2014 Northeastern Division Meeting Abstracts

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Updating the status of the re-emerging and damaging bloat nematode on garlic

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The stem and bulb (bloat) nematode *Ditylenchus dipsaci* continues to be a major constraint to garlic production and marketing since it was first observed causing severe damage in a commercial field in western New York in June 2010. It is widely distributed throughout the production areas in NY and many other states, as documented by survey results and the subsidized diagnostic testing of several hundreds of garlic samples conducted under a project funded by the Specialty Crop Block Grant Program through the NYS Dept. of Agriculture and Markets. The genetic characterization of selected populations from garlic samples that tested positive is in progress. Results obtained to-date suggest that all populations recovered exhibited little polymorphism. Severely infected plants exhibit stunting, yellowing, collapse of outer leaves and such plants may eventually die. Infected bulbs initially exhibit light discoloration. They later become dark brown, shrunken, soft, light in weight, and with cracks around the basal plate. Decay symptoms usually develop on such bulbs due to the involvement of various saprophytic soil organisms. During 2011–2014, eight workshops on the biology and management of the bloat nematode and general garlic production were offered and attended by >350 growers and industry personnel. Information provided included appropriate garlic and soil sampling protocols, interpretation of testing results, and the implementation of appropriate management options against this nematode for both conventional and organic production. The latter included the use of nematode-free planting seeds, planting in bloat nematode-free or treated soil, use of appropriate crop rotations, use of effective bio-fumigant cover crops and others.

Comparison of nematode communities between organically and conventionally managed golf courses

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Free-living and plant pathogenic nematodes play important roles in plant health. Free-living nematodes can increase nutrient cycling and available nitrogen to plants. They can aid in distributing microbes throughout the soil and they can consume beneficial and deleterious bacteria, fungi, algae, insects, and other nematodes. Plant pathogenic nematodes are known for their ability to destroy healthy plant roots and as possible vectors for other pathogens. Many golf course superintendents are in need of more sustainable ways to manage nematodes on their turf, especially with the banning and restricted use of nematicides. However, little is known on how synthetic pesticides versus organic pesticides affect free-living and plant pathogenic nematode communities. The goal of this study is to understand soil nematode communities on an organically (non-synthetic pesticides or fertilizers) and two conventionally managed golf courses and among roughs, fairways, and putting greens. The three golf courses were located within 10 km of one another. Soil samples were systematically collected using cores and the samples were processed for nematode communities and soil properties. Our preliminary results show significantly lower abundances of plant pathogenic nematodes on the organic putting greens compared to the other two courses, which corresponds to a significant increase in the frequency of free-living nematodes found on the organic course, especially the bacteriovores. The lowest abundance of fungivores was on the putting greens, regardless of organic versus conventional. An increase in soil organic matter correlated with an increase in plant pathogenic nematodes on the greens, whereas a decrease in soil organic matter correlated with an increase in bacteriovores and carnivores. Understanding how management strategies affect nematode communities will help in developing new control measures to decrease plant pathogenic nematodes and increase beneficial nematodes.

A portable field pathogen-detection system for disease-free planting materials

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Cassava frogskin disease is characterized by the presence of woody roots that are cork-like, brittle, and opaque. The peel is thick and will not lift off easily. It is marked by lip-like depressions that join each other in such a way as to resemble a net or honeycomb. The disease disseminates through the use of vegetative seed from fields of infected cassava. A diagnostic technique is needed that will guarantee cassava seed health in the field. The use of deep sequencing indicated that the best region for developing primers for the loop-mediated isothermal amplification kit (LAMP) is the 16S rDNA gene because it is a tandem region (more than one copy of the gene per cell) that is polymorphic for different phytoplasma groups. For LAMP reactions, fluorochrome hydroxynaphthol blue, which does not need observation under UV light, was used. For reactions in the field, a prototype incubator was developed, involving a 5-W solar panel, 12V 12Ah battery, voltmeter, and

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mini dry bath with a 35-sample capacity. The kit's sensitivity was equal to that of the qPCR technique and 1000 times that of the nested PCR technique. This LAMP kit could process 35 samples in 90 minutes without requiring electrical connections or any need to leave the field.

Characterization of the *Colletotrichum* species infecting apple and other fruit crops in the northeastern United States

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The genus *Colletotrichum* comprises a diverse group of endophytic and pathogenic ascomycetes that are capable of utilizing a wide array of plants as hosts. This fungal group is responsible for a variety of diseases that have the potential to cause significant economic losses, including anthracnose, bitter rot, and leaf spot. Three taxa, *Colletotrichum gloeosporioides*, *C. acutatum*, and *Glomerella cingulata*, are currently associated with bitter-rot of apple (*Malus domestica*) with *C. acutatum* typically being the dominant species found in the northeastern United States. However, a recent phylogenetic study reclassified the global population of *C. acutatum* into a species complex, comprised of 29 different species, of which 10 species were reported to infect apple globally. Therefore, the objective of this study was to complete a survey of the molecular diversity of *Colletotrichum* associated with apple and other fruit in the eastern United States. Isolates of *Colletotrichum* were collected from apple, apricot, blueberry, blackberry, plum, strawberry, and watermelon from across New Hampshire, Massachusetts, New York and Indiana. The multi-gene phylogenetic analysis was completed using ITS, β -tubulin and GADPH gene sequences. Preliminary results indicate that species diversity on apple was limited, as *C. fioriniae* was the dominant species recovered from both apple leaves and fruit in the northeastern U. S. In addition, *C. fioriniae* was frequently recovered from other fruit species including apricot, blueberry and blackberry. This study demonstrates that *C. fioriniae* is the primary pathogen causing both bitter rot and Glomerella leaf spot in the Northeast and may be present on a number of plant species in the area.

***In vitro* isolation of a phytoplasma associated with frogskin disease of cassava (*Manihot esculenta* Crantz)**

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In Colombia, frogskin disease is a limiting factor of the cassava crop, causing as much as 90% losses of roots. Recent studies at CIAT, Colombia, indicate an association of a phytoplasma with diseased plants. To advance knowledge on the disease and the role of the phytoplasma in its development, this study aims to isolate the microorganism *in vitro*. Fragments of roots, petioles, stems, leaves, and embryos from diseased cassava plants were planted in Phytoplasma *in vitro* liquid medium (PivL) and incubated at 25°C. When the PivL changed color from red to orange, an aliquot of 50 μ L was then transferred to Phytoplasma *in vitro* solid medium (PivS). This medium was kept under anaerobic conditions and at one atmosphere at 95% N and 5% C. The presence of phytoplasmas was verified, using the techniques of nested PCR, qPCR, RFLP, and sequencing. Moreover, optical and transmission electron microscopy was used to examine the solid medium. The PivL medium changed color between 5 and 10 days when root and embryo tissues were used, and colonies on PivS were observed after 12 to 15 days. The molecular tests showed 450-bp bands with primers M2/M1, polymorphic patterns similar to those of group III, and sequences with 99% homology with cassava frogskin disease phytoplasma from both media. Photographs of colonies of 1-mm diameters (20X) were also taken. Pleomorphic cells without walls and measuring between 0.5 and 2 microns were obtained from the solid medium. This is the first report on the isolation of a phytoplasma associated with cassava frogskin disease, using an artificial culture medium.

***Phytophthora* species baited from the Connecticut River Valley in Massachusetts and discovery of a putative novel species from the *P. citricola* s.l. complex**

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Phytopathology 105(Suppl. 1):S1.6

Phytophthora species were surveyed at 17 sites in the Connecticut River Valley in Massachusetts to assess the overall assemblage of native and non-native species. Many of the sampled waterways were adjacent to active agricultural lands, yet were buffered by mature floodplain forests composed of *Acer*, *Platanus*, *Populus* and *Ulmus*. Isolates were collected at one to two

week intervals from May through October in 2013 and 2014 using three types of baits (rhododendron leaves, pear and green bell pepper) and water filtration through 5 μ m membranes. Field soils were also baited from after drying and flooding in the greenhouse. To date, over 400 oomycete isolates have been recovered and 253 isolates of *Phytophthora* have been identified. Based on morphological characters and DNA sequences (ITS, β -tub and *cox1*), 12 species have been identified and include (in decreasing order of abundance): *P. hydropathica*, *P. plurivora*, *P. irrigata*, *P. lacustris*, *P. taxon* PgChlamydo, *P. pini*, *P. sp.*, *P. citrophthora*, *P. gonapodyides*, *P. citricola* MA, *P. hydrogena* and *P. riparia*. Four species of *Pythium* (*Py. litorale*, *Py. vexans*, *Py. undulatum* and *Py. sp.*) were also recovered. Three species in the *P. citricola* s.l. complex were identified: *P. plurivora*, *P. pini*, and a putative novel species, referred to here as *P. citricola* MA. To determine the host specificity of *P. citricola* MA, one-year-old twigs from 12 potential host tree species, representing nine genera, were under-bark inoculated and assessed for lesion formation. Inner bark and sapwood lesions were detected only on species of *Carya* and *Juglans*, and the pathogen was re-isolated from stained sapwood tissue. Inoculation trials on *Carya* and *Juglans* saplings will take place to confirm the preliminary results and fulfill Koch's postulate. The results illustrate a high level of native and non-native *Phytophthora* species diversity in the Connecticut River Valley.

Preliminary evaluation of four decision support systems for management of apple scab in the northeastern U.S.

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Apple scab (causal agent *Venturia inaequalis* Cke.) generates more fungicide use in commercial production in the northeastern U.S. than any other disease. Management focuses on primary infections caused by ascospores. The length of primary season depends on ascospore availability, which can be determined by direct observation or by using ascospore maturity models driven by environmental parameters, primarily temperature. Models based on temperature and leaf wetness evaluate whether an infection occurs. These models can use predicted weather data to forecast ascospore maturity and apple scab infections. Producers can use such forecasts to determine the need for fungicide applications, possibly making treatments more effective and efficient. Four such decision support systems (DSS) available in the Northeast include the Network for Environment and Weather Applications (NEWA) at Cornell University; AgRadar at the University of Maine; SkyBit at ZedX, Inc, (PA); and RIMpro at Bio Fruit Advies (NL). In 2014, these four DSS's were compared in terms of the number of primary infection periods and the length of the entire primary season from 0 to 100% ascospore maturation and release. The number of primary infection periods ranged from six to ten. The date of the last ascospore release varied from May 28 to June 3. The number of fungicide applications recommended was either 6 or 7. Three of the DSS's (NEWA, SkyBit and RIMpro) were used to time fungicide treatments to manage apple scab in a test block of McIntosh at the University of Massachusetts Cold Spring Orchard. Treatments were compared to a non-sprayed control and a standard application regimen timed without using a DSS. There were no significant differences between the DSS's or the standard treatment schedule in terms of disease incidence or severity. All treatments reduced scab significantly compared to levels in the control.

***Diplodia cupressi* and other canker pathogens on Leyland cypress in Long Island, NY nursery and landscape settings**

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Leyland cypress [$\times$ *Hesperotropsis leylandii* (A.B. Jacks. & Dallim.) Garland & Gerry Moore (*Hesperocyparis macrocarpa* $\times$ *Callitropsis nootkatensis*)] has become widely used in Long Island landscapes as a living screen between properties. Before 2012, few samples of this tree were submitted for diagnosis, but its popularity and problems have escalated. Pathogens have included species of *Botryosphaeria*, *Seiridium*, *Phomopsis*, and *Pestalotiopsis*. In 2012, a fungus with morphology consistent with *Diplodia cupressi* was isolated from cankers on Leyland cypress. Wound-inoculation of potted Leyland cypress 'Leighton Green' in a greenhouse led to shoot death and the fungus was reisolated. Sequences of ITS1, 5.8S and ITS2 regions of nuclear rDNA were found to match the *D. cupressi* holotype. Environmental stress due to shading and competition for water in closely-spaced plantings is typical for Leyland cypress in LI landscapes. Continued problems with *D. cupressi* and other canker fungi are anticipated for this ornamental under these conditions.

Using nanoparticles of metallic oxides to suppress soilborne diseases of eggplants and tomatoes

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Materials at the nanoscale or nanoparticles (NP) possess unique properties not observed in equivalent bulk materials. We hypothesized that NP of certain metal oxides applied foliarly may allow a slow release of ions and/or particles that may be loaded into the phloem for transport to disease-susceptible root tissues. NP of Al, Cu, Fe, Mn, Ni, and Zn oxides were foliarly applied to tomatoes to assess their effect on growth and Fusarium wilt. Six weeks later, NP of Cu and Mn were associated with less disease; NP of Al, Fe, and Ni had no effect or were associated with increased disease. Subsequent greenhouse studies compared bulked oxide equivalents to NP of Cu, Mn, and Zn for their effect on Fusarium wilt of tomato and Verticillium wilt of eggplant. Disease development was lowest and plant weights were highest on tomatoes and eggplants treated with NP of Cu. Root digestions revealed that Cu levels were highest in plants treated with NP when compared to the bulked Cu equivalent or untreated plants. Field studies were conducted with eggplants in soil naturally infested with *Verticillium dahliae* in 2013 and 2014. Three to 4 wk.-old eggplant transplants were foliarly treated once with NP of Cu, Mn, and Zn or their bulked equivalents and set into the field plots. Yield, growth, and disease were measured over the season. Only NP of Cu increased the plant canopy and increased yield when compared to controls. One possible explanation may be the increased basipetal translocation of Cu ions from NP as opposed to bulked equivalents to roots where activation of host defense products like lignin and phenolic products occur. These findings suggest the unique size of NP of Cu may favor their entry into the phloem and transport in plants and may have a future role in disease management.

Turbulent wind in a vineyard canopy

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The spread of disease caused by pathogens which are disseminated via airborne spores is critically dependent on the details of air flow within and immediately above the plant canopy. For field crops having a relatively homogenous canopy structure the details of the wind field has been well studied. Trained trellised grapes, however, have a unique "elevated hedgerow" structure. The foliage along a row is limited to a height of between 1 and 2 meters and is trained using catch wires to extend less than half a meter perpendicular to the row. Cross-row wind is characterized by a blow-through under canopy air flow and intermittent circulatory eddies between rows. Down-row wind flow is very similar to the wind field above bare ground with some enhanced turbulence. Preliminary measurements using six 3D Sonic anemometers are presented to illustrate the various air flow patterns. The impact of the observed wind fields on the spread of grape diseases will be discussed.

Population genomics of *Phytophthora infestans*

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There have been major advances in our understanding of the genomics of *Phytophthora infestans* and its interactions with potato and tomato in the past decade. This organism was recently ranked as the most important oomycete plant pathogen in terms of molecular studies. Interestingly, it was not too long ago that, *P. infestans* had been regarded as being recalcitrant to basic studies. Initial major applications of this information have been in taxonomy and population genetics. From such studies, we now understand Oomycetes to be 300–350 million years old, and the debate concerning the center of origin of *P. infestans* has been fueled by genomic data. Another major contribution of genomic studies is to identify hypotheses concerning the biology and pathogenicity of *P. infestans*. The discovery of the RxLR motif as a signal for oomycete effectors has enabled investigators to predict more than 500 effectors in a single individual. Importantly, the availability of a sequenced genome has also enhanced the interpretation of gene expression studies. However, phenotypic analyses indicate that some predictions from only genomic analyses may be inaccurate. Thus both genomic and phenotypic analyses are required for accurate understanding. Illustrations of how genomic/phenotypic analyses have enhanced our understanding will be described in three general areas: i) the role of specific effectors; ii) fungicide resistance in the pathogen and iii) additional interpretations of host responses to infection.

Replacement of chlorothalonil for cranberry fruit rot control

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In response to increasing concern with regard to minimum residue limits (MRLs), an Organic Materials Research Institute (OMRI) approved polyoxin-D zinc salt fungicide with a 0 day pre-harvest interval (PHI) was tested as a possible replacement for chlorothalonil in a standard fruit rot fungicide regime on *Vaccinium macrocarpon* (large-fruited American cranberry). A standard fungicide regime for *V. macrocarpon* is typically two sprays of azoxystrobin and fenbuconazole followed by three sprays of chlorothalonil. In this study one, two, or three of the chlorothalonil applications were replaced with polyoxin-D zinc salt. The field trial was designed as a randomized complete block design with eight replications and was conducted under high disease pressure on the cultivar Stevens at the Phillip E. Marucci Center for Blueberry and Cranberry Research and Extension in Chatsworth, New Jersey. Replacement of the final chlorothalonil spray with polyoxin-D zinc salt proved as effective at controlling fruit rot as the standard fungicide regime and increased the pre-harvest interval for chlorothalonil from 65 days to 79 days. Although replacing two or three chlorothalonil sprays with the polyoxin-D zinc salt showed higher average rot when compared to the standard regime, these treatments were significantly lower in relation to treatments that used only two sprays of azoxystrobin and fenbuconazole, as well as in relation to completely untreated controls. Further rot assessments performed at harvest will determine the ultimate effectiveness of the chlorothalonil replacement treatments at suppressing cranberry fruit rot. Should polyoxin-D prove sufficient at controlling rot, it will provide an important tool for matching cranberry disease management programs with current MRL restrictions.

Behavior of *Phytophthora erythroseptica* in plant infection mediated by microbe-secreted compounds

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Phytophthora erythroseptica is a soilborne pathogen causing pink rot of potato. Its zoospores serve as inocula for host infection, which can be regulated by self or other environmental factors. In this study we focused on the chemical compounds secreted from both *P. erythroseptica* and other soil microbes, and determine how the microbial environment impact the pathogen. Zoospore exudates (ZE) of *P. erythroseptica* were collected from high-density zoospore suspension (10^4 zoospores/ml) by filtration. Freshly produced zoospores of *P. erythroseptica* at 10^2 and 10^4 zoospores/ml were treated either with water (control), ZE, or soil extract. The treated zoospores were either incubated in a depression well (100 μ l per well), or inoculated on potato tuber slides (10 μ l for each concentration per inoculation), which were incubated at 22°C. Zoospore germination and host infection were observed. *Phytophthora erythroseptica* at 10^4 zoospores/ml germinated and successfully infected potato tuber slides in all treatments. In contrast, at 10^2 zoospores/ml, zoospores neither germinated nor infected potato tuber slides when treated with water. However, zoospores germinated and successfully infected potato tubers when treated with ZE and soil extract. The results indicated that zoospore behavior is mediated by compounds from *P. erythroseptica* and possibly other soil microorganisms. Results from thin layer chromatography assays showed that there were at least three possible compounds in ZE. These compounds will be further determined using liquid chromatography and mass spectra analysis.

Molecular diagnostics for the boxwood blight pathogen, *Calonectria pseudonaviculata*

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Since first detected in Connecticut and North Carolina in October 2011, *Calonectria pseudonaviculata*, the fungus that causes boxwood blight, has been found in 13 additional U.S. states and three Canadian provinces. The disease has affected boxwood and other members of the Buxaceae, including *Pachysandra* spp., in both nurseries and landscapes, and has caused significant economic losses. First observed in the U.K. in the 1990s, it is now widespread throughout Europe and New Zealand. Two genetic clades occur in Europe: the predominant G1 clade is the only clade identified to date in the U.S.; the G2 clade, more restricted in its distribution, demonstrates higher thermotolerance and resistance to at least two fungicide classes. The disease is noteworthy for its potential to kill plants in as little as two weeks, making rapid, accurate and early detection a critical component of all management strategies, and a principal objective of this study. Real-time PCR primers and probe were designed for a 97-bp region of the histone (H3) gene containing an

intron highly variable among *Calonectria* species, resulting in probe hydrolysis and fluorescence only in the presence of *C. pseudonaviculata* DNA. The assay is sensitive down to 10 pg of target DNA, even when in the presence of boxwood DNA. When assaying DNA extracted directly from putatively infected plants, the H3 assay can be duplexed with universal plant cytochrome oxidase (COX) primers and probe, providing an important internal control on DNA quality. We demonstrated through artificial inoculations of boxwood plants that *C. pseudonaviculata* can be reliably detected from asymptomatic plants one day after infection. We have also developed probe-based SNP allelic discrimination assays based on H3, calmodulin, and beta-tubulin, that distinguish between the G1 and G2 clades; no G2 isolates have been detected yet in North America, making early detection critical.

Status of fungicide sensitivity in *Podosphaera xanthii* and impact on managing cucurbit powdery mildew in New York

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Effectively managing powdery mildew in cucurbit crops necessitates applying fungicides at risk for resistance development because their mobility enables movement to the lower leaf surface where the pathogen develops best. Efficacy of such fungicides was determined by applying them at highest label rate weekly a total of 5 times with a tractor-sprayer to field-grown pumpkin in a replicated experiment in 2013. A leaf disk bioassay was used to determine fungicide sensitivity of isolates collected after treatment was completed. Currently-registered fungicides were effective. Based on AUDPC values for severity on lower leaf surfaces in the field experiment, control was 93% for Pristine (FRAC Code 7 and 11), 95% for Procure (FRAC 3), and 99% for Quintec (FRAC 13). The bioassay revealed that all isolates tested were resistant to FRAC code 1 and 11 fungicides; 23% (6 of 26 isolates) were resistant to boscalid (FRAC 7 ingredient in Pristine); 27% were able to grow on leaf disks treated with 80 ppm myclobutanil (FRAC 3); and 81% on disks treated with 40 ppm quinoxyfen (active ingredient in Quintec). All 4 isolates from pumpkin treated with Pristine alone were resistant to boscalid (tolerated 500 ppm). This adds to previous observations that using at-risk fungicides alone during a growing season can select for resistant strains. In this case product efficacy was not impacted. Boscalid resistance was detected in 1 of 3 isolates from pumpkin treated once with Pristine applied in alternation with Quintec and Procure. An isolate tolerating 80 ppm quinoxyfen was obtained from a Quintec plot.

The causal agent(s) of blueberry stem blight disease in New Jersey

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Blueberry stem diseases are not controlled by currently available pesticide programs. One of the most serious of these diseases in highbush blueberry is stem blight (commonly referred to as Botryosphaeria stem blight). Symptoms of stem blight include color change and/or drying of the leaves on one or more canes. Infected canes can die rapidly with brown leaves remaining attached to the stem. The causal agent was first described in 1958 as a species of *Botryosphaeria* distinct from that which causes stem canker (*B. corticis*). The species was later described as *B. dothidea*. Differences in both symptomatology and fungal morphology suggest that other species may be involved. A study of the causal agents of the disease in southern highbush blueberry in Florida identified two primary fungal species (*Lasiodiplodia theobromae* and *Neofusicoccum ribis*). These species are in the Botryosphaeriaceae and are closely related to *B. dothidea*. We collected samples exhibiting symptoms of stem blight from two counties and 13 different commercial farms in New Jersey. Samples were collected throughout the season (May-August), but symptoms were most apparent in July-August when the majority of samples were collected. A total of 262 fungal isolates were cultured from 210 stem samples. The isolates were separated by

morphotype and selected representatives of each morphotype were sequenced. The primary causal agents of classic stem blight in New Jersey were identified to be *B. dothidea* and *Neofusicoccum* sp., based on ITS sequence analyses. *Phomopsis vaccinii* was also frequently isolated. This species (*P. vaccinii*) is the causal agent of twig blight and canker in highbush blueberry and as such, these isolates were typically originated from stems exhibiting tip dieback. Some species (e.g., *Pestalotia vaccinii*) not thought to cause stem blight were also isolated. Confirmation of pathogenicity of all isolates is in progress.

Biological control of blueberry and cranberry fruit rot targeting host plant floral-extracts

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Phytopathology 105(Suppl. 1):S1.8

Colletotrichum acutatum and *Coleophoma empetri* are two of the most important plant pathogens affecting blueberry and cranberry production in the Northeast. Effective disease control has only been achieved when applications of fungicides are made around the time of bloom. Our previous research has demonstrated that water-soluble floral-extracts from both host species will induce and increase appressorial formation, enhance microcyclic conidiation as well as increase hyphal growth. The purpose of this study was to evaluate a novel target, that includes water-soluble floral compounds critical for pathogenesis, for biological control. Selected *Bacillus* and *Paenibacillus* isolates, including some registered biological controls, were tested for the ability to utilize and inactivate floral-extracts. *In vitro* assays were used to screen for digestion and inactivation of the stimulatory principle of the extracts. Some of the bacteria collected from cranberry tissues also possessed strong antifungal attributes, which were evaluated via inhibition assays on growth media. Replicated field trials and associated storage tests were conducted on two cultivars of blueberry, early season cv Duke and mid-season cv Bluecrop and one cultivar of cranberry, cv Stevens. Bacterial suspensions were applied during and immediately following the bloom period in both blueberry and cranberry. The field trials demonstrate that some control is achieved comparable to established biological controls available on the market, especially in the early blueberry cv Duke. This research aims at development of screening procedures and applications of biological control bacteria that will be available for future research.

Characterization of fungi associated with needle defoliation of eastern white pine (*Pinus strobus*)

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Eastern white pine is a crucial ecological and economic component of forests in the northern USA and eastern Canada, and is facing an emerging problem in white pine needle defoliation (WPND). It is unclear whether WPND is caused by one or a combination of multiple fungal pathogens. Therefore, the objective of this study was to characterize the fungi associated with WPND in the northeastern United States. To date 16 species of fungi, either cultured from diseased pine needles or formed fruiting bodies on pine needles, were identified based on morphology and sequence data. *Lecanosticta acicola* (*Mycosphaerella dearnessii*), a historically southern pine pathogen, and a putative new species of *Septorioides* were the species most frequently recovered from diseased needles. We also provide the first phylogenetic analysis of *Canavirgella banfieldii* and *Bifusella linearis*, two obligate biotrophic fungi frequently observed on pine needles in the northeast, for which no sequence data was previously available. In addition, putative new species of *Stagonospora* and *Hemiphacidium* found on eastern white pine are described. While *L. acicola* appears to be the primary pathogen causing WPND several new emerging pathogens as well as other common needle pathogens are being more frequently observed. Current research is investigating the role of climate on epidemics of WPND, the epidemiology, and potential northerly migration of *L. acicola*.