2019 Research Symposium
Wednesday June 19
9:00am-3:30pm

Organized and hosted by members of S.A.G.E.S.
Schedule of Events

8:30 – 9:00 a.m.
Light Breakfast and networking

9:00 – 10:00 a.m.
**Keynote Address: James Livengood, Radicle Farm Co.**
*The Future of Food is Precarious (and Hopefully Not Local): Lessons from a Local Farm*

10:00 – 10:30 a.m.
Poster Session and coffee break

10:30-10:45 a.m.
**Samantha Willden**
*A biological survey of common strawberry pests found on low tunnel versus open-field grown strawberry in New York*

10:45-11:00 a.m.
**Zachary Stansell**
*Understanding Broccoli: Complex horticultural quality traits are illuminated by evaluating the immortal BolTBDH mapping population*

11:00-11:15 a.m.
**Dustin Wilkerson**
*Using the Salix F1 hybrid common parent mapping population to map resistance to Melampsora leaf rust*

11:15 – 11:30 a.m.
Break

11:30-11:45 a.m.
**Ashley Jernigan**
*Invertebrates strengthen the linkage between soil microbial activity and crop productivity*

11:45-12:00 p.m.
**Rey Cotto**
*Identifying the genetic association between the ABCC2 gene and the down regulation of the APN1 protein*

12:00 – 1:20 p.m.
Lunch at Jordan Hall Pavilion (rain location: Jordan Hall Staff Room/Auditorium)
1:30-1:45 p.m.
**Gregory Vogel**
*Genotyping-by-sequencing of Phytophthora capsica isolates from New York farms enables the discovery of loci associated with mating type and mefenoxam sensitivity*

1:45-2:00 p.m.
**Christopher Peritore-Galve**
*Characterizing xylem colonization and infection of Clavibacter michiganensis subsp. michiganensis in tolerant wild tomato species*

2:00-2:15 p.m.
**Larissa Osterbaan**
*Grapevine fanleaf virus vein clearing symptoms in Nicotiana benthamiana are modulated by a single residue of a viral protein*

2:15-2:30 p.m.
**Al Kovaleski**
*Progress in modeling grapevine bud cold hardiness*

2:30-2:45 p.m.
Break

2:45-3:00 p.m.
**Laura Dougherty**
*Exploring DNA variant segregation types enables identification of columnar apple recessive repressors and a Co-gene network*

3:00-3:15 p.m.
**Bill Weldon**
*Early season infection of hop powdery mildew (Podosphaera macularis) chasmothecia*

3:15-3:30 a.m.
**Katrin Ayer**
*Preserving fungicide efficacy in the field: managing resistance of V. inaequalis to SDHI fungicides*

3:30 – 4:30 p.m.
Reception and networking at Jordan Hall Pavilion
Hosted by the Student Association of the Geneva Experiment Station (SAGES)
James Livengood is Co-Founder and Owner of Radicle Farm Company in Newark, NJ, and Utica, NY, a year-round hydroponic grower of baby greens and herbs. He has built and/or refurbished more than 60K square feet of greenhouse space, designed and implemented a range of diverse production systems, and facilitated a variety of school- and community-focused training programs on local food production. Since its inception in 2014, Radicle has produced and sold roughly three-quarters-of-a-million pounds of greens and herbs. James believes the ideal food system is diverse, resilient, and equitable. James likes a good salad, but not as much as he likes building the systems, or working with the people, that grow that salad.
An evaluation of potential terroir-based differences in New York State hops
Gaëlle Vier1, K. Kirkpatrick1
1Cornell University, Department of Food Science, Cornell AgriTech, Geneva, NY 14456

Driven by the new Farm Brewery legislature passed in 2012, New York State (NYS) is now home to more than 5400 acres of hops, one of the defining elements of beer. With diverse growing conditions across the state, hop growers wonder what makes their hops different from their neighbors. The objective of this study is to determine if terroir has an impact on the chemical composition, and ultimately flavor potential, of hops. This research focused on the hop variety Cascade, popular for its sensory qualities in beer and agronomic value. Cascade hops originating from five different farms located across NYS were evaluated. Several points including the geographical location, elevation, climate, soil and its characteristics, post-harvest processing and storage were considered as potential factors contributing to terroir. To evaluate chemical differences, steam distillation was performed in order to collect essential oil, a component relating to hop aroma. The percentage of alpha and beta acids, responsible for bittering potential, were also analyzed by spectrophotometry. Hops essential oil was further analyzed by gas chromatography; 15 flavor compounds known to be important to hoppy beer flavor were quantitated using calibration curves of known chemical standards. Findings from this study can benefit both hop growers and brewers; hop terroir may add value to regional products and more consistent products may be achieved with a better understanding of the varietal differences in hops. A follow up study taking into account year to year variation will help establish the significance of this preliminary work.

Effects of pH, storage temperature, and alcohol content on foodborne pathogens in dry-hopped beer
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Hoppy beers have gained popularity in the beer market in recent years. On farm, hops must first undergo a kilning step to preserve quality and microbial stability during storage. Unlike the traditional kilning method, which subjects hops to temperatures between 60 – 80°C, new techniques boast temperatures below 60°C and in some instances, air drying and dehumidification is used. Hops may come in contact with food borne pathogens on farm and in processing; therefore, it is important to evaluate the risks associated with handling this material. While beer offers protective qualities against food borne pathogens, gram-negative bacteria such as E. coli, and Salmonella have shown resistance towards the bacteriostatic effects of hop acids. In this experiment, a risk assessment was carried out to identify the parameters which offer protection for and from three foodborne pathogens (E. coli O157:H7, S. enteritidis, and L. monocytogenes). The effects of ethanol, pH, and storage temperature were explored for the gram-negative bacteria (E. coli O157:H7 and S. enteritidis), whereas hop acids affected gram-positive (L. monocytogenes) bacterial growth. The low alcohol beer (3.2% ABV) showed an inhibitory effect on the growth of E. coli and Salmonella, and Listeria had the highest CFU/ml reduction over the incubation period (63 days). In addition, cold storage at 4°C resulted in a lower bacterial count as compared to 14°C. The gram-negative pathogens revealed growth in non-alcoholic beer (<0.5% ABV) and storage at 14°C, whereas cold storage (4°C) and high pH (4.8) had a shielding effect on L. monocytogenes. The results of this risk assessment will better inform safe practices for handling hops on farm and using this essential ingredient in beer.
Monitoring onion thrips (Thysanoptera: Thripidae) susceptibility to spinetoram in New York onion fields

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Onion thrips (Thrips tabaci Lindeman) is a severe pest of onion (Allium cepa L.). Their management relies on frequent applications of foliar insecticides, including spinetoram (Radiant®SC), which has a novel mode of action and is effective at controlling large populations. However, despite being widely used for the past 10 years, susceptibility to spinetoram has not been evaluated formally in New York state, where nearly 3,000 hectares of onion are planted annually. Over two years (2017-2018), the susceptibility of onion thrips to spinetoram was assessed from populations collected in commercial onion fields in New York. LC₅₀s for adults were generated from feeding assays and ranged from 2.07-5.08 ppm, indicating that onion thrips populations continue to be susceptible to spinetoram. Moreover, there was little regional or temporal variation in susceptibility among these populations. These results serve as a valuable reference for the continued monitoring of onion thrips susceptibility to spinetoram, contributing to ongoing efforts to manage insecticide resistance in this system.

Systemic seed treatment uptake: relationship of the fluorescent tracer, Coumarin 120 and water uptake in corn seeds

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Seed coat permeability regulates the rate of water and systemic seed treatment uptake during the first stage of germination. The objective of this study was to evaluate the effect of corn varietal differences on uptake during imbibition. The fluorescent tracer, coumarin 120 was used to mimic a systemic seed treatment. In addition, correlations were calculated between fluorescent tracer uptake and water uptake. Nine corn inbred lines and 1 variety were examined, and water uptake during the first 24 hours was quantified. Coumarin 120 was chemically extracted from imbibed seeds and analyzed with a spectrofluorometer. Water uptake had a significant linear relationship with the imbibition time (Log 10 transformed) for all 10 lines/variety. The inbred line, OH7B had the highest concentration of coumarin 120, while B73 has the lowest concentration after 14 hours of imbibition. The uptake of coumarin 120 had a significant linear correlation with the uptake of water at 4 or 24 hours of imbibition time. Collectively, there are large genotypic differences in corn seed with respect to both water and coumarin 120 uptake. Systemic seed treatment uptake and consequently early season pest management may vary by variety due to differential uptake of active ingredients. This material is based upon work that is supported by the National Institute of Food & Agriculture, US Department of Agriculture, Federal Capacity Multi-State Fund, under W-3168.

Biostimulant seed coating to enhance Italian ryegrass seedling stand establishment

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Italian ryegrass, Lolium multiflorum is noted for its high forage quality, and is also grown as a cover crop. Biostimulants can enhance the physiological mechanisms resulting in increased plant growth. Biostimulants are commonly applied as foliar treatments, but pioneering research in the Taylor Seed Technology Lab at Cornell AgriTech has focused on biostimulants applied as seed treatments. In the present study, novel seed coating formulations were developed by using biostimulant components, including soy flour, a plant-derived protein and micronized vermicompost. Soy flour also served as a seed coating binder or adhesive to maintain the seed coating strength.
Ryegrass seeds were coated with different combinations of soy flour and micronized vermicompost. All coatings were applied with a rotary pan seed coater with a 1:1 (seed : coating material). The mechanical properties of coated seeds are important indices to evaluate the quality of seed coating formula. As the proportion of soy flour ratio increased from 30 to 50%, the mechanical strength of coated seeds increased as measured by a TA.TX-PlusC analyzer (Texture Technologies Corp.). This also resulted in a longer time for coatings to disintegrate in water. The coated seeds were tested in the lab under controlled conditions of 15/25 °C with a 16/8 h photoperiod. All coated treatments improved seedling growth compared to the non-treated control. Biostimulant coatings increased shoot height by 22 to 29% and root length by 18 to 23% compared to a non-treated control. Biostimulant coating have the potential to effectively promote seedling growth and early stand establishment of Italian ryegrass. This material is based upon work that is supported by the National Institute of Food & Agriculture, US Department of Agriculture, Federal Capacity Hatch Funds, under Accession #1017599.

Super absorbent polymer seed coating to mitigate drought stress and improve cover crop stand establishment
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Early season drought threatens seedling establishment of all seeds, including cover crops. Development of a seed coating system containing a super absorbent polymer (SAP) was proposed as a method to decrease the risk of soil moisture deficit at the soil surface. The objective of this project was to develop seed coating formulas using a SAP to protect the germinating seeds against a soil moisture deficit. Red clover seeds were coated using laboratory-scale rotary pan coater in the Taylor Seed Technology Laboratory with 1:1 build-up of different proportions of SAP components (0, 1, 10 and 20%). The SAP, ‘Stockosorb’, is a cross-linked polyacrylate polymer (Evonik Corp., Greensboro, NC). The SAP coated seeds imbibe water rapidly and causing the seed coat to swell while maintaining integrity. Seeds were sown on the surface of a Montmorillonite clay (40/100 LVM) with 95% moisture content in plastic containers in a growth chamber. To simulate drought stress during germination, soil media was air dried for 24h after sowing and the containers were sealed. Maximum seedling emergence was 50% for the non-treated control compared to greater than 90% for the seed coated with 10 or 20% Stockosorb. Seedling drought survival was 20% for the non-treated control compared to 70% for the seed coated with 10 or 20% Stockosorb. Novel seed coating technologies using SAP materials could potentially be an effective strategy to minimize early season drought stress and enhance seed germination. This material is based upon work that is supported by the National Institute of Food & Agriculture, US Department of Agriculture, Federal Capacity Hatch Funds, under Accession #1017599.

Selection of switchgrass genotypes for cold tolerant and rapid germination from native populations in the Northeast USA
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Switchgrass seed harvested from individual genotypes from a cool temperature breeding population selected from switchgrass breeding nurseries was evaluated for cold tolerant germination in a series of germination tests. The switchgrass nurseries were established in 2008 and 2009 from seed collected from native stands of switchgrass in the Northeast USA (NE) between 1991 and 2008. Cold tolerant seed
germination of switchgrass genotypes was evaluated (with and without stratification) using a 10/15 °C cycle and 12-hour photoperiod. Germination tests showed that several lines from the cool season breeding nursery had significantly higher maximum percentage germination as well as faster germination rates expressed as T50 (number of days required to reach 50% maximum germination) when compared to control lines. The breeding lines also had significantly higher vigor index, an index that incorporates both the total percent and rate of germination compared to the non-selected control. In addition, a final germination test was conducted using seed collected from the original switchgrass breeding nurseries established in 2008 and 2009 (cycle 0), a top performing cool season breeding line, and a commercial cultivar 'Espresso' developed for rapid germination and low dormancy. In this test, both the breeding line and Espresso had significantly higher maximum and more rapid germination than the cycle 0 seed. These data indicate successful selection for cold tolerance and more rapid germination in switchgrass genotypes from native germplasm collected in the NE. This material is based upon work that is supported by the National Institute of Food & Agriculture, US Department of Agriculture, Federal Capacity Multi-State Funds, under NE-1010 and W-3168.

Toward identification of TAL effector targeted susceptibility genes in black rot of cabbage caused by Xanthomonas campestris pv. campestris

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Transcription activator-like effectors (TALEs) are a large family of type III secreted effectors present in some Xanthomonas species that specifically target and directly upregulate plant host genes. Xanthomonas campestris pv. campestris (Xcc) causes black rot of crucifers, one of the most important Brassica diseases worldwide. The first three complete Xcc genome sequences published had no TALE-encoding genes. However, more recent work and reclassification of Xanthomonas campestris pathovars have revealed that many Xcc strains do encode, and express, TALEs. By PCR and western and Southern blotting we surveyed 124 Xcc isolates from a 10-year New York State collection and found that 30% encode and express TALEs. Across the New York Xcc isolates, TALE repertoires differ, even between isolates found by multi-locus sequence analysis to be closely related. By targeted mutagenesis, we have found that multiple TALEs from different New York Xcc strains contribute to virulence in cabbage. We are sequencing TALE containing strains and identifying the brassica susceptibility genes targeted by these TALEs by binding site prediction and by using RNA-Seq and qRT-PCR. Identification of susceptibility genes could inform breeding of cruciferous vegetable crops for resistance to black rot.
Oral presentations

A biological survey of common strawberry pests found on low tunnel versus open-field grown strawberry in New York
Samantha A. Willden1, G. Loeb1
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Growing strawberries under plastic low tunnels is a new trend occurring in the northeastern United States. Although low tunnels extend the growing season of day-neutral variety strawberries, they may also provide good habitat for some pests. Indeed, this has been realized for the two-spotted spider mite (*Tetranychus urticae*), which can achieve especially high densities on protected cultures. The effect of plastic tunnels on the presence of other pests, however, has not been quantified for low tunnel strawberry although there is anecdotal evidence that several arthropod, mollusk, pathogen and weed pests establish well under plastic tunnels. This study presents the results of a broad biological survey quantifying the presence and severity of common strawberry pests found on open-field versus low tunnel grown strawberries in New York during the growing season of 2018. Monitoring of arthropods included the weekly deployment of pitfall and sticky card traps and counts of pests present on strawberry flowers and fruits. Slugs were monitored using beer baited slug traps. Presence/absence surveys were conducted to quantify the presence of common strawberry pathogens on a random subset of leaflets and fruits. Finally, weeds rooted within plots were identified, counted and dried overnight to determine both the number and dry weight of weed species in both open-field and low tunnel systems. The results of this research will benefit New York low tunnel strawberry growers by providing needed information on general pest incidence under plastic tunnels and specific targets for pest management.

Understanding broccoli: complex horticultural quality traits are illuminated by evaluating the immortal BolTBDH mapping population
Zachary Stansell1,2*, Mark Farnham3, Thomas Björkman1,2
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Improving horticultural quality in regionally adapted broccoli (*Brassica oleracea var italica*) and other *B. oleracea* crops is a challenging due to the complex genetic control affecting morphology, development, and yield. Mapping horticultural quality traits to genomic loci is an essential step in these improvement efforts. By unraveling the molecular mechanisms underlying horticultural quality and enabling multi-trait marker-assisted selection, improved, resilient, and regionally adapted *B. oleracea* germplasm may be developed. The publicly-available biparental double-haploid BolTBDH mapping population (Chinese kale x broccoli; *N* = 175) was evaluated by multiple quantitative trait loci mapping using 1881 genotype-by-sequencing derived single nucleotide polymorphisms. The physical locations of 56 single and 76 epistatic QTL were identified via multiple QTL mapping within 25 horticultural traits in six trait classes (architecture, biomass, phenology, leaf morphology, flower bud morphology, and head quality). Several key genomic hotspots associated with the broccoli heading phenotype and other quality traits are identified: four QTL (OQ_C03@57.0, OQ_C04@33.3, OQ_C08@25.5, OQ_C09@49.7) explain a cumulative 81.9% of variance (PVEtot) in the broccoli heading phenotype, contain the FLC homologs (*Bo9g173400* and *Bo9g173370*), and exhibit epistatic effects. Two phenology QTL (DF_C03@6.4 and DF_C09@50.0) reduce days to flowering by 7.0 and 8.3 days (PVEtot = 54.0), contain the FLC homolog *Bo3g024250* and the FLC homologs identified in OQ_C09@49.7. Strong candidates *BoLMI1* (*Bo3g002560*), and leaf apex shape, *BoCCD4* (*Bo3g158650*), implicated in flower color, and *BoAP2* (*Bo1g004960*) implicated in the hooked sepal horticultural defect, were also identified. The BolTBDH population
provides a framework for the improvement of broccoli and other B. oleracea crop groups by targeting key molecular mechanisms and enabling marker-assisted selection contributing to high-quality horticultural quality phenotypes.

Using the *Salix* F₁ hybrid common parent mapping population to map resistance to *Melampsora* leaf rust
Dustin Wilkerson¹, L. Smart¹
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Breeding programs benefit from knowledge of the genomic architecture of traits targeted for selection. In perennial crops like shrub willow (*Salix* spp.), developing genetic maps can help reduce the time between crossing and cultivar release that could otherwise take many years. We have developed the resources to take a multifaceted approach for mapping leaf rust resistance, including eight interspecific F₁ common parent families, and a *S. purpurea* F₂ mapping population. These populations have been planted in separate fields with four randomized complete blocks and have all been genotyped using genotyping-by-sequencing (GBS). The interspecific F₁ families have either a common female or male *S. purpurea* parent crossed to individuals of *S. suchowensis*, *S. viminalis*, *S. integra*, *S. udensis*, *S. koriyanagi*, and *S. alberti* and are being used to develop F₁ back cross maps for joint linkage QTL analysis. Phenotypes related to biomass, physiology, and pathology have been targeted with the purpose of developing molecular tools to advance shrub willow breeding. Description of the F₁ hybrid population, strategies used to construct the maps, and identified QTL will be presented.

Invertebrates strengthen the linkage between soil microbial activity and crop productivity
Ashley Jernigan¹, K. Wickings¹
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Soil and crop management practices can alter relationships between the soil food web, soil processes, and agroecosystem function. In 2005, the Cornell Organic Grain Cropping Systems Experiment was established in central New York State. Four organic grain cropping systems that varied in crop rotations, fertilizer inputs, tillage practices, and weed control were compared. In 2017, the experimental site was moldboard plowed and seeded with sorghum sudangrass as part of a uniformity trial to assess legacy effects of past management practices. Prior to initiating the uniformity trial, soil samples were collected and analyzed for soil health indicators. Soil samples were also collected to assess soil invertebrate abundance and community structure at two time points during the uniformity trial. Sorghum sudangrass and weed biomass were sampled at the end of the uniformity trial. Piecewise structural equation modeling (SEM) was used to quantify relationships between these different response variables. Results from SEM show that soil phosphorus, soil aggregate stability, and soil respiration explained variation in abundance of some invertebrates and that aggregate stability, soil respiration, soil moisture, weed biomass, and a select group of invertebrates affected the sorghum sudangrass biomass production. Our results provide evidence that soil invertebrates facilitate linkages between microbial communities and crop yield that may go undetected otherwise. In addition to illustrating relationships between crop productivity and soil health indicators, this research provides support for including direct measurements of soil invertebrates in soil health assessments due to their cross sensitivity to multiple soil health traits.
Identifying the genetic association between the ABCC2 gene and the down regulation of the APN1 protein
Rey Cotto1, P. Wang1
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Insecticidal proteins from the soil bacterium *Bacillus thuringiensis* (Bt) in genetically engineered crops has revolutionized the pest management practice in agriculture. Bt-crops have the potential to contribute with solutions to our world’s growing population, food demand and conversely provide significant environmental and economic benefits. However, development of resistance to Bt-toxins in insect pests threatens the sustainable application of this biopesticide in agriculture. The molecular mechanism of insect resistance to the Bt-toxin Cry1Ac has been identified to be associated with midgut brush border proteins aminopeptidase-N (APN) and the ATP-binding cassette (ABC) transporter ABCC2 in Cry1Ac resistant *Trichoplusia ni*, but whether APN1 expression is regulated by or associated with the ABC transporter is unknown. In this study, we seek to investigate if the high level resistance to Cry1Ac involves two genes, the ABCC2 gene and the gene controlling the APN1 down-regulation. Understanding the genetic association of ABCC2 and APN1 in field-evolved resistance to Bt toxins is crucial for understanding the complex genetic basis of Bt resistance in Lepidopteran pests.

Genotyping-by-sequencing of *Phytophthora capsici* isolates from New York farms enables the discovery of loci associated with mating type and mefenoxam sensitivity
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2Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

*Phytophthora capsici* is a soil-borne oomycete pathogen that causes fruit, root, and stem rots on several economically important vegetable crops, such as squash and pepper. Assaying pathogen isolates for mating type and fungicide sensitivity provides growers with information that has important implications for disease management, but can be time-consuming and laborious. With the goal of designing molecular markers for these traits, we phenotyped and genotyped using genotyping-by-sequencing a panel of 243 pathogen isolates, collected mostly from New York farms in recent years. These isolates were resolved into 127 unique genotypes after identifying clonal lineages that consisted of multiple isolates. Clonal lineages were unique to individual fields and isolates belonging to the same clonal lineage were consistent in terms of mating type and mefenoxam sensitivity. Using over 80,000 single-nucleotide polymorphisms (SNPs) and the clone-corrected dataset of 127 isolates, we performed a genome-wide association study for these two traits. A single locus was found to be highly associated with mating type and co-localized with the mating type region previously mapped using biparental crosses. Sensitivity to mefenoxam was associated with SNPs on several scaffolds, which may be physically linked or represent independent loci. This research represents the first use of a genome-wide association study to identify trait-associated molecular markers in a plant-pathogenic oomycete. Based on these results, we will develop PCR-based markers for these traits and validate their predictive ability in additional isolates.
Characterizing xylem colonization and infection of *Clavibacter michiganensis* subsp. *michiganensis* in tolerant wild tomato species

F. Christopher Peritore-Galvez¹, Christine Miller¹,², Christine D. Smart¹

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*Clavibacter michiganensis* subsp. *michiganensis* (Cmm) is the gram-positive causal agent of bacterial canker of tomato, an economically devastating disease with a worldwide distribution. Cmm colonizes the xylem, leading to unilateral wilt, stem canker, and eventually plant death. Splash dispersal of Cmm can also infect developing tomato fruit, forming bird’s-eye lesions. There are no documented sources of qualitative resistance, however, QTL that confer tolerance from *Solanum arcanum* and *S. habrochaites* have been identified. We hypothesized that complex morphological, genetic and metabolic factors of wild *Solanum* spp. would contribute to tolerance. In planta colonization and spread was measured and contrasted to Cmm growth in extracted xylem sap. Cmm aggregates in xylem vessels were observed using laser scanning confocal microscopy and scanning electron microscopy. These analyses demonstrated preferential colonization of protoxylem vessels in wild tomato species and limited spread to metaxylem vessels and parenchyma cells. Finally, we used untargeted metabolomics of xylem sap from *S. lycopersicum* and *S. habrochaites* to understand changes Cmm might be inducing in the xylem environment during infection. Preliminary metabolomic data demonstrate provide evidence for breakdown of sugars and defense compounds. Foundational studies of Cmm-tolerant host interactions may contribute to future development of strategies for prevention and management of bacterial canker.

Grapevine fanleaf virus vein clearing symptoms in *Nicotiana benthamiana* are modulated by a single residue of a viral protein

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Grapevine fanleaf virus (GFLV) is one of the most adverse viral pathogens of grapevine. It causes fanleaf degeneration disease of grapevine, which is characterized by developmental malformations, foliar symptoms such a yellow mosaic and leaf banding, uneven and poor berry set, and overall decline and premature death of the vine. The molecular mechanisms underlying symptom development are not well understood. In the herbaceous host *Nicotiana benthamiana*, most strains of GFLV produce asymptomatic infections. However, strain GFLV-GHu produces distinct vein clearing on apical leaves. A reverse genetics screen determined that vein clearing caused by GFLV-GHu in *N. benthamiana* is modulated by a single residue: lysine 802 of protein 1EPol. Substitution of this residue with other amino acids can attenuate or abolish vein clearing symptoms, though lysine 802 is not sufficient to produce vein clearing in an asymptomatic strain of GFLV. Furthermore, vein clearing development was not correlated with overall virus titer. The GFLV variants produced in this study will be used in a proteomics-based approach to identify potential protein interaction partners of 1EPol. Understanding the virus-host interactions which lead to symptom development can help guide the development of GFLV-resistant grapevines for the control of fanleaf degeneration.
Progress in modeling grapevine bud cold hardiness
Al Kovaleski1, J. Londo1
1USDA-ARS Grape Genetics Research Unit

Low winter temperatures frequently cause bud damage in vineyards of the Finger Lakes region, especially those located further from the lakes. A model based on field data was developed in 2011 in Washington State and further enhanced and expanded in 2014. This model is based on linear rates of gain (acclimation) and loss of cold hardiness (deacclimation) that have a discrete change between endo- and ecodormancy – where typically acclimation is enhanced during endodormancy and deacclimation during ecodormancy. The WA model, however, is not a good descriptor of bud cold hardness in the NY climate. Using growth chambers, we have shown that loss of cold hardness follows kinetics similar to enzyme temperature responses, but at any given temperature this response increases logistically with chill accumulation during the winter. Acclimation in growth chambers appears to respond to temperature, daily thermal amplitude, and chill accumulation, but responses are challenging to untangle. Based on measured deacclimation and estimated acclimation response curves, we have produced a new Eastern climate grapevine model for bud cold hardness that outperforms the currently available model.

Exploring DNA variant segregation types enables identification of columnar apple recessive repressors and a Co-gene network
Laura Dougherty1, Tuanhui Bai1,2, Susan Brown1, and Kenong Xu1
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Apple fruit production is a labor intensive practice. The columnar growth habit, first identified in a ‘McIntosh’ somatic mutation ‘Wijcik McIntosh’, is characterized by reduced branching, upright structure and exclusive spur bearing. These characteristics make columnar apple trees a good candidate for orchard mechanization, therefore reducing labor. Many studies have shown that the apple columnar trait is controlled by a single dominant gene, called Co (columnar) and a retroposon insertion present in ‘Wijcik McIntosh’ but not ‘McIntosh’ causes changes in the Co gene expression near the insertion. The Co gene was identified downstream the insertion and is upregulated in ‘Wijcik’ when compared to ‘McIntosh’. In addition to the Co gene, other genes have long been speculated to be involved in the columnar trait. This is particularly clear in a Coco x Coco F₁ population segregating for the columnar insertion, as a subset of trees carried the insertion exhibit standard phenotype. Using pooled genome sequencing approach and DNA variant analysis, we mapped two recessive loci (c2 and c3) that can repress the Co gene. RNA seq analysis revealed that Co and differentially expressed genes within c2 and c3 form a Co-expression gene network associated with growth habit.

Early season infection of hop powdery mildew (Podosphaera macularis) chasmothecia.
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Hop powdery mildew, caused by the ascomycete fungus Podosphaera macularis, is currently one of two major pathogens threatening the sustainability of the New York hop industry. The fungus causes economic damage when it grows on hop cones, rendering the cones physically deformed, discolored and with unacceptable secondary metabolite profiles for use in the brewing process. P. macularis can overwinter in one of two ways; i) when vegetative mycelia grow on to hop buds that reside just below the soil line, go dormant during the winter, and then emerge infected in the spring (termed a flag shoot), or ii) through sexually produced overwintering structures called chasmothecia, which house ascospores that are released in the spring. It was recently
demonstrated that *P. macularis* overwinters as a flag shoot with a success rate around one percent. The extent to which chasmothecia successfully overwinter and cause early season infection is not well described. We designed a pot-in-pot style hop yard for which potted hop plants were populated exclusively with *P. macularis* chasmothecia as an overwintering source. Spring 2019 disease incidence counts indicate that chasmothecia forming in the late fall of 2018 successfully overwintered and caused disease in 63.3% of hop plants, with an average disease severity per pot of 8.1%. The striking difference in overwintering success between asexually infected flag shoots and chasmothecial release of ascospores has major implications in how aggressively hop growers must manage the pathogen in the early spring, making it crucial to know which overwintering sources are possible within a given yard.

**Preserving fungicide efficacy in the field: managing resistance of *V. inaequalis* to SDHI fungicides**

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Apple scab, caused by the ascomycete fungus *Venturia inaequalis*, is one of the most economically devastating diseases of apple, causing lesions on both leaves and the fruit. In order to attain acceptable control in cool and wet climates, management relies on repeated applications of fungicides. With this high use of single-site fungicides comes the risk of resistance, which has become an increasing issue, limiting options for rotation. This research aims to evaluate resistant management strategies to the class of next generation Succinate Dehydrogenase Inhibitors (SDHIs); a group of single-site fungicides that inhibit fungal respiration. The effect of fungicide application rate (high vs. low rate) was evaluated over the course of three years in a repeated measures experiment using the SDHI fungicide fluxapyroxad. Following the completion of fungicide applications each year, isolates were collected from the field and subject to fluxapyroxad sensitivity assays. Trends show that application with a low rate of a single-site fungicide may result in more rapid selection for reduced-sensitivity isolates. However, to date, no isolates with full resistance have been identified. This selection experiment is ongoing in the fourth year and is similarly being conducted in other pathosystems to test broad applicability.
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