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Characterization of two new ...
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Against these isolates, the background polygenic resistance was inadequate to prevent severe disease. These results indicate that sole reliance upon this single dominant gene-based resistance is not sustainable.

Fusarium stem rot of vanilla in North Sulawesi. E. C. Y. LIEW (1), F. Rondouwu (2), A. Pinaria (2), D. T. Sembel (2), B. A. Summerell (3), and L. W. Burgess (1). (1) Faculty of Agriculture, Food & Natural Resources, The University of Sydney, NSW 2006, Australia; (2) Department of Pests & Diseases, Faculty of Agriculture, Sam Ratulangi University, North Sulawesi, Indonesia; (3) Royal Botanic Gardens, Sydney, NSW 2000, Australia. Phytopathology 94:S61. Publication no. P-2004-0409-AMA.

Vanilla is an important and popular cash crop offering high economic returns to smallholder farmers in North Sulawesi. However, the production of vanilla in this region is greatly constrained by *Fusarium* stem rot. Although the disease is most severe on the stem of the vanilla vine, it is also found on the leaves and roots. On the stem internode, small brown water-soaked spots or lesions initially appear, which enlarge and become necrotic, eventually girdling and shriveling up the stem. The lesion often expands to adjacent internodes and develops along the vine. In a recent disease survey of vanilla farms on 12 sites throughout North Sulawesi, the disease was detected at incidences of 20-78% on each site. Several *Fusarium* species were isolated from various plant parts of diseased vines. Only *F. oxysporum* was shown to be pathogenic in greenhouse experiments. *Colletotrichum* was also isolated from diseased tissue but at a lower frequency.

Ceratocystis associated with clove decline in North Sulawesi. E. C. Y. LIEW (1), B. Assa (2), M. J. Wingfield (3), D. T. Sembel (2), B. A. Summerell (4), and L. W. Burgess (1). (1) Faculty of Agriculture, Food & Natural Resources, The University of Sydney, NSW 2006, Australia; (2) Department of Pests & Diseases, Faculty of Agriculture, Sam Ratulangi University, North Sulawesi, Indonesia; (3) Forestry & Agricultural Biotechnology Institute (FABI), University of Pretoria, Republic of South Africa; (4) Royal Botanic Gardens, Sydney, NSW 2000, Australia. Phytopathology 94:S61. Publication no. P-2004-0410-AMA.

Clove decline is the most serious of clove diseases in North Sulawesi, Indonesia. Despite its devastating impact on one of the most important cash crops in this region, the aetiology of this disease has yet been established until recently. Infected trees show symptoms of wilt and defoliation, which often lead to the death of whole trees. In a recent disease survey of 17 sites and more than 100 farms throughout North Sulawesi, clove decline was observed on all sites, with disease incidence of greater than 90%. A fungus, closely resembling the wilt pathogen, *Ceratocystis fimbriata*, was consistently isolated from wood tissues of infected trees. This fungus appears to be associated with a wood-boring beetle, *Hexamitodera semivelutina*. The larvae bore into trees forming extensive galleries within the trunks. All isolates of this fungus were obtained from stained wood tissue adjacent to these wood-borer galleries. Multiple pathogenicity tests confirmed the pathogenicity of this fungus on both seedlings and mature clove trees. Molecular studies are being conducted on these isolates to confirm their identity.

Expression of Soybean mosaic virus (SMV) HC-Pro in transgenic soybean plants enhances SMV symptoms. H. S. LIM (1), T. S. Ko (2), L. L. Domier (1,3), H. G. Kim (4), and G. L. Hartman (1,3). (1) University of Illinois Urbana, IL; (2) University of Minnesota, St. Paul, MN; (3) USDA-ARS Urbana, IL; (4) Chungnam National University, Daejeon, Korea. Phytopathology 94:S61. Publication no. P-2004-0411-AMA.

Transgenic soybean lines expressing the helper component-protease (HC-Pro) coding region of SMV G5 were produced by *Agrobacterium*-mediated transformation of immature soybean cotyledons. Homozygous transgenic lines were recovered with single copy insertions that expressed SMV HC-Pro mRNA at levels ranging from 5 to 34% of that found in SMV-infected plants. Ten days after inoculation with SMV, all HC-Pro transgenic lines had symptoms more severe than *uidA* transgenic plants. Symptom severity was related to HC-Pro expression levels in the transgenic lines, but SMV RNA titers did not differ among the lines. Similar levels of small interfering RNAs were detected in SMV-infected HC-Pro and *uidA* transgenic plants. Starting at 20 days after inoculation, new leaves of the transgenic line that expressed the highest level of HC-Pro mRNA no longer showed symptoms, and SMV RNA titers were drastically reduced. The titers of coat-protein and HC-Pro coding regions declined at similar rates suggesting that the HC-Pro coding region was not preferentially targeted. In soybean lines that expressed lower levels of HC-Pro, symptoms remained severe at all sampling dates and no reductions in SMV RNA titers were observed. These results show that HC-Pro enhances SMV symptom severity in transgenic plants and that even potyvirus HC-Pro transgenes are susceptible to virus-induced gene silencing when expressed at high levels.

Characterization of two new strains of grapevine rupestris stem pitting associated virus. M. F. LIMA (1), R. Alkowni (2), D. Golino (1), J. K. Uyemoto (1), and A. Rowhani (1). (1) Department of Plant Pathology, University of California, Davis, CA; (2) Arab American University, Jenin, Palestine. Phytopathology 94:S61. Publication no. P-2004-0412-AMA.

Grapevine rupestris stem pitting associated virus (GRSPaV) is graft-transmissible and associated with rupestris stem pitting disorder. GRSPaV is detected by indexing on *Vitis rupestris* cv. St. George, in which it induces pittings below the graft union. GRSPaV belongs to the genus *Foveavirus* in the family *Flexiviridae*. In field surveys in California, two new strains of GRSPaV from a *V. vinifera* cv. Syrah (SY-RSP) and cv. Pinot Noir (PN-RSP) were identified. CDNA libraries were made from dsRNA, using random primers. Selected cDNA clones were sequenced and specific primers were designed and used in RT-PCR to fill the gaps. Sequences were compared with the published sequences of GRSPaV. Both isolates showed similar genome organization, comprising six ORFs. Nucleotide and amino acid analysis showed 76-89% and 85-96% (SY-RSP), and 79-89% and 83-93% (PN-RSP), respectively, to published isolate. Specific detection primers for both isolates were designed for a survey to determine their rate of spread in the field.

Genotyping and assessing genetic diversity in the PD strains of *Xylella fastidiosa* by simple sequence repeat (SSR) DNA markers. H. LIN (1), M. Francis (2), S. Barros (2), R. Hu (2), E. L. Civerolo (1), and A. M. Walker (2). (1) ARS-USDA, 9611 S. Riverbend Avenue, Parlier, CA 93648; (2) Department of Viticulture & Enology, University of California, Davis, CA 95616. Phytopathology 94:S61. Publication no. P-2004-0413-AMA.

The insect-transmitted bacterium, *Xylella fastidiosa* (Xf), causes diseases in many economically important plants, including Pierce's disease in grape. Understanding the genetic diversity and population structure of the pathogen are critical steps in managing disease outbreaks. With the recently available genomic sequencing of four Xf strains, Pierce's disease of grapevine (PD), citrus variegated chlorosis (CVC), almond leaf scorch (ALS), and oleander leaf scorch (OLS), identification of repeated sequence loci is facilitated. A genome wide search was performed for identifying Simple Sequence Repeat (SSR) motifs among the all four strain sequence databases, and 60 SSR loci were selected for primer design. These simple repeat motifs consist of 2-8 bp repeat units and were distributed across the whole genome. We evaluated these SSR primers with 21 Xf isolates collected from Napa Valley, San Joaquin Valley and southern California vineyards. Seventy percent of these SSR primers were highly polymorphic and distinguished genetically close strains. This PCR-based SSR marker is a precise and repeatable marker system. The power of this polymorphic detection system makes it a useful tool for population structure, genetic diversity and epidemiological risk assessment analyses.

Formulating locally effective integrated management packages for tomato bacterial wilt. C.-H. Lin and J.-F. WANG. AVRDC-The World Vegetable Center, Tainan, Taiwan. Phytopathology 94:S61. Publication no. P-2004-0414-AMA.

Bacterial wilt, caused by *Ralstonia solanacearum*, is an endemic and important tomato disease worldwide. Efficacy of reported control methods, including tolerant cultivars, resistant rootstocks, and soil amendments, could be variable over strains, locations or soils. A case study was conducted on formulating effective management packages for a production area in Taiwan. First 52 local strains were profiled based on their aggressiveness. Representative strains were selected for evaluating commercial tolerant cultivars and resistant rootstocks. Eggplant and tomato varieties, EG203 (mean percent wilting 0%) and Hawaii7996 (mean percent wilting 21%), were selected as potential rootstocks. All tolerant cultivars tested were susceptible. Local soil samples were collected to evaluate the efficacy of a soil amendment consisting urea (825 kg/ha) and slaked lime (3993 kg/ha). The amendment could reduce the pathogen density from 7.0 to 4.7 log (cfu/g dry soil) and the disease incidence from 60% to 3% at 28°C in the greenhouse. A field trial was conducted in fall 2003 consisting of 6 treatments combining the soil amendment and 3 planting materials (ASVEG10, ASVEG10 grafted on EG203 or on Hawaii7996). At 105 days after transplanting, about 90% of ASVEG10 was wilted, while treatments with eggplant rootstock showed only 1 to 3% wilting. The soil amendment effect was only observed on the treatments with tomato rootstock, which provided additional 29% reduction of incidence. The results show that applying a pre-selection scheme could ensure the success of local integrated management package.

Rice bacterial blight resistance genes *Xa7*, *xa5*, and *Xa4* confer resistance during all developmental stages. K. M. LINHOLM (1,2), E. Garcia (2), C. M. Vera Cruz (2), and J. E. Leach (1). (1) Kansas State University, Manhattan, KS; (2) International Rice Research Institute, Manila, Philippines. Phytopathology 94:S61. Publication no. P-2004-0415-AMA.