

been to collect fruiting bodies of fungi associated with cankers and isolate fungi and oomycetes from diseased tissues. The putative pathogens have been identified based on DNA sequence homology and standard morphology, and species of interest have been included in inoculation trials on one to three species of alder in replicated plots in two or more field locations of pathogen origin. The pathogens that have demonstrated significant virulence include *Valsa melanodiscus*, *Melanconis alni*, and *M. stilbostoma*. Pathogens of trees generally cause disease on stressed host plants and therefore inoculation trials often do not adequately reflect the virulence of a pathogen. Our index of putative pathogens on alder will include listing of other fungi in the inoculation trials as well as numerous wood decay fungi.

#### **Phosphonate, carboxylic acid amide, and benzamide treatments for pre- and postharvest management of citrus brown rot**

J. E. Adaskaveg (1), H. FORSTER (1), M. Vilchez (1)

(1) University of California, Riverside, CA, U.S.A.

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Brown rot of citrus fruit caused by species of *Phytophthora* is common in California during the winter season when high rainfall may occur. Copper and phosphonates are the only effective registered preharvest treatments. Recently, phosphonates were classified as exempt from tolerance in the U.S., we supported postharvest registration of phosphonates, and evaluated the efficacy of new pre- and postharvest treatments. In preharvest studies, incidence of brown rot of fruit harvested 2 weeks after application (3330 L/ha) and inoculated with zoospores of *P. citrophthora* was 44.2% for fluopicolide (37 mg/L), 2.0% for mandipropamid (38 mg/L), 6.8% for potassium phosphite (620 mg/L), 5.6% for copper-lime (670 mg mce/L), and 77.0% for the control. Incidences after 6 weeks were 75.9%, 8.3%, 62.5%, 27.5%, and 95.9% respectively. In postharvest studies, fruit were dip-treated with aqueous solutions and then inoculated. Brown rot incidence was 0.7% for fluopicolide (300 mg/L), 0% for mandipropamid (310 mg/L), 1.3% for potassium phosphite (1242 mg/L), and 85.5% for the control. When fruit were first inoculated and treated after 12 h, only potassium phosphite was effective and incidence of decay was reduced to 5.0% as compared to the control with 82.3%. International tolerances are being established for phosphonates. Fluopicolide and mandipropamid are proposed for integrated pre- and postharvest use on citrus to ensure resistance management and long-term usage of these compounds.

#### **Eight new viruses identified in bioenergy switchgrass**

B. O. AGINDOTAN (1), L. L. Domier (1), M. E. Gray (1), C. A. Bradley (1)

(1) University of Illinois, Urbana, IL, U.S.A.

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*Panicum virgatum* (switchgrass), a potential bioenergy crop, was investigated for virus infections that could reduce its biomass yield. In addition to Barley yellow dwarf viruses (BYDVs), *Sugarcane mosaic virus* (SCMV), *Panicum mosaic virus* (PMV), and recently, *Switchgrass mosaic virus* (SwMV), were reported to infect the crop. To determine if other RNA viruses infect switchgrass, five young leaves were collected from 18 switchgrass varieties with different foliar symptoms ranging from necrotic spots to mosaic from a five-year old switchgrass plot. Pieces (about 3-cm) were cut from the tips of symptomatic leaves and pooled. To enrich for viruses, virus particles were partially purified from 5 g of the ground pooled leaf tips. Total RNA extracted from the preparation was treated with DNase I, reverse transcribed, and high-throughput sequenced. Eight new RNA viruses and one unexpected DNA virus were identified. The replicase or coat protein amino acid sequences of the eight viruses were 30% to 52% identical to the most closely related polerovirus, tenuivirus, ctyorhabdovirus, ourmavirus, foveavirus, fijivirus, cripavirus or mastrevirus in GenBank. The viruses were detected in 5 to 18 of the original 18 varieties of switchgrass and are being further characterized.

#### **Myxomycetes on *Orbygnia* sp. (Arecaceae) from the Brazilian Cerrado**

L. A. N. Agra (1), J. C. DIANESE (1)

(1) Departamento de Fitopatologia, Universidade de Brasília, Brasília, Brazil

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An intensive survey of the Cerrado Myxomycetes is on the way, but in an early stage. However about 70 species has already been described for this entire Biome. On host species belonging in Arecaceae these organisms are commonly found. However, little is known about the Myxomycetes on a common *Orbygnia* species present on dense Cerrado areas close to dry forests. A first sample indicated the presence of four different species of myxomycetes, three more abundant belonging in the *Physarales* and one in *Trichiales*. However, the most notorious event was the presence of *Badhamia viridescens*, for the first time found in the Neotropica.

#### **Glancing at host adaptation in *Ralstonia solanacearum* through comparative genomics of highly host-adapted lineages**

F. AILLOU (1), G. Cellier (2), D. Roche (3), C. Allen (4), P. Prior (5)

(1) CIRAD, Saint-Pierre, France; (2) ANSES, Saint-Pierre, France; (3) Genoscope, Evry, France; (4) University of Wisconsin-Madison, Madison, WI, U.S.A.; (5) INRA, Saint-Pierre, France

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*Ralstonia solanacearum* is a vascular soil-born plant pathogen with an unusually broad host range. This globally distributed, economically destructive organism has thousands of distinct lineages within a heterogeneous and taxonomically disputed species complex. Some of those lineages can be assigned to ecotypes that include highly host-adapted strains such as the banana Moko disease-causing strains, the cold-tolerant potato brown rot strains (R3bv2) and the recently emerged NPB strains (Not Pathogenic to Banana). The polyphyletic nature of the Moko ecotype and the unexpected closeness of some its lineages to the paraphyletic brown-rot and NPB ecotypes make those highly adapted strains a robust model for study of host adaptation and speciation in general. Genomes of 10 new strains were produced to complement the 12 publicly available ones. Using a panel of bioinformatics methods, we looked for genetic or evolutionary features that discriminate between ecotypes. There were relatively few divergent features. Those related to known virulence factors were further analysed for functional clues about host adaptation and ecotype emergence mechanisms. These analyses yield no clear signal, suggesting that the large biological differences between these closely related strains result from differences in gene expression rather than from differences in gene content. Transcriptomic analyses of these strains during host infection are underway to test this hypothesis.

#### **Identification of resistance to *Rhizoctonia* root rot in mutant and wild barley (*Hordeum vulgare* subsp. *spontaneum*)**

O. O. AJAYI (1), T. C. Paulitz (2), K. G. Campbell (2), K. M. Murphy (1), S. E. Ullrich (1)

(1) Washington State University, Pullman, WA, U.S.A.; (2) USDA ARS, Pullman, WA, U.S.A.

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Direct seeding cereal crops into non-tilled fields is a practice that is gaining importance in the Pacific Northwest region of the United States. Unfortunately, *Rhizoctonia* root rot and bare-patch caused by *Rhizoctonia solani* AG-8 limits the yield of direct-seeded cereals in this region. No resistant germplasm is available, and other available control methods have not been effective in preventing yield losses. To identify potential sources of resistance, M<sub>2</sub> populations of two barley lines treated with sodium azide and wild barley (*Hordeum vulgare* subsp. *spontaneum*) accessions from the Wild Barley Diversity Collection (WBDC) were evaluated in controlled environments. Ten putative M<sub>3</sub> mutants were identified and reciprocal crosses to their wild-type progenitors were carried out for genetic analysis. The findings that not all BC<sub>1</sub>F<sub>1</sub> plants evaluated were susceptible suggest that resistance to *Rhizoctonia* root rot in the mutant barley is inherited as a dominant trait. Observed segregation ratios of progeny of BC<sub>1</sub>F<sub>1</sub> plants are currently being tested against several gene models of inheritance to determine the number of genes conferring resistance. Of 317 wild barley accessions that were screened for resistance, six accessions showed potential as gene donors for *R. solani* resistance with one accession, WBDC 021, showing the greatest potential by displaying moderate resistance. Research is underway to test WBDC 021 for its reaction to *R. solani* under field conditions.

#### **Survey for Grapevine red blotch-associated virus in the Foundation Plant Services vineyards at the University of California-Davis**

M. Al Rwahnih (1), V. Klaassen (1), C. Islas (1), K. Umeda (1), D. GOLINO (1), A. Rowhani (1)

(1) University of California-Davis, Davis, CA, U.S.A.

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In 2008, a new disease characterized by red blotches along leaf margins and red veins under the leaf surface was observed in red grape varieties in a few vineyards in Napa Valley, CA. A new DNA virus, *Grapevine red blotch-associated virus* (GRBaV) was identified in these vines. Given the apparent widespread incidence of GRBaV and the unknown nature of its origin and mode of transmission, we decided to screen a majority of the planting stock at Foundation Plant Services for GRBaV. This planting stock included all the vines in our newly established Russell Ranch vineyard in addition to more than 1,600 vines from our Classic Foundation vineyard. Comparison of the real-time PCR test results with those from conventional PCR for the 1,102 Russell Ranch vines verified that our new assay was highly sensitive and specific for GRBaV and indicated that all Russell Ranch vines were negative for GRBaV. More than 1,600 vines from the classic Foundation Vineyard are