2012 Pacific Division Meeting Abstracts

Abstracts presented at the APS Pacific Division meeting in Sacramento, California, June 27–29, 2012. The abstracts are arranged alphabetically by the first author's name. Recommended format for citing division meeting abstracts, using the first abstract below as an example, is as follows: Aegerter, B., Miyao, E., Turini, T., Stoddard, S., and Le Strange, M. 2012. Control of tomato powdery mildew (*Leveillula taurica*) and impacts on fruit yield and quality in central California. (Abstr.) *Phytopathology* 102(Suppl. 6):S6.7. <http://dx.doi.org/10.1094/PHYTO-102-11-S6.7>.

Control of tomato powdery mildew (*Leveillula taurica*) and impacts on fruit yield and quality in central California

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Powdery mildew (*Leveillula taurica*), known in California since 1978, became more severe on tomatoes in California's Central Valley during the 2007 through 2011 seasons. Sporulation of the pathogen is now more abundant, symptoms and damage more severe, and outbreaks now progress faster than prior to 2007. Fourteen uniform field trials evaluating chemical control programs were conducted over a three-year period to identify economical and effective control programs, but also to better understand the impact of this aggressive powdery mildew on yield and fruit quality in processing tomatoes. Of the three trial years, disease pressure was highest in 2009; and lighter in the two subsequent years. Data will be presented from the eight trials where mildew was present. Disease severity and foliar necrosis at harvest were always significantly reduced by the fungicide programs. Programs which emphasized early applications (6 weeks post-transplanting through mid-season) were more effective in reducing necrosis than those programs which relied more heavily on late-season applications. Sulfur dust was found to be the most effective, although other materials provided a benefit. Mildew reduced fruit yield by 52% in one trial where disease pressure was highest; in all other trials where disease pressure was either moderate or appeared late, there was no yield effect. Soluble solids were decreased by an average of 0.5° Brix in non-treated plots compared to sulfur-treated plots; the greatest reduction was 1.4° Brix in one trial. There was a significant correlation between AUDPC and reduced soluble solids. Increasing disease only one month prior to harvest may affect soluble solids without affecting yield, while earlier high disease pressure may significantly reduce both yield and soluble solids.

Gibberellic acid-3 mimics the symptoms of twister disease of onion

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Nueva Ecija is the leading province in onion production in the Philippines. However, onion production is marked by fluctuations because of pests and diseases. Onion anthracnose-twister disease, which involves fungal pathogens such as *Colletotrichum gloeosporioides* and *Gibberella moniliformis*, is the most destructive disease of onion in the country and is often associated with poor bulb development with distinct twisting, and curling of leaves and neck elongation. This study was conducted to determine if gibberellic acid-3 (GA3) is associated with neck elongation and twisting in onion. Seedlings (45-day-old) were transplanted in sterilized soilless mix, and treated 24 h later with GA3 at concentrations: 0 (control), 0.1, 1.0, 10.0, 100.0 and 1000.0 µg/plant diluted in 20 µL of solution to the neck of onion seedlings. All seedlings were maintained inside the greenhouse with temperature within 27–30°C. Prior to GA3 application and at 4, 8, 12, 24, 48, 72, and 96 h after application, seedlings were measured for the length of the neck from cotyledon axil to the base of the apical bud. Two weeks after application, neck elongation and twisting were observed in plants treated with 100 µg and 1000 µg of GA3. Similarly, the longest leaves and neck were also observed in the same treatments. Cells were longer and wider in tissues treated with GA3 than in untreated tissues. Symptoms in plants treated with GA3 mimicked those exhibited by onion plants affected by twister disease under field conditions. Thus, gibberellic acid may be associated with twister disease in onion.

A shift in species dominance of FHB fungi in southern Idaho

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Cereal grain production in southern Idaho is being threatened by *Fusarium* head blight (FHB). Since 1991, maize acreage has more than doubled in southern Idaho, providing excellent substrate for the increasing the populations of pathogenic fungi capable of causing FHB. During the 2011 growing season, FHB was observed under field conditions and deoxynivalenol toxins were detected above 5 ppm at local grain elevators. FHB symptomatic wheat heads from five locations and grain samples from elevators across southern Idaho were collected in the summer of 2011. Fungi contaminating the grains were cultured and identified to species using Qiagen DNeasy kits and species-specific primer pairs for *Fusarium graminearum* and *F. culmorum*. Of the more than 700 samples collected, 64.7% were identified as *F. graminearum* and only 12.1% were identified as *F. culmorum* with the remaining 23.2% attributed to various other *Fusarium* species. The percentage of each species of *Fusarium* from sample sites differed, but *F. graminearum* was the dominant species at all but one location. A previous study in the mid-1980s had identified *F. culmorum* as responsible for 76.2% of all infections and *F. graminearum* for 2.3% of all infections, with 21.5% of all infection attributed to various other *Fusarium* species. The switch in dominance of *Fusarium* species in southern Idaho is likely attributed to the increases in maize acreage in the region recorded over the past two decades. Limited crop rotation and poor crop management practices have the potential to severely impact the presence of FHB and the future of cereal grain production in southern Idaho.

The abstracts are published as submitted. They were formatted but not edited at the APS headquarters office.

Effectiveness of a Swiss needle cast disease management program in controlling disease development in U.S. Pacific Northwest Douglas-fir Christmas tree plantations

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Swiss needle cast (SNC), caused by *Phaeocryptopus gaeumannii*, has been a major problem on Douglas-fir Christmas trees in the U.S. Pacific Northwest. A survey of Christmas tree plantations in 1981 found that about 90% of the plantations and 84% of trees inspected had SNC. Approximately 11% of the infected trees were unmarketable, because they only retained a single year's worth of needles. This equated to a \$3.4 million loss to growers. In addition, the presence of infected needles on marketable trees was shown to increase the rates of moisture and needle loss once the trees were harvested, thus reducing the postharvest quality of trees available to consumers. As a result, in the early 80's a disease management program was developed that was based on monitoring trees in plantations for the presence of infected needles and then making one or two applications of a chlorothalonil-based fungicide during shoot elongation if the disease was present during the 3 to 4-year period prior to harvest. In the 20-year-long period between 1987 and 2007, yearly surveys of Douglas-fir Christmas tree plantations in Oregon were done to determine the effectiveness of this SNC disease management program. This survey found that only 37.7% of the 465 plantations examined had any SNC-diseased trees. The overall incidence of infected trees during this time was 13%, compared to 84% in 1981. These results indicate that the disease management program established in the early 80's has effectively reduced the incidence and severity of SNC on Douglas-fir Christmas trees in the PNW. Although chlorothalonil-based fungicides have consistently been the most effective materials in controlling this disease, recent studies have shown that trifloxystrobin, and caprylic acid also have the potential to provide effective control of SNC.

Quantitative molecular assays for investigating virus-host and virus-virus interactions using negative-stranded RNA viruses as a model system

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Tospoviruses (*Tospovirus*; *Bunyaviridae*) affect crop productivity in numerous field and horticultural crops worldwide. Sensitive molecular assays were developed to investigate virus-host and virus-virus interactions in planta using *Iris yellow spot virus* (IYSV) and *Tomato spotted wilt virus* (TSWV) as model tospoviruses, with *Datura stramonium* as the model host. The distribution and accumulation of the nucleocapsid (N) gene of each virus were determined in individually inoculated *D. stramonium*. To investigate the interactions between the two viruses in the same host, the viruses were simultaneously inoculated and the distribution and levels of each virus determined. Quantitative real-time PCR showed that TSWV was capable of suppressing the host defense system as it was detected in all the inoculated as well as in non-inoculated leaves. In contrast, the host restricted IYSV only to inoculated leaves; no IYSV N gene was detected in the non-inoculated leaves. There was no change in terms of distribution or titer levels of TSWV in dually infected plants. However, in the presence of TSWV, IYSV managed to overcome the host defense system and spread to some non-inoculated leaves. In addition, IYSV titers increased more than 1000-fold in inoculated leaves in the presence of TSWV. These results suggest a unilateral synergistic interaction between IYSV and TSWV, where only the former benefits. This interaction could have economic and epidemiological impact by significantly reducing yield and increasing vector transmission efficiency. The assays and the model system developed would be useful in studying virus-host interactions at the molecular level.

Modeling uncertainty in grapevine powdery mildew

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Erysiphe necator (Schwein.) is an important pathogen that affects cultivated grapevines around the world. Several epidemiological models have been developed to predict disease onset and disease intensity based on weather conditions, most notably the Gubler-Thomas (GT) model. The GT model uses hourly temperature data to predict disease development based on duration of optimum and lethal conditions for the pathogen, and produces advisory forecasts for disease management. However, scattered weather stations and microclimates lead to uncertainty in hourly weather data. We used fuzzy arithmetic to modify the GT model to account for uncertainty in weather data. The fuzzy GT model maintained the same disease control as the original GT

model and comparatively reduced the number of fungicide applications in a location with a relatively distant weather station. While the fuzzy GT model helps to adapt to weather data uncertainty, there is still uncertainty in the basic biology of *E. necator*. Relatively little is known about the effects of consecutive exposures to abiotic stress in fungi. To address this, detached leaf co-culture assays of three-day-old single colonies of *E. necator* were exposed to one, two or three consecutive days of heat stress. While there was a consistent decrease in colony growth after a single heating event, each subsequent heating event had less effect on colony growth and delay in sporulation date. Colonies appeared to adapt to heat stress rapidly, with no significant additional effects by the third treatment. Colonies also appeared to recover from consecutive heat stress, with no significant differences in colony diameter between treatments by eleven days after inoculation. These data suggest that *E. necator* is able to rapidly adapt to heat stress.

Scientific method and *habeus corpus*: Assessing the significance and management of seedborne *Verticillium* in spinach

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Seedborne *Verticillium dahliae* directly impacts the international seed industry because of phytosanitary regulations. *V. dahliae* has been demonstrated to be prevalent in commercial spinach seed lots from all seed production regions in the world, and is readily seed transmitted in spinach. Although symptoms of *Verticillium* wilt of spinach have not been observed in vegetative crops, symptoms are evident in spinach seed crops after the onset of bolting (initiation of reproductive growth). Prevalence of the pathogen on spinach seed has raised concern that planting infested spinach seed lots at dense populations (up to 9 million seed/ha) in baby leaf production may infest soils and provide inoculum for susceptible crops rotated with spinach. To address these concerns, short term research efforts have focused on identifying conventional and organic seed treatments that mitigate the potential role of spinach seed in infesting soils with *V. dahliae* by eradicating the pathogen from seed or reducing the rate of seed transmission and soil infestation. Although none of the highly effective treatments identified was registered for use on spinach seed in 2011, seed treatment registrations are in progress in the U.S.A. Longer-term research efforts are investigating the complexity of conditions that influence the significance of infested spinach seed relative to other sources of inoculum, including soil pH, soil microbial activity (affected by fumigation), spinach germplasm resistance, scientifically-based thresholds for soilborne vs. seedborne inoculum, and the VCG and host range of *V. dahliae* isolates from spinach seed. Complicating these efforts is the lack of a standardized, internationally accepted spinach seed health assay for *V. dahliae* that accommodates the necessity of testing treated and non-treated seed. Establishment of an assay is being addressed in collaboration with the International Seed Health Initiative. Scientific method will help avoid violation of the *habeus corpus* of this highly controversial, seedborne pathogen.

Population biology of *Verticillium dahliae* associated with potato and mint: Implications for *Verticillium* wilt management

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Verticillium wilt, caused by the fungus *Verticillium dahliae*, is an economically important disease of many crops. The wide host range and long persistence of the pathogen in field soils makes crop rotation and control of *Verticillium* wilt difficult. Potato and mint, two economically important hosts of *V. dahliae*, are grown in the Columbia Basin of the U.S. Pacific Northwest on relatively large scales and can be rotated in the same fields. Despite its wide host range, *V. dahliae* isolates from potato and mint in North America typically belong to different vegetative compatibility groups (VCGs) and are often more aggressive on their respective hosts. Isolates of *V. dahliae* from potato and mint belong to VCG4A and VCG2B, respectively, and are genetically distinct, indicating that these two hosts are susceptible to different populations of the fungus. Genetic differentiation between isolates from potato and mint may be due to the occurrence of host-adapted haplotypes belonging to different VCGs and the prevalence of a single mating-type (*MATI-2*) leading to clonal reproduction. Perennial crops, such as mint, may also contribute to the increase and persistence of host-adapted strains after each cropping season. Vegetative propagation of potato and mint, and the practice of increasing planting materials in the field, may aid in the dispersal of *V. dahliae* via propagative materials. Tare dirt associated with certified seed lots of potato can contain *V. dahliae* at levels well above the inoculum threshold required to incite *Verticillium* wilt. Infested dirt associated with seed tubers can contribute to inoculum levels of *V. dahliae* in field soils and greater plant infection, particularly when levels of inoculum in field soils are low. The transport and introduction of infested dirt with seed tubers is

especially important considering the widespread use of expensive fumigants to reduce *V. dahliae* levels in fields prior to planting.

Genome sequences of two field isolates of *Bean common mosaic virus*

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In 2011, two isolates of *Bean common mosaic virus* (BCMV) were collected in the Willamette Valley of Oregon from bean plants exhibiting mild mosaic and stunting symptoms. Both isolates appeared to be seedborne in the line L192, a brown-seeded dry bean with determinant growth habit. Based on a biological characterization on twelve bean differential lines, these two BCMV isolates were classified as belonging to the non-necrotic pathotype VII, similar to a control isolate US10. Both isolates had B-serotype but exhibited serology distinct from the isolate US10 (pathotype VII). Both isolates were subjected to cDNA cloning and sequencing and were found to be 98% identical to the BCMV isolate RU1 originally intercepted in the mid-1980s in a dry bean entry imported from Russia. However, the original RU1 isolate was classified as a non-necrotic strain belonging to pathotype VI. It is possible that the weekly expressed, attenuated symptoms are responsible for the spread of these isolates in beans. This is the first report of a BCMV RU1-like strain isolated from field plants in the U.S.

Fitness and competitiveness of *Penicillium* spp. isolates with reduced sensitivity to fludioxonil and pyrimethanil

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Isolates of *Penicillium expansum* (Pe) and *P. digitatum* (Pd) resistant to the postharvest fungicides fludioxonil (EC50 values 0.1 to >10 mg/L; baseline: <0.02 mg/L) and/or pyrimethanil (EC50 values 2 to >10 mg/L; baseline: <0.7 mg/L) were selected in packinghouses or in the laboratory from natural populations of each species. Isolates were demonstrated to be pathogenic on their respective hosts and were evaluated for their fitness based on growth rate and conidial production as well as on competitiveness in co-inoculations with sensitive wild-type isolates. Isolates of both species resistant to pyrimethanil were mostly similar in growth and sporulation rate to the wild type sensitive isolates, whereas isolates resistant to fludioxonil displayed a range of growth and sporulation rates. Isolates of both species highly resistant or isolates of Pd moderately resistant to fludioxonil were not recovered from decaying fruit after co-inoculation with sensitive isolates. Isolates of both species highly resistant to pyrimethanil and isolates of Pe moderately resistant to both fungicides, however, were recovered at a high frequency. Thus, fitness differences occur for different modes of action among resistant isolates of the two species. Fitness penalties exist for fludioxonil resistance but are less apparent for pyrimethanil resistance or for moderate double resistance. These results may reflect qualitative and quantitative types of resistance between the two fungicides.

Colonization of sclerotia of *Sclerotinia sclerotiorum* by a fungivorous nematode

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Some members of the genus *Aphelenchoides* are known to feed on hyphae of both beneficial and plant pathogenic fungi. However, no information is available to date about their potential for biological control of the plant pathogen *Sclerotinia sclerotiorum*. We tested colonization of sclerotia of *S. sclerotiorum* by a known fungivorous *Aphelenchoides* sp. (Y. S. Bae & G. R. Knudsen, 2001, Phytopathology 91:301-306). Nematodes (20 or 50 individuals, mixed males and females) were inoculated into 5-day-old fungal cultures growing on potato dextrose agar that had been inoculated with sclerotia, mycelium, or alginate-formulated pellets of *S. sclerotiorum*, or with mycelium of the biocontrol agent *Trichoderma harzianum* (ThzID1), or with mycelium of ThzID1 plus sclerotia of *S. sclerotiorum*. Nematodes were extracted using the Baerman funnel method and counted after 1, 2, 4, 6, and 8 weeks. Sclerotia that developed in plates containing *S. sclerotiorum* were dissected and observed microscopically, and nematodes found colonizing them were counted. The experiment was analyzed as a pooled complete randomized design with repeated measures. Nematodes fed on hyphae of both fungi and also on sclerotia. Nematode populations initially increased in all treatments ($P < 0.0001$), then decreased again by about week 10. Highest numbers of nematodes were observed after two weeks on mycelium of *S. sclerotiorum* ($P < 0.0001$), and lowest numbers on ThzID1 cultures after 8 weeks. By week 6, nematodes were observed colonizing sclerotia (300–

600 nematodes per sclerotium). Our results suggest that fungivorous nematodes may potentially play a role in biological control of *S. sclerotiorum* in the field. In a subsequent experiment, preliminary results indicated that sclerotia were colonized by *Aphelenchoides* sp. in both sterile and nonsterile soil, and also that apothecial production was inhibited when nematodes were present.

Managing *Verticillium* wilt in strawberries with and without fumigation

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The adoption of pre-plant fumigation in the 1960s largely eliminated *Verticillium* wilt as a concern to the strawberry industry in California. However, the risk of damage from *Verticillium* wilt has increased recently for two reasons: 1) reduced access to methyl bromide means more growers rely on less effective fumigants and 2) fumigants are often now delivered to individual beds via drip lines, which fails to fully treat the soil. As a consequence of these changes, suppression of soil populations of *Verticillium dahliae* is less effective and inoculum density may ultimately increase to damaging levels. Regulatory restrictions on fumigation will continue to intensify and management of *Verticillium* wilt will be increasingly dependent on alternative practices. Central to future management efforts will be the use of resistant cultivars. For this reason, resistance to *Verticillium* wilt was included as a selection criterion in the University of California breeding program beginning in the early 1990s. As a consequence, the average resistance score of genotypes used as parents has steadily increased and most recently released cultivars are significantly more resistant than those developed prior to adoption of the current program. Although it is reasonable to expect a continuation of this trend, it seems doubtful that resistance alone will be sufficient to prevent economic damage from *Verticillium* wilt. For this reason, it will be important to adopt practices that minimize the abundance and efficacy of inoculum in soil. One important consideration is the potential for crops grown in rotation with strawberries to support development of *V. dahliae* and thus contribute to soil populations of the pathogen. For example, recent work has shown that *V. dahliae* will extensively colonize and form microsclerotia in a number of legumes, all of which remain symptomless. A better understanding of the risk posed by other rotation crops is also needed.

Diversity of *Agrobacterium tumefaciens* found in Yuba County California

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Agrobacterium tumefaciens biovar 1 is the causal agent of crown gall, a serious disease of walnut in California. To investigate the diversity of *A. tumefaciens* in Yuba County, a total of 446 random isolates were collected from 12 healthy galls on walnut trees grown from 3 different nursery sources. Isolations were performed using 1A, a modified semi-selective medium for *Agrobacterium*. One hundred and seventy-three of the 446 isolates (38.8%) were confirmed *A. tumefaciens* biovar 1, and 273 isolates (61.2%) were Benedict's negative (i.e. *A. tumefaciens* negative). Only 12 (2.7%) of the 173 *A. tumefaciens* biovar 1 isolates were confirmed virulent. Surprisingly, we did not find any Ti-plasmid positive isolates from six of the galls examined. DNA sequence analysis of the *recA* gene in 44 biovar 1 virulent and avirulent isolates revealed members of genomovar 1, 2, 4 and 7. In addition, three previously undescribed genomovars were discovered (N1, N2, N3). The group of virulent isolates contained 5 members of genomovar 1, 6 members of genomovar 4, and one isolate belonging to a newly discovered genomovar N1. Repetitive sequence-based PCR (Rep-PCR) genomic fingerprinting using the BOX A1R primer revealed 4 unique fingerprints present in the virulent isolates and 12 unique fingerprints among the avirulent isolates. Each genomovar contained 1 to 4 unique fingerprints. All *A. tumefaciens* isolates also were screened for their sensitivity to the agrocin 84 producing strain K84. Resistance to K84 was found in 91.7% of the virulent and 75.8% of the avirulent isolates. Both *recA* and Rep-PCR analysis revealed a high degree of genetic diversity of *A. tumefaciens* collected over a limited geographic range. This diversity is being exploited to develop forensic tools for strain genotyping, tracking and inoculum source detection.

Verticillium wilt: Disease development in potato and mint

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Verticillium wilt, caused by *Verticillium dahliae*, is a major disease of potato, mint and a variety of other hosts. The soilborne fungus infects plant roots, increases exponentially in invaded xylem elements, disrupts water transport and causes vascular wilt and death of susceptible hosts. Despite the broad host

range of *V. dahliae*, distinct vegetative compatibility groups (VCGs) have been recognized which contain host-adapted pathotypes that are aggressive and prevalent on particular hosts. Isolates of *V. dahliae* collected from potato in North America mostly belong to VCG4A and are highly aggressive on potato, while VCG2B isolates are more prevalent and aggressive on mint than other VCGs. Initial inoculum of *V. dahliae* for potato is primarily soilborne microsclerotia. *Verticillium dahliae* can be transmitted in potato seed tubers and, although this source of infection appears to have little effect on wilt symptoms and potato yield compared to soilborne inoculum, tuber-borne inoculum may potentially introduce inoculum to soils not previously cropped to potato. Severity of *Verticillium* wilt increased in non-fumigated potato fields with increasing number of prior potato crops, whereas it remained constant in fumigated fields after an initial reduction. In commercial mint fields, infected plants were demonstrated to be spatially aggregated within and between plant rows. More disease aggregation was found within than between rows, indicating spread within rows during the life of the perennial mint crop, possibly through cultivation practices and irrigation water. Some perennial *Mentha arvensis* and *M. longifolia* genotypes were demonstrated to recover from initial infections by the mint pathotype of *V. dahliae* when allowed to regrow after harvest. Employment of resistance that favors plant recovery from infection may be an effective tactic in managing *Verticillium* wilt in perennial mint crops.

Vert. in the dirt: Status of Verticillium wilt in the fields of coastal California

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The string of coastal California counties that includes Santa Cruz, San Benito, Monterey, San Luis Obispo, Santa Barbara, and Ventura makes up the state's major cool season vegetable and strawberry production region. Total value for all agricultural commodities here exceeds \$6.7 billion. *Verticillium* wilt affects dozens of these crops and is particularly threatening to lettuce and strawberry, which are commonly grown in rotation with each other. Over the last few years, growers are observing the steady spread of this disease in lettuce plantings, and there is also a possible resurgence in *Verticillium* wilt in strawberry. Several factors account for the persistence of *Verticillium* wilt as a production challenge on the coast: limited crop rotations, movement of infested soil, lack of resistant cultivars, high cost of tarped flat fume applications, changes in pre-plant fumigation options, and increasing regulatory restrictions for fumigants. The phase out of flat fume applications with methyl bromide + chloropicrin and the use of less effective fumigants applied only to pre-formed beds is associated with several recent soilborne disease developments. In addition, the discovery that spinach seed can harbor *V. dahliae* inoculum adds another possible factor to the epidemiology of *Verticillium* wilt in coastal California. Because *Verticillium* wilt symptoms can resemble those caused by other diseases, growers, pest control advisors, field managers, and extension personnel should exercise caution in diagnosing these problems based only on symptoms.

Proteomic study of white pine-blister rust interaction

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The proteomic profiles of primary needles from Cr2-resistant and susceptible *Pinus monticola* seedlings were analyzed post *Cronartium ribicola* inoculation by 2-DE. One hundred and five protein spots exhibiting significantly differential expression were identified using LC-MS/MS. Functional classification showed that the most numerous proteins are involved in defence signalling, oxidative burst, metabolic pathways, and other physiological processes. Our results revealed that differential expression of proteins in response to *C. ribicola* inoculation was genotype and infection stage dependent. Responsive proteins in resistant seedlings with incompatible white pine blister rust (WPBR) interaction included such well-characterized proteins as heat shock proteins (HSPs), reactive oxygen species (ROS) scavenging enzymes, and intermediate factors functioning in the signal transduction pathways triggered by well-known plant R genes, as well as new candidates in plant defence like sugar epimerase, GTP-binding proteins, and chloroplastic ribonucleoproteins. Fewer proteins were regulated in susceptible seedlings; most of them were in common with resistant seedlings and related to photosynthesis among others. Quantitative RT-PCR analysis confirmed HSPs and ROS-related genes played an important role in host defence in response to *C. ribicola* infection. To the best of our knowledge, this is the first comparative proteomics study on WPBR interactions at the early stages of host defence, which provides a reference proteomic profile for other five-needle pines as well as resistance candidates for further understanding of host resistance in the WPBR pathosystem.

Oxalic acid production and mycelium pigmentation in relation to pathogenicity of Sclerotinia sclerotiorum on Valencia peanut

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Sclerotinia sclerotiorum attacks a broad range of plant hosts, and has been described as a fungal pathogen that produces white mycelium. Recently, darkly-pigmented isolates of *S. sclerotiorum* have been found on Valencia peanut in New Mexico and Texas. It has been shown in some pathogenic fungi that melanin and oxalic acid play a role in pathogenicity. In much of the literature on non-pigmented, pathogenic *S. sclerotiorum* isolates, oxalic acid has been demonstrated as the major determinant for pathogenicity. Studies were initiated to assess the effects of pure oxalic acid and an oxalic acid precursor, arabinose, on oxalic acid production in pigmented (SD) and mutant non-pigmented (SW) isolates of *S. sclerotiorum*. Oxalic acid production was assessed by transferring SD and SW isolates to 9-cm diameter petri plates containing potato dextrose agar (PDA) amended with bromophenol blue. The presence of yellow halo on this medium signifies acid production. The SD isolate produced a yellow halo within two days and reached the edge of the petri plate within four days. The mutant SW isolate did not produce a yellow halo when grown on PDA only, PDA amended with pure oxalic acid, or PDA amended with the oxalic acid precursor. Valencia peanut leaflets were inoculated with a mycelium plug of the SD or SW isolates grown on PDA, PDA amended with pure oxalic acid, and PDA amended with oxalic acid precursor. Regardless of the type of medium, the SD isolate caused lesions on leaflets within 72 h. However, no such effects were observed with the SW isolate. Results suggest that oxalic acid is produced by the SD isolate while the SW isolate doesn't produce or uptake any measurable amounts of oxalic acid. These findings may explain why the SD isolates are pathogenic while the SW isolates are not.

Wheat root defense gene induction by biocontrol Pseudomonas fluorescens

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Plant-growth promoting rhizobacteria, including strains of *Pseudomonas fluorescens*, can protect host plants by inducing systemic resistance against foliar pathogens. We are seeking to understand how root-colonizing pseudomonads impact molecular responses in wheat roots. The aggressive and persistent biocontrol strain *P. fluorescens* Q8r1-96 colonized wheat roots and deposited the antifungal metabolite 2,4-diacetylphloroglucinol (DAPG) on roots in a cultivar-dependent manner. This strain also induced differential expression of defense gene homologues in roots of cultivar Finley relative to those of 442 and 443, two lines near-isogenic for the vernalization *vrn1A* locus. The induced genes were components of pathways involved in basal defense, or innate immunity, such as the hypersensitive response, oxidative stress, and jasmonic acid signaling. We recently extended gene expression studies to two additional cultivars, Tara and Buchanan, which differed from cv. Finley in root colonization and DAPG accumulation. We tested the hypothesis that DAPG production and/or the type III secretion system (T3SS) of *P. fluorescens* Q8r1-96 are required for induction of root gene expression. Both a DAPG non-producer and a T3SS mutant of strain Q8r1-96 retained some of the transcriptional responses of the wild type, indicating that neither DAPG nor T3SS were key single inducers of global wheat root defense. However, cv. Buchanan showed more changes in gene expression than cv. Tara. Progress on wheat root defense gene induction by soilborne pathogens will be reported.

Efficacy of iodomethane against Armillaria root rot of cherry and peach rootstocks

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Armillaria root rot caused by *Armillaria mellea* is a major problem in establishing new orchards in riparian areas and when re-planting at locations where the disease occurred previously. *A. mellea* can persist in the soil for many years as mycelium in infested dead roots or as rhizomorphs. In laboratory tests, the effect of iodomethane (IM) on viability of *A. mellea* in naturally infested root segments of Lovell peach and Mahalab cherry was tested. Incubation at 100 mg/L and 20°C for 5 or 8 h resulted in 17% or 12% and 60% or 17% viability for peach and cherry, respectively, as compared to the untreated control with 100%. At 10°C, incubation of peach roots for 4 or 16 h resulted in 75% or 12% viability, respectively. In a rate test with 7-h incubations, 8% of roots yielded viable *A. mellea* at 75 or 100 mg/L IM, and

100% were viable at 25 or 50 mg/L. In field fumigation trials, infested roots were buried 0.3 m or 1.2 m deep before treatment. Probe site injection with IM:chloropicrin-CP (98:2, 454 g IM/site) was as highly effective in inactivating the pathogen as MB:CP (98:2, 454 g MB/site). In broadcast treatments, IM:CP (33:67) at 100 kg IM/ha and MB:CP (98:2) at 400 kg MB/ha were less effective in reducing *A. mellea* at the lower depth. Still, IM only slightly reduced viability at the upper depth; whereas MB was highly effective. This emphasizes the need for a high rate of IM:CP (400 kg IM/ha) that is limited to only probe injections with the current U.S. label.

Field flooding for controlling soilborne potato pathogens in western Washington

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A research project has been in place in WWA since 2009 to investigate whether the practice of flooding agricultural fields to provide habitat for shorebirds may be used as an alternative crop rotation for managing certain soilborne plant pathogens. Sclerotia of *Colletotrichum coccodes* were buried in flooded and non-flooded soils at 62°F in greenhouse cone-tainer experiments. At 3, 6 and 9 months there was no recovery of viable colonies from flooded soils. Similarly, 3 weeks to 3 months of flooding resulted in 80% less germination of recovered sclerotia of *Sclerotinia sclerotiorum*, and loss of viability between 3 and 6 months. Exposing sclerotia of *S. sclerotiorum* to flooding at 39, 52, and 68°F resulted in loss of viability at 4.5 months, but only at the two higher temperatures. Six percent of sclerotia retained viability after 4.5 months if at 39°F but none could be recovered at 9 months. In contrast, microsclerotia of *Verticillium dahliae* appeared to be resistant to flooding. In greenhouse soils at 62°F, *V. dahliae* was readily recovered, even after 6 months of flooding. A similar result occurred in Verticillium-inoculated field microplots which were flooded or fallowed from 24 Apr to 9 Oct in 2009. Soil populations of *V. dahliae* did not change for either treatment after one year (Apr 2009 to Apr 2010). Further, Russet Norkotah potatoes planted 24 May 2010 into treatment areas flooded or fallowed the previous year, did not reveal significant differences, respectively, in incidence of plants with Verticillium wilt (96 and 91%), recovery of *V. dahliae* from sampled potato stems (100%), or total yield (0.95 and 0.85 lb per plant). Flooding may be useful in WWA for managing black dot and white mold, but not Verticillium wilt.

Post-harvest storage diseases of onion in Utah

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Onion is the second largest vegetable crop produced in Utah. In the spring of 2011, onion planting was delayed by ~ 4 wks in some locations due to prolonged cold and wet weather. Because of the delayed planting, harvest was either delayed or onions were harvested prematurely (i.e. tops were not down and necks were green). Upon removal from storage, up to 95% loss from postharvest rots occurred. Culled onions were collected from two packing sheds in Utah. The culls were cut in half with a sterile knife and bacteria and fungi were isolated from symptomatic areas on nutrient agar, LB agar and PDA. The plates were incubated at room temperature. Fungi were identified to genus morphologically and to species by sequencing the internal transcribed spacer (ITS) region. To identify bacteria, the 16S gene of each isolate was sequenced and when further characterization was necessary physiological tests were conducted. The majority of onions had neck rot (*Botrytis aclada*). Other fungal pathogens we isolated included *Botrytis cinerea*, *Fusarium oxysporum*, *F. proliferatum* and *Penicillium* sp. Bacterial pathogens found included soft rot bacteria such as *Serratia* sp. and *Enterobacter cloacae*. The center rot pathogens *Pantoea ananatis* and *P. agglomerans* were also recovered. The large losses in storage might have been significantly reduced if onions had been harvested at optimum maturity with dry necks and properly cured which is one of the best controls for *Botrytis* neck rot.

The *phoP/Q* two-component regulatory system plays important roles in *Xylella fastidiosa*'s colonization of *Vitis vinifera* grapevines

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Xylella fastidiosa (*Xf*) is a gram-negative, xylem-limited plant pathogenic bacterium that causes disease in a variety of economically important agricultural crops including Pierce's disease of grapevine, citrus variegated chlorosis, and almond leaf scorch. *Xf* is transmitted in nature by xylem-feeding leafhoppers. Once introduced into the xylem vessels, *Xf* cells form aggregates leading to fruit desiccation and plant dieback. *Xf* biofilms formed in the xylem vessels of plants play a key role in early colonization and

pathogenicity by providing a protected niche and enhanced cell survival. Biofilm formation is induced by the process of quorum sensing and may be mediated by two-component regulatory systems. Like many other bacteria, *Xf* possesses homologs to the two component regulatory system *phoP/Q* which differentially regulates genes in responses to divalent periplasmic cation concentration and other environmental stimuli. *Xf* knockout mutants deficient in the production of *phoP* and *phoQ* exhibit phenotypic differences in cell dispersal and clumping when grown in liquid culture. *Xf phoP/Q* mutants had a 42% and 47% reduction in biofilm formation, and a 42% and 36% reduction in cell-cell aggregation, respectively. Dispersed growth and lack of cell clumping are phenotypes of *Xf* mutants deficient in hemagglutinins; however western blot analysis showed both *Xf* hemagglutinins are expressed in the *Xf phoP/Q* mutants. Grapevine pathogenicity assays showed *phoP/Q* mutants are non-pathogenic and are unable to successfully colonize or move within the xylem vessels. These results may be due to the inability of *Xf* to successfully sense, respond and adapt to the nutrient-poor environment of the xylem. This regulatory system, essential for *Xf* to cause Pierce's disease, is a novel target for disease control through anti-*PhoP/Q* peptides or other compounds produced by transgenic grapevines.

Lettuce diseases observed in high tunnel and open field organic production in western Washington

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Lettuce diseases occurring in high tunnel (HT) and open field (OF) production were compared during 2010 and 2011 growing seasons in western Washington (WWA). Six cultivars from 3 lettuce types were planted: Adriana, Ermosa (Boston); Coastal Star, Jericho (Romaine); Green Star, New Red Fire (Leaf). Plots were managed organically, and rated weekly for disease incidence and severity following transplanting on 22 Apr both years, and at all harvest times. Gray mold (*Botrytis cinerea*) incidence was similar for production systems in 2010, but significantly ($P = 0.004$) higher in HTs in 2011. Coastal Star and Jericho had significantly ($P = 0.0001$) higher gray mold incidence than the other cultivars in 2010, but not in 2011; Green Star had significantly less gray mold incidence each year ($P = 0.0001$ and $P = 0.007$, respectively). Lettuce drop (*Sclerotinia sclerotiorum*) was observed on all cultivars in HTs and OFs but no significant differences existed by location or cultivar either year. Verticillium wilt symptoms were observed on 3 plants at final harvest in 2010, and in 2011, 25 plants (16 from HT, 9 from OF) exhibited symptoms but 15 were still marketable. Coastal Star and Jericho were significantly ($P = 0.0001$) more affected than other cultivars. *V. tricornutum* was isolated from infected crowns both years and pathogenicity was later confirmed on 5 cultivars. Disease severity per infected plant ranged from 1–100% for gray mold, 5–100% for lettuce drop, and 1–50% for Verticillium wilt. Disease did not translate into loss of yield for either HT or OF production system. Green Star is an ideal cultivar for WWA as this loose leaf type had high yields and showed some resistance to gray mold, and was not seriously affected by lettuce drop or Verticillium wilt.

Fruit infection and postharvest decay of greenhouse tomatoes caused by *Penicillium* species in British Columbia

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In 2009 to 2011, a previously undescribed spotting of tomato fruits was observed in the greenhouse and packinghouse of a commercial organic greenhouse producer in the Fraser Valley of British Columbia. Symptoms initially appeared as small black spots on the tomato surface that were barely visible at harvest. The spots expanded after 5–10 days of cold storage to form larger gray and yellow lesions with evidence of mycelial growth in the center. Isolations from symptomatic skin and pericarp tissues from early and expanded lesions yielded three species of *Penicillium*. These species were identified following PCR amplification and sequencing of regions of the β -tubulin gene, the ITS region (ITS1-ITS4) and the cytochrome oxidase gene. Healthy tomato fruits inoculated with isolates identified as *P. olsonii* developed black spots which progressed to form larger gray lesions, typical of symptoms observed in the commercial greenhouse. Isolates identified as *P. solitum* and *P. polonicum* only caused soft rot and decay. Swabs of tomato fruit surfaces and calyx tissues taken from fruit developing on the vine, followed by plating onto PDA, revealed that high populations of *P. olsonii* were present (> 40 CFU/fruit). Similar populations were recovered from calyx tissues plated directly onto agar media. Wounding significantly enhanced disease severity compared to unwounded treatments, suggesting that the mode of entry of *P. olsonii* resident populations may be through naturally occurring cracks or wounds on the fruit surface. Lesion development occurred at low (12°C) temperatures and when *P. olsonii* conidia were inoculated onto the

shoulder region of ripe tomato fruits. To our knowledge, fruit spotting and postharvest decay of tomato fruits caused by *P. olsonii* has not been previously reported.

Early infection events in tomato roots predisposed to *Phytophthora capsici* by salt stress

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Plants respond to a wide range of abiotic and biotic stresses with complex signaling networks, often under the control of phytohormones. These networks are impacted by many factors, as well as by positive and negative crosstalk that can occur among downstream effectors of the response. The phytohormone, abscisic acid (ABA), plays a central role in adaptation to water stress, such as imposed by water deficit or high salinity. Stress events, even those from which the plant fully recovers, elevate ABA levels to predispose plants to levels of pathogen inoculum they would normally resist. ABA's role in induced susceptibility to *Phytophthora* species is now generally recognized, but the underlying mechanisms and impact on host defense responses are unresolved. This study examines early infection events in tomato roots predisposed by salt stress to *P. capsici*. Confocal microscopy was used to examine if the hemibiotroph, *P. capsici* displays an altered infection strategy in predisposed roots. A change in the rate of root colonization and associated cell death was apparent in infected salt stress roots. Abiotic and biotic stress related gene expression was profiled in predisposed roots following infection. Unlike some bacterial pathogens, *P. capsici* does not appear to be manipulating the ABA signaling pathway during infection. However, defense related gene expression is strongly suppressed in predisposed tomato roots relative to *P. capsici* infected controls.

Fungi associated with palm dieback and palm wilt symptoms in California

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Palm wilt, caused by *Fusarium oxysporum* f. sp. *canariensis* was first detected in California in the 1970s and is a lethal, vascular disease primarily of Canary Island Date Palm (*Phoenix canariensis*). In 2007, the Plant Pest Diagnostics Lab at CDFA began testing for Palm wilt and other palm diseases from samples exhibiting one-sided petiole, rachis and leaflet dieback. Samples were submitted by county agriculture agents, arborists and homeowners. Palm species included *Phoenix canariensis*, *P. reclinata*, *P. dactylifera*, *P. roebelenii*, and *Howea forsteriana*, with *P. canariensis* representing more than 95% of the total samples. Between 2007 and May 2012, the lab processed a total of 595 nursery and residential samples from 17 counties in California and 2 in Nevada. Samples were isolated onto half-strength acidified potato dextrose agar. Palm wilt was confirmed from 47% of the samples using a strain-specific PCR for *F. oxysporum* f. sp. *canariensis*. Pink rot caused by *Nalanthamala vermoeseni* was detected in 16% of the samples, and members of the Botryosphaeriaceae in 7%. Fungi, not known to be pathogens of palm or not known to occur in California were also identified by sequence analysis and morphological characters, including *Fusarium proliferatum*, *Phaeoacremonium parasiticum*, *P. fuscum*, *Neodeighonia phoenicum*, *Neofusicoccum australe*, *Neofusicoccum luteum*, *Exserohilum rostratum*, and *Cytospora eucalypticola*. Three undescribed species, including two *Fusarium* and one *Phaeoacremonium* species were also detected. Pathogenicity of 12 isolates was tested by inoculating wounds with colonized agar plugs on *P. canariensis* rachises and incubating them in moist chambers. After 1-2 months, *Neofusicoccum australe*, *N. luteum* and the two *Fusarium* species caused the longest lesions with the most extensive decay. All of the tested fungi were reisolated from symptomatic tissue. This survey confirms that multiple fungi are capable of causing localized symptoms similar to palm wilt and disease diagnosis cannot be made solely on field symptoms.

Effect of two soil inoculants on seed germination and infection of chile seedlings by *Phytophthora capsici*

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Seed germination is critical in stand establishment, and therefore various seed treatments are used to enhance seed germination and seedling vigor. In growth chamber studies (26°C/20°C, day/night temperature), two microbial formulations, approved for organic production, were applied to soil as an aqueous solution (2 g/liter), one (Piranha) containing a combination of nine fungal species including mycorrhizae (*Trichoderma* spp, *Glomus* spp, and

Rhizopogon spp.) and two species of bacteria (*Pseudomonas* spp.), and the other (Tarantula) containing a combination of bacteria including nine species of *Bacillus*. Two soil mixtures were formulated from sand, soilless mix, and vermiculite at volume ratios of 2:1:1 and 2:1:2. Plastic pots (500 cm³) were filled with either soil mixture, and seeds of chile pepper (*Capsicum annuum*) cultivar AZ-20 were planted in a circular fashion around the rim of each pot (10 seeds/pot). Pots were sub-irrigated with 100 ml of each formulation as needed. One week after sowing, a set of pots were infested with *Phytophthora capsici* by burying a 1-cm mycelium plug in the center of each pot at 1 cm below the soil surface. Seed germination was similar for both microbial formulations across both soil mixtures. Plant development, as gauged by height, number of fully expanded leaves, and leaf size was also similar for both soil inoculants. None of the formulations prevented seedling infection and mortality by *P. capsici*. Further research will focus on rate and timing of application of the soil inoculants.

Evidence of inhibitory volatiles of London rocket and flaxweed against three soilborne pathogens of chile pepper

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London rocket (*Sisymbrium irio*) and flaxweed (*Descurainia sophia*) are weeds with a wide geographical distribution belonging to the family brassicaceae, which includes several cruciferous plant species that contain glucosinolates. During degradation glucosinolates release bioactive volatile and non-volatile compounds with inhibitory activity against pests such as weeds and pathogens. Plant samples of London rocket and flaxweed were collected from various locations in agricultural fields and along roadways in southern New Mexico. The plants were processed by separating leaves from mature inflorescences with young to mature pods. Leaves and pods were dried in an oven at 60–65°C for 48–72 h, and then ground with a coffee grinder. The powdered products were evaluated for volatile activity against mycelial growth of *Phytophthora capsici* and *Rhizoctonia solani*, and *Verticillium dahliae*, three soilborne pathogens of many vegetable crops including chile pepper (*Capsicum annuum*). Mycelium plugs from a culture of each pathogen grown on water agar were placed onto potato dextrose agar (PDA) in 9-cm plastic petri plates, which were inverted and sealed in place over petri plates containing 0 or 2 g of ground leaves or pods mixed with 25 ml of sterile distilled water. All plates were maintained in darkness at 25°C. Mycelium growth was inhibited in the presence of ground tissues from flaxweed and ground reproductive tissues from London Rocket. However, mycelial growth was recorded in the presence of ground leaves tissues of London Rocket. These results suggest that *S. irio* and *D. sophia* do produce fungicidal volatiles, especially in reproductive tissues including seeds.

Verticillium wilts and management with special emphasis on lettuce

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Verticillium wilt is a devastating disease of many crops causing billions of dollars in annual losses. In cotton, pepper, strawberry and tomato, Verticillium wilt has historically been among the most important diseases. Despite their well-known plastic host range, Verticillium species have recently experienced sudden host range expansions. Recent examples include Verticillium wilt of cauliflower caused by *V. longisporum* that was unknown before 1990 and Verticillium wilt of lettuce and artichokes caused by *V. dahliae*, crops that were immune prior to 1995 and 1999, respectively. Using phylogenetic analyses, morphological investigations and comparisons to herbarium material and the literature, the taxonomy of the genus Verticillium was revised to include ten species, five of which are new to science. Of the different species that cause the disease, *V. dahliae* is the most notorious. Once introduced, *V. dahliae* is difficult to eradicate as it persists in the soil in absence of a host for many years by producing microsclerotia that are clusters of specialized, thick-walled and highly melanized fungal cells. Cultural practices offer limited control owing to the existence of cross-pathogenic isolates. Fumigation is uneconomical in most crops and its continued availability to crops that can afford fumigation is also in doubt. Development of cultivars resistant to Verticillium wilt is the optimal choice but is also the most difficult to accomplish. The talk will focus on the host range expansion, recent successes in identifying resistance to Verticillium wilt in lettuce, how this led to the discovery of the presence of two races, the uniqueness of this finding relative to the evolution of races in other pathosystems, relative proportion of the two races in sampled populations, parallels to the tomato system, and our recent discovery of the molecular determinant of race in *V. dahliae* and its implications to breeding programs.

The ecology of tree-seedling immunity: Symptomless *Fusarium circinatum* infection as a trigger for enhanced pathogen resistance in *Pinus radiata* seedlings

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Trees are highly susceptible to disease at the seedling stage, and it is commonly assumed that survival depends primarily on pathogen avoidance. Exposure of native Monterey pine (*Pinus radiata*) to *Fusarium circinatum*, the cause of pitch canker, is known to enhance resistance to subsequent infections in mature trees. *Fusarium circinatum* can cause rapid mortality of *P. radiata* seedlings, but can also cause cryptic infections, which may induce systemic resistance, providing a potential alternative to escape. The goals of this study were to (1) estimate the proportion of symptomless *P. radiata* seedlings that are infected in native stands, (2) determine if colonization in the absence of symptoms can induce systemic resistance in seedlings subject to either artificial or quasi-natural infections, and (3) evaluate the relative importance of escape vs. induced resistance in seedling survival. Surveys in native forests indicate that up to 70% of symptomless second year trees are infected by *F. circinatum*. Symptomless seedlings grown in infested sand or emerging through infested litter have significantly shorter lesions and enhanced survival following stem-challenge inoculations, compared to non-induced plants. Across infestation levels, 63–80% of seedlings died, 4–20% sustained symptomless infection, and 0–20% were not infected within the first four months after emergence. Together these results indicate that symptomless interactions between this pathogen and host occur commonly in native stands, can result in enhanced seedling resistance, and may have a protective function that is equal to, if not more important than, escape. Microbe-mediated induced resistance has not been previously shown to occur in tree seedlings, and further studies are needed to better understand the role of microbes, both as individuals and communities, in contributing to seedling survival.

NPDN expands analysis of the national repository

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For eight years the National Plant Diagnostic Network (NPDN) National Repository has been maintained by the Center for Environmental and Regulatory Information Systems (CERIS) at Purdue University. The NPDN Repository collects results from NPDN member laboratories and contains over 720,000 diagnostic records to date. Pilot projects using the NPDN analysis tools were conducted on virus diseases of wheat, soybean rust, late blight, and *Phytophthora ramorum* blight as well as others. New analysis tools include the host/pest index report, expanded weather-based models using a Google maps interface, the pest groups/synonyms tool, and additional nematode data fields. First submission reports are now available to all NPDN diagnosticians for data from their laboratory and/or their state (in the case that other labs may have done a diagnosis for a sample originating from the same state).

Constitutive plasmid-based protein expression in *Xylella fastidiosa*

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Production of some recombinant *Xylella fastidiosa* (Xf) proteins has proven difficult in commercially available *E. coli* and *P. pastoris* expression systems. Xf polygalacturonase (PG) is one of these proteins. Xf possesses a single PG gene and it was shown that if the gene encoding Xf PG was disrupted, the resulting PG-mutant was completely non-pathogenic in grapevines. Thus, identifying peptides or proteins that could inhibit the activity of Xf PG may provide a viable means for protecting grapevines from Pierce's disease. To identify such PG inhibitors, it is necessary to produce adequate quantities of

enzymatically active Xf PG. Unfortunately, our numerous attempts to produce enzymatically active Xf PG in *E. coli* and *P. pastoris* expression systems were unsuccessful. These results suggest that over expressing recombinant Xf PG in Xf may be a viable approach for producing enzymatically active Xf PG. Unfortunately, there are no inducible and very few constitutive plasmid or chromosomal based expression systems for the production of recombinant proteins in Xf. In order to express active Xf PG, we constructed a plasmid-based Xf protein expression system. These expression plasmids are based on the pBBR1MCS and pPROBE broad host range cloning vectors and use the constitutive nptII promoter to drive protein expression. Green fluorescent protein (GFP) reporter constructs made using this system expressed GFP in Xf under antibiotic selection. We are currently screening our Xf PG constructs to determine if they will express biologically active Xf PG.

***Verticillium dahliae* in production fields of the ornamental nursery industry**

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Verticillium dahliae is a common soilborne pathogen affecting numerous woody ornamental plant species. However, there is little information regarding the prevalence of the pathogen in nursery production fields or about the incidence of verticillium wilt among susceptible woody plant species in the industry. Fifteen fields (10–180 acres in size, 3040 acres total) from six nurseries specializing in woody ornamentals were surveyed in 2008–2009. One-acre plots, consisting of a single susceptible woody plant host species, were established to represent 10% of the acreage in each field. Disease incidence was recorded from 50–100 host plants within each plot and the presence of *V. dahliae* was confirmed from plant samples; the amount of *V. dahliae* inoculum was quantified in each plot by assessing soil samples. *Verticillium dahliae* was detected from soil and/or plant samples in 11 fields and the incidence of verticillium wilt in infested plots ranged from 1–100%. Inoculum density in infested plots ranged from 1–109 propagules/gram dry weight soil, although in some cases *V. dahliae* was not detected from soil in plots with infected plants. The pathogen was isolated from 15 plant taxa (different species and/or cultivars). The most commonly infected hosts included Japanese maples (*Acer japonicum* and *Acer palmatum*, 38% across both species), sugar maple (*A. saccharum*, 15%), Norway maple (*A. platanoides*, 15%), red maple (*A. rubrum*, 8%), and redbud (*Cercis canadensis*, 13%). Results indicate that *V. dahliae* is prevalent in many nursery production fields and can cause significant damage to several susceptible ornamental hosts, even at low population levels. Once infected, plants cannot be cured and must be rogued. Because many woody ornamentals are field-grown for more than one year, the presence of *V. dahliae* represents a continual and cumulative threat to susceptible plant species.

Grape mealybug ecology and its role in grape leafroll associated virus epidemiology

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Grapevine leafroll-associated viruses (GLRaV) are a complex of viruses that cause leaf discoloration and leaf margins to "roll" downward, and can reduce yields, delay fruit maturity, and impede fruit pigmentation. Vector-borne GLRaVs are transmitted by mealybug insects, including the grape mealybug, *Pseudococcus maritimus*. In field studies, we evaluated grape mealybug transmission of species GLRaV-3 with regard to vector seasonal behavior and population dynamics. Acquisition and inoculation of GLRaV-3 from trunks, spurs, canes, and leaves was evaluated in July 2010 and 2011, the peak time for first instar emergence. An estimated 2.3% of mealybug first instars transmitted GLRaV-3, with no differences in acquisition or inoculation efficiency among feeding tissues on the vine. However, insect survival was higher on leaves as compared to canes, cordons, or trunks. Surveys of grape mealybugs from five Napa County vineyards were taken monthly, from May 2011 to April 2012, to assess changes in seasonal populations and viral acquisition efficiency throughout the year. Preliminary analysis indicates that 50% (n = 117) grape mealybug groups collected from leafroll-infected vines tested positive for GLRaV-3, compared to 7% (n = 19) collected from leafroll-negative vines. The viral detection rate in collected mealybugs was highest in June and August, while few mealybugs collected between November and March tested positive for GLRaV-3. The proportion of GLRaV-3-positive mealybugs was correlated to the number of GLRaV-3-positive vines in the vineyards surveyed. Implications for disease spread will be discussed with regards to timing of vector control and removal of diseased vines.