plant health 2021 online
August 2–6, 2021
Seismic Shifts in Disease Risk

Plant Health 2021
Abstracts of Presentations

Abstracts submitted for presentation at the APS Plant Health 2021 Annual Meeting held virtually, August 2–6, 2021. The recommended format for citing annual meeting abstracts, using the first abstract below as an example, is as follows:

Yang, L. 2021. A molecular mechanism of age-related resistance. (Abstr.) Phytopathology 111:S2.1. https://doi.org/10.1094/PHYTO-111-10-S2.1

The abstracts are published as a supplement to *Phytopathology* for citation purposes. They were not reviewed by the *Phytopathology* Editorial Board and were not edited by the APS editorial staff.

https://doi.org/10.1094/PHYTO-111-10-S2.1

A molecular mechanism of age-related resistance
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Age-related resistance (ARR) refers to a gain of disease resistance during shoot or organ maturation. ARR associated with vegetative phase change, a transition from the juvenile to the adult vegetative phase, is a widespread agronomic trait in fruits, vegetables, and row crops, affecting resistance against viruses, bacteria, fungi, oomycete and insects. However, it is still unclear how innate immunity is differentially activated in successive stages of shoot maturation on a plant. MicroRNA156 (miR156) and its targets, the SQUAMOSA-promoter binding protein-like (SPL) transcriptional factors, are conserved regulators of vegetative phase change. We found that *Arabidopsis thaliana* (Arabidopsis) showed ARR against its bacterial pathogen *Pseudomonas syringae pv. tomato* DC3000 (*Pto* DC3000) during a transition from the juvenile to the adult stage. The timing of ARR activation was associated with a temporal drop of miR156 level. A systematic analysis of the loss- and gain-of-function mutants of 11 *SPL* genes revealed that a subset of *SPL* genes, including *SPL2*, *SPL10*, and *SPL11* activated ARR in the adult stage. The immune function of SPL10 was independent of its function in regulating morphogenesis. In addition, we found that the SPL10-mediated age-dependent activation of the salicylic acid pathway contributes to ARR. Disrupting SA biosynthesis or signaling abolished the age-dependent gain of resistance against *Pto* DC3000. Given the conserved roles of miR156 in regulating developmental timing in plants, miR156 may contribute to age-related resistance in various pathosystems.

Exploration of a novel density-dependent volatile-induced antimicrobial compound produced by *Xanthomonas perforans*
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For most of the 20th century, *Xanthomonas euvesicatoria* (*Xe*) was the only known causal agent of bacterial spot of tomato (BST) in Florida. *X. perforans* (*Xp*) was first isolated in 1991 from Florida tomato fields and quickly replaced *Xe* via production of bacteriocins (BCNs) against *Xe*. However, in a previous study, a *Xp* mutant with nonfunctional BCNs was still able to outcompete *Xe* in the field. We discovered that the BCN mutant produced an antimicrobial compound that is effective against *Xe* in vitro. This compound was volatile-induced, cell density-dependent, and expressed under limited nutritional conditions and at a later growth stage than the previously described BCNs in *Xp*. Production of the volatile-induced antimicrobial compound was not conserved across *Xp* field strains, but other *Xanthomonas* species (*X. gardneri*, *X. vesicatoria*, *X. cynarae*, *X. campestris* pv. *campestris*) also produced a similarly expressed antimicrobial compound against *Xe* and elicited production of the antimicrobial compound by *Xp*. A wide range of other plant pathogenic bacteria, including *Clavibacter michiganensis* subsp. *michiganensis*, *Pantoea stewartii*, and *Pseudomonas cichorii*, also elicited production of this antimicrobial compound by *Xp*. To identify the antimicrobial compound, we performed mass spectrometry of agar where the antimicrobial was present, compared with agar from lower cell density Petri plates where the antimicrobial was not

and “C” respectively, whereas 87KEN3018 comprised the “C” haplotype (85 Mb, 24 contigs) and a new haplotype “D” (88 Mb, 57 contigs). For verification of the haplotype assignments of these assemblies, sequence alignments were done against haplotypes “A” and “B” (21-0), and “A” and “C” (Ug99). In addition, pairwise diversity analysis of alleles from 1,299 conserved BUSCO genes further verified that the “C” haplotype in the Ug99 lineage (clade I) was derived from clade II lineage as represented by isolate 87KEN3018. Genomic tools are now available to elucidate the recombination events leading to the evolution of lineages of *P. graminis*.

Deciphering the *Chaetomium globosum* induced defense signaling network in tomato against early blight disease
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Chaetomium globosum is a potential biological control agent against various plant pathogens. While most studies report on the mycoparastism and antibiosis of *C. globosum* against plant pathogenic fungi, only a few reports on its induced resistance. To gain insights into the induced defense mechanisms of *C. globosum* (Cg-2) against early blight of tomato, the suppression of disease by Cg-2 was evaluated and RNA-seq performed. There was a 30.9% reduction in disease severity in the Cg-2-treated plants. The expression of hormone signaling marker genes was analyzed by qPCR to determine the best time point for RNA sequencing. The transcriptome data revealed that 22,473 differentially expressed genes (DEGs) were expressed in tomato at 12hpi compared to control plants, of which, 922 DEGs had a two-fold up- or downregulation ($P < 0.05$). The KEGG pathway analysis revealed that most of the DEGs represented metabolic pathways, biosynthesis of secondary metabolites, plant-pathogen interaction, chlorophyll metabolism and plant hormone signal transduction. GO analysis revealed that DEGs were mainly related to the binding and catalytic activities, metabolic processes, response to stimulus and biological regulation. The gene modulations in hormone signaling transduction, phenylpropanoid biosynthesis and MPK signaling indicated their involvement. The results revealed the activation of JA and SA signaling pathways indicating the potential involvement of both induced systemic resistance (ISR) and systemic acquired resistance (SAR) in the resistance activated by Cg-2 in tomato against early blight.

Susceptibility to azoles of *F. musae*, agent of crown rot disease of banana
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Crown rot disease is one of the main post-harvest diseases of banana. It is a devasting disease that causes important losses every year. The rot is not visible when the bananas are boxed, and symptoms generally appear only after shipping to banana-consuming countries. *Fusarium musae* is a pathogenic species belonging to the *F. fujikuroi* species complex. It is a novel species firstly described in 2011. It contributes especially in central American countries to crown rot disease. In addition, it has also been found on human patients as a saprophytic agent. Given the potential risk of this novel pathogen to spread from food to clinical settings and the unknown mechanisms of transmission from one host to the other, knowledge on its susceptibility to widely used agricultural azole fungicides was investigated. Eight DMIs used in crop protection (prochloraz, tebuconazole, epoxiconazole, difenoconazole, propiconazole, tetraconazole, flusilazole, and fenbuconazole) were tested using the CLSI protocol methodology on 11 *F. musae* strains collected worldwide from infected bananas. The goal of the work was to define the level of susceptibility of the population to different drugs currently used in agriculture. Overall results show that the agricultural azole fungicides tested need to be applied at higher concentrations to inhibit the grow of *F. musae* compared to its sister species *F. verticillioides*.

Identification of a suppressor of RNA silencing encoded by Grapevine fanleaf virus
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RNA silencing is an effective antiviral defense mechanism utilized by plants to fight virus infections. To counteract this defense response, plant viruses encode viral suppressors of RNA silencing (VSRs). VSRs have been identified in most plant viruses, but it is unclear whether nepoviruses in the family *Secoviridae* possess VSRs, although the coat protein of Tomato ringspot virus, a subgroup C nepovirus, has been demonstrated to interact with Argonaute-1 protein to potentially prevent translation repression. No VSR has been reported yet for subgroup A nepoviruses, including Grapevine fanleaf virus (GFLV). We aim to identify a VSR encoded by GFLV, the causative agent of fanleaf degeneration, which is one of the most devastating viral diseases of grapevine. Following silencing of the enhanced green fluorescent protein (eGFP) in transgenic *Nicotiana benthamiana* expressing eGFP by *Agrobacterium tumefaciens*-mediated delivery of a dsRNA hairpin eGFP construct, chimeric constructs containing individual GFLV proteins or fused GFLV proteins were transiently expressed in eGFP-silenced plants via *A. tumefaciens*-mediated delivery. Local and systemic suppression of eGFP silencing by GFLV proteins was evaluated and quantified using fluorescence imaging, spectrometry, and RT-qPCR with specific primers. In addition, we probed the GFLV genome for the conserved tryptophan-glycine (WG)/glycine-tryptophan (GW) motif, which has been detected in numerous plant VSRs. The identification of a VSR of GFLV will enhance our understanding of virus-host interactions.

First report of oxytetracycline and streptomycin resistance genes in *Xanthomonas arboricola* pv. *pruni*, the causal agent of bacterial spot in peach
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