drought.**
2. A. Chini, I. Monte, AM. Zamarreño, M. Hamberg, S. Lassueur, P. Reymond, S. Weiss, A. Stintzi, A. Schaller, JM. García-Mina and R. Solano. **An OPR3-independent pathway uses 4,5-didehydrojasmonate for jasmonate synthesis.**
3. Andreu Paytuví i Gallart. **PRGdb 3.0: a comprehensive platform for prediction and analysis of plant disease resistance genes.**
4. Aurélia Emonet, Feng Zhou and Niko Geldner. **Cell-specific FLS2 expression impacts spatiotemporal compartmentation of PAMP-Triggered Immunity in *Arabidopsis thaliana*.**
5. Rosany Camargo-Ramírez, Beatriz Val-Torregrosa and Blanca San Segundo. **Regulatory function of miR858 during pathogen infection in *Arabidopsis thaliana*.**
6. Diego López-Márquez, Ángel Del-Espino Pérez, Nieves López-Pagan, Edgar A. Rodríguez-Negrete, Adela Zumaquero, Javier Ruíz-Albert, Ignacio Rubio-Somoza, Eduardo R. Bejarano and Carmen R. Beuzon. **Regulation of plant defense response against *P. syringae* via miRNA/phasRNA.**
7. Dousheng Wu, Orlando de Lange, Niklas Schandry, Alvaro L. Perez-Quintero, Boris Szurek, Edda Von Roepenack-Lahaye and Thomas Lahaye. **Identification of host target genes of *Ralstonia solanacearum* TAL like effector Brg11.**
8. Elwira Smakowska-Luzan, G. Adam Mott, Katarzyna Parys, Martin Stegmann, Karin Grunwald, Mathias Madalinski, Cyril Zipfel, Darrell Desveaux, David S. Guttman and Youssef Belkhadir. **Cross-talk between PSK- and flg22- signalling pathways attuned by scaffolding APEX and APEX-2 receptor kinases.**
9. Cristina Peris-Peris, Albert Serra-Cardona, Ferran Sánchez-Sanuy, Sonia Campo, Joaquin Ariño and Blanca San Segundo. **The Metal ion transporter NRAMP6 is associated to Disease Resistance in Rice.**
10. Guillermo Jimenez, Sandra Scholz, Ralf Ölmüller, Roberto Solano and Wilhem Boland. **Small molecules as molecular probes to understand plant signaling: the JA pathway as a case study.**
11. Hicham Chahtane, Thanise Nogueira Füller, Pierre-Marie Allard, Laurence Marcourt, Jacques Falquet, Emerson Ferreira Queiroz, Jean-Luc Wolfender and Luis Lopez-Molina. **A specific quorum sensing dependent molecule inhibits *Arabidopsis* germination through DELLA and ABA signaling.**
12. Inmaculada Sánchez Vicente, Pablo Albertos, Isabel Mateos, Brecht Wybouw, Bert De Rybel and Oscar Lorenzo. **Reversible S-Nitrosylation control of seed developmental programs.**
13. Jordi Gamir, Zhivko Minchev, Juan M. Garcia, Giulia de Lorenzo and Maria J. Pozo. **Differential local and systemic immune responses to oligogalacturonides in tomato roots and shoots.**
14. Martin Weyhe, Lennart Eschen-Lippold, Pascal Pecher, Dierk Scheel and Justin Lee. **Regulation of plant biotic stress through MAPK-mediated phosphorylation of WRKY-interacting factors.**
15. Ka-Wai Ma and Paul Schulze-Lefert. **Modulation of plant innate immunity during root microbiota establishment.**
16. Mireia Bundó and María Coca. **Rice calcium dependent protein kinases as signaling nodes in stress responses and development.**
17. Maria C. Salazar-Rondon, Carolin Seyfferth and Kenichi Tsuda. **Role of the evolutionarily conserved C-terminal regions of *Arabidopsis* MAPKs, MPK3 and MPK6, in transcriptional activation.**
18. Martin Mecchia, Mar Ferreira, Lluís Civera Cantó and Ana I. Caño-Delgado. **Evolutionary origin of steroid signalling in plants.**

19. Vilde Olsson, Mari-Kristine Anker, Maike Breiden, Elwira Smakowska, Youssef Belkhadir, Rüdiger Simon and Melinka A. Butenko. **The secreted peptide IDA amplifies immunity in *Arabidopsis*.**
20. Miguel Ángel Torres, Viviana Escudero, Magdalena Delgado, Sara Sopeña-Torres, Sanjay Swami, Jorge Morales, Antonio Muñoz-Barrios, Hugo Mérida, Lucía Jordá and Antonio Molina. **Mitogen-activated protein kinase phosphatase 1 (MKP1) negatively regulates Microbe-Associated Molecular Pattern-triggered immunity in *Arabidopsis*.**
21. Michael Karampelias, Fidel Lozano-Elena, Norma Fàbregas Vallvé and Ana I. Caño-Delgado. **Novel protein regulators of the Brassinosteroid receptors upon drought stress conditions.**
22. Sandra Fernández-Piñán, Pau Boher, Marçal Soler, Marisa Molinas, Mercè Figueras and Olga Serra. **Transcriptomic profiling highlights biotic stress genes for cork development.**
23. Tamara Lechón, María Guadalupe Fernández-Espinosa, Luis Sanz and Oscar Lorenzo. **Nitrosative stress impairs root stem cell niche homeostasis.**
24. Selena Gimenez-Ibanez and Roberto Solano. **Molecular Basis of Plant Resistance to Pathogens in Early Land Plants.**
25. C. Cabot, R. Bosch, S. Martos, C. Poschenrieder and A. Perello. **Alleviation of wheat blast disease in plants treated with biocontrol agents and affected by salt stress.**
26. Svenja Saile, Vera Bonardi, Lisa Wünsch, Pierre Jacob, Paulo J. P. L. Teixeira, Elke Sauberzweig, Jeffery L. Dangl and Farid El Kasmi. **Functional Characterization of helper NLRs in *Arabidopsis thaliana* immunity.**
27. Talia L. Karasov, Juliana Almario, Claudia Friedemann, Wei Ding, Michael Giolai, Darren Heavens, Sonja Kersten¹, Derek S. Lundberg, Manuela Neumann, Julian Regalado, Richard A. Neher, Eric Kemen and Detlef Weigel. **Distinct *Pseudomonas* pathogen evolution in agricultural versus wild plant populations.**
28. Tatsuya Nobori and Kenichi Tsuda. **Transcriptome landscape of bacteria under plant immunity.**
29. Toby Parkes, Sung Un Huh, Abigail Cooper, Oliver Furzer, Sebastian Fairhead, Jorge Carlier, Panagiotis F. Sarris, Jonathan D. G. Jones, Eric Holub and Volkan Cevik. **Distinct *Arabidopsis thaliana* resistance genes arrest development of the oomycete rust *Albugo candida* at different infection stages.**

PRACTICAL INFORMATION

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Agora Room (-3 floor)

Free wifi

1. Select [wifi_cosmocaixa_bcn](#)
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Contact persons during the event



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SUGGESTED READING

- **Mechanisms to mitigate the trade-off between growth and defense.**
Karasov, T., Chae, E., Herman, J. and Bergelson, J. (2017). *The Plant Cell*, 29(4), pp.666-680.
- **Should I fight or should I grow now? The role of cytokinins in plant growth and immunity and in the growth–defence trade-off.**
Albrecht, T. and Argueso, C. (2016). *Annals of Botany*, 1, pp. 725-735.
- **Trade-off between growth and immunity: role of brassinosteroids.**
Lozano-Durán, R. and Zipfel, C. (2015). *Trends in Plant Science*, 20(1), pp.12-19.
- **Disease resistance or growth: the role of plant hormones in balancing immune responses and fitness costs.**
Denancé, N., Sánchez-Vallet, A., Goffner, D. and Molina, A. (2013). *Frontiers in Plant Science*, 4.
- **The impact of temperature on balancing immune responsiveness and growth in Arabidopsis.**
Alcázar, R. and Parker, J. (2011). *Trends in Plant Science*, 16(12), pp.666-675.
- **Genetic and evolutionary perspectives on the interplay between plant immunity and development.**
Alcázar, R., Reymond, M., Schmitz, G. and de Meaux, J. (2011). *Current Opinion in Plant Biology*, 14(4), pp.378-384.
- **Organ-specific regulation of growth-defense tradeoffs by plants.**
Smakowska, E., Kong, J., Busch, W. and Belkhadir, Y. (2016). *Current Opinion in Plant Biology*, 29, pp.129-137.
- **The growth–defense pivot: crisis management in plants mediated by LRR-RK surface receptors.**
Belkhadir, Y., Yang, L., Hetzel, J., Dangl, J. and Chory, J. (2014). *Trends in Biochemical Sciences*, 39(10), pp.447-456.
- **uORF-mediated translation allows engineered plant disease resistance without fitness costs.**
Xu, G., Yuan, M., Ai, C., Liu, L., Zhuang, E., Karapetyan, S., Wang, S. and Dong, X. (2017). *Nature*, 545(7655), pp.491-494.

OUTCOMES

B·Debateca

On the website of **B·Debate**, you will find all the information related with the celebration of the meeting that includes reports, conclusions, scientific documents, interviews with the experts, speaker's CVs, videos, images, press documentation and other related materials. We invite you to visit the section **B·Debateca** on www.bdebate.org

Contents of the meeting: "When development meets stress: Understanding developmental reprogramming upon pathogenesis in plants"

The screenshot shows the B·Debate website interface. At the top left is the B-DEBATE logo with the text "International Center for Scientific Debate BARCELONA". To the right are logos for "biocat" and "Obra Social 'la Caixa'". A navigation menu includes "INICI", "B-DEBATE", "CONVOCATÒRIA", "DEBATECA" (circled in red), "NOTÍCIES", "SINOPSIS", "PREMSA", and "CONTACTE". Below the menu, a breadcrumb trail reads "Inici / Debateca / Programa anual 2017/2018". A dropdown menu for "DEBATECA" is open, listing "PROGRAMA 2017/18", "PROGRAMA 2016/17", "HISTÒRIC DE DEBATS", and "CICLES DE DEBATS". The main content area features two event listings. The first is titled "Programa anual 2017/2018" and "20/04/2017 a 21/04/2017" with the headline "The Genotype Tissue Expression (GTEx) Project Community Meeting. Enhancing the Usage of Human Genomics for the benefit of all". It includes a small image of a human silhouette and a DNA helix, and a brief description of the project. The second listing is dated "23/05/2017 a 24/05/2017" with the headline "Zika virus and other mosquito-borne viruses. Science for preparedness and response in the Mediterranean region" and a small image of a globe. On the right side, a "DEBATECA" sidebar lists links for "Programa 2017/18", "Programa 2016/17", "Històric de debats", and "Cicles de debats".

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More info: www.bdebate.org



The **Centre for Research in Agricultural Genomics (CRAG)** is an independent research institution located in the area of Barcelona (Spain), and devoted to leading-edge research in the molecular basis of genetic characters of interest in plants and farm animals and in the applications of molecular approaches for breeding of species important for agriculture and food production. Research at CRAG spans from basic science to applied studies in close collaboration with industry.

The CRAG forms part of the CERCA system of research centers of the Government of Catalonia, and is established as a partnership of four institutions: the Spanish National Research Council (CSIC), the Institute for Agri-Food Research and Technology (IRTA), the Autonomous University of Barcelona (UAB) and the University of Barcelona (UB). CRAG has been recognized as "Centro de Excelencia Severo Ochoa 2016-2019" by the Spanish Ministry of Economy and Competitiveness.

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