

Hahn, with some modifications in fungicide concentrations in the media. Resistance to anilinopyrimidines was present in some samples, but degree and frequency were uncertain, in part because a subset of isolates grew poorly on sucrose medium; assays were supplemented by inoculation of treated and untreated table grapes. Resistance to benzimidazoles was widespread, and a low level of resistance to iprodione (residual germ tube growth on 5 mg/L iprodione) was common as well. The many boscalid-resistant isolates in the survey, most of which also had resistance to QoI, were not cross-resistant to fluopyram. Fenhexamid resistance was rare in Virginia grape isolates (4 isolates from 2 sites), but has been reported elsewhere in 45% of Florida strawberry isolates, 17% of Carolina strawberry isolates, and was detected in samples from two of three Virginia strawberry fields tested.

New rice resistance genes via targeted genome editing

S. Baufumé (1), D. Meynard (2), M. Reschke (3), M. Solé (3), S. Cunnac (1), B. Szurek (1), E. Guiderdoni (2), J. Boch (4), R. KOEBNIK (1)

(1) Institut de Recherche pour le Développement, Montpellier, France; (2) Centre de Coopération Internationale en Recherche Agronomique pour le Développement, Montpellier, France; (3) Martin Luther University, Halle (Saale), Germany; (4) Martin Luther University, Halle (Saale), France
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Rice is one of the most important food crop in the world providing the principal source of calories for nearly half of its population. Bacterial Leaf Blight (BLB) of rice, caused by *Xanthomonas oryzae* pv. *oryzae*, depends on direct induction of host susceptibility genes by bacterial TAL (Transcription Activator-Like) effectors. So far, efficient control of this disease relies on the use of resistant varieties. Since bacterial ability to induce specific host susceptibility genes is critical for disease development, we wish to create mutations in rice susceptibility gene promoters using the TALEN (TAL Effectore Nuclease) technology, in order to make them unresponsive to bacterial infection. We show that (i) designer TALENs cleave DNA target sites in a predictable manner, (ii) engineered bacteria secrete TALENs into culture supernatants, and (iii) engineered TALEs injected into rice embryogenic tissues are able to induce their target genes efficiently. Based on the DNA recognition code, designer TALENs were created to induce site-specific protective mutations and thus mimic the natural evolution of resistance genes on a much faster scale. With this approach, we hope to provide breeders with new strategies to generate broad and durable resistance to bacterial infections, thus reducing chemical use, providing yield stability, and increasing profitability of rice farming, in particular for smallholder farmers.

Defining the stages of infection of grapevine stems with the trunk disease Botryosphaeria dieback

K. BAUMGARTNER (1), R. Travadon (2), E. Galarneau (1), A. McElrone (1)

(1) USDA ARS, Davis, CA, U.S.A.; (2) University of California, Davis, CA, U.S.A.

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Detection of *Neofusicoccum parvum*, one of the causal agents of Botryosphaeria dieback of grapevine, is limited to the late stage of infection, when the wood canker is well-established. Early detection is hampered by the internal nature of the canker, which is revealed only by cutting into the wood. A detection tool for the early stage of infection, and from leaves instead of the trunk or cordon, would inform management decisions. We defined early and late stages of infection of inoculated vs. non-inoculated (both wounded and non-wounded) plants at 2-week intervals for 2 months, based on: recovery of *N. parvum* in culture, xylem occlusions as measured by light microscopy, and xylem embolism as measured by high-resolution x-ray computed tomography (HRCT). Incubation of 1.5 months was required for recovery at 2 cm from the inoculation site (late stage). In contrast, occlusions and embolized vessels, which were significantly more frequent in inoculated plants, were found at only 2 weeks post-inoculation and up to 4 cm from the inoculation site (early stage). Our findings show that these changes in xylem anatomy occur in advance, both in terms of time and position relative to the inoculation site, of colonization. The next step is to identify candidate genes, as identified by RNAseq and confirmed by qRT-PCR, the expression of which in grape leaves corresponds with the early timing of occlusions and embolisms in the woody stem.

Evaluation of fungicides and biorational products for management of Pythium and Rhizoctonia damping-off in greenhouse-produced vegetables

F. Baysal-Gurel (1), S. A. MILLER (1)

(1) The Ohio State University, Wooster, OH, U.S.A.

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Damping-off, caused by *Pythium* spp. and *Rhizoctonia solani*, can cause significant losses in transplant and micro-vegetable production in protected

environments. Experiments were performed in a greenhouse to determine the efficacy of biopesticides and fungicides against *Pythium* and *Rhizoctonia* damping-off in lettuce and pepper. Treatments applied were Rootshield Home and Garden, Rootshield PLUS WP, Rootshield WP, Prestop, Actinovate, Mycostop, Serenade Soil, Subtlex, Regalia, SoilGard and the fungicides Double Nickel LC, Previcur Flex, Banrot and Phosphite. The center 48 cells of 288-cell trays were filled with *P. ultimum* or *R. solani*-infested potting mix (0.5 g inoculum/100 ml Fafard's Superfine Germinating mix) and the remaining cells of each flat were filled with non-inoculated potting mix. Treatments were applied to the entire flat, with the exception of the Root Shield Home and Garden, Rootshield PLUS WP and Rootshield WP treatments, which were only applied to the center 48 cells of each flat. Rootshield Home and Garden, Rootshield PLUS WP, Rootshield WP and Double Nickel LC were consistently effective in reducing *Rhizoctonia* damping-off in pepper and lettuce. While no product was effective in reducing *Pythium* damping-off in pepper, Prestop, Double Nickel LC, Rootshield Home and Garden, Rootshield PLUS WP, Mycostop, Previcur Flex, Serenade Soil and Regalia effectively controlled *Pythium* damping-off in lettuce.

Mosquito midguts and the trichomycete fungi that don't live there

C. E. BEARD (1)

(1) Clemson University, Clemson, SC, U.S.A.

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Trichomycete fungi live symbiotically in the guts of many aquatic insects. They are especially common in larval Diptera such as chironomids, black flies, and mosquitoes. Two host habitats are used by these fungi: the midgut and hindgut. Each habitat has characteristic groups of trichomycetes. *Smittium* spp. are common in the hindguts of all three insect groups. Chironomids host *Stachylina* spp. in their midguts and black flies are the only known suitable midgut habitats for *Harpella* spp. Mosquitoes have never been documented to host trichomycetes in their midguts. We asked why trichomycetes have not been found in the mosquito midgut even though they are common in the hindgut. To test the suitability of mosquito midguts to fungi, we exposed them to unculturable *Harpella melusinae* trichospores (asexual) obtained from wild larval black flies. The spores were ingested by *Aedes albopictus* mosquitoes and exhibited growth. They tended to colonize larval mosquitoes *Aedes albopictus* more readily than *Culex quinquefasciatus* or *Aedes aegypti*. We suspect that environmental factors might be more important than physiology in explaining the lack of midgut trichomycetes. Mosquitoes tend to inhabit still waters, while black flies are found exclusively in running water.

Molecular and genetic basis guiding the establishment of a mutualistic relationship between *Epichloë festucae* and perennial ryegrass

S. BEC (1), J. Liu (2), C. Scharld (2)

(1) University of Kentucky, Department of Plant Pathology, Lexington, KY, U.S.A.; (2) University of Kentucky, Lexington, KY, U.S.A.

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The relationship between *Epichloë festucae* and *Lolium perenne* is a model system for studying mutualism between endophytes and cool season grasses. During the reproductive phase of growth, the fungus exhibits a dual nature: benign endophytic growth and seed transmission, or forming external stromata and suppressing seed production. We have identified a number of genes encoding small secreted proteins (*ssp*) that are highly up-regulated in benign infected inflorescences. The preliminary data suggest that two genes, *sspB* and *sspX*, may play a role in host specificity. Although *E. festucae* is reported to be compatible with *L. perenne* and *L. pratense*, strains generated from a series of crosses and backcrosses showed a range of compatibility with *L. perenne*, but were consistently compatible with *L. pratense*. One such strain, E2368, had low compatibility with *L. perenne*, whereas a subculture (variant E4844) showed improved compatibility with this host. Genomes of E4844 and E2368 were compared, revealing the loss of subtelomeric region containing *sspB* and *sspX* in E4844. The possible roles of *sspB* and *sspX*, and of other genomic changes in the variant, are under investigation. The set of progeny strains has been screened for the establishment of stable mutualistic symbioses with perennial ryegrass, and is slated for Illumina genome sequencing and subsequent bulk segregant analysis to identify SNP markers correlated with host-specificity phenotypes.

Host specificity of fungal phyllosphere communities of tropical trees

D. BEGEROW (1), T. Wubet (2)

(1) Ruhr-Universität Bochum, Bochum, Germany; (2) Helmholtz Centre for Environmental Research GmbH (UFZ), Halle, Germany

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Tropical microorganisms in the phyllosphere such as epiphyllous yeast and endophytic filamentous fungi contribute substantially to global organismic