2016 IS-MPMI XVII CONGRESS PORTLAND, OREGON

XVII Congress on Molecular Plant-Microbe Interactions Meeting Report

Reports by travel awardees for the 2016 IS-MPMI XVII Congress

July 16–21, 2016, Portland, Oregon, U.S.A.

PLENARY SESSION 1

Summarized by: Gayani Ekanayake (University of Missouri, U.S.A.), Chenglong Liu (Texas A&M, U.S.A.), Barbara Franco (James Hutton Institute, U.K.), Shuai Huang (University of British Columbia, Canada)

As the first plenary session speaker, Dr. **Jeffrey Dangel** (University of North Carolina, Chapel Hill, U.S.A.) talked about mechanisms of effector-triggered immunity. They are looking at how bacterial type III effectors activate nucleotide-binding leucine-rich repeats (NLR) guarding RPM1 interacting protein4 (RIN4) proteins at the plasma membrane. They found that the *Pseudomonas syringae* effector HopBA triggers cell death and resistance in Arabidopsis. Structural and biochemical analyses indicate that RBA1 as a toll and interleukin-1 receptor (TIR)-domain only protein is able to self-dimerize using distinct interfaces, reminiscent of those in R proteins L6 and RPS4. HopBA1 interaction with RBA1 requires RBA1 self-association and functional L6 interface residues G151 and K149. The interface mutants of RBA1 were defective in activating HopBA1-triggered defense responses, indicating that the homodimerization of RBA1 is required for activating an immune response.

The session continued with a talk by Dr. **Uta Paszkowski** (University of Cambridge, U.K.), who talked about arbuscular mycorrhizal (AM) symbiosis with cereals. The rice (*Oryza sativa*) mutant, *hebiba*, was identified as more resistant to pathogens. Using this mutant, they showed that α/β Hydrolase DWARF14-LIKE (D14L) is required for AM symbiosis. D14L is the homolog of Arabidopsis karrikin receptor KAI2. This

karrikin receptor complex is required for rice perception of AM fungi. She also talked about an arbuscule receptor kinase, called ARK. The expression level of ARK dramatically increases in the late stage of symbiosis, suggesting that ARK may contribute to the life-span, senescence and nutrition acquisition of the fungi.

Dr. **Sally Miller** (Ohio State University) shared her excellent work on translating basic knowledge of plant pathology into food security improvement in developing countries. She described her work on improving tomato production in Morogoro by optimizing the integration of plant pathology study into breeding, culture and harvest practices. In developing countries, there is strong resistance to technologies like GMO. There are major yield gaps in developing countries and it is important for researchers to clearly understand the reality. She focused on education and knowledge transfer as a solution to achieve food security.

Dr. **Giles Oldroyd** (John Innes Institute, U.K.) introduced how they identified nuclear-localized cyclic nucleotide-gated channels (CNGCs) that mediate symbiotic calcium oscillations in *Medicago truncatula*. Using genetic and biochemical approaches, they showed that CNGC16a/b/c forms a complex with the potassium-permeable channel and modulates nuclear Ca^{2+} release as a key event during symbiosis with rhizobia.

PLENARY SESSION 2

Summarized by: Thomas Liebrand (University of California Davis, U.S.A.), Martin Stegmann (The Sainsbury Laboratory, U.K.), Xiaoxiao Zhang (CSIRO, Australia), Anna Joe (University of California Davis, U.S.A.) and Joji Grace Sernestrand (Forschungszentrum Juelich, Germany)

The first talk in the Plenary 2 session was the EMBO keynote lecture, given by Dr. **Ulla Bonas** (Martin Luther University, Halle, Germany). The Bonas group studies secreted effector proteins from the bacterial spot pathogen *Xanthomonas campestris* pv. *vesicatoria* (Xcv) and their interaction with the host plants pepper and tomato. The function of the studied

Travel awardees were supported by grants from the National Science Foundation (IOS-1608266) and from the Agriculture and Food Research Initiative of the USDA National Institute for Food and Agriculture (2016-67013-24728).

This meeting report is published as submitted. It was formatted but not edited at the APS headquarters office.

<http://dx.doi.org/10.1094/MPMI-29-12-S1>
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Xop effectors are characterized through a pipeline which includes the generation of deletion mutants, transient effector expression in planta and the identification of plant targets. These studies are combined with protein 3D structure analysis. In her talk, she presented findings about the biochemical activities of several Xcv effectors with diverse biological functions.

Microbes evolve faster than plants, so why are not all plants susceptible and conquered by microbes? To answer this question, Dr. **Fumiaki Katagiri**'s research group (University of Minnesota, St. Paul, U.S.A.) investigates plant immune signaling networks by using quadruple mutants lacking the well-studied *DDE2* (Delayed Dehiscence 2), *EIN2* (Ethylene Insensitive 2), *PAD4* (Phytoalexin Deficient 4) and *SID2* (Salicylic Acid Induction Deficient 2) genes that represent four defense signaling sectors. They found that 1) the *Arabidopsis* transcriptome response to flg22 treatment is highly resilient; and 2) there is a special expression sector named "sector X" that can compensate for the four known sectors in regulating the effector-induced Hypersensitive Response (HR). In addition, sector X was found to be inhibited by pattern-triggered immunity (PTI).

The root-infecting fungal pathogen *Fusarium oxysporum* shows a broad host range and strong host-specific pathogenicity with over 120 forms displaying compatible and incompatible host interactions. Dr. **Li-Jun Ma**'s research group (University of Massachusetts, Amherst, U.S.A.) developed a novel *Arabidopsis*-*Fusarium* pathosystem where an incompatible *Fusarium* bio-control strain grows outside of *Arabidopsis* cells whereas a compatible virulent strain invades into the host cells. Genome analysis showed that both strains display similarities including the same lineage-specific genomic regions and the same number of effectors. RNA-seq analysis showed that the bio-control strain expresses more effector proteins which may contribute to the non-pathogenic phenotype of this strain.

PLENARY SESSION 3

Summarized by: Kwasi Adusei-Fosu (Nottingham University, U.K.), Matthew Helm (Indiana University, U.S.A.), Margarita Marroquin-Guzman (University of Nebraska Lincoln, U.S.A.), Jeannette Rapicavoli (University of California Riverside, U.S.A.), Teja Shidore (Connecticut Agricultural Experiment Station, U.S.A.)

Dr. **Barbara Baker**, from the University of California at Berkeley, opened the session. Baker presented her work focusing on the regulation of plant innate immunity through microRNA (miRNA). Plant miRNAs and small interfering RNAs (siRNAs) guide sequence-specific silencing of *R* genes, thereby reducing fitness costs due to high copy genes. Her talk highlighted the role of DCL4 (Dicer like protein 4)-dependent novel miRNA families whose members silence genes encoding immune receptors, including those that confer resistance to the major pathogens of *Solanaceae* crops. Notably, DCL4-generated miRNAs silence two *Solanaceae* family *R* genes, *Cf9* and *Tm2*; and DCL4 is required for the biogenesis of miR6021 and miR6023 in tobacco and tomato. Many of these novel miRNAs amplify gene silencing by triggering the production of secondary trans-acting siRNAs (tasiRNAs). Baker further showed that miRNA overexpression leads to attenuated R-gene mediated resistance. Her work highlights the evolution of the plant innate immunity, incorporating small RNAs and a regulatory silencing network to fine tune pathogen defense responses.

Dr. **Steven Lindow**, from the University of California at Berkeley, presented viable strategies for the biological control of Pierce's disease of grapevine, caused by the xylem-limited bacterium *Xylella fastidiosa*. These strategies functioned through exploitation of the pathogen's quorum sensing system,

leading to pathogen confusion. RpfF of *X. fastidiosa* encodes a quorum sensing signal synthase that synthesizes a fatty acid diffusible signaling factor (DSF), which is produced and sensed by components of the regulation of pathogenicity factors (*rpf*) cluster. Lindow explained that the accumulation of DSF represses virulence in *X. fastidiosa*. DSF accumulation suppresses the release of outer membrane vesicles, which contributes to enhanced stickiness of *X. fastidiosa*. At high cell densities, DSF accumulates, leading to reduced cell mobility and limiting the spread of disease. Conversely, at low cell densities, reduced DSF levels induce the expression of virulence genes associated with systemic colonization, which is critical for successful infection. His group demonstrated that transgenic lines expressing *X. fastidiosa* RpfF are significantly more resistant to Pierce's disease than wild type plants. Another strategy he presented utilized the endophyte *Burkholderia phytofirmans*, which greatly reduced Pierce's disease severity when co-inoculated with *X. fastidiosa*.

Plant microbiome research studies the interactions between plants, their environments, and their associated communities of microorganisms. Plants grow in association with complex microbial communities, which can influence the health and productivity of plants and their responses to abiotic and biotic stresses. Advances in systems biology approaches and supporting technologies (e.g. high-throughput sequencing and "omics" technologies), are contributing to a greater understanding of the composition and function of these microbiomes. Dr. **Paul Schulze-Lefert**, from the Max Planck Institute for Plant Breeding Research in Germany, described reductionist approaches to explore microbiota functions utilizing a Microbiota Reconstitution Biology system. After establishing a reference culture collection of *Arabidopsis thaliana* root-associated microbes (based on culture dependent and independent techniques), his group assesses the impact of complex microbial synthetic communities (SynCom) on plant growth. This process begins with axenic or "germ-free" *Arabidopsis*, followed by controlled re-population of microbiota into the soil. Using this system, Schulze-Lefert presented strong evidence that re-introduction of microbiota into the soil, as a complete community, fully rescued plant growth phenotypes. He also demonstrated that rhizobial nodules contain distinct microbial communities and disabling nodulation results in a drastic shift in the composition of the microbial community. This implies a function of the nodulation pathway in the assembly of root-associated microbiota.

PLENARY SESSION 4

Summarized by: Susanna Harris (University of North Carolina Chapel Hill, U.S.A.), Xiaoyu Liu (University of Alabama at Birmingham, U.S.A.), Li Zhang (Michigan State University, U.S.A.), Kaitlin McNally (University of Zurich, Switzerland).

Dr. **Dong Wang** (University of Massachusetts, Amherst, U.S.A.) is the young investigator Awardee for the 2016 MPMI congress. His group focuses on understanding the membrane interface between rhizobia and their legume hosts during nodulation. They found that the maturation of symbiosomes into functional forms is mediated by one isoform of the *Medicago truncatula* SYNTAXIN 132 (SYP132), called SYP132A. The SYP132 transcript is able to produce two target-membrane soluble NSF attachment protein receptor (t-SNARE) isoforms by undergoing alternative cleavage and polyadenylation. SYP132A localizes to the peribacteroid membrane and the SYP132A-silenced plants exhibit immature symbiosomes. SYP132A is also required for arbuscular mycorrhizae colonization, suggesting a general role in plant-microbe symbiosis. The other isoform, SYP132C, localizes to the plasma membrane and regu-

lates root development that is unrelated to symbiosis (Pan et al. 2016). In addition, they discovered that the DEFECTIVE IN NITRIGEN FIXATION2 (DNF2) protein, which is required for rhizobial survival inside the host cell, belongs to a novel class of phosphatidylinositol-specific phospholipase Cs (PI-PLC) and cleaves glycosylphosphatidylinositol (GPI) anchored proteins. As such, DNF2 evades the host defense response via suppressing the release of defense proteins from the symbiosome membrane.

Using fluorescent labeling and confocal laser scanning microscopy (CLSM), Dr. **Savithramma P. Dinesh-Kumar's** lab (University of California Davis, U.S.A.) was able to observe induction of stromules, the tubular projections from chloroplasts, during N-mediated defense against *Tobacco mosaic virus* (TMV) or bacteria-induced immune responses. They detected stromule-to-nuclei associations, indicating pro-defense signal transportation between chloroplasts and the nucleus, e.g. chloroplastic N Receptor Interacting Protein 1 (NRIP1) and ROS accumulation in nuclei during N-mediated defense. The formation of stromules was shown to enhance programmed cell death (Caplan et al. 2015). They then investigated how stromules are formed, and their significance. Using a combination of specific fluorescent labels they showed that stromules extend along microtubules and through the endoplasmic reticulum (ER). Treatments that stabilize/increase microtubules increased the stromules' extensions, indicating that microtubules are the major factor for the extension mechanism, while actin is important for stromules to anchor to the microtubules.

Dr. **Alisa Huffaker's** (University of California San Diego, U.S.A.) talk focused on Plant Elicitor Peptides (Peps) and their role in the plant immune response. Peps, released after MAMP- or HAMP- triggered immunity, are recognized by Pep receptors (PEPRs) and function to amplify the immune signal. Peps are ubiquitous throughout angiosperm and gymnosperm plants but interfamilial recognition is not detected. Peps regulate defenses against both pathogens and herbivores. ZmPep1 activates jasmonate (JA) and ethylene biosynthesis and stimulates the accumulation of defense-related proteins and chemical compounds. Pre-treatment with ZmPep1 enhances plant resistance against *Cochliobolus heterostrophus* and *Colletotrichum graminicola* (Huffaker et al. 2011). ZmPep3 is induced in response to *Spodoptera exigua* oral secretions and mediates direct or indirect defense against *S. exigua*. Protease inhibitors induced by ZmPep3 directly reduce larval growth, while volatile compounds recruit the parasitoid natural enemy *Cotesia marginiventris* (Huffaker et al. 2013). Peps and their receptors form complexes with additional co-receptors (e.g. BAK1) which lead to phosphorylation of downstream signal components. In order to define novel downstream signaling components, her lab screened for proteins that rapidly changed in phosphorylation state upon Pep treatment in maize and Arabidopsis. Candidates discovered using this approach include a RNA recognition motif (RRM)-containing protein and a DNA-binding protein (PDBP1), both of which were confirmed to negatively regulate Pep and PAMP-mediated immune responses.

The last talk in this plenary session was from Dr. **Diane Saunders** (Genome Analysis Centre and John Innes Centre, U.K.). Dr. Saunders reported recent advances in the pathogenomics of wheat yellow (stripe) rust pathogen *Puccinia striiformis* f. sp. *tritici* (PST). PST has emerged over the past decade as a serious threat to wheat production (Hubbard et al. 2015). The goal of her project is to develop an international surveillance program to track pathogen races. Her lab initiated transcriptome sequencing of infected wheat leaves collected from the field. This pathogenomics approach could overcome the limitations associated with traditional methods involving culturing of PST. In addition, pathogen diversity can be assessed

quickly, which is a benefit to farmers. Comparisons of PST populations collected over 30 years in the U.K. showed a dramatic shift in 2013. This might be due to a recent introduction of a diverse set of exotic PST lineages. Four distinct lineages were characterized from the screen, and a correlation of genotype to virulence patterns on different wheat varieties was detected. In 2014, lineage 4 became dominant and continued to evolve into dominant sub-lineages in 2015. During the season, isolates from other lineages were found only in the summer months while lineage 4 was otherwise always dominant. They also surveyed isolates around the world and found that lineage 4 is present world-wide. More information for yellow rust disease can be found in U.K. Cereal Pathogen Virulence Survey and Wheat Yellow Rust Genomics.

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PLENARY SESSION 5

Summarized by: Laura A. Fleites (University of Florida, U.S.A.), Steen Hoyer (Donald Danforth Plant Science Center, U.S.A.), Paolo Margaria (Pennsylvania State University, U.S.A.), Mina Ohtsu (Nagoya University, Japan)

This session included three scientists working on diverse areas of research, from pathogenic to symbiotic interactions, with a central theme of exploring the perception of plant-associated microbes.

Dr. **Simona Radutoiu** (Aarhus University, Denmark) described the characterization of a LysM family receptor kinase from the model legume *Lotus japonicus*. Transcriptional analyses identified specific expression patterns of the kinases in *L. japonicus* roots in the absence or presence of the microsymbiont *Mesorhizobium loti*. In particular, a specific candidate gene showed the highest expression in the root zone most susceptible to nodulating bacteria, and remained unchanged in the presence of *M. loti*. The N-terminal ectodomain of the encoded protein was tested for Nod-factor binding, and the full-length protein tested for activation of NIN, a transcription factor involved in downstream signaling and nodulation. Differences between NIN activation via the Nod-factor receptor (NFR1) versus other candidate receptors were identified. The discovery of these differences will aid further investigations of the complex interplay between host and symbiont.

Dr. **Xinnian Dong** (Duke University, U.S.A.) presented new developments from genetic analyses initiated over 20 years ago, which identified an *Arabidopsis* mutant called *constitutive pathogenesis response (cpr)-5*. The story built on recent work in the Dong lab showing that CPR5 is a nuclear-membrane-localized protein that inhibits effector-triggered immunity through the cell cycle machinery. Mass spectrometry analysis of the CPR5 complex, pairwise protein interaction analysis, subcellular localization analysis, and genetic analysis all sup-

port a role of CPR5 as a specific nuclear pore component that alters protein transport into the nucleus upon perception of pathogen effectors. This work offers a new angle on the long-standing mystery of how plant immune receptors trigger downstream molecular events leading to immunity, and has parallels to exciting new findings in the field of animal immunity.

Dr. Saskia Hogenhout (John Innes Centre, U.K.) focused on effectors encoded by phytoplasmas, wall-less phloem-limited bacterial pathogens transmitted by sap-feeding insects. The effector SAP54 is produced by diverse phytoplasmas and responsible for inducing disease symptoms in *Arabidopsis* including leaf-like flowers and a bushy phenotype. SAP54 causes down-regulation of many genes involved in defense, especially NB-LRRs and MAPKs. It also promotes phytoplasma transmission by enhancing insect vector colonization and oviposition in the absence of any additional phytoplasma proteins. SAP54 can interact with MADS-box transcription factors: in particular, MAF5 and SVP1 are involved in attraction of leafhoppers to healthy plants, whereas AGL24 and FUL promote the attraction of leafhoppers to phytoplasma-infected plants. They have also demonstrated that female leafhoppers prefer to feed and lay eggs on SAP54-expressing plants only when males are also present. Intriguingly, the presence of males causes expression changes of a larger number of genes than females. In the proposed model, SAP54 causes down-regulation of MAF5 and SVP1 and up-regulation of AGL24 and FUL, resulting in a less efficient plant defense response, higher attraction of female leafhoppers, thus promoting colonization and propagation of phytoplasmas.

PLENARY SESSION 6

Summarized by: Beverly Agtuca (University of Missouri-Columbia, U.S.A.), Adam Bentham (Flinders University, Australia), Volker Hegenauer (University of Tuebingen, Germany), Sarah Hind (Boyce Thompson Institute, U.S.A.), Fabien Lonjon (LIPM, Université de Toulouse, INRA, CNRS, France)

Dr. Guo-Liang Wang from The Ohio State University (U.S.A.) studies the interaction between rice plants and the fungal pathogen *Magnaporthe oryzae* which causes the important rice blast disease. In particular, Wang elucidates the molecular mechanisms underlying the virulence activities of the effector protein AvrPiz-t, including its recognition by the rice resistance protein Piz-t. They identified the E3 ligases APIP6 and APIP10 as well as the bZip transcription factor APIP5 as interactors of AvrPiz-t. APIP6/10 are positive regulators of pattern-triggered immunity (PTI) as silencing of *APIP6/10* in a non Piz-t background enhanced susceptibility to *M. oryzae*. AvrPiz-t facilitates infection by promoting the degradation of APIP6/10 via the 26S proteasome. On the other hand, AvrPiz-t suppresses the transcription regulation activity of APIP5, which functions as a negative regulator of plant cell death. Interestingly, Piz-t stabilizes APIP5 and prevents its degradation mediated by AvrPiz-t.

Next, **Dr. Linda Kinkel** from the University of Minnesota (U.S.A.) talked about pathogen-suppressive soil microbes. In healthier plants, *Streptomyces* species could be found at higher densities with more diverse populations and increased inhibitory activities. Interestingly, Kinkel observed local selection for more intense inhibition of sympatric isolates, suggesting that antibiotics can be used against sympatric competitors.

Dr. Christian Voigt from the University of Hamburg, Germany, showed that overexpression of the *Arabidopsis thaliana* callose synthase PMR4 leads to resistance to powdery mildew. He shared high-resolution images showing cell wall reinforcement after pathogen infection using dSTORM microscopy. Voigt was able to resolve that callose biosynthesis co-occurred

at the sites of pathogen infection and demonstrated that the rosette formation at the site of polymer formation was comprised of an octamer complex. The cytosolic domain of PMR4 is sufficient for callose synthesis.

The final talk of the session was given by **Dr. Yuanchao Wang** from Nanjing Agricultural University, China. Wang studies apoplastic effector proteins produced by *Phytophthora sojae*, an important oomycete pathogen of soybean. One particular effector called XEG1 induces cell death in diverse plants and has been shown to be an essential virulence factor through its hydrolase activity. The soybean protein PLP1 contributes to disease resistance by binding to and inhibiting the hydrolase activity of XEG1. As a consequence of the plant-pathogen arms race, another *P. sojae* effector, XP1 acts as a paralog decoy of XEG1 and contributes to virulence by competing for PLP1 binding with better affinity than XEG1. Finally, XEG1 is recognized by a conserved plant receptor called RXEG1, which requires the co-receptor BAK1.

PLENARY SESSION 7

Summarized by: Jose Pedro Fonseca (Noble Foundation, U.S.A.), Mael Baudin (University of California Berkeley, U.S.A.), Joren Salazar (California State University Bakersfield, U.S.A.), Tongjun Sun (University of British Columbia, Canada)

Dr. Ken Shirasu (RIKEN, Japan) studies the interactions between parasitic and host plants using the facultative parasitic plant *Phtheirospermum japonicum* as a model. In order to recognize and invade a host plant, parasitic plants develop specialized structures called haustoria, which are formed upon detection of haustorium-inducing factors produced by the host plants. A large screening of EMS mutants identified mutants with an altered haustorium-related phenotype (Cui et al 2015). The Shirasu group identified genes affecting haustorial hair defect, specialized root hairs that support parasitism in *P. japonicum*, and is currently cloning these candidates. *P. japonicum* protrudes the haustorium upon induction by DMQB, a natural quinone. Transcriptome analysis was used to pinpoint genes differentially expressed upon DMQB treatment and host root exudate. *PjYUC3* is expressed at haustorium hairs and epidermal layer cells specifically and can be induced by host root exudates, which can also induce haustoria formation. The *yuc3* mutant produces a reduced number of haustoria. Additionally, *PjYUC3* expression at epidermal cells induces cell division. Expression pattern of *P. japonicum* genes involved in auxin signaling and cytokinin synthesis during haustorium development was determined. In particular, parasites produce cytokinins to induce host hypertrophy.

Dr. Gitta Coaker (University of California, Davis, U.S.A.) studies kinase mediated regulation of plant innate immune responses. Receptor-like cytoplasmic kinases (RLCKs) are important components involved in recognition of microbial patterns and also in NLR perceptions. Coaker's talk focused on the SIK1 Kinase in *Arabidopsis*, which belongs to the MAP4K protein family and is highly conserved in both monocot and dicot plants. Analysis of *sik1* mutant plants revealed that they were specifically compromised in the RPS5-mediated HR. SIK1 was shown to associate with PBS1. Silencing of the *SIK1* homolog in *Nicotiana benthamiana* led to reduced accumulation of PBS1. SIK1 also associates with RBOHD; consistently, the *sik1* mutant was compromised in the ROS burst. The Coaker group also characterized another kinase PBL13, which is a negative regulator of plant defense. The *pbl1-3* mutant exhibited an enhanced ROS burst and resistance to bacterial infection.

Dr. Eva Stukenbrock (Christian-Albrechts University of Kiel and Max Planck Institute of Evolutionary Biology, Kiel

and Ploen, Germany) studies fungal pathogen and host evolution using *Zymoseptoria tritici* as a model. *Z. tritici* displays both a biotrophic and necrotrophic infection stage. It generates and maintains high levels of genetic variation in uniform agro-systems. The authors selected three isolates from Iran, Holland and Denmark, displaying three distinct karyotypes, and analyzed gene expression profiles during wheat infection. Transcriptome analysis showed strong differences in these isolates, approximately 50% of the differentially expressed genes were isolate-specific, indicating a high genetic variation. Histone modifications contribute to regulation of putative effector genes although a core set of effector candidates was identified. The three isolates also show distinct colonization patterns based on microscopy analysis.

Dr. Laurent Deslandes (INRA, France) talked about the activation of the Arabidopsis resistance protein RRS1-R, which recognizes the *Ralstonia solanacearum* type III effector PopP2. RRS1-R is a nucleus-localized NB-LRR protein that contains a WRKY domain. Modification of the amino acid sequence to include an extra codon that inhibits DNA binding mediated by the WRKY domain leads to autoimmunity. RRS1-R has been shown to interact with PopP2, which functions as an acetyltransferase. EMSA assays show that acetylation of RRS1-R at the WRKY domain disrupts DNA-binding activity, leading to activation of PopP2-triggered immunity. An amino acid substitution that mimics RRS1-R acetylation by PopP2 also activates immunity. These results suggest that RRS1-R is an integrated decoy system that detects PopP2 activity. Around 10% of all NLRs have domains that may function as decoys, indicating that it is a widespread mechanism in plant defense.

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CONCURRENT SESSION 1 SYMBIOSIS AND MUTUALISM I

Summarized by: Kevin R. Cope (University of Wisconsin-Madison, U.S.A.), Michael Paries (Ludwig Maximilian University of Munich, Germany), Alex Greenspan (University of California Davis, U.S.A.), Akira Akamatsu (John Innes Institute, U.K.), Carol Ibe (University of Cambridge, U.K.).

In the first talk, Dr. **Jens Stougaard** from Aarhus University (Denmark) provided insight into the family of LysM receptor-like kinases of the model legume plant, *Lotus japonicus* using LORE1 retrotransposon insertion mutants (Urbanski *et al.* 2012) and biochemical characterization. Members of this protein receptor family provide a main interface in the signaling between mutualistic or pathogenic microbes and the plant (Lohmann *et al.* 2010). Besides the new findings that the receptors LYS6/CERK6 and LYS12 are involved in the defense response against necrotrophic fungi or oomycetes, respectively, the characterization of *Lys11* marked another highlight of this talk. Expression of this receptor was undetectable during root nodule symbiosis with nitrogen-fixing rhizobia but highly upregulated in arbusculated and adjacent cortical root cells (Rasmussen *et al.* 2016). Furthermore, overexpression of *Lys11* was able to complement the nodulation defective phenotype of a mutant of its closest paralog NFR5 (Radutoiu *et al.* 2003, Madsen *et al.* 2003). In light of these findings it is very interesting that the *lys11* mutant is not obviously impaired in either root nodule or arbuscular mycorrhizal symbioses. Additionally, two other receptors were found to be involved in root

nodule symbiosis: LYS1 and EPR3 (Kawaharada *et al.* 2015), which are expressed upon Nod factor perception and control rhizobial infection, delineating the formation of infection threads.

Dr. Caroline Gutjahr from Ludwig Maximilian University of Munich (Germany) gave an update on karrikin signaling in arbuscular mycorrhiza (AM) development. Previously in the Paszkowski lab, she showed that the alpha/beta-fold hydrolase DWARF14LIKE is required for arbuscular mycorrhizal fungi to colonize rice (Gutjahr *et al.* 2015). D14L is an orthologue of KAI2 in *Arabidopsis* which, in complex with the F-box protein DWARF3, is involved in the perception of karrikins, compounds found in smoke that are structurally similar to strigolactone. In that study, she also found that a paralog of DWARF3, i.e. MAX2, is required for colonization. Here, she outlined the progress her lab has made in elucidating the role of the karrikin receptor complex in AM development in *Lotus japonicus*. By phylogenetic analysis, they found that D14L is duplicated in the genomes of various legumes, including *L. japonicus*, but only one copy of MAX2 is present in the *L. japonicus* genome, suggesting that the karrikin receptor complex is conserved in legumes. They have acquired mutants for these genes and are now beginning to establish a model for how the karrikin binding complex regulates AM symbiosis.

Dr. Michelle Lum from Loyola Marymount University (U.S.A.) presented her lab's work on nitrogen-fixing bacteria. The symbiotic association between legumes and alphaproteobacteria has been studied extensively; however, the Lum lab has placed their focus on the association of legumes with betaproteobacteria, such as *Burkholderia tuberum*. This species of nodulating bacteria likely acquired nod genes through horizontal gene transfer, although the canonical *nodABC* operon encoding core Nod factor synthesis is rearranged. The Lum lab employed forward and reverse genetics approaches to determine the similarities between alpha- and beta-rhizobia. They have found that, similar to alpha-rhizobia, lipopolysaccharide is important for nodulation and that flavonoids regulate *nod* gene expression. They also observed that although multiple copies of *nodC* and *nodD* are present, not all of them are required for nodulation and may in fact be pseudogenes.

Dr. Akihiro Yamazaki from the Hayashi Lab at the RIKEN Center for Sustainable Resource Science in Japan presented his work on Nod factor perception by NFR1 and NFR5 in *Lotus japonicus* and how this leads to activation of the symbiosis signaling pathway. Downstream of NFR1 and NFR5 is a third receptor-like kinase, SYMRK, which is required for the activation of calcium spiking. It has recently been proposed that SYMRK activates the accumulation of mevalonate and either mevalonate or a product of this compound might act as a secondary messenger to initiate calcium spiking (Venkateshwaran *et al.* 2015). However, how the signal is transmitted from NFR1/5 to SYMRK, and how mevalonate activates calcium spiking is still not well understood. Yamazaki *et al.* found a new interacting protein, Avr9/Cf-9 Rapidly Elicited Protein 76 (ACRE76), which can interact with both NFR1 and SYMRK and has a positive role for nodulation. It might function as a scaffold protein or enhancer of mevalonate production. This work will likely provide important new insights into the signaling processes that occur during rhizobial infection.

Phytohormones play an essential role in development and environmental adaptation of plants. It has been shown that they are also involved in the establishment of plant root endosymbiosis. Prominent examples for this are the suppression of mycorrhizal colonization by gibberellic acid (El Ghachtouli *et al.* 1996) or the involvement of cytokinin in the root nodule symbiosis with nitrogen-fixing bacteria (Libbenga *et al.* 1973). With the new findings of Dr. **Sonali Roy** from the group of Dr.

Jeremy Murray at the John Innes Centre (U.K.) the phytohormone auxin was confirmed as a member of this collection. She found that the cellular auxin influx transporter LAX2, a *Medicago truncatula* orthologue of *Arabidopsis thaliana* AUX1, is involved in the successful establishment of root nodule symbiosis with nitrogen-fixing rhizobia. In the roots of the *lax2* mutant, a weaker and restricted pattern of auxin accumulation was observed, concomitant with the formation of fewer lateral roots than in the wild-type. Interestingly, the *lax2* mutant also displayed a decreased nodule number and reduced nodule size upon infection. From these results it seems likely that polar auxin transport is essential for the formation of nodules.

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CONCURRENT SESSION 2 GENOMES, GENOMICS, AND EPIGENOMICS

Summarized by: Maryn Carlson (Cornell University, U.S.A.), Hao-Xun Chang (University of Illinois Urbana-Champaign, U.S.A.), Samriti Midha (CSIR-Institute of Microbial Technology, India), Benjamin Schwessinger (Australian National University, Australia), Hester J Van Schalkwyk (University of the Free State, South Africa)

The topics of this session spanned plant, bacterial, fungal, and oomycete genome structure and evolution. This session demonstrated that the field has moved far beyond genome annotation, with six talks emphasizing structural and evolutionary analysis of plant and microbial genomes.

Dr. **Valerie Geffroy** (Institute of Plant Sciences Paris-Saclay, France) described features of the approximately 400 putative NB-LRR resistance genes in the common bean (*Phaseolus vulgaris*) genome. These genes predominantly colocalize in complex clusters in subtelomeric regions. Within these heterochromatic regions NB-LRR genes are targeted by 24 nucleotide small RNAs, associated with satellite DNA *khpu* and exhibit DNA methylation patterns similar to those of transposable elements (TE).

Methylation has additionally proved to play a significant role in pathogenicity. Working with the soil-borne fungal pathogen *Verticillium dahliae*, Dr. **David Cook** (Wageningen University, The Netherlands) demonstrated that DNA and histone methylation regulate genome structure and gene expression. The *V. dahliae* genome encodes three DNA methyltransferases, which when silenced minimally effect overall fungal growth and development. In the core genome, which consists of regions conserved within the species complex, methylation is predominantly associated with repetitive DNA and TEs. In contrast, lineage specific (LS) genomic regions are depleted of methylation and linked to high gene expression and potentially increased TE activity. Dr. Cook suggests that these observations connect the chromatin structure of LS regions with the concept of a two-speed genome.

Dr. **Julie Gervais** (INRA, France) focused on the expression of virulence related effector candidates at different infection stages of the blackleg fungus *Leptosphaeria maculans*. *L. maculans* colonizes canola and displays two distinct infection strategies. Biotrophic early infection often does not induce symptoms on young leaves. Later in plant development necrotrophic infection causes lesions and damping off of the stem. Gervais studied the expression patterns of candidate effectors during these two distinct infection stages. She identified over 300 effector candidates that are highly expressed specifically during infection of canola stems, but not young leaves. These effector candidates predominantly localize to the GC-isochore gene-dense euchromatic regions. As previously discussed by Dr. Cook, Dr. Gervais highlighted the potential of DNA methylation to serve as a primary regulator of effector gene expression and virulence in the context of the two-speed genome model.

Dr. **Peter Dodds** (CSIRO, Australia) did not observe clear signatures of the two speed genome in the dikaryotic fungal rust pathogens *Puccinia graminis* of wheat or *Melampsora lini* of flax. Dr. Dodds generated a high quality linkage map for *M. lini* by utilizing restriction site associated DNA sequencing (RAD-seq) of historic selfed populations developed in the last century. The genetic map anchored approximately 70% of the genome, enabling cloning of three new flax rust avirulence (*avr*) genes. Identification of *avr* genes in *P. graminis* is currently focused on mutants pathogen strains able to grow on wheat lines carrying the resistance gene *Sr50*. Virulence of these mutants is associated with large DNA deletions. The confirmation of candidate genes within these regions is well underway.

Next Dr. **David Guttman** (University of Toronto, Canada) shifted gears to talk about bacterial pathogens and his work on 'Comparative and Evolutionary Genomics of the *Pseudomonas syringae* Species Complex'. In an attempt to understand the basis of niche specificity, Guttman and his group took a population genomics approach where they sequenced 284 strains of *P. syringae* and analysed them alongside other publicly available genomes using a new analysis pipeline, DeNo-GAP. Four different types of type III secretion systems were identified among the 391 strains of *P. syringae*: canonical, rhizobial, S-PAI and atypical. They identified the composition of ecologically associated, evolutionarily related and recombinant loci, both inter-pathogroup and intra-pathogroup, demonstrat-

ing a strong correlation between virulence associated genes with loci under positive selection.

In oomycete pathogens such as *Bremia lactucae*, polyploidy may play a role in adaptation and speciation as illustrated by Dr. **Lien Bertier** (UC Davis, U.S.A.). To estimate ploidy level Bertier combined multiple approaches: flow cytometry, whole genome sequencing, and SNP allele frequencies. Applying these techniques, Bertier demonstrated multiple ploidy states among *B. lactucae* isolates: diploid, triploid, or tetraploid. Intriguingly, in some cases SNP allele frequencies did cohere with increases in genome size measured by flow cytometry.

Bertier's talk closed this exciting session. All talks illustrated how the field has moved beyond model systems toward applying novel, state of the art technologies to a vast array of important crop pathogens.

CONCURRENT SESSION 3 TRANSLATIONAL RESEARCH: DEVELOPING WORLD NEEDS

Summarized by: Kwasi Adusei-Fosu (Nottingham University, U.K.), Matthew Helm (Indiana University, U.S.A.), Margarita Marroquin-Guzman (University of Nebraska Lincoln, U.S.A.), Jeannette Rapicavoli (University of California Riverside, U.S.A.), Teja Shidore (Connecticut Agricultural Experiment Station, U.S.A.)

We live in a world that is expected to exceed 9 billion people by the year 2050. To meet this surge in population growth, food production needs to increase by at least 70%. This is a formidable task that is made more difficult by the fact that plant diseases destroy nearly 30% of the global harvest. The demand is urgent for translational research to provide technologies and approaches to the developing world to increase crop productivity in a safe and sustainable manner.

Dr. **Ricardo Oliva** at the International Rice Research Institute (IRRI) in the Philippines, opened the session. Oliva characterized the populations of *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) in the Philippines archipelago. *Xoo* is the causal agent of bacterial leaf blight, which is the most important bacterial disease of rice. Analysis of *Xoo* collections showed three genetic lineages that experienced different adaptation processes to rice. Comparative genomics demonstrated positive selection, recombination, and diversification of effector genes within *Xoo* lineages, suggesting that understanding these genotype-specific interactions is pivotal to developing resistance rice cultivars. Oliva's work demonstrates a high-throughput strategy to monitor emerging *Xoo* clones and supports breeding programs in one of the world's most important rice growing regions.

Dr. **John McDowell**, from Virginia Tech University (U.S.A.), presented work on exploiting effector biology for durable disease management of soybean root rot disease caused by the oomycete pathogen *Phytophthora sojae*. *P. sojae* is a devastating pathogen of soybean responsible for significant yield losses in major soybean-growing areas. During infection, *P. sojae* translocates effectors containing the amino acid motif RxLR (i.e. RxLR effectors) into the host cell, thereby promoting virulence. Thus, R proteins recognizing core RxLR effectors would confer durable resistance, as it would be difficult for *P. sojae* to mutate without compromising virulence. In the presented work, three *P. sojae* RxLR effectors Avh16, Avh180, and Avh240 were identified as core effectors that contribute to *P. sojae* virulence. These effectors are highly expressed and strictly conserved among characterized *P. sojae* isolates. Using the Effector Detector Vector (EDV) system, 31 *Glycine max* and 17 *Glycine sojae* accessions were determined as being resistant to *P. sojae* expressing either Avh16, Avh180, or Avh240.

Further screening identified 14 *G. max* and 3 *G. sojae* accessions that respond to all three effectors. Taken together, this effector-based screening approach discovered novel resistance genes in commercially cultivated and wild soybean germplasms. Introducing soybean R genes that recognize conserved RxLR effectors may provide resistance to *P. sojae*.

Dr. **Dean Gabriel** (University of Florida, U.S.A.) presented work on controlling the Pierce's disease (PD) of grapevine by targeting the TypeI efflux pump of the causal agent *Xylella fastidiosa* (*Xf*). Gabriel explained that a single gene (*tolC*) is responsible for the function of the *Xf* Type I efflux system (TIS), which increases its vulnerability to inhibition by small molecule treatments. Utilizing a *tolC* mutant, Gabriel demonstrated that loss of TIS increases sensitivity of *Xf* to the surfactant Silwet L-77. Using *Xf*-GFP, and a high-throughput fluorescence assay to evaluate cell viability, small molecules were screened for activity against *Xf*. Significant growth inhibition of *Xf* was observed with 209 chemicals, 150 of which exhibited growth inhibition enhanced by Silwet L-77, indicating that these chemicals possibly target TIS efflux. Future experiments will explore dose-dependent effects of selected chemicals and the influence of sap and crude extracts from PD resistant grapevines on *Xf* viability and TIS.

Dr. **Ralph Panstruga** (RWTH Aachen University, Germany) discussed the use of TILLING (targeted induced local lesions in genomes) to select spring wheat lines with an ethane substitution mutation in the gene *Mlo*. Panstruga and collaborators selected single amino acid mutations in *Mlo* genes with transient expression analysis. They combined multiple mutant alleles using intermutant crosses and marker-based selection, leading to double and triple mutant combinations. The resulting wheat lines were resistant to powdery mildew, without pleiotropic effects that have been previously observed in the barley *mlo* mutants.

Matthew Helm (Indiana University, U.S.A.) from the Innes laboratory presented work on expanding the recognition specificity of a plant NLR protein using synthetic 'decoys'. Prior work demonstrated that swapping the endogenous protease cleavage site within the *Arabidopsis* PBS1 protein substantially expanded the recognition specificity of the "guarding" *Arabidopsis* R protein RPS5, thereby conferring resistance to multiple pathogens. The specificity of RPS5 can be changed simply by altering the protease cleavage sequence in PBS1. Here, this technology is used to engineer resistance in soybean (*Glycine max*) to the *Soybean Mosaic Virus* (SMV) based on the activity of the viral protease, NIa. Helm replaced the endogenous protease cleavage site in *Arabidopsis* PBS1 with the cleavage sequence recognized by NIa. Transient expression of the modified *Arabidopsis* PBS1 along with the NIa protease and RPS5 in *N. benthamiana* resulted in NIa-dependent cleavage of the PBS1 derivative, triggering an RPS5-dependent defense response. Next, Helm identified three genes in soybean that are orthologous to *Arabidopsis* PBS1. He replaced the native protease cleavage site in each soybean PBS1 ortholog with the NIa cleavage sequence. Transient expression of the modified soybean PBS1 along with the NIa in *N. benthamiana* again resulted in NIa-dependent cleavage, confirming the potential of using synthetic decoys to accomplish resistance.

Dr. **Rebecca Bart** (Donald Danforth Plant Science Center, U.S.A.) presented work on dissecting the disease triangle of plant pathology. The "disease triangle" is the concept that plant disease is not necessarily caused by a single organism but affected by the combination of three major factors: 1) a virulent pathogen, 2) a susceptible host, and 3) dynamic environmental conditions. The Bart laboratory studies the various ways plants and microbes interact and how dynamic environmental conditions influence such interactions. Cassava (*Mani-*

hot esculenta) is a staple food crop for an estimated 800 million people, and this crop is prized for its drought tolerance and ability to grow under adverse conditions. However, there are several diseases that impact this crop: cassava bacterial blight (CBB), caused by the bacterial pathogen *Xanthomonas axonopodis* pv. *manihotis*, is one of the most devastating diseases. Currently, there are no characterized *R* genes effective against CBB, and chemical application methods are not financially feasible. Bart applied image-based phenotyping methods to study the cassava-CBB pathosystem. The Raspberry Pi computer and camera captures and quantifies infection over a given period of time, thus significantly limiting bias during disease scoring. The second method uses a bioluminescent reporter system within the bacteria to monitor pathogen spread throughout the plant. The combination of the two image-based phenotyping methods enhanced the resolution and the sensitivity for quantifying spatial and temporal disease progression.

CONCURRENT SESSION 4 MOLECULAR ECOLOGY OF HOST-MICROBE INTERACTIONS

Summarized by: Bruna Gonçalves Coutinho (University of Washington, U.S.A.), Sebastià Lòpez-Fernández (Fondazione Edmund Mach, Italy), Tiffany M. Lowe-Power (University of Wisconsin, U.S.A.), and Onur Oztas (University of Massachusetts Amherst, U.S.A.).

The research described in this session integrated the natural ecology of organisms with reductionist experimental systems to test hypotheses. The research foci spanned from small-scale (identifying novel secondary metabolite synthesis enzymes) to medium-scale (bipartite interactions between bacterial competitors or tripartite interactions between a beneficial symbiont, a pathogen, and plant hosts), to large-scale (high throughput screening by laser ablation-electrospray ionization mass spectrometry and in situ analysis of microbial metabolites in agricultural fields). Although many of the presentations focused on metabolite-mediated ecological interactions, one presentation focused on a protein-mediated interaction.

Dr. **Dimitri Mavrodi** (University of Southern Mississippi, U.S.A.) provided a reminder that antibiotics produced by soil microbes often have complex roles in the biology and ecology of the producing microbe. Although phenazines produced by *Pseudomonas fluorescens* are well-known as antibiotics, Mavrodi's work shows that phenazines also function as alternate electron acceptors to support bacterial growth in waterlogged, anoxic soil. This function of phenazine is supported by its chemical ecology as phenazine accumulates in the soil under wet conditions at the beginning of the growing season.

Dr. **Choong Min Ryu** (Korea Research Institute of Bioscience and Biotechnology, Korea) identified an airborne molecule (2,3-butandiol) that both promotes plant growth and antagonizes *Pectobacterium* virulence. Because volatile molecules accommodate long distance signaling between organisms, these molecules can easily shape interactions in physically and biologically complex environments like the rhizosphere.

Dr. **Andrew Klein** (Stanford University, U.S.A.) identified the plant enzymes responsible for synthesizing antimicrobial indole glucosinolates. Although his research is not primarily ecology, these antimicrobial compounds can drive ecological interactions between plant hosts and interacting microbes.

Dr. **Kevin Hockett** (University of Arizona, U.S.A.) is interested in understanding how microbe-microbe interactions influence plant-microbe interactions. His work shows that some strains of *Pseudomonas syringae* are able to produce a tailocin (bacteriocin derived from domesticated bacteriophage) that kills other *P. syringae* pathovars. Lipopolysaccharide (LPS)

was shown to be the tailocin receptor and LPS mutants were resistant to the bacteriocin activity. However, these mutants have a reduced ability to proliferate in host plants. This study shows how the production of bacteriocins can be an effective mechanism for niche competition.

It was evident from this session that small molecules play important ecological roles in host-microbe interactions, however the detection of these molecules can be difficult and this hampers progress. Dr. **Rachel Okrent** (USDA-ARS, U.S.A.) described a new detection approach for small metabolites. She used laser ablation-electrospray ionization mass spectrometry (LAESI-MS) to detect 4-formylaminoxyvinylglycine (FVG) produced by *P. fluorescens*. FVG is an amino acid analog that inhibits germination of weeds and growth of the fire blight pathogen *Erwinia amylovora*. This method could be used for the identification of new products of biotechnological interest.

In summary, this session highlighted the importance of different types of metabolites in plant-bacteria interactions and their role in microbial competition for plant colonization. The next step will be to determine the role of these molecules in shaping the complex microbial communities associated with plants.

CONCURRENT SESSION 5 MICROBIAL MANIPULATION OF HOST I

Summarized by: Ryan Kessens (University of Wisconsin Madison, U.S.A.), Arun Kumar (University of Wisconsin Madison, U.S.A.), Sowmya Ramachandran (Washington State University, U.S.A.), Robyn Roberts (University of Wisconsin Madison, U.S.A.).

Dr. **Thomas Baum** (Iowa State University, U.S.A.) is interested in identifying host targets of effector proteins secreted by heterodera cyst nematodes during syncytial formation. Using a combination of yeast two-hybrid and bifluorescence complementation assays, a novel effector from *Heterodera schachtii* was found to interact and co-localize with an *Arabidopsis* histone chaperone (FKBP53) and the histone deacetylase HDT1. This effector, 32E03, prevents HDT1 from deacetylating H3K9 acetylated histones. Interestingly, nematode infection in *Arabidopsis* is accompanied by a shift in the ratio of 45S rRNA variants, and H3K9 acetylation is known to regulate rRNA transcription. Expression of 32E03 in *Arabidopsis* resulted in derepression of rRNA transcription due to increased H3K9 acetylation levels. This work provides insight into how effectors are utilized by pathogens to induce epigenetic changes for a more suitable host environment.

While Dr. Baum has shed light on protein modifications and transcriptional changes induced by effectors, work by Dr. **Lindsay Triplett** (Connecticut Agricultural Experiment Station, U.S.A.) suggests that effectors may directly target small molecules. Dr. Triplett's study focused on identifying the target of AvrRxo1, a type III effector from *Xanthomonas oryzae* pv. *oryzicola* that suppresses plant immunity. Structural studies on AvrRxo1 revealed similarities to Zeta-toxin, a sugar-nucleotide kinase in prokaryotes. Overexpression of *AvrRxo1* in *E. coli*, yeast, and tobacco resulted in the accumulation of phosphorylated NAD (NADP) as detected by mass spectrometry. Interestingly, this form of NADP turned out to be 3'-NADP, a phosphorylated molecule that has never been detected in nature before. Furthermore, an ATPase mutant was still able to suppress ROS accumulation and increase pathogen virulence, indicating that 3'-NAD phosphorylation is not the only function of AvrRxo1.

The stylet of nematodes and the Type III secretion system of bacteria provide effective means of intracellular effector delivery for these pathogens. However, less is known about the

mechanisms of effector entry from fungi and oomycetes. Previous work by Dr. **Brett Tyler**'s lab (Oregon State University, U.S.A.) showed that RxLR effectors from *Phytophthora* species can bind phosphatidylinositol-3-phosphate (PI3P) in lipid membranes in a RxLR motif dependent manner. To validate their hypothesis that RxLR effector binding to PI3P at the host plasma membrane was important for their entry into the host cell, they replaced the RxLR motif of the effector Avr1b with VAM7p, a PI3P binding protein in yeast. The Avr1b-VAM7p chimera was successfully delivered into soybean cells by *P. sojae* during infection, suggesting a role of PI3P-binding in effector delivery.

As the smallest plant pathogens, viroids rely almost solely on host factors for successful pathogenesis. Dr. **Ying Wang** (Ohio State University, U.S.A.) uses Potato spindle tuber viroid (PSTVd) as a model to identify host factors required for RNA-dependent RNA polymerase (RdRP) activity, which some DNA-dependent RNA polymerases (DdRP) have been shown to possess. He showed that the canonical 9-zinc finger (ZF) Transcription Factor IIIA (TFIIIA-9ZF) and its variant TFIIIA-7ZF are able to interact with the (+) form of the viroid while only TFIIIA-7ZF can interact with the (–) form. Silencing of *TFIIIA-7ZF* resulted in decreased viroid accumulation while overexpression resulted in increased accumulation *in planta*. This study identified TFIIIA-7ZF as a factor required for the RdRP activity of a plant DdRP that benefits the propagation of a plant pathogen.

Dr. **Anna Joe** (University of California Davis, U.S.A.) recently identified a small sulfated protein from *Xanthomonas oryzae* pv *oryzae* (Xoo) that acts as an elicitor of XA21-mediated immunity in rice. This effector, called RaxX, shares similarity to PSY1, a plant peptide containing sulfated tyrosine residues. PSY1 is a hormone that promotes plant cell proliferation and expansion, and suppresses immunity. They found that RaxX binds to PSY1 receptors and has evolved to mimic PSY1 in order to suppress host defenses, facilitate infection, and enhance plant growth. This study provided an interesting example of a pathogen effector (RaxX) that serves as a molecular mimic of a small peptide hormone (PSY1) and a resistance gene that has evolved to specifically recognize the mimic, thus avoiding auto-activation of immunity in response to the native host peptide.

CONCURRENT SESSION 6 SYSTEMS BIOLOGY AND MODELING

Summarized by: Hiroaki Adachi (Nagoya University, Japan), David E Cook (Wageningen University, The Netherlands), Marcella Teixeira (University of California Riverside, U.S.A.), Jessie K Uehling (Duke University, U.S.A.)

This session was all about generating and analyzing big data sets to get a broad view of how plants interact with associated microbes. A major theme was the use of *transcription profiling during plant-microbe interactions to establish networks* aimed at understanding plant immune response or characterizing pathogen virulence. Using *Arabidopsis* responses to bacterial and fungal pathogens, Dr. **Katherine Denby**'s group (University of Warwick, U.K.) identified host transcription factors that regulate plant defense gene networks, and discovered new regulators of these responses. Dr. **James Elmore** (USDA-ARS, U.S.A.) combined transcriptome and proteome data using a Barley-*Blumeria pathosystem* to identify stage specific effectors and establish effector functions. One interesting question to address in the future is how rapid co-evolution between plants and microbes impacts gene network regulation, structure, and usage.

Another prominent use of transcriptional profiling and systems biology was to tackle the *genomics of quantitative re-*

sponses during plant-pathogen interactions. Dr. **Dave Berger**'s lab (University of Pretoria, South Africa) combined co-expression networks with quantitative disease resistance traits to identify the genetic under-pinning of quantitative disease resistance in *Maize* against *Cercospora* spp. Dr. **Dan Kleibenstein**'s lab (University of California Davis, U.S.A.) collected transcriptional response data of 96 diverse *Botrytis* strains on various *Arabidopsis* ecotypes. A major finding was that both the pathogen and host genotype greatly influenced the quantitative output of the interaction. That is, genomic variation in the pathogen largely affected host response and *vice versa*. An important future goal will be translating these findings into meaningful resistance in an agronomic setting.

Dr. **Elwira Smakowska** (The Gregor Mendel Institute of Molecular Plant Biology, Austria) discussed a high-throughput screen based on ELISA-AVEXIS technology to establish *an interaction network for the extracellular domains* of more than 200 leucine-rich repeat containing proteins. The interaction network has identified new potential cell-surface receptors important for host defense. These and other future, high-throughput, genome level screens will provide guidance to our search for genetic targets for modification during efforts to create crop plants with greater disease resistance.

CONCURRENT SESSION 7 COMMONALITIES BETWEEN MUTUALISTS AND PATHOGENS

Summarized by: Mael Baudin (University of California Berkeley, U.S.A.), Jose Pedro Fonseca (Noble Foundation, U.S.A.), Joren Salazar (California State University Bakersfield, U.S.A.), Tongjun Sun (University of British Columbia, Canada)

Dr. **Shin Okazaki** (University of Agriculture and Technology, Japan) gave the first talk about the role of the type III secretion system (T3SS) in the symbiotic bacterium *Bradyrhizobium elkanii*. The *hrcC* mutant of this bacterium, which is unable to secrete effectors, shows reduced nodule formation on the efficient soybean host, BARC-3. However, the same mutant shows significantly increased nodule formation on the non-efficient cultivar BARC-2. Both of these phenotypes are mainly due to the type III effector, ORF5208. There is no predicted function for this effector but it is conserved among nitrogen-fixing bacteria and some plant pathogenic bacteria like *Xanthomonas*. Restriction of nodulation is mediated by the presence of Rj4 in the non-efficient BARC-2 host. In the absence of Rj4, *B. elkanii* is able to bypass the nod factor pathway and nodulate the *nfr1* soybean mutant in a T3SS-dependent manner. Transcriptomic analyses revealed similarities between the defense mechanisms induced by symbiotic and pathogenic bacteria. Therefore efficient rhizobial colonization requires the suppression of plant immunity in legumes.

Dr. **Catherine Masson-Boivin** (Laboratory of Plant-Microbe Interactions, France) presented the experimental evolution from a pathogen to a symbiont. The pathogenic bacterium *Ralstonia solanacearum* was transformed with the symbiotic plasmid of the nitrogen-fixing, mimosa-symbiotic bacterium, *Cupriavidus taiwanensis*, and then inoculated on *Mimosa* plants. After phenotyping over 16 cycle-evolved clones, the transformed pathogenic bacterium acquired symbiotic features like the formation of infection threads, induction of nodule formation, and colonization of the nodules. However, no nitrogen fixation phenotype was acquired over the course of the relatively short evolutionary experiment. Mapping of the mutations that occurred during the experimental evolution process revealed that the virulence pathways of *R. solanacearum* were targeted.

Dr. **Sebastian Schornack** (The Sainsbury Laboratory, U.K.) described experiments comparing colonization requirements

for the oomycete root pathogen *Phytophthora palmivora* and the beneficial arbuscular mycorrhizal (AM) fungus, *Rhizophagus irregularis*. Genome-wide association studies (GWAS) of ecologically diverse genotypes of the model plant *Medicago truncatula* allowed the authors to identify *RAD1*, a GRAS-type transcription factor involved in the colonisation by *R. irregularis* as well as *P. palmivora*. Knock down of *RAD1* significantly impaired both the pathogenic and symbiotic interactions. Authors also showed that *RAD1* was locally induced during *P. palmivora* infection. Another approach discussed in this talk was the expression profiling of effectors from the pathogen and/or the symbiotic fungus in *N. benthamiana* roots to evaluate their impacts on root colonization. The effector R5 from *R. irregularis* promotes the development of AM symbiosis but also *P. palmivora* colonization.

Dr. **Timothy Tschaplinski** (Oak Ridge National Laboratory, U.S.A.) presented a metabolomic analysis, which revealed the impact of the introduction of a symbiotic receptor in the non-ectomycorrhizal host *Arabidopsis*. In wild-type *Arabidopsis*, *Laccaria bicolor* induces a strong defense response, resulting in a non-host interaction. In poplar (*Populus trichocarpa*), the lectin receptor-like kinase (*LecRLK8*) enhances root colonization by *L. bicolor*. Expression of *LecRLK8* in *Arabidopsis* enabled interaction with the fungus and induced a strong metabolic reprogramming. Transgenic *Arabidopsis* plants expressing *LecRLK8* showed increased *L. bicolor* colonization. Host defense was downregulated in the transgenic *LecRLK8* line. Particularly, the expression of defense genes like *PR1*, *NPR1* and *WRKY70* was reduced. Consistently, the authors found decreased levels of salicylic acid and azelaic acid in the transgenic plant. In conclusion, *LecRLK8* suppresses the defense response induced by potential fungal symbionts and facilitates symbiosis.

Dr. **Cara Haney** (University of British Columbia, Canada) presented her work about the role of microbiome in plant defense and nutrient acquisition. Studying the rhizosphere microbiome of a natural population of *Arabidopsis* revealed the presence of *Pseudomonas* species that can induce systemic susceptibility (ISS) or systemic resistance (ISR). The authors measured the impact of a collection of *Pseudomonas* strains on plant defense and growth. *Pseudomonas* can promote plant growth by improving nitrogen or iron uptake. ISS was correlated with the capacity of the bacteria to promote nitrogen uptake while ISR was correlated with ion uptake. A change in the nitrogen status of plants can impact defense. The tradeoff between plant growth and defense could be partially explained based on nitrogen content.

Dr. **Roeland Berendsen** (Utrecht University, The Netherlands) closed the session with a presentation about the role of microbiome in disease suppressive soils. The disease suppression capacity of a soil usually requires a previous crop with major disease development, suggesting that the plant upon attack play an active role in establishing suppressive capacity. In order to screen the rhizosphere microbiome present in suppressive soils, the authors isolated bacteria present in soil from plants infected by the oomycete pathogen *Hyaloperonospora arabidopsidis* (*Hpa*). Bacteria from three different operational taxonomic units (OTUs) were more abundant upon *Hpa* infection. Interestingly, the bacteria recruited upon *Hpa* infection could inhibit oomycete growth *in vitro*. Specific recruitment of these three OTUs was also observed upon aboveground defense activation.

CONCURRENT SESSION 8 HOST-MICROBE CO-EVOLUTION

Summarized by: Hiroaki Adachi (Nagoya University, Japan), David E Cook (Wageningen University, The Netherlands),

Marcella Teixeira (University of California Riverside, U.S.A.), Jessie K Uehling (Duke University, U.S.A.)

This was a diverse session covering oomycete, fungal, and viral interactions on various plant hosts. Two talks in this session centered on the theme of *host variation affecting disease outcomes*. Dr. **Laura Rose** (University of Duesseldorf, Germany) presented data on a class of microRNAs (miRNAs) found across diverse tomato species that are predicted to target 20% of the host *R* genes. The Rose lab is currently focusing on understanding how these miRNAs are differentially expressed in response to *Phytophthora* infection and how this response influences the interaction. Dr. **Peter Moffett** (Sherbrooke University, Canada) presented data showing that variation of the ARGONAUTE 2 (AGO2) protein in *Arabidopsis* corresponds to its susceptibility to *Potato virus X* (PVX). Data from a heterologous system suggests that PVX is able to suppress certain alleles of AGO2, allowing viral infection.

Another prominent theme addressed in this session was how *pathogens evolve to manipulate their hosts*. Dr. **Suomeng Dong** (Nanjing Agricultural University, China) presented research on the *Phytophthora sojae* effector Avr3c. Using a variety of approaches, his group showed that this effector likely influences host RNA splicing and/or stability by interacting with a RNA-binding protein in plants. Dr. **Alvaro Perez-Quintero** (UMR IPME Universite Montpellier, France) presented new bioinformatic tools and analysis on the evolution and function of transcription activator-like (TAL) effectors of *Xanthomonas* spp. His research suggests that TAL effectors undergo evolutionary shuffling of their tandem repeats to manipulate new targets in the hosts. Dr. **Shirin Seifbarghi** (Agri-Food Canada) presented how the *Sclerotinia sclerotiorum* transcriptome changes throughout the course of fungal infection on *Brassica napus*. In particular, they analyzed genes differentially expressed during early and late stages in the infection.

A common theme throughout the meeting, *how a molecule's structure influences its function*, was present in this session as well. Dr. **Yi Xu** (Cornell University, U.S.A.) addressed how a stem-loop structure in the RNA genome of potato leafroll virus was essential for infection. The stem-loop structure is needed for the translation of a viral protein, which is required for cell-to-cell movement of the virus.

CONCURRENT SESSION 9 RECOGNITION IN PLANT IMMUNITY I

Summarized by: Gayani Ekanayake (University of Missouri, U.S.A.), Chenglong Liu (Texas A&M, U.S.A.), Barbara Franco (James Hutton Institute, U.K.), Shuai Huang (University of British Columbia, Canada)

The session started with Dr. **Mark Banfield** (John Innes Centre, U. K.) who talked about direct recognition of the AVR-Pik effectors from the rice blast pathogen *Magnaporthe oryzae* by the NLR immune receptors encoded by Pik alleles in rice. Effector and receptor genes display nucleotide polymorphisms reflective of pathogen-host evolution. For example, co-expression in *N. benthamiana* revealed that Pikm differentially recognises and responds to products of the AVR-Pik alleles. The integrated heavy metal associated (HMA) domain of Pikm binds to the product of AVR-D, E and A alleles *in vitro* but not to AVR-C, which evades host recognition. This work may lead to engineering novel integrated HMA domains to enhance resistance to rice blast disease.

The session continued with a talk from Dr. **Xiangxiu Liang** (Chinese Academy of Sciences, China), who works on the regulation of plant immunity by heterotrimeric G-proteins. He showed that G proteins composed of the G α protein XLG2, the G β protein AGB1, and the G γ proteins AGG1 and AGG2

are required for FLS2-mediated immunity in *Arabidopsis*. Both XLG2 and AGB1 are also required for flg22 induced RbohD phosphorylation on the Ser39 residue. Simultaneously, flg22 induces XLG2 N-terminal phosphorylation by BIK1/PBL kinases. XLG2 separates from the FLS2-BIK1 pattern recognition receptor complex after flg22 treatment and further regulates ROS production through interaction with RbohD.

The next talk was given by Dr. **Isabel Saur** (Max Planck Institute for Plant Breeding Research, Germany) who identified a leucine rich repeat-receptor like protein (LRR-RLP) that is required for recognition of the bacterial cold shock protein, csp22. In her experiments, the co-receptor BAK1 was transiently expressed in *Nicotiana benthamiana* plants and immunopurified after the treatment with csp22. Identification of proteins co-immunoprecipitated with BAK1 using mass spectrometry revealed a LRR-RLP named NbCSPR. Expression of this receptor in *Arabidopsis* conferred response to csp22 that limited bacterial growth.

PhD student **Shuai Huang** (University of British Columbia, Canada) presented his work on the function of Tumor necrosis factor receptor-associated factor (TRAF) proteins in regulating NLR immune receptors. Two redundant TRAF proteins, MUSE13 and MUSE14, contribute to the maintenance of NLR homeostasis by associating with a E3 ubiquitin ligase and promoting degradation of NLRs.

Next, Dr. **Sarina Schulze** (ZMBP-Centre for Plant Molecular Biology, Germany), discussed BAK1-interacting receptor-like kinase 3 (BIR3) as a negative regulator of PAMP-triggered immunity (PTI) in *Arabidopsis*. BIR3 interacts with PAMP/DAMP receptors and antagonizes their interaction with BAK1. BIR3 positively contributed to the stability of BAK1 and its localization to plasma membrane. Interestingly, overexpressing *BIR3* also suppresses the dephosphorylation/activation of the transcription factor BES in brassinosteroid (BR) signaling.

The final talk of the session was given by **Zane Duxbury** (The Sainsbury Laboratory, U.K.) from Dr. Jonathan Jones' group whose work is directed at understanding and engineering immune receptor complexes in plants. A series of chimeric and truncated mutants of the R protein pair RRS1/RPS4 were constructed and tested for their function in hypersensitive response triggered by the corresponding type III effectors PopP2 and AvrRps4. Interestingly, AvrRps4 disrupts the association of the WRKY with the nearby DOM4 domain in RRS1, which also interacts with RPS4.

CONCURRENT SESSION 10 MICROBIOME AND PHYTOBIOME I

Summarized by: Fernanda R Rezende de Castro Moretti (Universidade de Sao Paulo, Brazil and The Ohio State University, U.S.A.), Alfredo Mari (Max Planck Institute for Plant Breeding Research, Germany), Marco E Mechan Llongtop (Virginia Polytechnic Institute and State University, U.S.A.), Sergey Ivanov (Boyce Thompson Institute, U.S.A.)

During the Microbiome and Phytobiome I concurrent session, multiple interesting updates were provided. Dr. **Sarah Lebeis** (University Minnesota, U.S.A.) presented research on the duckweed's leaf microbiome, which involves species like *Wolffia*, *Wolffia*, *Spirodella*. Of these, particularly, Proteobacteria seem to affect overall plant biomass production. Understanding the mechanisms underlying microbiome formation and dynamics would be extremely useful from an industrial perspective, especially for biofuel production and bioremediation purposes.

Dr. **Davide Bulgarelli** (University of Dundee, U.K.) reported his current studies on the barley root microbiome. The experi-

ments involved testing barley accessions from Israel, the original area of domestication, in different soil types. The bacterial community was profiled by 16S rRNA shotgun sequencing and the results reinforced the hypothesis that host genotypes drive fluctuations within the root microbiome composition.

Dr. **Samuel Kroll** (Max Planck Institute for Plant Breeding Research, Germany) reported on a study employing microbial network analysis as a powerful tool to investigate microbe-microbe interactions within the plant host. This study focused on *Arabidopsis* and analyzed sample sets made from a series of different times. He showed how microbial networks were changing on the same leaf, underpinning the hypothesis of a major role for microbe-microbe interactions in shaping the leaf microbiome.

Dr. **Dawn Chiniquy** (Joint Genome Institute, Lawrence Berkeley National Labs, U.S.A.) presented research aimed at characterizing the sorghum microbiome for improved biomass production. This study used interdisciplinary approaches to understand the basic interactions among the sorghum plant, its microbiome, and the environment. The authors used different sorghum genotypes grown in water- and nitrogen-limited environments and evaluated the microbiome composition at two time points. Their results showed that the sorghum rhizosphere has a variable microbial diversity in soils with high or low nitrogen concentration. Additionally, the microbiome composition depends on the season. For example, high microbial diversity was found in soil compared with the rhizosphere during July.

Dr. **Sebastian Lopes-Fernandez** (Fondazione Edmund Mach, Italy) reported on the transport of bacterial symbiont communities into plants. The system studied consisted of micro-propagated grapevines and the transporting agent, *Scaphoideus titanus*, which is a sap-feeding insect. The study concluded that the bacterial endophytic community is plant host-dependent. It also highlighted that plant microbiome development results from complex interactions between the plants and the insects that feed on them.

CONCURRENT SESSION 11 IMPACTS OF VESICULAR TRAFFICKING AND CYTOSKELETON DYNAMICS ON MICROBE-HOST INTERACTIONS

Summarized by: Teura Barff (Universite de Sherbrooke, Canada), Meltem Cavdar (RWTH Aachen University, Germany), Julie Gervais (INRA, France), Yohann Petit (INRA, France).

Continuously threatened by infectious pathogens from the environment, plants have evolved strategies to defend themselves. This session summarized recent studies dealing with vesicular trafficking and cytoskeleton dynamics during host-microbe interactions.

Early immune responses are initiated by direct contact of microbes or microbe-derived patterns with pattern recognition receptors (PPRs) at the plasma membrane of plant cells (Smith et al 2014). Little is known about the components of vesicular trafficking that contribute to PPR trafficking to and from the plasma membrane. The Group of Dr. **Antje Heese** (University of Missouri, U.S.A.) focuses their work on clathrin-coated vesicles (CCVs), which are involved in intracellular cargo transport at the plasma membrane and the trans-Golgi network (TGN), and studies the role of CCVs in plant immunity. They showed evidence of epsin N-terminal homolog (ENTH) domain proteins contributing to CCV formation. In their study, the *enth-2* mutant *Arabidopsis* showed reduced MAMP-related responses and a decreased level of the PPR FLS2 protein abundance at the plasma membrane.

A main goal of Dr. **Christopher Staiger**'s (Purdue University, U.S.A.) group was to determine if cytoskeletal rearrange-

ment is involved in PAMP-triggered immunity (PTI) in *Arabidopsis* (Li et al 2015). They showed that the movement of actin filaments can be divided into three phases including convolutedness, elongation and severing. In addition, their findings demonstrated that MAMP-related responses like Ca^{2+} transients and accumulation of reactive oxygen species (ROS) lead to increased density of actin filaments. Actin assembly is regulated by several innate immune responses that target capping proteins (CPs). One of the key findings highlighted the necessity for the interaction of phosphatidic acid (PA) and CP for the immediate cytoskeletal responses that take place during the immune response.

Immune responses like the recognition of PAMPs at the plasma membrane are taking advantage of the microtubule network to propagate defense signals to diverse cellular compartments. The microtubule network is also used to secrete defense compounds like antimicrobial compounds or other defense-related molecules. HopE1 is a *Pseudomonas syringae* type III effector with PTI-suppressing activity that significantly contributes to virulence. Dr. **Ming Guo** (University of Nebraska, U.S.A.) from the Alfano laboratory reported that HopE1 interacts with the plant protein MAP65-1, which is implicated in microtubule crosslinking in a calmodulin-dependent manner. Analyses of *Arabidopsis* lines either overexpressing HopE1 or deleted for *MAP65-1* showed that HopE1 dissociates MAP65-1 from the microtubule network, leading to microtubule network disruption. HopE1 has also been shown to inhibit PR-1 secretion. Together those results support a model where HopE1 interferes with PTI-associated trafficking by disrupting the microtubule network leading to interruption of immune signaling and cell-wall associated defenses (Guo et al 2016).

In barley, the protein RACB is required for susceptibility to the fungal pathogen *Blumeria graminis* f. sp. *hordei* (*Bgh*) (Opalski et al 2005). The team of Dr. **Christopher McCollum** (Technical University of Munich, Germany) showed that the *Bgh* effector ROPI1 interacts with RACB and induces its activation. They demonstrated that the activated RACB impacts the cellular localization of three ROP inducing proteins (RIPs), leading to microtubule depolymerization, probably through the kinase 13A (Mucha et al 2010). They also showed that overexpression of one of the RIPs leads to increased susceptibility of barley to *Bgh*. This work suggests that *Bgh* may manipulate RACB to interfere with microtubule organization.

All in all, the presenters from this session were able to give deep insights regarding the impact of vesicular trafficking and cytoskeletal dynamics on plant immunity and the significance of endocytic and exocytic processes in evolving resistance to pathogens.

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CONCURRENT SESSION 12 PLANT HORMONES AND REGULATORS IN SYMBIOSIS AND DEFENSE

Summarized by: Jixiang Kong (Gregor Mendel Institute, Austria), Aldo Seguel (Pontificia Universidad Católica de Chile, Chile), Ka-Wai Ma (University of California Riverside, U.S.A.) and Brenden Barco (Yale University, U.S.A.).

The complex network of hormone signaling pathways in plant immunity

Plant hormones are central to regulating developmental processes and also involved in plant immunity. The important roles of jasmonic acid (JA), salicylic acid (SA) and ethylene (ET) in plant immunity have been extensively studied (Robert-Seilaniantz et al. 2011). In addition, crosstalk between these hormones and auxin, cytokinin, and gibberellin has been uncovered. Finally, a role for brassinosteroid signaling in MAMP triggered immunity was proposed in several studies (Smakowska et al. 2016). Pathogens can also manipulate plant hormone signaling to promote infection (Ma and Ma 2016). However, the nexus between different hormone responses and different pathogen infections is not well understood even though it is critical to understanding the disease outcome in the context of a given pathosystem.

Dr. **Mary Wildermuth** (University of California Berkeley, U.S.A.) started this session emphasizing the importance of the temporal and spatial SA concentration for its function (Dempsey et al. 2011). As a node in signaling plant immunity, mutating the *Arabidopsis* GH3 acyl adenylase gene (*PBS3*) led to reduced SA total levels, lower *PR-1* expression and higher susceptibility to *Pseudomonas syringae* infections (Nobuta et al. 2007). In addition, a conversion of SA into an inactive conjugated form, SA-Asp, was detected in *pbs3* mutants. These results suggest that PBS3 acts downstream of stress-induced SA synthesis and that the amino acid modification of SA is a regulatory mechanism for its activity. However, it is unclear whether formation of SA-Asp in *pbs3* mutants is entirely responsible for the enhanced susceptibility to pathogens.

Dr. **Tina Kyndt's** (Ghent University, Belgium) group reported the important role of the ascorbate oxidation level and its regulation of JA signaling during parasitic root-knot nematode (RKN) infection of rice plants (Escobar and Fenoll 2015). Combined transcriptome data and hormone measurements showed that ascorbate oxidation levels in plants are altered during RKN infection. They further suggested that elevated ascorbate oxidation levels strongly correlate with an increase in JA biosynthesis. Additionally, ascorbate-deficient mutants developed more galls during infection. This phenotype could be rescued by the application of ascorbate. This study provides insights into the interaction between JA signaling, ascorbate status/level, and RKN parasitism.

Another interesting study presented by Dr. **Gerhard Adam** (University of Natural Resources and Life Sciences, Austria) showed how *Fusarium graminearum* may hijack auxin signaling to promote susceptibility (Svoboda, T; Parich, A; Michlmayr, H; Schöfbeck, D; Schmeitzl, C; Krska, R; Schuhmacher, R; Wiesenberger, G; Adam, G. 2015). *F. graminearum* infection leads to up-regulation of tryptophan biosynthesis genes and the synthesis of hydroxycinnamic acid amides (e.g. coumaroyl-tryptamine) by cereal hosts. Yet, *F. graminearum* can hydrolyze these antifungal compounds and convert released tryptamine to auxin at high yields. Highly elevated auxin and auxin-conjugate (IAA-Asp, IAA-Glc) levels were detected in infected wheat heads. However, whether auxin production promotes virulence still remains unclear because the high redundancy of auxin biosynthesis genes prevents the construction of *Fusarium* mutants deficient in auxin production.

The *in vivo* detection of pathogen-induced hormone responses at the cellular level is a challenging task. In contrast to auxin reporters that have long been available, *in planta* visualization of SA and JA has lagged behind. Dr. **Hassan Ghareeb** working in Volker Lipka's group (Goettingen University, Germany) developed a "Colorful" toolkit (Ghareeb et al. 2016) using different fluorescent markers. This toolkit allows visualization of SA and JA/ET responses upon pathogen infection with cellular resolution and can be used for studying hormone crosstalk in the context of plant-microbe interactions.

The final talk was given by Dr. **Brenden Barco** (Yale University, U.S.A.) who introduced the topic of plant secondary metabolites and their importance for defense response (Rajniak et al. 2015). Canonical Trp-tryptophan-derived pathway compounds such as glucosinolates and camalexin were shown to be involved in plant defense. With the regulon approach by which certain transcription factors activate numerous metabolic pathways, they discovered a new compound, 4-hydroxyindole-3-carbonyl nitrile (4-OH-ICN), that contributes to the defense system, which added a new branch to the Trp-derived secondary metabolism pathway. This research provides insights into the function of secondary metabolites in the *Arabidopsis* immune system.

Hormone signaling pathways involved in plant immunity: A, PBS3-mediated SA signaling pathway in immunity; B, the interaction between RKN and JA signaling pathway; C, the manipulation of auxin levels by *F. graminearum* to control plant defense response. Dash line: the crosstalk might differ between organs or species.

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CONCURRENT SESSION 13 SYMBIOSIS AND MUTUALISM II

Summarized by: Kevin R. Cope (University of Wisconsin-Madison, U.S.A.), Michael Paries (Ludwig Maximilian University of Munich, Germany), Alex Greenspan (University of California Davis, U.S.A.), Akira Akamatsu (John Innes Institute, U.K.), Carol Ibe (University of Cambridge, U.K.)

Dr. **Joel Griffitts** (Brigham Young University, U.S.A.) discussed his recent work on understanding symbiotic pairs in the rhizobia-legume symbiosis (Price et al. 2015). Some legumes, like the model plant *Medicago truncatula*, impose terminal differentiation in their nitrogen-fixing bacterial partner by releasing nodule-specific cysteine-rich (NCR) peptides. The Griffitts lab found that *Sinorhizobium meliloti* strain B800 exhibits reduced terminal differentiation in *M. truncatula* genotype A20 by producing host range restriction peptidase (*hrrp*), an M16A metalloprotease which is encoded on an accessory plasmid. This phenotype is lost in the host genotype A17, perhaps indicating that NCR peptides in the latter genotype are resistant to *hrrp*-mediated proteolysis. When NCR peptides are degraded, as in A20, it inhibits nitrogen fixation and the bacteria are able to proliferate more extensively. Their data also suggest that *hrrp* in *Rhizobium leguminosarum* is the ancestral form, as it is a chromosomal gene. The *R. leguminosarum hrrp* contains a signal peptide which is absent in the *S. meliloti* strain B800 *hrrp*. When the signal peptide is restored, catalytic activity on A20 NCR peptides is lost.

Dr. **Ronelle Roth** from the Paszkowski Lab (University of Cambridge, U.K.) introduced an impressive high-resolution method for visualizing arbuscule development in rice roots. Using multi-photon laser scanning microscopy, she was able to monitor periarbuscular membrane (PAM) dynamics during arbuscule branching. By imaging live cells with time-lapse capture, she found that OsPT11 (Phosphate Transporter 11)

Fig. 1. Summary of the hormone signaling pathways in plant immunity discussed at the Concurrent Session 12 of IC-MPMI 2016.

fused to eGFP localized to distinct PAM foci and that these foci were highly dynamic as the arbuscule developed into the mature, highly-branched state. Essentially, they observed that PT11 is highly abundant at lateral PAM loci and this phenomenon precedes arbuscule branching through every stage of arbuscule development. By anti-GFP immuno-gold labeling, they confirmed that PT11 localizes not only to the PAM, but also to multivesicular bodies near the PAM. They also found that the PAM arbuscule-specific receptor-like kinase (ARK) does not co-localize with PT11 at these foci but do once PT11 was distributed around the branches. Based on these results, they proposed that Pi-uptake at the PT11 foci drives reiterative arbuscule branching.

A very promising approach for *in situ* metabolic profiling in root nodule symbiosis was introduced by Dr. **Beverly Agtuca** from the laboratory of Gary Stacey (University of Missouri, U.S.A.). In depth profiling of soybean root nodules was carried out by laser ablation-electrospray ionization mass spectrometry (LAESI-MS). As a 'proof of concept' approach, lateral profiling by sectioning root nodules was done to validate in-depth profile analyses. By targeting different localization areas of the section relative to nodule anatomy, tissue specific metabolic profiling was established, allowing the comparison of carbon and nitrogen fluxes between soybean and wild-type or *nifH* mutant *rhizobia*. We are looking forward to the development of this technique with higher resolutions, perhaps fine-tuned to the scale of a single-cell.

Dr. **Maria Harrison** (Boyce Thompson Institute, U.S.A.) discussed the discovery of new structures both in and around the periarbuscular membrane (PAM) as well as the regulation of arbuscule degeneration during arbuscular mycorrhizal (AM) symbiosis. Although much is known about the PAM in terms of content and development, little is known about the periarbuscular matrix. Using high-pressure freezing transmission electron microscopy and 3D-electron tomography, her group found membrane vesicles/tubules in the periarbuscular space that are contiguous with the PAM. They also found tubular structures extending from the fungal plasma membrane that proliferated extensively into the space between the fungal wall and fungal plasma membrane. The function of these two types of tubular structures remains unknown, which reflects how little we know about the plant-fungal interface in AM symbiosis. Harrison also summarized our current understanding of arbuscule degeneration and how her lab is beginning to extend our knowledge of this topic. Using promoter fusions to fluorescent proteins, they were able to visualize arbuscule degeneration in colonized *Medicago truncatula*. As shown previously (Javot *et al.* 2007), degeneration is linked to the loss of PT4 function and now they showed that arbuscule degeneration is suppressed in a *pt4/myb1* double mutant. The MYB1 transcription factor regulates expression of hydrolase genes associated with arbuscule degeneration.

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CONCURRENT SESSION 14 RNA-MEDIATED INTERACTIONS

Summarized by: Ryan Kessens (University of Wisconsin Madison, U.S.A.), Arun Kumar (University of Wisconsin Madison, U.S.A.), Sowmya Ramachandran (Washington State Uni-

versity, U.S.A.), Robyn Roberts (University of Wisconsin Madison, U.S.A.)

Dr. **Fontes** (Universidade Federal de Vicosa, Brazil) and her group recently demonstrated inverse functions of a NB-LRR gene *NIK1* during viral and bacterial infection. Using *NIK1* overexpression lines, it was shown that NIK1 suppresses global translation, consequently leading to viral immunity. NIK1 translocated the ribosomal RPL10 protein to the nucleus where it interacted with MYB-like protein LIMYB to fully downregulate the plant translational machinery. Begomoviruses on the other hand, have evolved effectors that can suppress NIK1 activity and promote viral replication. Interestingly, constitutive expression of *NIK1* had an opposite effect on bacterial infection since NIK1 is also involved in suppression of PAMP-immune responses. Together these results demonstrate a novel paradigm of antiviral defense in plants and a dual role for a single NB-LRR family member in pathogen defense.

Small RNAs (sRNAs) constitute a class of non-coding RNAs that are central to gene regulation through RNA silencing. One such class of small RNAs, called phasiRNAs, are triggered by microRNA cleavage of target transcripts. In his insightful talk, **Qili Fei** (University of Delaware, U.S.A.) from Dr. Blake Meyers's laboratory discussed the biogenesis of these phased, secondary small RNA molecules generated from NB-LRR genes of *Medicago truncatula* and the mechanism by which microRNAs trigger phasiRNA production. Interestingly, the 3' terminal pairing, and not the 10th position, is essential for phasiRNA generation. This work provides useful information for miRNA-mediated regulation defense genes.

Blumeria graminis f. sp. *hordei* (Bgh), the causal agent of barley powdery mildew, encodes over 500 candidate secreted effector proteins (CSEPs), a majority of which await functional characterization. Dr. **Ali Ahmed** (University of California, Davis, U.S.A.) from Richard Michelmore's group identified four CSEPs that decreased the rate of haustorial formation, a key step in fungal pathogenesis. Using various protein-protein interaction approaches, two heat shock proteins—Hsp16.9 and Hsp17.5—were found to interact with CSEP0105 and CSEP0162. Additionally, CSEP0105 compromised the chaperone activity of Hsp16.9. Because Hsp 16.9 is involved in the activation of plant defense, these results demonstrate a novel strategy by which effectors modulate plant immunity.

While it has been shown that sRNAs can act as effector molecules and inhibit host defense genes, the opposite also seems to be true. In their study, Dr. **Ming Wang** at UC Riverside (U.S.A.) demonstrated that *Arabidopsis* expressing sRNAs that target *Botrytis cinerea* dicer-like proteins (Bc-DCL) are more resistant to infection, suggesting sRNA movement is bidirectional during host pathogen interactions. Furthermore, to demonstrate that *B. cinerea* could take up sRNA and dsRNA from the environment, Bc-DCL dsRNA and sRNA was applied to fruits and shown to significantly reduce grey mold infection. In addition to advancing our knowledge of the fungal RNAi mechanism, these results also provide a non-transgenic approach for fungal disease management.

Triticum mosaic virus (TriMV) is a recently-emerged *Potyvirus* virus that contains an unusually long internal ribosome entry site (IRES) compared to other members of the same family. Using bio-layer interferometry, Dr. **Robyn Roberts** (University of Wisconsin-Madison, U.S.A.) demonstrated that the mRNA cap-binding complex, eIF4F and its isoform eIFiso4F, both bind to the viral IRES, though eIF4F binds with higher affinity. Binding is dependent on a stem loop structure located within the 5' UTR, and both complex isoforms can be used for TriMV translation. These findings represent the discovery of a novel plant viral IRES which may aid in the development of stable viral resistance.

CONCURRENT SESSION 15 SIGNAL TRANSDUCTION FOR SYSTEMIC DEFENSE

Summarized by: Brenden Barco (Yale University, U.S.A.), Ka-Wai Ma (University of California, Riverside, U.S.A.), Jixiang Kong (Gregor Mendel Institute, Austria) and Aldo Seguel (Pontificia Universidad Católica de Chile, Chile)

Systemic defenses: old friends with different looks

Systemic acquired resistance (SAR) is a long-lasting, systemically-induced defense effective against a broad spectrum of pathogens. Traditionally, SAR is known to require salicylic acid (SA) as the major signaling molecule, which facilitates the monomerization and nuclear localization of the coactivator protein, NPR1 in the regulation of SA-responsive defense genes including *PR-1* (Spoel and Dong 2012). Another similar systemic defense known as induced systemic resistance (ISR) is triggered by non-pathogenic soil-born microbes and is mainly dependent on jasmonate (JA) and ethylene (ET) signaling (Pieterse et al. 2014). Over the years, pipecolic acid (Pip), glycerol 3-phosphate (G3P), and azelaic acid (AzA) have emerged as new players in defense priming, a process by which the plants prepare to quickly and robustly respond to a future stimulus such as pathogen challenge (Reimer-Michalski and Conrath 2016). Some exciting findings regarding the induction, signaling and regulation of systemic defenses were presented in this session (Fig. 2).

Dr. Corina Vlot (Helmholtz Zentrum München, Germany) began the session by showing that putative sugar binding proteins (lectins) including LLP1, LEC1, and LEC2 are essential for SAR (Breitenbach et al. 2014). By using petiole exudate extract from different genetic backgrounds as direct inocula, these lectins were shown to act in systemic tissues during SAR signal perception, possibly in cooperation with Pip. This study suggests that sugar metabolism is probably an underappreciated area in SAR signaling (Figure 2, #1).

Dr. Ivan Baccelli (University of Neuchâtel, Switzerland) next demonstrated the use of ultra-high pressure liquid chromatography tandem mass spectrometry (UHPLC-MS/MS) to

quantify the priming molecule β -aminobutyric acid (BABA). BABA treatment induces an increase in primary metabolites that prepares plants to quickly activate stress-related signaling pathways upon exposure to stimuli (Baccelli and Mauch-Mani 2016). In contrast to the previous studies demonstrating a role of BABA as a xenobiotic that is recognized and responded to by the plant, BABA was found to be naturally produced by different plant species under abiotic and biotic stress in both leaf and root tissues (Fig. 2, #2). Future studies in the metabolism of this molecule will help to enhance plant resistance in response to different stresses.

Modulation of chromatin configuration by different epigenetic modifications plays dramatic roles in the regulation of the global transcriptome (Ding and Wang 2015). By using formaldehyde-induced cross-linking and a two-phase extraction method, Dr. Eva Reimer-Michalski (RWTH Aachen University, Germany) was able to separate DNA associated with open and closed chromatin states and showed that the induction of *WRKY6/29/53* under SAR is indeed correlated with an open chromatin configuration (Figure 2, #3). This study again reminded us of the significance of chromatin regulation in the induction of SAR.

Shifting to the realm of ISR, Dr. Suruchi Roychoudhry (University of Chicago, U.S.A.) characterized the involvement of lipid transfer proteins AZI1 and EARLI1 in AzA-dependent resistance in *Arabidopsis* roots (Figure 2, #4) (Cecchini et al. 2015). AZI1 localizes to the plasma membrane and exists as small punctate structures in root cells in a way similarly observed in leaf tissue. Additionally, AZI1 also partially co-localizes with root plastids. Further studies will provide more insight into the roles of lipid transfer processes common to both ISR and SAR.

On a final note, Dr. Steven Spoel (University of Edinburgh, U.K.) showed his interesting finding on the roles of reversible polyubiquitination in the regulation of NPR1 function (Furniss and Spoel 2015). The E4 polyubiquitin ligase mutant *ube4* had an opposite phenotype to the E3 ligase mutant *crl3*, exhibiting higher *PR-1* expression compared to wild-type *Arabidopsis* plants. Furthermore, the use of specific deubiquitinase inhibitors also affected the ability of NPR1 to induce SAR, suggesting that concerted ubiquitination initiation and ubiquitin chain elongation processes play a fundamental role in regulating NPR1 activity (Fig. 2, #5).

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Fig. 2. Summary of topics discussed at Concurrent Session 15 of IC-MPMI 2016. Topics are illustrated in grey and include (#1) promotion of SAR in parallel with SA by lectins, (#2) accumulation of BABA in stress response, (#3) changes in chromatin configuration at the DNA regulatory elements of defense genes under SAR, (#4) involvement of lipid transfer proteins in AZA-induced ISR, and (#5) control of NPR1 coactivation activity by reversible processive ubiquitination.

CONCURRENT SESSION 16 TRITROPHIC INTERACTIONS AND BIOCONTROL

Summarized by: Beverly Agtuca (University of Missouri-Columbia, U.S.A.), Adam Bentham (Flinders University, Australia), Volker Hegenauer (University of Tuebingen, Germany), Sarah Hind (Boyce Thompson Institute, U.S.A.), Fabien Lonjon (LIPM, Université de Toulouse, INRA, CNRS, France)

Dr. **Clare Casteel** from the University of California, Davis (U.S.A.) shared her work on the impact of the viral protease Nla-Pro from *Turnip Mosaic Virus* on feeding by *Myzus persicae*, the green peach aphid which vectors the virus. The protease can induce changes in plant physiology impacting *M. persicae* fecundity, and its intracellular localization in the plant cell is dependent on the presence of aphid feeding. Trapping Nla-Pro in the plant nucleus had a negative impact on its ability to increase aphid fecundity through blocking host defenses. Similar results were obtained with a protease encoded by the potato virus Y, which also underwent relocalization to the vacuole after aphid feeding. Work from Casteel's lab supports the importance of persistent viruses recognizing their aphid vectors during plant-aphid interactions.

Next, Dr. **Trisna Tungadi** from the Carr lab at the University of Cambridge (U.K.) explained how *Cucumber mosaic virus* (CMV) inhibits prolonged phloem feeding by *Myzus persicae*. They identified three CMV proteins that act on *Arabidopsis* plants to induce the accumulation of a feeding deterrent (4-methoxy-indolyl-3-methyl glucosinolate), which in turn encourages aphid dispersal from the host plant. Shuffling of CMV RNA products from two CMV strains helped identify an elicitor of aphid resistance in tobacco, and it appears that a combination of multiple viral products is needed to condition the plant-aphid interaction. Elucidating the functions of different CMV RNA products will be important for better understanding the transmission of the virus by aphids.

Dr. **Christine Vogel** from the Vorholt lab (ETH Zurich, Switzerland) described the diversity of *Arabidopsis* phyllosphere bacteria, and the identification of two main genera of bacteria, *Sphingomonas* and *Methylobacterium*. *Methylobacterium extorquens* PA1 did not suppress disease symptoms when co-inoculated with *Pseudomonas syringae* pv. *tomato* (*Pst*). However, co-inoculation of *Sphingomonas melonis* Fr1 with *Pst* leads to transcriptional reprogramming of plant host genes related to defense responses, including those encoding putative pathogen recognition receptors (PRRs). *Sphingomonas* induction of *Arabidopsis* genes depended on BAK1/BKK1, demonstrating that functional PTI signaling is important for this protection. These experiments support a role of bacterial phyllosphere communities in impacting the success of some pathogens.

Dr. **Martin Filion** from Université de Moncton (Canada) described an antibiotic called phenazine-1-carboxylic acid (PCA) produced by *Pseudomonas fluorescens* LBUM223. LBUM223 acts as a biocontrol agent for common scab of potato caused by *Streptomyces scabies*. PCA alters the pathogen's gene expression rather than directly causing cell death. RNA-seq analyses of *S. scabies* incubated with wild-type LBUM223, a PCA-deficient mutant of LBUM223 (*phzC*-), or purified PCA shown that PCA impacted 12-14% of *S. scabies* genes. Functional categories of these up or down-regulated genes included those involved in metabolism, pathogenesis, transport, and oxidation-reduction processes. Since LBUM223 decreases the mycelium/spore formation and virulence of *S. scabies*, these findings support its use as a biocontrol agent to potato scab disease.

Dr. **Christoph Keel** from the University of Lausanne (Switzerland) explained the oral insecticidal, infection route from a

subgroup pseudomonads, that included *Pseudomonas protegens* and *Pseudomonas chlororaphis*. There are rhizosphere pseudomonads with a plant beneficial lifestyle, because they harbor an insecticidal activity. In this study, an insecticidal protein, known as Fit toxin, produced by the pseudomonads was determined to be a major factor of insect pathogenicity. Comparative genomics and targeted mutational analyses revealed that lipopolysaccharide O-antigen of the bacteria also contributed to insect pathogenicity. These pseudomonads strains were also determined to be resistant to insect antimicrobial peptides. Overall, this is the first study of molecular and genetic analyses of the O-antigen gene in pseudomonads and demonstrated that plants can be protected from pests through the development of a beneficial rhizosphere.

CONCURRENT SESSION 17 MICROBIAL MANIPULATION OF THE HOST II

Summarized by: Susanna Harris (University of North Carolina Chapel Hill, U.S.A.), Xiaoyu Liu (University of Alabama at Birmingham, U.S.A.), Li Zhang (Michigan State University, U.S.A.), Kaitlin McNally (University of Zurich, Switzerland)

Dr. **Yi Li** from Peking University (China) talked about small RNA-mediated host antiviral defense in rice. Major reductions in rice crop yield in Asia are due to a prevalent disease called rice stripe, caused by the insect-transmitted virus *Rice stripe Tenuivirus* (RSV). Plants utilize RNA interference to detect and degrade viral RNA molecules as a resistance mechanism. Argonaute 1 (AGO1) binds small-interfering RNAs (siRNAs) to cleave the target RNA and is post-transcriptionally regulated by miR168. Dr. Li described how a new AGO member, AGO18 from rice, contributes to antiviral defense by regulating AGO1 accumulation (Wu et al. 2015). AGO18 has binding affinity towards miR168 and outcompetes AGO1 for miR168 binding during RSV infection. Similarly, transgenic expression of a miR168-resistant form of AGO1 restored the resistance of *ago18* towards RSV, further supporting that AGO18 induces the accumulation of AGO1 by sequestering miR168 to confer antiviral activity. Dr. Li also reported unpublished data suggesting that AGO18 competes with AGO1 for miR528 binding to regulate ascorbic acid accumulation upon viral infection. Genetic analysis demonstrated that miR528 negatively regulates the antiviral response. RNA-seq and qPCR analysis revealed that miR528 targets the *L-Ascorbate Oxidase* (AO) mRNA. Overexpression of a miR528-resistant form of AO leads to enhanced viral resistance, supporting an antiviral effect of AO. During viral infection, AGO18 binds to miR528 to release AO mRNA. The accumulation of AO enhances ascorbic acid degradation and ROS accumulation, potentially contributing to antiviral defense.

The talk of Dr. **Wenbo Ma** (University of California Riverside, U.S.A.) focused on *Phytophthora* RxLR effectors promoting infection by suppressing small RNA silencing in plants. The Ma lab recently reported that the *Phytophthora sojae* effector Phytophthora suppressor of RNA silencing 1 (PSR1) suppresses host small RNA (sRNA) accumulation to promote susceptibility (Qiao et al. 2013; Qiao et al. 2015). Here, she presented an in-depth analysis of PSR2, which has the capacity to specifically affect small interfering RNAs (siRNAs). PSR2 contains tandem repeats of seven L-W-Y motifs and each is about 80 amino acids in length. Crystal structure analysis of an N-terminal truncation of PSR2 (78-670 aa) revealed a necklace-like structure where each L-W-Y motif forms a conserved fold with five α -helices. Functional analysis revealed that the N-terminus of PSR2 possesses cell death suppression activity and all L-W-Y motifs except the fourth one contribute to RNA silencing suppression activity. Characterization of an

Arabidopsis transgenic line expressing PSR2 revealed that PSR2 contributes to disease susceptibility by suppressing phased siRNAs in the host during infection. Y2H analysis identified a RNA-binding protein, DRB4, that interacts with PSR2 and further analysis revealed that the first three L-W-Y motifs of PSR2 are sufficient for DRB4 binding. DRB4 potentially works together with Argonaute or Dicer-like Protein 4 (DCL4) to regulate phased siRNA production. Their work suggests that the *Phytophthora* effector PSR2 suppresses the accumulation of phasiRNAs, which may regulate defense gene expression, and therefore confers disease susceptibility.

Adam Bayless (University of Wisconsin Madison, U.S.A.) from Dr. Andrew Bent's laboratory presented work on the analysis of resistance to soybean cyst nematode (SCN). The SCN *Heterodera glycines* can manipulate soybean root cells to develop specialized feeding cells termed syncytia. *Rhg1* is a major resistance locus to SCN but the underlying molecular mechanisms remain unknown. It was previously discovered that SCN resistance associates with *Rhg1* copy number and alleles encoding distinct α -SNAP (α -soluble *N*-ethylmaleimide-sensitive factor attachment protein) proteins (Cook et al. 2014; Cook et al. 2012). α -SNAPs have a well-conserved function in stimulating NSF (*N*-ethylmaleimide-sensitive factor) ATPase activity to assist the recycling of SNAREs following vesicle-mediated transport. Recent work indicates that the C-terminus of the α -SNAP, which is essential for NSF interaction, carries differentially selected residues for resistance or susceptibility towards SCN. The SCN-resistant types of α -SNAPs are altered at a Leucine residue and are impaired in NSF interaction. Overexpression of the SCN-resistant type α -SNAP leads to cell death, suggesting a deleterious effect of these α -SNAPs. However, this effect can be rescued by co-expressing wild-type α -SNAPs in a dosage-dependent manner. Though balanced under a steady state, nematode infection leads to the hyper-accumulation of SCN-resistant type α -SNAPs at the feeding site and disrupting SNARE recycling. This work demonstrates that the presence of the SCN-resistant type α -SNAPs within the *Rhg1* locus disrupts SNARE trafficking to enhance resistance against nematodes.

Post-transcriptional gene silencing (PTGS) is a critical regulatory component of plant immunity. Bacterial effectors have previously been implicated in suppressing host silencing pathways to contribute to virulence (Navarro et al. 2006). Dr. **Lionel Navarro** (IBENS-CNRS, France) presented mechanism by which two *Pseudomonas syringae* pv. *tomato* type III effectors, HopU1 and HopT1-1, suppress RNA silencing (RNAi) in *Arabidopsis*. HopU1 was shown to promote bacterial infection by suppressing AGO1 function. They found that HopU1 has ADP-ribosyltransferase activity and targets Glycine-rich RNA Binding Protein 7 (GRP7), which interacts directly with AGO1 via the GW/WG motif. RNA binding analysis revealed that 30% of the AGO1-loaded RNAs associate with GRP7, suggesting that GRP7 participates in the AGO1-mediated RNA processing to contribute to resistance. Similarly, a GRP7 loss-of-function mutant, which is more susceptible to bacterial infection, mimics the miRNA-deficient plants. Thus, HopU1 targets GRP7 to reduce its binding affinity towards RNA, limiting AGO1-mediated gene silencing activity. Another *Pseudomonas* effector HopT1-1 directly targets AGO1 in the cytosol and also suppresses AGO1-mediated RNA silencing.

Dr. **Tolga Bozkurt** (Imperial College London, U.K.) recently published their work on the *Phytophthora infestans* effector PexRD54, which could bind to the autophagy-related protein ATG8CL to stimulate autophagosome formation (Dagdas et al. 2016). Crystal structure analysis of PexRD54 revealed N-terminal W-Y repeats and a C-terminal ATG8-interacting motif (AIM). *In planta* and *in vitro* assays demonstrated that

PexRD54 interacts with ATG8CL at the AIM motif to induce autophagosome formation around the haustoria. More intriguing, this interaction can outcompete ATG8CL binding with the autophagy cargo receptor Joka2. Similarly, PexRD54 counteracts the Joka2-mediated enhanced resistance against *P. infestans*. Dr. Bozkurt then discussed their unpublished data on the interaction of the N-terminal WY domains of PexRD54 with the host Rab GTPase, Rab8, which is involved in vesicle trafficking and fusion. The WY domains are essential for the co-localization of Rab8 and PexRD54. Interestingly, PexRD54 mediates the interaction and co-localization of Rab8 and ATG8CL. A Rab8 dominant-negative form or *Rab8*-silenced plants abolished autophagosome formation induced by PexRD54, supporting the hypothesis that PexRD54 requires functional host Rab GTPase to stimulate autophagosome biogenesis. These findings suggest the striking possibility of pathogen manipulation of host autophagosome formation and trafficking as a mechanism of nutrient uptake.

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CONCURRENT SESSION 18 CELL WALL-MEDIATED RESISTANCE

Summarized by: *Gazala Ameen (North Dakota State University, U.S.A.), Wenjun Xie (University of Copenhagen, Denmark), Chih-hang Wu (The Sainsbury Laboratory, U.K.), Ana Bossa-Castro (Colorado State University, U.S.A.)*

Cell wall-mediated warfare between plants and pathogens

The outcome of the battle between plants and pathogens is highly dependent on their ability to arm themselves and strike hardest for their survival. In this battle, plant cell wall plays a pivotal role, as the first challenge for a pathogen is to breach the cell wall and plants use it as a source for non-self-recognition. The results of this war can govern the final relationship between plants and pathogens.

Stomatal closure is one of the earliest defense responses against bacterial pathogens. **Li Zhang** in Dr. Sheng Yang He's group (Michigan State University, U.S.A.) discovered a cell wall-based mechanism for regulating stomatal defense in *Arabidopsis*. Two genes, *SCORD6* and *SCORD7* (susceptibil-

ity to a cor-deficient), involved in cell wall biosynthesis are important for stomatal closure. *SOCR6* encodes a GDP-D-mannose-4, 6-dehydrolase (GMD2), while *SCORD7* encodes a Trichome Birefringence-Like (TBL) family protein which is proposed to be a xyloglucan-specific O-acetyltransferase. Both *scord6* and *scord7* mutants are defective in stomatal defense and are more susceptible to the coronatine-deficient mutant of *Pseudomonas syringae* pv. *tomato*. In addition, *scord6* is defective in salicylic acid (SA)-mediated stomatal closure whereas *scord7* is defective in both SA and abscisic acid (ABA)-mediated stomatal closure. These results shed light on the plant cell wall-based regulation of stomatal defense and the interplay among different host defense mechanisms against pathogen infection in plants (Zeng et al 2011).

Plant pathogens enzymatically digest plant cell walls to facilitate infection. However, breaking down pectin, one of the major components of the plant cell wall, leads to the production of oligogalacturonides (OGs) that act as DAMP (damage associated molecular pattern) signals which activate plant defense responses. Dr. **Giulia De Lorenzo's** group (Sapienza University of Rome, Italy) found that wall-associated kinase 1 (WAK1) is the receptor of OGs (Ferrari et al 2013). Two cytosolic proteins, GRP3 (glycine-rich protein 3) and KAPP (kinase-associated protein phosphatase), govern OG-mediated responses by negatively regulating WAK1-mediated signalling. The Lorenzo group created an "OG-generating machine" by fusing a pathogen polygalacturonase (PG) to a plant polygalacturonase-inhibiting protein (PGIP). This "OG-machine" released bioactive OGs *in vivo* to trigger plant immunity. Transgenic plants expressing the "OG-machine" under the control of a pathogen inducible promoter are more resistant to several fungal and bacterial pathogens, highlighting the value of DAMP signaling as a mechanism to protect plants against a wide range of pathogens (Gramegna et al 2016).

In another talk, **Gerit Bethke** (University of Minnesota, U.S.A.) in Dr. Jane Glazebrook's group talked about the research conducted on the two epimerases, UDP-D-glucuronate 4-epimerases 1 and 6 (GAE1 and GAE6), which are important in pectin biosynthesis (Molhoj et al 2004). Plants lacking these two enzymes showed altered OG production when treated with macerozyme or challenged by the fungal pathogen, *Botrytis cinerea*. Macerozyme-induced immunity, but not OGs-induced immunity, was compromised in the *gae1/gae6* double mutant, emphasizing the contribution of releasing OGs from pectin to immunity during plant-pathogen interactions (Bethke et al 2016).

In addition to OGs, plant WAKs are also capable of sensing other biotic and abiotic stresses that impact the cell wall. This mechanism is not limited to model systems but can also translates to important crops. Utilizing map-based cloning, Dr. **Kostya Kanyuka's** group at Rothamsted Research Institute (U.K.) identified that *Stb6*, a resistance gene to Septoria tritici blotch in wheat, encodes a member in the WAK family. Functional analyses using *Barley Stripe Mosaic Virus*-induced gene silencing (VIGS) and EMS mutagenesis confirmed that wheat *TaWAKL4* is the *Stb6* gene. The STB6 protein consists of a predicted apoplastic WAK/GUB domain, a transmembrane domain, and a cytoplasmic kinase domain. The ability of WAKs to perceive abiotic and biotic response other than their role in cell expansion during plant development suggests functional diversification of this conserved class of genes. However, pathogens have armed themselves with novel virulence factors to remain elusive to plants cell surface receptor detection.

A talk with a different perspective was given by Dr. **Georg Jander** from the Boyce Thompson Institute (U.S.A.), who highlighted the role of cytokinins in plant-insect interactions. Jander's team combined different strategies to understand the effects of proteins and small molecules identified from *Myzus*

persicae saliva on the aphid's growth *in planta*. They individually overexpressed some *M. persicae* salivary effector proteins and demonstrated that each one has a different effect on aphid fecundity. Interestingly, a fraction of small molecules of less than 3 kDa from the aphid saliva have 100 fold more cytokinin hormone derivatives than plants. By feeding aphids a diet containing isotope-labeled ATP, they demonstrated that these cytokinins are aphid derived. Dr. Jander further hypothesized that aphids inject cytokinins into their feeding sites to delay host senescence as a way to counteract the localized defense responses induced by plants (Elzinga et al 2014).

In the 2016 International Society for Molecular Plant-Microbe Interactions conference, the concurrent session on cell wall-mediated resistance had great talks about the interaction between diverse pathogen groups with their corresponding host plants. The interesting discoveries reported in these talks evoke discussions on cell-wall based defense regulation. The role of SA was central in most of the talks, which reassured its importance in the multi-layered, multi-faceted immune response in plants. SA not only governs many biochemical defense responses but also directs the physiology of stomatal closure. We also learned about the evolutionarily recent roles of wall associated kinases in disease resistance, which identify the intruder outside the cell and induce cellular events for defeating pathogens.

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CONCURRENT SESSION 19 MICROBIOME AND PHYTOBIOME II

Summarized by: Fernanda R Rezende de Castro Moretti (Universidade de Sao Paulo, Brazil and The Ohio State University, U.S.A.), Alfredo Mari (Max Planck Institute for Plant Breeding Research, Germany), Marco E Mechan Llonetop (Virginia Polytechnic Institute and State University, U.S.A.), Sergey Ivanov (Boyce Thompson Institute, U.S.A.)

Angela Sessitsch (AIT Austrian Institute of Technology, Austria), Carolyn Young (The Samuel Roberts Noble Foundation, U.S.A.), Devin Coleman-Derr (USDA-ARS, U.S.A.), Cindy Given (University of Jyväskylä, Finland) and Oliver Ellingham (University of Reading, U.K.) updated the congress in the Microbiome and Phytobiome II session with progress made toward understanding how microbial communities affect plant productivity and resistance to biotic and abiotic stresses. In addition, examples of how aerial and geospatial tracking can assist in understanding these affects were presented.

Dr. **Angela Sessitch**'s project aims to characterize the plant microbiomes associated with different plant tissues, specifically the seed-associated microbiome. The research is focused on *Setaria viridis* and *Setaria pumila* seed endophytes. It has been found that the seed endophyte communities could be engineered to integrate any strain of interest into the seed with an aim to establish them in the next plant generation.

Dr. **Carolyn Young** reported on a two-year field experiment on the progression of root rot disease of alfalfa. Alfalfa is a major stock feed of beef cattle in Oklahoma, U.S.A. and the root rot disease is caused by the ascomycete fungus *Phymatotrichopsis omnivore*, whose infection is characterized by rapid spreading in the field. The study employed drone aerial imaging and GPS-tracking with subsequent computational analyses to measure the speed of pathogen spread. Coupled with molecular biological methods, these techniques are aimed at generating tools to minimize the impact of the disease in agricultural settings.

Dr. **Oliver Ellingham** reported on a survey aimed at assessing the variety of powdery mildew species in U.K. This study employed a citizen science scheme, which intended to promote science communication and involvement of the general public in scientific research. Over 500 survey samples were obtained from the public from different parts of U.K. and analyzed to either genus or species level using morphological and genetic techniques. Results of the identifications were communicated back to public participants.

Dr. **Devin Coleman-Derr** reported on the association between bacterial microbiome changes and water stress on grass roots. In this study, eighteen species of C3 and C4 grasses were evaluated under irrigated and drought conditions. Three different samples were collected: root, root rhizosphere and soil, during early and late growth stages, pre and post-flowering. This research concluded that under irrigated conditions, Proteobacteria is the most dominant phylum. On the other hand, as drought stress is induced, there is an increase in the phylum Actinobacteria. This was observed on roots at the early and late growth stages and was less pronounced in the rhizosphere and soil samples.

CONCURRENT SESSION 20 APOPLASTIC INTERACTIONS

Summarized by: Teura Barff (Universite de Sherbrooke, Canada), Meltem Cavdar (RWTH Aachen University, Germany), Julie Gervais (INRA, France), Yohann Petit (INRA, France).

Molecular plant-microbe dialogue in the apoplastic space during infection.

The apoplastic space serves as one of the first interaction sites between plants and microbes (Doehlemann and Hemetsberger, 2013). Those interactions include recognition of microbe-associated molecular patterns (MAMPs) by pattern recognition receptors (PRRs) and the subsequent immune responses like secretion of antimicrobial compounds. Pathogens in turn secrete effector proteins in order to circumvent plant defenses (Macho and Zipfel, 2014).

Dr. **Thorsten Nürnberger** (University Tübingen, Germany) reported on two novel leucine-rich receptor proteins RLP23 and RLP32 that are able to sense protein PAMPs from various microbes and contribute to plant innate immunity (Albert et al 2015). Both PRRs were shown to constitutively interact with and require SOBIR1 as a co-receptor. Another highlight of the group's findings was that the co-receptor BAK1 seems to be recruited into the RLP/SOBIR1 complex in a ligand-dependent manner. Additionally, the two RLPs are specific to *Brassica*

ceae. In their studies, they showed evidence that RLP23 recognizes a peptide motif within the necrosis-and-ethylene-inducing protein 1 like proteins (NLPs). On the other hand, RLP32 recognizes protein patterns from the bacteria *Ralstonia solanacearum* or *Escherichia coli*.

The apoplastic pathogenesis-related protein 1 (PR-1) was discovered in 1970 in pathogen-challenged tobacco plants (Van Loon and Van Kammen, 1970). An antimicrobial activity was proposed for this protein and the *PR-1* gene is often used as a marker for defense-related responses. Despite its importance in defense, no mode of action has been found for PR-1. PR-1 is a member of the CAP-family of proteins involved in sterol-binding, inciting Dr. **Jordi Gamir** (University of Fribourg, Germany) to hypothesize a sterol-binding activity for PR-1. This hypothesis was validated by the finding that PR-1 complements yeast *pry1* and *pry2* (pathogen-related yeast) mutants, allowing restoration of sterol export. Moreover, an *in vitro* interaction was demonstrated between PR-1 and diverse sterols. This sterol-binding activity is necessary for PR-1 antimicrobial activity, as shown by the titration of its antimicrobial activity by addition of sterols. Two modes of actions of PR-1 can thus be hypothesized: either PR-1 interferes with sterol uptake by the pathogen or it directly binds sterols of the pathogen's plasma-membrane to cause damage.

Nematodes are known to infect both plants and animals, but the way they suppress the immune response is poorly understood. The group of Dr. **Lozano-Torres** (Wageningen University, The Netherlands) recently showed that the apoplastic effectors, venom allergen-like proteins (VAPs), are able to repress plant defense response (Lozano-Torres et al 2014). By expressing heterologous VAPs from nematodes in plants, they observed increased susceptibility toward various pathogens, indicating a compromised plant basal immunity. The induction of ectopic VAPs seems to act on cell surface localized proteins. Furthermore, their release into plants tissue is synchronized with the enzymatic breakdown of the plant cell wall. Taken together, these results suggest that VAPs inhibit early activation of immune responses and damage plant tissue.

Dr. **Lay-Sun Ma** (Max Planck Institute for Terrestrial Microbiology, Germany) from Dr. Regina Kahmann's laboratory reported the identification of a new apoplastic effector Rsp3 from the fungal pathogen *Ustilago maydis*. Rsp3 was specifically expressed during infection and required for *U. maydis* virulence. Ma demonstrated that Rsp3 attached to the outside of fungal hyphae and interacted with maize DUF26 domain-containing proteins that belong to a family of antifungal proteins. The antifungal activity of the DUF26 proteins was blocked by Rsp3. Results thus suggested that the apoplastic effector Rsp3 protects *U. maydis* from host antifungal activity, presumably by inhibiting DUF26 domain-family proteins from binding to the fungal cell wall.

To summarize, speakers of this session presented evidence for a large array of strategies associated with the plant-pathogen interactions in the apoplastic space, either from the plant perspective with RLPs and secretion of PR proteins or from the pathogen side with various apoplastic effector proteins.

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CONCURRENT SESSION 21 EMERGING SYSTEMS

Summarized by: Laura A. Fleites (University of Florida, U.S.A.), Steen Hoyer (Donald Danforth Plant Science Center, U.S.A.), Paolo Margaria (Pennsylvania State University, U.S.A.), Mina Ohtsu (Nagoya University, Japan)

This session featured a particularly diverse set of plant parasites, including nematodes, parasitic plants, aphids, pathogenic fungi, and bacteria. Each speaker found suitable methods for their system and approached plant-microbe interaction from a unique direction.

Dr. **Godelieve Gheysen** (Ghent University, Belgium) presented evidence that SA, ET, and JA pathways in rice (*Oryza sativa*) cooperatively contribute to resistance against the root-knot nematode (*Meloidogyne graminicola*) whereas GA signaling enhances susceptibility. Moreover, they showed that the nematode strongly and rapidly suppressed systemic defense, resulting in significantly enhanced susceptibility to rice blast (*Magnaporthe oryzae*). While *M. graminicola* predisposed rice for rice blast disease, other filamentous pathogens such as the oomycete *Pythium* spp. could act antagonistically with the nematode infection.

Dr. **Christopher Clarke** (Virginia Tech, U.S.A.) presented analyses of the interaction between the parasitic plant *Phelipanche aegyptiaca* and the model host *Arabidopsis thaliana* to find key factors determining resistance or susceptibility. On the parasite side, Clarke and colleagues found five new effector candidates that suppress flg22-triggered ROS production or promote infection by other nonhost pathogens. On the host side, they revealed that the auxin pathway is involved in resistance, while the GA pathway is required for attachment of the parasitic plant to host roots and thus enhances susceptibility.

Dr. **Thomas Vincent** (John Innes Centre, U.K.) presented his work on plant-aphid interactions using the green peach aphid (*Myzus persicae*) as a model. Vincent et al. used *in vivo* high-resolution imaging techniques to reveal a clear and rapid calcium wave that moves from the vacuole and apoplast to the cytosol of plant cells. This wave is regulated by calcium channels located in the vacuole and plasma membrane. Moreover, the calcium burst seems to be BAK1-dependent. Overall, the authors provided greater knowledge of the role of calcium signaling in plant defense response to aphids.

Dr. **Jan Bettgenhaeuser** (Sainsbury Laboratory, U.K.) presented recent progress in using rust-cereal interactions as a model for dissecting mechanisms of nonhost resistance. This conceptual framework uses barley as an intermediate host and the small panicoid grass model *Brachypodium distachyon* as an intermediate nonhost to characterize genes affecting wheat stripe rust infection at different stages. By quantitative trait locus analysis (enabled by the high-quality reference *B. distachyon* genome), two mapping intervals have been narrowed to *NB-LRR* genes, suggesting a mechanistic connection to classical gene-for-gene host-type resistance.

Dr. **Elizabeth Savory** (Oregon State University, U.S.A.) presented research on the Gram-positive phytopathogen *Rhodococcus fascians*. This bacterium causes an array of symptoms, including phyllody, witches' broom and leafy galls, on several hosts, which are believed to be primarily caused by

plasmid-borne cytokinin biosynthesis (*fas*) genes. The virulent strain D188 and a series of mutants were used to dissect the role of individual *fas* genes in disease symptom development. This work allowed the identification of a small number of *fas* genes as possible virulence determinants in *R. fascians*, and calls into question aspects of the current model for virulence.

CONCURRENT SESSION 22 INTER-KINGDOM SIGNALING

Summarized by: Bruna Gonçalves Coutinho (University of Washington, U.S.A.), Sebastián López-Fernández (Fondazione Edmund Mach, Italy), Tiffany M. Lowe-Power (University of Wisconsin, U.S.A.), and Onur Oztas (University of Massachusetts Amherst, U.S.A.)

The session "interkingdom signaling" gathered presentations detailing the intimate interactions of microorganisms with their hosts. Some molecular interactions in nature rely on chemical cues produced by components of a multi-partite system. Although most paracrine signaling depends on molecules from microorganisms, the host plant can also trigger biochemical phenomena through its own molecules.

Dr. **Vittorio Venturi** (ICGEB, Italy) described a case study where two bacteria, *Pseudomonas savastanoi* and *Erwinia toletana*, are able to communicate using *N*-acyl homoserine lactones (AHL) and regulate virulence phenotypes. As an endophyte, *E. toletana* lives harmlessly inside plants whereas *P. savastanoi* lives as a symbiont in the phyllosphere. Whenever there is a wound on the plant, *P. savastanoi* enters and teams up with *E. toletana* switching both lifestyles to pathogenic. In this interaction it is not known if other factors like metabolic syntrophy or more signaling circuits are involved.

Dr. **Barbara Valent** (Kansas State University, U.S.A.) showed another type of interaction where the translocation of effectors regulates access of the rice blast fungus *Magnaporthe oryzae* to the host plant. A candidate effector known as Bas55 is a model for studying Golgi-independent effector translocation. Valent elegantly showed how the effector accumulates in the contact zone of the invasive fungal hyphae and the plant cell membrane via small vesicles that are delivered rapidly from the pathogen to the host.

Dr. **Goncalves Coutinho** (University of Washington, U.S.A.) on the other hand, presented a scenario where the molecule regulating lifestyle options derives from the plant host. In experiments directed at finding the nature of the signaling molecule, Coutinho explains how a bacterial signaling system, evolved from quorum sensing, is LuxR (receptor) dependent but AHL (signal) independent. Several experiments revealed that the signaling molecule is a non-diffusible peptide that is actively transported from the plants and regulates a variety of phenotypes crucial for bacterial colonization.

Megan O'Malley (Oregon State University, U.S.A.) from Dr. Jeff Anderson's lab proposed that a GacS/GacA two-component system might be involved in perceiving specific organic acids exuded by *Arabidopsis* which induce Type III Secretion System (T3SS)-associated genes in *Pseudomonas syringae* pv. *tomato* DC3000. She found that the absence of GacA function increased the expression of T3SS-associated genes and the delivery of Type III effectors into the host cells, while, surprisingly, reducing bacterial virulence. This observation requires further investigation.

Finally, Dr. **Naweed Naqvi** (Temasek Life Sciences Laboratory, Singapore) reported a novel enzyme secreted by *Magnaporthe oryzae* during rice infection that modifies host jasmonic acid and blocks the pathogen recognition and defense system in rice. His research implies that a change in only a single bond of jasmonic acid is sufficient to suppress immunity.

It is clear from the session that evolution of microbes and plants is a parallel process that has shaped the ecological roles of both types of organisms. The mechanisms that bacteria and fungi use for colonization of their hosts arise from the overlapping of habitats where strategies necessary for adaptation are developed.

CONCURRENT SESSION 23 POPULATION GENOMICS

Summarized by: Maryn Carlson (Cornell University, U.S.A.), Hao-Xun Chang (University of Illinois Urbana-Champaign, U.S.A.), Samriti Midha (CSIR-Institute of Microbial Technology, India), Benjamin Schwessinger (Australian National University, Australia), Hester J Van Schalkwyk (University of the Free State, South Africa)

In the first IS-MPMI 'Population Genomics' session, four speakers presented population analysis of various plant pathogens, including *Pseudomonas syringae*, *Xanthomonas perforans*, *Phytophthora* species and *Puccinia striiformis* f. sp. *tritici*. One speaker covered population studies of *NB-LRR* resistance genes in a wild tomato species.

First, Dr. **Boris Vinatzer** (Virginia Tech, U.S.A.) showed that host specificity of *Pseudomonas syringae* varies across strains. A previous comparative genomic study between *PtoT1*, an efficient colonizer of tomato but not *Arabidopsis thaliana*, and the model strain *P. syringae* pv. *tomato* DC3000, which is capable of infecting both tomato and *A. thaliana*, suggested that differences in effector repertoire may determine host specificity. Several strain-specific effectors were identified in the study, and one effector AvrRpt2 in *PtoT1* was involved in triggering the hypersensitive response in *Arabidopsis* to *PtoT1* (Almeida et al. 2008). As *PtoT1* has become predominant in agronomic fields, Vinatzer et al. compared its virulence genes to those of strains from non-agricultural environments. A previous study led by the Vinatzer group discovered that crop pathogens such as *PtoT1* have higher recombination frequencies than *P. syringae* isolates from non-agricultural environments. Crop pathogenic *P. syringae* strains likely evolved from environmental strains, which generally displayed less virulence and broader host range (Monteil et al. 2013)). Vinatzer et al. further pointed out two effectors, HopD1 and HopQ1, that were absent in non-agricultural isolates. As in *P. syringae*, effector repertoire differences among races of *Xanthomonas* spp. also effects host specificity.

Then, Dr. **Erica Goss** (University of Florida, U.S.A.) discussed monitoring *Xanthomonas perforans* races in Florida from 1991 to 2012. Over time, race T4 emerged as the dominant *X. perforans* race. Based on a core genome phylogenetic analysis, *X. perforans* race T4 strains consist of two distinct phylogenetic groups, with sub-grouping within each group (Schwartz et al. 2015). By 2010, *X. perforans* race T4 (*XpT4*) gained a loss of function mutation in the Type III effector gene AvrXv3 and replaced race T3 (*XpT3*). In addition, most isolates of *XpT4*, with exception of three strains of group 2 *XpT4*, also gained another Type III effector AvrBsT (Timilsina et al. 2016). The population-level observations were experimentally supported by examining knockout mutants of *avrBsT* and another effector, *XopQ*. Deletion mutants of *X. perforans* exhibited an expanded host range from tomato to pepper and tobacco (Schwartz et al. 2015). Phylogenetic and genomic comparison further suggested that the second group of race *XpT4* may have arisen through a hybridization with *Xanthomonas euvesicatoria* 85-10, which was dominant prior to 1991 and before the appearance of *XpT3*.

Many plant resistance genes encode a class of proteins called Nod-Like Receptors (NLRs) that are involved in plant resistance signalling. As there is high divergence and copy

number variation in the NLR repertoire in plants, Dr. **Remco Stam** et al. (Technische Universität München, Germany) explored the NLR diversity in the wild tomato species, *Solanum pennellii*. Using the *R*-gene Enrichment Sequencing (RENSeq) approach, Stam identified 220 NLRs in *S. pennellii*. The number of NLRs identified was fewer than shown for closely related species, but a phylogenetic reconstruction demonstrated representation of all *Solanum* NLR families. Examination of short term evolutionary changes led to the identification of NLR candidates exhibiting variation and signatures of selection. Stam extended the analysis to another species, *Solanum chilense*, where distinct pathogen pressures should result in differences in the NLR complement.

Dr. **Niklaus Grünwald** (USDA ARS, U.S.A.) described mechanisms of *Phytophthora* spp. emergence as elucidated through the application of evolutionary, population genetic and bioinformatic approaches. Emergence of these pathogens involves a wide range of mechanisms including hybridization, migration, and adaptation. In both North America and Europe, *Phytophthora ramorum* populations remain clonal. Despite the fact that both mating types coexist in North America, sexual reproduction has not been observed. *Phytophthora infestans* populations show a similar pattern, but clearly undergo an apparently 'random' succession of clonal lineages. The South American tomato tree pathogen *Phytophthora andina* emerged via hybridization between *P. infestans* and another unknown *Phytophthora* species.

Lastly, Ph.D student **Hester van Schalkwyk** (University of the Free State, South Africa) shared results from a genomic characterization of *Puccinia striiformis* f. sp. *tritici* (PST) races found in South Africa. Since the first occurrence in the country of stripe rust of wheat in 1996, only four races of PST have been identified based on virulence and microsatellite marker analysis. A whole genome analysis was conducted to derive a possible origin, evaluate the hypothesis of stepwise evolution, and understand the influence of effector proteins on increases in virulence over time. To do comparative candidate putative effector expression profiling, susceptible wheat lines were inoculated with PST and infected leaf material were collected at different time points of fungal development. Additionally, profiling of putative effectors and transcriptomic analysis of field isolates from the past three years, coupled with virulence tests on a large set of wheat differentials (lines capable of differentiating pathogen isolates based on *R*-gene complement) shed light on PST temporal genetic diversity. South African stripe rust races are all closely related, and most closely related to isolates from Ethiopia and Kenya. These results suggests that South African isolates may have originated from East Africa, or share an origin with East African isolates. The current population in South Africa is genetically distinct from historical races but does exhibit the same virulence profiles, which raises the question of what selection pressures are involved in shaping their evolution.

In summary, Vinatzer et al. and Goss et al. demonstrated the power of population genomics to explore virulence reservoirs and highlighted the importance of effectors in determining host specificity. Stam et al. provided a method to understand NLR diversity in wild tomato that can be extended to various crop species. He showed that understanding the variability of *R* genes may lead to identification of potential candidates for durable resistance breeding. In-depth *Phytophthora* genomic analyses by the Grünwald group facilitates the development of translational approaches such as targeted best management practices; and van Schalkwyk et al. employed pathogenomic approaches contextualize the South African PST population within the global populations, providing a platform for further investigation of the population's genetic diversity.

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CONCURRENT SESSION 24 RECOGNITION IN PLANT IMMUNITY II

Summarized by: Thomas Liebrand (University of California Davis, U.S.A.), Martin Stegmann (The Sainsbury Laboratory, U.K.), Xiaoxiao Zhang (CSIRO, Australia), Anna Joe (University of California Davis, U.S.A.), and Joji Grace Sernestrand (Forschungszentrum Jeulich, Germany)

The research group of Dr. **Aska Goverse** (Wageningen University, The Netherlands) investigates how plant immune receptors mediate resistance against the plant parasitic nematode *Globodera pallida*. Work presented focused on resistance mediated by the NLR-type receptor GPA2. GPA2 recognizes RBP1, a secreted nematode effector protein containing a SPRY-domain. Interestingly, GPA2 shows strong homology to Rx1, an NLR involved in resistance against *Potato virus X*. Her research showed that GPA2 recognizes RBP1 in the cytoplasm and, similar to Rx1, GPA2 requires a nuclear and cytoplasmic pool to mediate resistance. However, subtle differences between Rx1 and GPA2 localization were observed. Additional work in the Goverse lab involves 3D computational modeling and subsequent mutational analysis of the effector protein RBP1.

Dr. **Dingzhong Tang** (Institute of Genetics and Development, Chinese Academy of Sciences, China) presented recent advances from his lab on the identification and characterization of suppressor mutants of *edr1* (enhanced resistance 1) in *Arabidopsis*. He presented unpublished data about a suppressor mutant that is affected in a Glycosylphosphatidylinositol (GPI)-anchored protein, which is involved in the regulation of PTI signalling. They are currently investigating the molecular mechanism of this novel PTI regulator.

Dr. **Simon Williams** from the Kobe lab (University of Queensland, Australia) presented their investigation on signalling domains of plant NLRs immune receptors. Plant NLRs possess either a TIR or CC domain at their N-termini. These domains are critical for the activation of defense signaling and the hypersensitive response (HR). The wheat CC-NLR protein Sr33 confers resistance to wheat stem rust. The NMR structure of the CC domain (a four-helix dimer) of Sr33 shows similarities to the CC domains of the potato NLR Rx and the barley NLR MLA10. Biophysical assays suggest that all three proteins are monomeric in solution. Deletion studies combined with in planta cell death assays suggest that the currently known MLA10 CC structure may not represent the active form of the NLR and that crystallization may have caused a domain swap in the earlier solved CC domain structures.

Dr. **Koki Fujisaki** from the lab of Dr. Ryohei Terauchi (Iwate Biotechnology Research Center, Japan) presented their work on the *Magnaporthe oryzae* effector AVR-Pii, which forms a complex with the homologous exocyst subunits Exo70F2 and Exo70F3. Interestingly, the corresponding rice resistance protein Pii does not directly interact with AVR-Pii, but indirectly interacts via the effector-associated Exo70F2/F3. Knockdown of *Exo70F2/F3* specifically impairs Pii-mediated resistance, suggesting that they might act as a helper or guarder for AVR-Pii recognition. The lab is currently trying to further dissect this recognition mechanism.

Dr. **Isgouhi Kaloshian** (University of California Riverside, U.S.A.) reported on the atypical pairing of the plasma membrane-localized receptor SERK1 with the cytoplasmic CC-NLR Mi-1.2 in mediating resistance to potato aphids. A potential aphid effector found in both the total protein extracts and aphid saliva can be recognized by Mi-1.2, which requires SERK1 for activating immunity. Overexpression of SERK1 enhances defense against aphids in tomato and *N. benthamiana* plants. Co-immunoprecipitation and BiFC studies revealed that, upon effector recognition, SERK1 and Mi-1.2 directly interact and co-localize to microsomes.