2021 Pacific Division Meeting Abstracts

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Development of specific PCR-based markers for the identification and detection of needle cast pathogens on *Pinus contorta* and *P. flexilis* in the USA

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Morphological similarities and fastidious development of increasingly emerging fungal needle pathogens impede accurate disease diagnosis and early detection. This study analyzed the specificity and sensitivity of PCR-based markers developed for emerging needle cast pathogens *Lophodermella concolor* and *L. montivaga* co-occurring on *Pinus contorta* and *Bifusella linearis* and *L. arcuata* on *P. flexilis*. We utilized sequences of the internal transcribed spacer (ITS) region and genomes of related species for primer design. DNA of target and non-target fungal species were used for primer assays. Additionally, DNA samples from asymptomatic and symptomatic *P. contorta* needles infected with *Lophodermella* pathogens and their ITS metadata from a previous study were used to evaluate primer sensitivity. Direct and nested polymerase chain reaction (PCR) primer sets for each pathogen were developed from the ITS region and singleton gene 2175, respectively. The ITS primer pairs successfully differentiated the needle pathogens. Exterior and interior 2175 primer pairs detected Rhytismataceae species and discriminated both *Lophodermella* pathogens on *P. contorta*, respectively. While sensitivity level varied, both ITS and 2175 primer sets for *L. concolor* and *L. montivaga* detected their respective pathogens in asymptomatic and symptomatic needles. These molecular tools can help monitor and assess needle diseases for forest management and phytosanitary regimes.

Haplotype analysis of *Fusarium* spp. collected from conifer tree nurseries of the contiguous U.S.A.

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Nursery pathogens can move undetected through latent infected nursery stock, causing seedling mortality after outplanting and increasing the risk of pathogen introduction into novel landscapes (e.g., restoration areas). Once introduced, these pathogens can persist in landscapes due to inefficient management practices. Targeted management strategies can be developed to mitigate pathogen introductions into novel landscapes if pathogen composition and pathogenicity are known. Our work has two objectives: 1) evaluate the diversity and occurrence of *Fusarium* spp. in conifer tree nurseries across the U.S.A. to identify host preferences and geographic

distribution among populations of pathogenic *Fusarium*; and 2) use population genomics to assess potential movement of pathogenic *Fusarium* among states. *Fusarium* isolates were collected from western, midwestern, and southern U.S.A. conifer tree nurseries to determine *Fusarium* spp. diversity. Based on DNA sequences of the translation elongation factor 1- α and RNA polymerase II second largest subunit, *F. oxysporum*, *F. commune*, *F. redolens*, *F. fujikuroi*, *F. proliferatum*, *F. solani*, *F. equiseti*, and *F. tricinctum* were among the 15 species identified. Our project, by understanding pathogen populations and their potential movements from nursery to natural areas, will aid in developing tools to quantify disease pressure.

Effect of rotation crops on survival of *Fusarium oxysporum* f. sp. *lycopersici* race 3 and development of Fusarium wilt in California processing tomato

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Fusarium wilt (FW) caused by *Fusarium oxysporum* f. sp. *lycopersici* race 3 (Fol3) is a primary driver of yield loss in California processing tomatoes. As a host-specific pathogen, Fol3 should be suppressed by crop rotation; however, even after several non-tomato years, FW still causes severe losses. In previous studies, some crops harbor systemic but symptomless Fol3 infections—these may promote pathogen persistence in soil. To determine whether rotation crops vary in their effects on FW loss in tomato, we evaluated 1) survival of Fol3 after incorporation of infested tissue of ten rotation crops in field soil (greenhouse pot study), and 2) the effect of one year rotation with six cool-season and five warm-season crops on FW development in tomato (field trial). Fol3 persisted in soil at least 4 months after incorporation of infested sunflower, melon, vetch, corn, pepper, wheat, and cotton tissue (high to low density) but was no longer detectable in rice, fava bean, and broccoli tissue treatments. Crops resulting in higher infestation levels typically had less tissue break down. In field trials, FW incidence in tomato was greatest following one year rotation to tomato, pepper, melon, sunflower, broccoli, lettuce, and vetch and least severe following cotton, lima bean, wheat, fava bean, and onion rotation, as well as summer fallow. These studies can be used to optimize crop rotation as a management tactic for FW in tomato producing regions in California and other states.

Propiconazole resistance in *Geotrichum citri-aurantii* causing sour rot in California citrus packinghouses

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Sour rot caused by *Geotrichum citri-aurantii* (*Gca*) is a major postharvest decay affecting California citrus. The single-site mode of action demethylation inhibitor (DMI) propiconazole (PPZ) was the first postharvest fungicide with high efficacy against sour rot and has been used exclusively since 2012. Development of sour rot on PPZ-treated fruit in 2020 initiated our surveys on fungicide resistance in *Gca*. We cultured *Gca* from decayed lemon fruit that were stored for several months in three packinghouses in Ventura Co., determined effective concentrations of PPZ for 50% inhibition of mycelial growth (EC_{50} values), and compared these to our baseline sensitivity of 0.10 to 0.83 $\mu\text{g/ml}$ for isolates collected prior to 2012. Of the 35 isolates obtained, the sensitivity of 21 isolates was within the baseline range, however, 12 isolates with intermediate (EC_{50} = 1.4 to 3.4 $\mu\text{g/ml}$) and 2 isolates with high resistance (EC_{50} > 36 $\mu\text{g/ml}$) to PPZ were identified. This sensitivity distribution represents a bimodal shift and possibly describes quantitative and qualitative mechanisms of resistance, or two different molecular mechanisms of resistance have developed in the pathogen. Resistance to DMIs is considered a gradual change to higher resistance levels. Thus, this type of resistance pattern to DMI fungicides in *Gca* has not been previously described for any fungal pathogen and will be investigated in future studies.

Detection of Soilborne wheat mosaic virus using hyperspectral imaging: From lab to field scans and from hyperspectral to multispectral data

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Hyperspectral imaging allows for rapid, non-destructive, and objective assessments of crop health, including signatures of plant disease. Soilborne wheat mosaic virus (SBWMV) is an emerging disease in the dryland PNW, and an ideal model system to apply hyperspectral imaging for potential early disease detection. We used narrowband-hyperspectral data to select wavelength regions that can be exploited to identify wheat infected with SBWMV. First, leaf samples were scanned in the lab to investigate spectral differences between healthy and SBWMV-infected leaves, including non-symptomatic and symptomatic areas within an infected leaf. Next, the classification models were validated on field data. Classification of hyperspectral data from two SBWMV disease nurseries were used to assess the outcome for varieties with known susceptibility levels. Moreover, classification outcomes for field transects, in the form of a thematic map, were compared to visual assessments of experts. We successfully classified for infection in the field using classifiers trained on the entire spectrum of the hyperspectral data acquired in a lab setting. This is an exciting first step for potential early disease detection technology for farmers and has open application for many other pathosystems.

The fitness differences of quinone outside inhibitor fungicide resistant *Erysiphe necator*

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In 2016 and 2017, western U.S. vineyards experienced significant crop loss due to quinone outside inhibitor (QoI) fungicide-resistant *Erysiphe necator*. Little is known about the fitness costs of QoI resistance in *E. necator*, making it difficult to determine the long-term

efficacy of QoI fungicides for grape disease management. Isolate fitness was explored using eight QoI resistant and sensitive *E. necator* isolates collected from the Willamette Valley and southern Oregon. Isolates were exposed to temperatures ranging from 10 to 34°C, and growth and developmental parameters, including conidium germination, latency, and colony expansion, were compared. Studies comparing conidium maturation and competitiveness of artificially mixed populations are in progress. No latent period or colony expansion differences were found; however, percent germination was greater for QoI-resistant isolates at 19°C ($P = 0.036$), and mating type 1 had greater overall germination than mating type 2 ($P < 0.001$). Preliminary results from competition assays indicate that the QoI resistance allele frequency increases over time at cool temperatures. Results from this study indicate that potential fitness differences associated with QoI-resistant *E. necator* are either neutral or beneficial and may partially explain observed increases seen in field populations of QoI-resistant *E. necator* over the growing season.

Elucidating the disease cycle of *Calosphaeria pulchella*, a major fungal canker pathogen of sweet cherry in California

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Calosphaeria canker, caused by *Calosphaeria pulchella*, is a ubiquitous canker disease of sweet cherry and limits orchard productivity and longevity. Ascospores of the fungus infect pruning wounds from which the pathogen causes vascular discolorations and branch dieback, eventually leading to the death of entire branches and scaffolds. Perithecia of *C. pulchella* are produced under the bark of infected trees. Past spore trapping studies suggest that ascospores are the main infectious propagules. Nonetheless, very little is known about Calosphaeria canker disease cycle, such as the timing of infections and the seasonal susceptibility of pruning wounds. We determined in vitro the optimal temperatures for *C. pulchella* mycelial growth and spore germination. In field assays, we compared the seasonal susceptibility of pruning wounds to infection. The highest spore germination rates occurred near 30°C; this temperature was also optimal for mycelial growth. Field assays revealed that inoculations made in summer yielded higher infection rates than in winter. These results suggest that most *C. pulchella* infections occur in summer months, which is in contrast to the other two main cherry canker diseases caused by *Eutypa lata* and *Cytospora* spp. Since distinct cherry canker pathogens vary in their seasonal infectivity, synchronizing maintenance pruning with low periods of inoculum pressure will be critical for canker disease management in sweet cherry orchards.

Rhizosphere community selection reveals bacteria associated with reduced root disease

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Microbes benefit plants by increasing nutrient availability and protecting against pathogens. However, it is largely unknown how plants change the root microbiome. In this study, we used a successive planting and infection by the soilborne pathogen *Rhizoctonia solani* AG8 (hereafter AG8) to examine how plants impact the rhizosphere microbiome. Analysis of the rhizosphere microbiome using next generation sequencing revealed distinct bacterial community profiles assembled over successive plantings. Moreover, the cluster of bacterial communities formed from the AG8-infected rhizosphere was distinct from those without AG8 infection. The bacterial communities from the rhizosphere with the lowest wheat root disease gradually separated from those with the worst wheat root disease over planting cycles. Successive monocultures and application of AG8 increased the abundance of some bacterial genera which have potential antagonistic activities. Furthermore, among 47 isolated bacteria, 11 and 5 exhibited antagonistic activities to AG8 and *Rhizoctonia oryzae* in vitro, respectively. Notably, *Janthinobacterium* displayed broad antagonism against *Pythium ultimum*, AG8, and *R. oryzae* in vitro, and disease suppressive activity to AG8 in soil. This study demonstrated that successive plantings and pathogen infection can shape the rhizosphere microbial communities and specifically accumulate a group of beneficial microbes.

Evaluating the efficacy of *Phytophthora* detection methods to support restoration nurseries best management practices

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California native nurseries provide plant material for restoration sites. Over the last decade, more than 50 *Phytophthora* spp. have been associated with native plant nurseries in California, creating concern about introducing pathogens into wildlands. To improve *Phytophthora* detection, we evaluated *Phytophthora* testing protocols to inform design of an accreditation program for restoration nurseries. The efficacy of three *Phytophthora* detection methods was compared: a leachate baiting method, immunostrips, and direct isolation from root tissue. Coffeeberry plants were inoculated with *P. cactorum* and arranged in three subsets of inoculated and noninoculated plants. Every 4 weeks post-inoculation (wpi) over 3 months, subsets of inoculated (20%) and noninoculated plants were tested with the three detection methods. *P. cactorum* detection success with the leachate baiting method was 66% at 4 wpi, and 100% at 8 and 12 wpi among the three subsets. With direct isolation, *P. cactorum* detection success rate increased over time, with 16% at 4 wpi and 50% at 12 wpi. *Phytophthora* detection with the immunostrips was highly variable, ranging from 0 to 33% detection. Results suggest that the leachate baiting method is the most effective at detecting *Phytophthora*, but this method did not discern between infected or noninfected plants in a subset. These baseline findings are being expanded upon to support monitoring protocols used in a pilot accreditation program for restoration nurseries.

Survey of nematode-transmitted viruses and vectors of small fruit crops in the Pacific Northwest (USA)

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The Pacific Northwest (PNW) maintains a \$840 million small-fruit industry susceptible to nematode-transmitted nepoviruses. Washington has reported nepoviruses on small fruit crops, including Grapevine fanleaf virus (GFLV) on juice and wine grapes, Tobacco ringspot virus (TRSV) on grape and blueberry, and Tomato ringspot virus (ToRSV) on raspberry. Tomato ringspot virus has been detected on wine grapes in Oregon. The dagger nematode vectors of these viruses (*Xiphinema americanum* sensu stricto, *X. californicum*, and *X. rivesi*) have been reported in the PNW, increasing the risk for nematode transmission among and between small-fruit hosts. The objective of this research is to assess the risk of nepoviruses to small fruit production in the PNW by conducting a survey of nematode-transmitted viruses and vectors of grape, raspberry, blueberry, blackberry, and strawberry. In May–June 2021, plant and soil samples will be collected from sites with and without known nepovirus infections for virus and vector screening. Plant samples will be tested for Arabis mosaic virus (ArMV), Cherry leaf roll virus (CLRV), GFLV, Peach rosette mosaic virus (PRMV), Strawberry latent ringspot virus (SLRSV), ToRSV, and TRSV. Nematodes will be extracted from soil and identified to species. Presence of nepoviruses and dagger nematodes will be reported and potential impact will be discussed. This comprehensive survey will ultimately inform risk and management practices for PNW small-fruit growers.

The role of irrigation in disease development and management of *Macrophomina* charcoal rot on strawberries

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Macrophomina charcoal rot (MCR; caused by the soilborne fungus *Macrophomina phaseolina*) is an economically significant disease threatening California strawberry production. This disease is typically associated with drought, and studies in other crops have shown that improved irrigation practices can reduce disease severity. The objective of this research was to evaluate the role of different irrigation practices in disease development and management of MCR on strawberries. A field study was conducted from October 2019 to June 2020 in Irvine, CA. Irrigation treatments were established at high, optimal, or low soil moisture content as determined by soil water potential thresholds monitored using tensiometers. Irrigation treatments were evaluated in a factorial split-plot design with two cultivars (Monterey, Fronteras) and two inoculation treatments (inoculated, control). MCR severity of each plant was assessed on an ordinal scale. Slicing the significant three-way interaction revealed evidence for an influence of irrigation on disease severity only for Fronteras inoculated plants ($P = 0.0003$). Among Fronteras-inoculated plants and when compared to optimal soil moisture, MCR severity was higher in the low soil moisture treatment ($P = 0.0019$) but similar to the high soil moisture treatment ($P = 0.4723$). This suggests high soil moisture may not alter disease severity and that the role of irrigation on MCR may be cultivar-dependent. The study is currently being repeated.

Impact of rotational crops on *Aphanomyces* root rot of pulses

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The increased production of pulse crops in the United States has led to a rise in new disease challenges over time. Root rots on pulses in Montana have risen in recent years due to a complex of species, including the soilborne oomycete *Aphanomyces euteiches*, on dry peas and lentils. This pathogen is particularly difficult to manage, as traditional fungicides are not effective, and prevention is key due to the long-lived nature of the oospore. In the greenhouse, plants were grown in soil inoculated with an *A. euteiches* isolate collected from a Montana pea field, using an oospore solution, to determine the impact of rotational crops on root rot propagules. The species selected are of interest for production in Montana and included flax, chia, canola, mustard, camelina, pea, wheat, and safflower. Plants were removed from pots and assessed, then a susceptible pea variety (cv. Majoret) was planted. Disease was rated on pea using a severity score as a measure of *A. euteiches* soil inoculum. Compared to the severe root rot witnessed on peas grown in a pea-pea sequence, planting wheat and safflower prior to pea lead to minor root rot symptoms, with data assessed using ordinal regression ($P < 0.001$). Other plant species grown initially showed moderate to severe symptoms on the following pea host plants. This preliminary research indicates that crop rotation is an important tool in the toolbox for management of *Aphanomyces* root rot on pulses.

Genome-wide association analysis of stripe rust resistance in a Chinese wheat landrace panel with 660K single-nucleotide polymorphism arrays

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Stripe rust (caused by *Puccinia striiformis* f. sp. *tritici*) is one of the most severe diseases affecting wheat production. Chinese wheat landraces have excellent resistance to stripe rust. The objective of this study was to identify wheat landraces and map quantitative trait loci (QTL) for stable resistance to stripe rust from 271 Chinese wheat landraces. A genome-wide association study was conducted to identify quantitative trait loci (QTL) associated with stripe rust resistance by genotyping the wheat landraces with the 660K wheat single-nucleotide polymorphism (SNP) array and phenotyping stripe rust responses in six field environments. Thirteen landraces with stable resistance were identified and seven QTL were found to be associated with stripe rust resistance, including three on chromosome 3B and one each on 2D, 4A, 5A, and 5B. These QTL explained 9.53 to 13.59% of the phenotype variation with the QTL on 5A having

the strongest affect on stripe rust reduction. The QTL on chromosome 4A was presumably new. The identified stable resistant landraces, significant QTL, and linked SNP markers should be useful for breeding wheat cultivars with resistance to stripe rust.

Illuminating grape disease management: Germicidal ultraviolet light as a tool to suppress powdery mildew

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Germicidal UV light (UVC) is an emerging method to suppress grape powdery mildew (*Erysiphe necator*) that is particularly relevant to managing fungicide resistance. In lab studies, we suspended two, 36-W low-pressure discharge UVC lamps above an adjustable conveyor system to apply controlled doses of UVC to *E. necator* conidia on Gelzan medium plates. UVC exposure occurred 1 h after simulated sunset; darkness during treatment being an essential feature of UVC-based suppression. After UVC exposure, plates were incubated in darkness for 7 h, then imaged 48 h after exposure, and germination was calculated. The half-maximal UVC dose (ED50) to inhibit *E. necator* conidia germination varied among isolates from 50 J/m² to 250 J/m². In vineyard studies, we deployed a tractor-drawn, over-canopy array of 12, 55-W UVC lamps to expose vines to nighttime weekly UVC doses of 80 or 120 J/m² (ground speeds of 4.8 and 3.2 kph, respectively). Applications began 1 h after sunset and were completed within 4 h of sunrise. UVC sub-plots also received supplemental applications of micronized sulfur, azoxystrobin, or water (a control treatment) at 7- to 14-day intervals. UVC significantly (TukeyHSD, $P < 0.05$) suppressed incidence of foliar powdery mildew. These results suggest that UVC treatments may substantially contribute to management of grapevine powdery mildew at doses that can be achieved with available technology.

Population structure and pathways of spread of an emerging tree root pathogen *Phellinus noxius* in Southeast Asia, Australia, and the Pacific Islands

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Over the last few decades, the root- and wood-rotting fungus *Phellinus noxius* has been causing extensive damage to diverse trees in tropical/subtropical regions. Little is known about pathogen's global population structure, diversity, and invasion routes. Using restriction site-associated DNA sequencing data, we characterized genetic relationships, pathways of spread, and evolutionary histories among *P. noxius* populations from 15 locations in Southeast Asia, Australia, and the Pacific Islands. Population structure analyses revealed five distinct genetic clusters of *P. noxius*, with signatures of a complex recent and ancient migration history among study locations. Approximate Bayesian computation (ABC) analyses indicated that the most probable scenario of pathogen spread is from north to south, moving from Malaysia to the Pacific Islands, and with subsequent spread to Taiwan and Australia. Furthermore, ABC analyses indicate that major spread by *P. noxius* occurred thousands of generations ago, contradicting previous assumptions that it is a recently introduced pathogen in many areas. Our results suggest that *P. noxius* has a long evolutionary history in Southeast Asia, Australia, and the Pacific Islands, and pathogen emergence is likely driven by anthropogenic and natural disturbances, including climate change, that affect forest and horticultural trees.

Fusarium present as seedborne inoculum in lentils

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Lentils are an important crop worldwide including the USA. Pests and diseases impact yield. Fungal pathogens such as *Fusarium* cause root rot. The role of seedborne *Fusarium* in lentils is unknown. In 2019 and 2020, 84 lentil fields were surveyed in MT, ND, WA, and ID for disease. Seed was hand-harvested at physiological maturity. Four hundred seeds/field were assayed following ISTA protocol. Isolates were identified morphologically and molecularly. Four hundred eighty-six (2019) and two hundred twenty-eight (2020) isolates were characterized. Twenty-one isolates representing seven predominant species were tested in the greenhouse. All isolates were virulent on a susceptible line ranging from 1.5 to 4.5 on a root rot severity scale of 0–5. *F. sporotrichioides*, *F. oxysporum*, and *F. graminearum* were the most virulent rating above 4. To further assess the components of lentil seed infested by *Fusarium*, 100 seeds from 18 seed lots collected from 2019 to 2020 with an over 6% infection rate were selected. Seed coat, cotyledon, and embryo were aseptically dissected, surface sterilized, incubated, and enumerated as described above. *F. equiseti* (30%), *F. acuminatum* (28%), *F. oxysporum* (10%), *F. tricinatum* (9%), *F. graminearum* (9%), *F. proliferatum* (8%), and *F. sporotrichioides* (6%) were predominant in 2019. In the component separation experiment (2019; 2020), the seed coat was highly infested (57%; 75%), followed by the cotyledon (23%; 19%) and the embryo (20%; 6%). Data from this study will be used for informed management decisions.

Testing efficacy of canopy sprays against the *Cytospora* canker pathogen, *Cytospora plurivora*, following freeze damage on peaches in Colorado

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Cytospora plurivora, responsible for *Cytospora* canker disease, is a fungal pathogen that has reached near epidemic levels in peach orchards on the Western Slope of Colorado. In 2020, an early freeze event occurred, which caused severe damage to shoots, buds and twigs of peach trees on the Western Slope. Environmental damage provides infection courts for *C. plurivora* that can occur on twigs,

buds and within frost cracks along the main stem and large scaffolds. This freeze event prompted growers to apply prophylactic chemical treatments last fall. There are no current best practices for chemical canopy sprays against *Cytophora*; therefore, efficacy of applied treatments Captan, copper hydroxide, and lime sulfur were tested. The objectives of this study were to test the efficacy of both conventional and organic chemical sprays in six Western Slope orchards during December 2020 and March 2021. First-year growth (3 branches per tree) displaying apparent damage were collected monthly from 25 trees per orchard. The apical bud, as well as four subsequent buds, was plated on PDA, and all fungal colonies were isolated, sorted by morphotype, and sequenced at the loci internal transcribed spacer region (ITS). Preliminary results suggest that fungal diversity and *Cytophora* isolates increased with time since application and vary with chemical treatment. Results of this work will help inform growers of the efficacy of chemical canopy sprays and length of time sprays are effective.

Spatial and temporal trends in G143A caused QoI resistance in *Erysiphe necator* across the growing season in the western US

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Since 2015, western grape growers have reported more control issues due to quinone outside inhibitor (QoI; FRAC 11) resistant *E. necator*. However, little is known about the spatiotemporal dynamics of QoI resistance in *E. necator* populations. Samples (9–48 per vineyard) were collected from 30-cm shoot length to harvest from 43 vineyards in OR (2018–2020; $n = 1,427$), 39 in CA (2019–2020; $n = 867$), and 25 in WA (2019–2020; $n = 523$). The G143A resistance mutation was monitored using a discriminatory TaqMan qPCR. Regardless of location, the G143A frequency was lowest pre-bloom at 26% (range: 11–63%) and increased throughout the growing season, with samples collected post-veraison averaging 79% (range: 56–100%). This result occurred irrespective of the fungicide classes used (eight organic vineyards sampled in OR 2018–2020). Among years, the overall frequency of the G143A varied, with OR seeing the lowest overall frequency (2018: 35%, 2019: 29%, 2020: 50%), WA in the mid-range (2019–42%, 2020–59%), and CA with the highest (2019–89%, 2020–72%). One vineyard sampled in OR 2020 applied a QoI, trifloxystrobin, on two blocks and metrafenone (FRAC 50) on two others. Following these applications, QoI treated block samples had 92% ($n = 59$) G143A, while the non-QoI treated blocks had 53% ($n = 34$) G143A. These data indicate that the frequency of QoI-resistant *E. necator* increases over the growing season and that factors other than direct selection by QoI treatments are involved.

Molecular characterization of international collections of wheat stripe rust pathogen *Puccinia striiformis* f. sp. *tritici*

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Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is one of the most important diseases of wheat worldwide. To understand the genetic structure and variability of the *Pst* populations from the international scale, 621 *Pst* isolates collected from eight countries (China, Pakistan, Egypt, Ethiopia, Italy, Ecuador, Mexico, and the U.S.) were genotyped using 14 codominant simple sequence repeat markers. A total of 509 multi-locus genotypes (MLGs) were detected, which were clustered into four molecular groups (MGs). Many isolates from different countries, especially the isolates from the U.S., Mexico, and Ecuador, were found to be identical or very closely related MLGs, and some of the MGs were present in all countries, indicating *Pst* migrations among different countries. Analysis of molecular variance revealed 85% variation among isolates, 11% variation among countries, and only 5% variation among isolates within countries. The study provides the information on distributions of various *Pst* genetic groups in different countries, which should be useful to develop strategies for managing stripe rust.

Effect of inoculum density on *Verticillium* wilt responses in commercially grown *Mentha* species and cultivars

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Verticillium wilt, caused by *Verticillium dahliae* (*Vd*), is a major constraint to mint (*Mentha*) production in the United States. Currently, there are no clear guidelines on what constitutes an economic action threshold for soilborne inoculum of *Vd* in mint. The objective of this study was to identify the levels of *Vd* required to incite *Verticillium* wilt in commercially grown mint cultivars. A greenhouse trial was conducted to evaluate the *Verticillium* wilt response of peppermint (*M. × piperita*), Scotch spearmint (*M. × gracilis*), native spearmint (*M. spicata*), and cornmint (*M. arvensis*) cultivars when grown in field soils artificially infested with 0, 1, 5, 10, 20, 50, or 100 microsclerotia/cm³ of soil. A significant effect of inoculum level was only observed for AUDPC values of peppermint ($P < 0.0001$). Native spearmint and cornmint cultivars were resistant at all inoculum levels. Overall yield reductions of peppermint cultivars ‘M-83-7’ (3%), ‘Todd’s Mitcham’ (16%), and ‘Redefined Murray’ (19%) were significantly less than ‘Black Mitcham’ (45%), and yields of Scotch spearmint ‘S770’ were significantly greater than the standard Scotch spearmint cultivar. In general, yield reductions were greater for the second and/or third cutting compared to the first, and in many cases yield reductions were the only observable effect of *Vd* infection in resistant cultivars. These results can help mint growers make critical replant management decisions to avoid or reduce *Verticillium* wilt.

Evaluating *Botrytis cinerea* sensitivity towards fungicides commonly used in pear orchards

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Botrytis cinerea causes gray mold in pears and can adapt to changes in its environment, enabling it to become resistant to fungicides. The sensitivity of 21 *B. cinerea* isolates towards fungicides used in pear orchards was evaluated. The fungicides Manzate Pro-Stick, Ziram 76DF, Ph-D, and Botran 5F, which contain the active ingredients of mancozeb, ziram, polyoxin D, and dicloran, respectively, were tested against the *B. cinerea* isolates at concentrations of 0, 0.1, 10, and 100 µg/ml and the maximum label rate. Isolates were grown on PDA plates and then transferred to PDA plates amended with the different fungicide concentrations. Fungal growth was measured after 3 days. EC₅₀ values ranged from 21.65 to 136.02 µg/ml for mancozeb, 25.33 to 156.77 µg/ml for ziram, 4.05 to 619.02 µg/ml for polyoxin D, and from 4.08 to 26.75 µg/ml for dicloran. For biological testing, Bosc fruits were harvested at commercial maturity, surface sterilized, and wounded with a sterile nail head. Wounds were treated with fungicides adjusted to their respective labeled rate followed by spore inoculation of isolates. After 5 days, lesion diameter was measured and the fungicide efficacy was calculated. Percent efficacy ranged from 32.31 to 99.22% for mancozeb, 61.39 to 96.15% for ziram, 76.35 to 100% for polyoxin D, and from 21.15 to 89.53% for dicloran. Overall, this study suggests differential sensitivities of *Botrytis* isolates to fungicides with different modes of action.

Biological control of fungi causing Botryosphaeria dieback of grapevines in British Columbia

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Botryosphaeria dieback (BD) is a grapevine trunk disease (GTD) caused by species in the *Botryosphaeriaceae*. The fungi infect grapevines through pruning wounds and affected vines show a rapid decline and eventual death. Currently, no commercial products are registered to manage BD in Canada. The main objectives of this study were i) to identify local biocontrol agents (BCA) with potential activity against BD fungi *Diplodia seriata* and *Neofusicoccum parvum*, and ii) to compare their performance against commercial products registered elsewhere. Seven BCA were isolated from grapevines in British Columbia and identified by morphological and molecular studies as *Trichoderma* spp., including two novel species for the scientific community. The antagonistic capabilities of *Trichoderma* isolates against *D. seriata* and *N. parvum* were screened in vitro via dual culture assay. The best performing isolates were further evaluated in planta under greenhouse conditions using a detached cane assay and in a 2-year field trial in a 'Merlot' experimental vineyard. Results showed that three local *Trichoderma* spp. were able to protect pruning wounds against BD fungi for up to 60 days after treatment. In addition, selected local *Trichoderma* spp. performed equally or better than some of the commercial products included in the study. This research represents the first steps toward the implementation of management solutions against these economically important diseases for Canadian growers.

Assessing the relative tolerance of pistachio rootstocks to *Phytophthora* species in California

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Phytophthora root and crown rot is an emerging disease and a new threat to pistachio trees in California. Newly reported oomycetes pathogens associated with this disease include *Phytophthora niederhauserii*, *P. taxon* walnut and *P. sp. ax*. To provide a sustainable management approach to Phytophthora crown and root rot we evaluated the susceptibility/tolerance of clonal UCB1, PG1, and Platinum rootstocks against *Phytophthora* species. Susceptibility/tolerance was assessed through a series of stem and soil inoculations using all three *Phytophthora* spp. for each rootstock. Stem inoculations were conducted using mycelial plugs (4 mm) of each *Phytophthora* species. Inoculated rootstocks were incubated for 10 months. Averaged lesion length from stem inoculations indicated that Platinum is the most tolerant rootstock against *Phytophthora* spp., followed by PG1, then UCB1 rootstocks. Soil inoculations were conducted using 25 ml of a zoospore suspension (10⁵ zoospores/ml) or 5 g of inoculated rice grains in combination with a 4-h flooding treatment following inoculation. Inoculated plants were incubated for 3 to 7 weeks respectively in a greenhouse. Plant-death ratio of soil-inoculated plantlets showed that Platinum was the most tolerant rootstock towards *Phytophthora* spp. compared to UCB1, reflecting the stem inoculation results. These findings indicate that Platinum might be the preferred rootstock when planting pistachio trees in areas at risk for Phytophthora diseases.

Evaluation of grapevine-derived microbes for sustainable pruning wound protection against grapevine trunk diseases

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The grapevine trunk diseases (GTDs) complex poses a major threat to the economic sustainability of wine and grape cultivation worldwide. Pruning wounds are the primary entry point for fungal pathogens responsible for these diseases and as such are the focus of preventative disease control. The need for sustainable practices has prompted huge interest in the use of biological control agents for pruning wound protection. The goal of this study was firstly to identify and characterize potential biocontrol agents isolated from

different grapevine and evaluate their antagonistic activity against GTDs fungal pathogens in vitro. Secondly, we would evaluate their efficacy as pruning wound protectants in greenhouse and field trials in major California grapevine production regions. Finally, we would record recovery of biologicals from treated wounds. Recovered *Trichoderma* and *Bacillus* isolates exhibited various mechanisms of antagonism in vitro including stopped growth, overgrowth, and likely antibiosis. In greenhouse and field trials, *Trichoderma*-based biological treatments and the chemical treatments, Topsin M + Rally and Luna Sensation could effectively protect wounds from GTDs infection. Moreover, *Trichoderma*-based treatments could be recovered from treated canes, 8 months from application suggesting that effective wound colonization by biologicals is likely tied to sustained pruning wound protection.