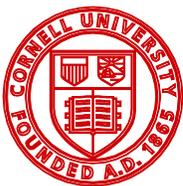


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These proceedings can be found on-line at

<http://www.scholars.pppmb.cals.cornell.edu/>

[1] Uncovering TAC1 and LAZY1 protein-protein interactions using a yeast-two-hybrid screen

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Shoot architecture can greatly influence both plant productivity and management. For example, peaches with a pillar phenotype allow growers to make more produce in a fixed amount of space, and trees with a weeping phenotype could make harvesting easier. Two closely related genes, *TAC1* and *LAZY1* control the angle of shoot branching. Mutations in the *TAC1* gene cause a pillar phenotype, while mutations in the closely related *LAZY1* gene lead to horizontal or weeping branches. We are interested in uncovering the molecular pathways that control branch angle. We used a yeast-two-hybrid screen to assay proteins that interact with TAC1 and LAZY1. Briefly, we used TAC1 or LAZY1 as a “bait” by fusing them to the binding domain (BD) of the yeast GAL4 transcription factor, and mated them with a library of peach proteins fused to the GAL4 activation domains (AD). When TAC1 or LAZY1 interact with a library protein, the GAL4 BD and AD will be reconstituted and can turn on a reporter gene. In this way, we can survey many peach proteins for interaction with TAC1 and LAZY1. Knowing these protein interactions will allow us to construct the molecular pathways controlling branch angle.

[2] Performance of open- and controlled-pollinated interspecific hybrids of shrub willow (*Salix* spp.) bioenergy crops

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Shrub willow (*Salix* spp.) is a high-yielding woody perennial that can be grown on underutilized agricultural land and is a proven feedstock for biofuels and bioproducts. The genus *Salix* includes at least 350 species, many of which can hybridize and display heterosis for yield. We aim to develop tools for genomics-assisted breeding and selection of higher-yielding *Salix* biomass crops. Six F₁ species hybrid families were generated using reference male or female genotypes of *Salix purpurea* as common parents crossed with diverse *Salix* spp. A greenhouse trial was established, using the parents and nine or ten random progeny from each of those six families, to determine the heritability of important biomass traits contributing to yield and whether there is heterosis for yield traits. Phenotypic measurements were recorded including stem lengths, specific leaf area, stomatal conductance, SPAD, above-ground biomass, and root biomass. Parent-offspring regression was used to test the performance of progeny relative to parental genotypes and comparisons between interspecific families were evaluated. Three families displayed significant mid-parent heterosis for above-ground biomass and stem length. Seedlings from 15 open-pollinated families of shrub willow that are putatively tetraploid or triploid were also grown in the greenhouse, and stem heights were measured to determine their relative performance. There was no significant difference based on the ploidy of the progeny, but there was significant variation between families. The best-performing parents were determined.

[3] Isolation and identification of fungi associated with tomato leaf mold in New York State

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Leaf mold of tomato is a fungal disease that is problematic for New York State tomato production in high tunnels and greenhouses due to the favorable high humidity conditions. The causal agent of Tomato Leaf Mold (TLM) is *Passalora fulva* (syn. *Cladosporium fulvum*), an asexual ascomycete fungus that infects and sporulates through open stomata thus affecting respiration. Single conidia isolates were cultured from tomato leaf samples displaying TLM symptoms from multiple New York State counties in 2015. Thirty-nine New York isolates were compared to 44 known species within the *Cladosporium* genus through phylogenetic analysis based on sequence data of the internal transcribed spacer regions ITS1, ITS2 and the 5.8S rRNA. In addition, five different cultivars of five-week old tomato plants were sprayed with conidial suspensions produced from three New York isolates. Results of the ITS sequence alignment data suggested that none of the isolates were *Passalora fulva*, but instead represented three haplotypes that are likely the saprophytic species *Cladosporium cladosporioides*. No TLM symptoms were found on the tomato plants sprayed with the conidial suspension after the expected incubation period of two weeks. Further analysis is necessary to confidently confirm the causal agent of Tomato Leaf Mold in New York State due to inconsistencies between the disease symptoms and the isolated saprophytic fungal species.

[4] Resistance of shrub willow to *Melampsora americana* rust pathogen

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Melampsora spp. rust fungi are the most threatening pathogens to the shrub willow biofuel crop, *Salix* spp., in the Northern Hemisphere. *Melampsora* spp. rusts are obligate biotrophs that can defoliate susceptible hosts and significantly reduce yield, up to 50% in extreme cases. Currently, the best method of reducing yield loss to *Melampsora* spp. is by breeding resistant willow lines. Therefore, we explored resistance in several *Salix* spp. diverse taxa to a single *Melampsora americana* isolate in order to elucidate the range of compatibilities present in these important breeding lines. In this experiment, the progeny of eight parent willow crosses were tested for resistance/sensitivity to *M. americana*. Six willow families, consisting of ten progeny each, were tested in this experiment. Detached leaves were inoculated with rust isolate R15-033-03, and the percent leaf coverages were measured each day for 15 days post-inoculation. Preliminary data suggests significant differences in sensitivity/resistance between and within willow families, indicating promising breeding opportunities for resistant cultivars. These assays will contribute to the selection of genotypes for eventual cultivar development.

[5] Determination of baseline sensitivity to fluxapyroxad and isolation of the *sdhC* gene in *Venturia inaequalis*.

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Apple scab is a disease of apples caused by the ascomycete *Venturia inaequalis*. Symptoms of the disease manifest as scabby lesions on the leaves and fruit, reducing photosynthesis and fruit quality, respectively. Fluxapyroxad is a new succinate dehydrogenase inhibitor fungicide used for managing apple scab. The site-specificity of the fungicide increases the risk that resistance could develop with increased field use. To establish a framework for evaluating the development of fungicide resistance, the fluxapyroxad EC₅₀ was determined for 22 baseline isolates. The mean EC₅₀ for these baseline isolates was found to be 0.259 µg ml⁻¹, which is similar to that of other SDHI fungicides. To further our understanding of the succinate dehydrogenase reductase target in complex II of the mitochondrial electron transport chain, the *sdhC* gene was cloned using a draft *V. inaequalis* genome in combination with *sdhC* homologs from related fungi. Putative *V. inaequalis* *sdhC* sequences obtained from field isolates displayed high levels of similarity to the draft genome despite the presence of some insertions and deletions. The amino acid sequence of SDHC indicated the absence of introns and only a few conserved regions between *V. inaequalis* and closely related fungi. Work is ongoing to better understand the genes of the enzyme target as well as monitor in vitro sensitivity to fluxapyroxad in field populations of *V. inaequalis*.

[6] Grapevine powdery mildew: the role of light in asexual sporulation

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Epidemics of grapevine powdery mildew (*Erysiphe necator*) are driven by the intense production of asexual spores. This essential process is regulated by light, resulting in a periodicity and mid-day peak in spore dispersal in vineyards. Prior genetic analyses have revealed genes associated with circadian clock regulation, as well as phytochrome and cryptochrome systems that may be involved in this process. However, the specific characteristics of light controlling conidiation are poorly understood. We determined the minimum duration of daylight exposure required to induce sporulation and the interactions of blue and red light in this process. Colonies of *E. necator* on *Vitis vinifera* 'Chardonnay' leaves that had grown vegetatively, but not yet sporulated, were exposed to natural sunlight, monochromatic blue, monochromatic red, or combined red and blue light for 15 seconds to 5 hours. Five hours after each light treatment, the colonies were scored for the production of mature conidia. Sporulation was induced after only 30 seconds of exposure to daylight. Additionally, blue light induced conidiation after 1 minute, while a minimum of 30 minutes of red light was required. Research in other biological systems have shown that lighting manipulation such as imperceptible pulsing of monochromatic lights can completely disrupt certain developmental processes. Thus, these experiments provide critical baseline data for the manipulation of light to disrupt the sporulation process in grapevine powdery mildew.

[7] Variations of the midgut cadherin protein in populations of *Trichoplusia ni*

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The cabbage looper moth (*Trichoplusia ni*) is a major pest to cruciferous crops and is one of the only two species that have developed resistance to Bt toxins in the field. The midgut cadherin is a known Bt toxin binding protein, and a major receptor for insecticidal Bt toxins in the detoxification pathway, thus mutations in the cadherin gene can cause insect resistance. Therefore, variations in this protein in insect populations provides genetic potential to develop resistance to Bt. This research is focused on analysis of variations in a specific Bt toxin binding site in the cadherin protein sampled from field populations of *T. ni*, captured using cabbage looper pheromone traps in different locations in the United States. A fragment of the cadherin gene, which includes an exon coding for the toxin binding region and its flanking intron regions, was amplified from *T. ni* individuals by PCR and sequenced. The variations of the amplified cadherin gene fragments and the protein sequences encoded by the exon in the PCR fragments were analyzed, and sequence variations of Bt toxin binding site in the cadherin were identified from the *T. ni* field populations. The results from this study provide information on the variation of a Bt toxin site in insects in the field, which is important for a better understanding of the development of insect resistance to Bt toxins.

[8] Cabbage susceptibility to black rot caused by the bacterium *Xanthomonas campestris* pv. *campestris*

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A field trial was conducted to test thirty-four different cultivars of cabbage commonly grown in Upstate New York, to assess the cultivar's resistance or tolerance to the bacterial disease black rot. Black rot is caused by the bacterium *Xanthomonas campestris* pv. *campestris* (Xcc) and is a serious disease of cabbage which is a high value crop in New York State. Growers have yield losses due to black rot outbreaks every year, and additional information about the relative resistance or susceptibility of cultivars is needed. The cabbage varieties were planted in the field on June 9, 2016 and two weeks later a NY strain of Xcc inoculum was sprayed to run-off just prior to sunset. Symptoms were recorded five days following the inoculation and a set of ratings were recorded over the next four weeks. All cabbage varieties displayed the typical V-shaped lesions associated with Xcc by the second rating but the severity varied from 1% to 20% of the leaf tissue infected. By the last rating the severity ranged from 2% to 45%. This information can help growers determine which cultivars will be most tolerant to black rot during a typical New York field season.

[9] Determination and characterization of a symptom determinant of *Grapevine fanleaf virus*

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Grapevine fanleaf virus (GFLV) causes fanleaf degeneration, one of the most damaging viral diseases among grapevines worldwide. GFLV is a bipartite (+) sense RNA nepovirus that is transmitted by the ectoparasitic nematode, *Xiphinema index*. In vineyards, GFLV infection reduces crop yields, lessens the quality of fruit and shortens the lifespan of the grapevine. In grapes, symptoms include fan-like leaves, vein yellowing, shortened internodes, and mosaics. RNA1 encodes proteins for viral replication and polyprotein maturation; RNA2 encodes proteins necessary for cell-to-cell movement and genome encapsidation. Little is known about the mechanisms of symptom expression arising from virus and host interactions. GFLV strain GHu causes vein-clearing symptoms in the model species *Nicotiana benthamiana* while GFLV-F13 causes asymptomatic infection. Recent work using GHu/F13 chimeras revealed a 408-nucleotide sequence at the 3' end of RNA1 of GFLV-GHu is necessary for symptom development. We validated that GHu RNA1 is capable of causing vein-clearing symptoms in agroinfection regardless of RNA2 identity. To narrow down the symptom determinant further, we used site-directed mutagenesis to mutate regions of the symptom determinant on RNA1. Systemic infection with these mutated constructs is challenging, something that warrants further study. Elucidating the mechanism of GFLV symptom expression in *N. benthamiana* will help us better understand how virus-host interactions lead to symptoms in grapes, and perhaps facilitate the development of new management strategies.

[10] Experimental assessment of attraction between *D. melanogaster* and fire blight pathogen, *Erwinia amylovora*,

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Erwinia amylovora is a bacterial phytopathogen that causes the necrogenic disease fire blight in apples and other rosaceous plants. Research suggests that fire blight can be transmitted by insects but in-depth knowledge describing interactions between the pathogen and potential vectors is lacking. To understand the baseline interactions between a potential vector, *D. melanogaster*, and the pathogen, we observed the fly location in a non-choice arena at 30-second intervals for one hour. Each arena consisted of five flies and either fire blight-inoculated media or control-inoculated media. There was a significant treatment effect and treatment-by-time interaction on location of flies, which depicted a strong initial affinity for fire blight-inoculated media that diminished over time. In contrast, the initial affinity for the control-inoculated media was significantly lower and increased slightly over time. Thus, this study suggests that flies exhibit a higher attraction to fire blight, but further baseline studies on the mechanism of this attraction are necessary. We hypothesize that the pathogen could either release an attractive volatile or serve as a higher quality nutrition source. Future studies will investigate these hypotheses through choice tests and insect performance assays.

[11] Characterization of an interspecific apple progeny (*Malus fusca* x *Malus domestica*) for fruit set, size, growth, deciduous calyx, and tree architecture

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The use of interspecific crosses will be important in the future to introgress traits of interest, such as disease resistance. Surprisingly, little is known about how different *Malus* species perform as parents in crosses to cultivated apples (*Malus* × *domestica*). In this research, we studied a cross between western crabapple (*M. fusca*) by an improved breeding selection (*M.* × *domestica*) with columnar architecture, NY 152. The progeny (138 seedlings) were sampled in their fifth growing season to study traits such as fruit set, fruit size, leaf lobing, stem juncture, calyx deciduousness and relation to tree architecture. Progeny fruit size (12 mm x 13 mm) was skewed toward small fruit, similar to the *M. fusca* parent (6.7mm x 6.8 mm), but the average number of fruit per spur (3) was more similar to fruit set in the columnar parent (3), than in *M. fusca* (6). Deciduous calyx appears dominant, with a 50% presence/absence ratio and stem length showed transgressive segregation, with stem lengths shorter and longer than either parent. Columnar fruit tend to have shorts stems, so the ability to enhance stem length is a positive discovery.

[12] Towards identification of the *Co2* locus of modifying effect on columnar growth habit in apple (*Malus domestica*)

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Compared with standard apple trees, columnar apple trees are characterized with thicker stems, shorter internodes and fewer branches. The columnar phenotype has been genetically mapped to the *Co* locus on linkage group (LG) 10, and the candidate genes responsible for the trait have also been reported. However, we observed in this study that the segregation of the columnar growth habit could not be completely explained by the *Co* locus in a population of 240 seedling trees derived from a cross between two different columnar apples. To search for other genes that might modify the expression of the columnar trait, we performed a bulked segregant analysis (BSA) with more than 100 SSR markers throughout the genome. Preliminary data analysis indicated that a genetic locus, tentatively named *Co2* on LG9 appeared to have significant genetic effect on modifying the expression of the trait. To characterize the *Co2* locus in more detail, several new markers have been developed in the region and analyzed in the population. The results suggested that more dedicated effort is required due to the inconsistent genomic assembly that spans the *Co2* locus in the apple reference genome.

[13] HPLC quantification of β -carotene levels in kale (*Brassica oleracea* var. *acephala*) market classes

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Carotenoids are organic, fat-soluble pigments responsible for the orange and red color of many vegetables. β -carotene, a carotene and vitamin A precursor found in large concentrations in kale (*Brassica oleracea* var. *acephala*), has been associated with reduced risk of oral, pharynx, and larynx cancers when included in the diet. Previous research indicates that β -carotene content in plants may be shaped by physiological and genetic factors. It was hypothesized that concentrations of β -carotene varied between different market classes of kale. Twelve cultivars of kale belonging to six market classes were grown under controlled conditions at the New York State Agricultural Experiment Station, harvested at four weeks as baby greens, and evaluated for β -carotene using high-performance liquid chromatography (HPLC). β -carotene content in above-ground kale tissue ranged from 1.622 mg/100g FW to 2.527 mg/100g FW. No statistically significant difference ($P < 0.05$) in β -carotene levels was observed among the six market classes of baby kale. These results suggest that variation in β -carotene levels across cultivars and market classes may not appear until kale reaches maturity, and warrants further competitive studies between juvenile and mature plant growth stages. Additionally, a lack of variation in β -carotene may not be representative of all carotenoid class compounds; evaluation of additional carotenoids, such as lutein and zeaxanthin may identify specific market classes of kale with the greater concentrations of these health-promoting plant compounds.

[14] Identifying root angle genes using a suppressor screen in Arabidopsis

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Root architecture is an important aspect of plant productivity since the shape of a plant's root system determines accessibility to water and nutrients. The gene *DROI*, which was first discovered in rice, has been shown to control the orientation or angle of root growth. *DROI* is a root-specific gene in the IGT family, which contains other genes known to control shoot architecture. In the model plant *Arabidopsis thaliana*, *DROI* mutant roots have much wider growth angles than wild-type roots. Little is known about the molecular pathways surrounding *DROI*, so our goal is to learn more about these pathways by performing a suppressor screen in *Arabidopsis*. We treated *dro1* mutants with the chemical mutagen EMS and screened for plants with normal root angles. We expect to find other genes that are involved in regulating root angle, and then be able to determine how they affect *DROI*. The implications of being able to control root growth could have tremendous ramifications for orchards. One possible result would be to create modified fruit trees that can thrive in water limited conditions.

[15] Phenotypic variations in shrub willow under water stress

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Shrub willow is a fast-growing, high-yielding crop that requires little maintenance, making it a favorable bioenergy crop for woodchips and biofuels. Shrub willow has a high water demand, and water availability can determine establishment success and potential yields. To evaluate heritabilities and to begin to map key traits of interest, we generated a series of F₁ species hybrid families with *Salix purpurea* as a common parent crossed with diverse *Salix* spp. Parents and one randomly selected progeny from each cross, 14 genotypes in total, were placed in a greenhouse trial to assess the impact of water stress on biomass yield. Each genotype was exposed to: no water stress, moderate and extreme water stress. Measurements of soil moisture, pot weight, chlorophyll content, specific leaf area, stem length, above ground biomass, and below ground biomass were collected to assess which parents and hybrids are more vulnerable or resistant to water stress and to see if hybrid vigor was present in any of the progeny. This is a first step in selecting genotypes that can produce high yields in water stressed conditions.

[16] Evaluation of parthenocarpy in summer squash varieties

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Modern crop production is heavily dependent on managed pollinators. With the decline of honeybees across North America, growers are concerned about their crops being adequately pollinated. For numerous years, squash growers have rented hives to pollinate their fields. However, there are fewer rental hives available and the price of hives have increased. To overcome these problems, a parthenocarpic squash, one that can produce marketable fruit without pollination, can be used. Prior research has shown that summer squash (*Cucurbita pepo* L.) varieties have variation in parthenocarpic fruit set, but there have been few evaluations conducted to test current varieties for parthenocary. In this study, 10 commonly grown varieties had female flowers bagged before opening to exclude pollinators. Bags were removed after 7 days and fruit was evaluated for its marketability. Varieties with marketable fruit were considered parthenocarpic and those with no marketable fruit were regarded non-parthenocarpic.

[17] Bacteria that affect grapevine health in the Finger Lakes region of New York

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Bacteria present both systemically and on the surface of grapevines can cause disease and decrease economic yields. Ice-nucleation active (INA) bacteria cause ice crystal formation on leaves and buds, leading to increased frost injury. Bacteria were collected from vineyards and cover crops and tested for INA. INA bacteria counts were found to be highest on grasses as compared to broadleaf plants. Therefore use of broadleaf cover crops may minimize chance of frost damage. *Agrobacterium vitis* causes crown gall disease on grapevines, producing damaging tumors. *A. tumefaciens* causes crown gall on other plants and only mild symptoms on grapes. We hypothesize that they respond to different plant wound signals, resulting in differences in virulence gene induction. Strains of *A. vitis* (S4) and *A. tumefaciens* (C58) were exposed to plant phenolic compounds to compare *virD2* induction, measured by RT-RT-PCR. In S4, *virD2* was upregulated 15-fold by 500, but not 100 μ M resveratrol, a known grape wound phenolic compound, but no induction was seen with exposure to acetosyringone. C58 induction will be measured in the future. In addition, the *virA* promoter region of another *A. tumefaciens* strain (CG978) was also determined to be significantly different from that of *A. vitis*, demonstrating another difference in virulence factor in grape. Understanding the differences in *vir* induction will inform future studies seeking to block virulence of *A. vitis* in grape.

[18] Genetics of sex determination in the dioecious shrub willow, *Salix purpurea*

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Members of the family *Salicaceae* are among the estimated 4-10% of all flowering plants that exhibit complete dioecy. This includes all *Populus* and *Salix*, woody perennials where male and female plants are discernable through clear morphological differences between staminate and pistillate catkins. Understanding the genetic basis of sex determination can provide insight for the evolutionary, ecological and molecular basis of sex differentiation, in addition to aiding in the development of molecular markers for plant breeders. Previous work in *Salix* has revealed that sex is determined by a ZW system. Genetic mapping results point to a putative sex determination region (SDR) on chromosome 15 in *S. purpurea*. We designed and tested PCR primers for five genes – REPA70, TFIID, TCP24, and mediator of RNA polymerase II - within this region. We PCR amplified portions of these genes in the SDR from a total of 14 *S. purpurea* genotypes, including parents and progeny representing six males, six females, and two hermaphrodites. The amplified PCR products from all individuals were sequenced and aligned to detect sequence polymorphisms whose segregation is consistent with the ZW model for the SDR. The female genotypes are heterozygous for SNPs, while the males are homozygous.

[19] Establishment and persistence of entomopathogenic nematodes in harvested sod

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Entomopathogenic nematodes (EPNs) can be an effective method for managing soil-dwelling pests, however, they are highly susceptible to environmental conditions. The goal is to test if growers can sell sod including EPNs as part of their product. To analyze the effectiveness of *Steinernema feltiae* (Filipjev) and *Heterorhabditis bacteriophora* Poinar as a control of sod pests, strips of sod were harvested and sprayed with EPN from mineral and muck soil fields in Batavia, NY. To determine if changes on soil conditions affect EPN infection, sod strips were rolled up and left outside for one week. Soil temperature and moisture content were determined for the surface and interior of the rolls. Soil samples from the roll surface and interior were extracted and used in laboratory bioassays with larvae of the greater wax moth, *Galleria mellonella* (L.), to assess EPN persistence. Secondly, to test EPN persistence after installing the sod, discs were cut from the strips of EPN-treated and untreated sod. The sod was planted on pots with soil and *G. mellonella* were confined in mesh sleeves in each pot. Later, the larvae were removed and observed for signs of EPN infection. We expect higher EPN infection in the pots with the EPN treated sod. We also expect EPNs to persist longer in the interior of sod rolls than on the surface, due to wetter and cooler conditions inside the rolls.

[20] Effects of corn grown in organically and conventionally managed soil on European corn borer searching behavior

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Organic soil management practices are frequently associated with increased insect pest control; however, there is little experimental evidence to support these largely anecdotal assertions. These claims rest in the principle that healthy soils promote healthy plants, which are more resistant to insect pests. Previous research with a generalist herbivore and pest of corn, the European corn borer, *Ostrinia nubilalis* (Hübner), showed that females preferentially oviposited on sweet corn grown in conventionally versus organically managed soil. Based on these host-acceptance findings, host-searching behavior of female *O. nubilalis* was assessed in no-choice tests for field corn grown in soil from five pairs of conventional and organic fields. Searching behavior scored included flight initiation time, orientation, and distance travelled toward plants grown in the two soil types. In only one of the five pairs, *O. nubilalis* oriented (40.6 vs. 17.1%) and travelled midway to plant (28.1 vs. 8.5%) more frequently in response to conventional than organic; the remaining pairs exhibited no difference. Flight initiation time was shorter for conventional in two field pairs. While these results demonstrated that *O. nubilalis* may discriminate between host plants of the same species, this difference is likely subtler than the distinction between “organic” and “conventional” soil management practices. Further investigation examining soil and plant health differences could elucidate the cause of *O. nubilalis* preference for corn grown in soil from one field versus another.

[21] Black stem borer trapping and management trials

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An ambrosia beetle known as the black stem borer (BSB), *Xylosandrus germanus*, (usually a pest in hardwoods and ornamental nurseries) has emerged as a pest on apple trees in New York State. From 2013-2015 BSB was determined to have a significant economic impact at more than 30 sites in New York. The wood-boring insect has been identified to cause tree decline and dieback, mainly in younger dwarf plantings with trees typically 5-25 cm in diameter. BSB are known to infest trees that are emitting ethanol volatiles due to stress. Traps baited with an ethanol lure were placed at 9 different sites in Wayne County and Geneva in order to assess timing of the BSB flight, as well as distribution of the insect. Management trials in the field were set up inside wooded areas at two different orchard locations in Wayne County. Trees were placed in groups of 5, 4 of which had different insecticidal trunk sprays, and one control. In addition, identical groups of trees were placed with a pheromone repellent Verbenone on a stake at the center of the grouping in order to see if the addition of Verbenone had any different effect on BSB.

[22] Confirmation of the *W* locus conferring weeping growth habit in apple

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The current apple production system is labor-intensive and costly due to lacking of mechanization of the routine tasks in orchard management, such as tree pruning and fruit harvesting, which are mostly conducted manually. One of the major challenges in mechanization of the orchard manual routines has been the high irregularity of tree canopy, which is tall, wide, dynamic, and highly variable depending upon the scion varieties as well as rootstocks. To address the challenge, we have initiated a comprehensive research project to understand the underlying mechanisms that control the directional growth of tree branches. As a part of the overall effort, this study focuses on the weeping growth habit in apple. We previously identified a genetic locus, designated *W*, on linkage group (LG) 13 using a small population of 38 seedling trees. To further confirm the finding, two additional populations segregating for the weeping trait were used in this study: one is of 140 seedlings from a bi-parental cross and the other comprises 47 seedlings from open-pollinated seeds of a weeping crabapple. Analysis of multiple DNA markers from LG13 in the two populations provided strong evidence that the *W* locus is largely responsible for the weeping growth habit in apple.

[23] **Contrasting the effects of two common systemic insecticides on soil microbial function**

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Imidacloprid and cyantraniliprole are commonly used insecticides in a wide variety of managed systems including vegetable crops and turfgrass. These insecticides are important tools for the management of soil-dwelling pests, but recent studies suggest they can have negative effects on beneficial soil organisms involved in decomposition and nutrient cycling. The objective of my project was to quantify the impact of systemic insecticides on soil microbial community function. Specifically, I investigated how imidacloprid and cyantraniliprole affect decomposition (carbon mineralization) and nitrogen mineralization in turfgrass soils. I conducted a short-term soil incubation to quantify differences in microbial respiration (carbon mineralization) in soils receiving an insecticide drench or insecticide-treated grass tissue. Microbial respiration (CO₂) patterns were quantified using infrared gas analysis. To assess nitrogen mineralization dynamics, I measured microbial urease production along with soil nitrate concentrations in the same soils at the conclusion of the incubation. Imidacloprid had initial suppressive effects on cumulative respiration over multiple dates. Soils amended with plant tissues treated with the different insecticides did not vary in cumulative respiration. Urease activity was higher in soils treated with imidacloprid. My data indicate that different insecticide use has varying effects on decomposition and nutrient cycling in soil and these differences are important to take into account when balancing pest control and soil health.

[24] **Using Fe₃O₄ superparamagnetic nanoparticles to extract DNA from soil for detection of root-knot nematode**

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Using DNA-based pre-plant soil tests to quantify levels of plant-parasitic nematodes could greatly contribute to effective treatment and prevention of crop damage or yield loss. However, current techniques for DNA extraction from soil such as commercial kits and phenol-chloroform methods have limitations on the volume of soil from which DNA may be extracted. They are also often difficult, time-consuming, and produce hazardous waste. An alternative method using Fe₃O₄ superparamagnetic nanoparticles and magnetic bioseparation was investigated. This method is potentially faster, produces less waste, and may allow for extractions from larger masses of soil. DNA was isolated from 1, 25, 50, and 100 g of soil containing *Meoloidogyne hapla* (root-knot nematode) using a constant mass of nanoparticles. Quality and quantity of the resultant DNA was then tested using spectroscopy (NanoDrop) and fluometry (Qubit®). The ability to amplify the internal transcribed spacer (ITS) region of *M. hapla* was also tested by PCR. DNA was extracted from all soil volumes and the ITS region was successfully amplified. However, the quantity of resultant DNA was significantly reduced when extracting from 50 and 100 g soil. Further amendments to the protocol would be required to optimize DNA extraction from 50 and 100 g soil for the detection of plant-parasitic nematodes and other soilborne pathogens.

[25] Exploration of alternative hosts for grapevine red blotch-associated virus

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Grapevine red blotch-associated virus (GRBaV) of *Vitis* sp. is a putative new member of the family *Geminiviridae*. The complete sequence of the GRBaV genome was published in 2012, and the virus has since been detected in all major grape-growing regions of the United States, likely due to transmission via infected propagation material and grafting. GRBaV is also transmitted by the three cornered alfalfa treehopper (*Spissistilus festinus* Say). *S. festinus* is not a pest of grapevine, but can cause economic losses in fabaceous crops, including soybean, alfalfa, and peanut. Some fabaceous species are sown in vineyard row middles as cover crops. This warrants the evaluation of their potential to host GRBaV. A major objective of this project was to inoculate fourteen varieties of fabaceous plants with an infectious bitmer clone of GRBaV via *Agrobacterium tumefaciens*-mediated infection. After two and four weeks, petioles were collected and tested for GRBaV by reverse transcription polymerase chain reaction (RT-PCR) to verify virus infection. Any legume species that tests PCR positive for GRBaV will be further examined for its potential as a reservoir for *S. festinus*-mediated transmission. This research is important to better understand the epidemiology of GRBaV.

[26] “Shocking Effects” of acute cold events in the suppression of hop powdery mildew

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Occurrence of favorable temperatures is often assumed to be a primary driver of epidemic rates for powdery mildews. Past research on forecasting of Hop Powdery Mildew (HPM) (*Podosphaera macularis*) has focused on optimal growth temperatures. Despite highly favorable temperatures, the severity of HPM can be slow to increase early in the growing season possibly due to acute overnight cold events. My objectives were to: (i) test for the occurrence of acute cold induced disease resistance, (ii) quantify germination and sporulation after acute low temperatures, and (iii) assess implications of natural overnight cold events in the field on pathogen establishment, growth, or survival. Young, detached hop leaves were exposed to either a single 4 hr event at 4°C 24 hr prior to inoculation, or to daily exposures of 4°C treatments 24 hr after inoculation. Colony establishment at 48 hr post inoculation and latency period were recorded. Exposure of hop leaves to both single or repeated acute cold events significantly reduced infection efficiency and extended latency. Hop leaf temperatures measured under clear-sky nights showed leaf temperatures 2°C below ambient air temperatures due to intense radiational cooling. Thus, in certain climates, or in conjunction with long periods of fair weather, the favorability of average daily temperatures may overpredict disease development. Inclusion of the quantitative effects of acute cold events in advisory systems will likely improve their performance as predictors of HPM severity.

[27] Characterization of NYS isolates of *Pseudomonas syringae* pv. *tomato* for the presence of the avirulence gene *AvrPto*

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Pseudomonas syringae pv. *tomato* (*Pst*) is a Gram-negative plant pathogenic bacterium that causes bacterial speck on tomatoes. New York State (NYS) is the fifth largest producer of fresh market tomatoes in the USA, which makes this study of pathogen diversity crucial to the success of the NYS industry. The pathogen enters the plant through the stomates and hydathodes during cool, wet conditions, where it can multiply within the host and cause devastating economic loss to growers. *Pst* uses a range of effectors secreted into the host by the type III secretion system to compromise the plant immune system. The *Pto* gene, a resistance gene present in some tomato varieties, is a defense mechanism which elicits the plant immune defense against *Pst* in the presence of *AvrPto*. A total of forty-seven isolates of *Pst* were collected previously from New York growers' fields and tested for the presence of the avirulence gene, *AvrPto* using gene specific primers. Pathogenicity assays with the isolates via inoculation on tomato plants were done to observe disease symptoms of each isolate. Knowing more about the diversity between *Pst* isolates with *AvrPto* will give insight to how effective the *Pto* resistance gene will against isolates present in NYS.

[28] Disrupting host landing and oviposition in *Drosophila suzukii*

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Spotted wing drosophila (SWD), *Drosophila suzukii* (Matsumura) (Diptera: Drosophilidae), causes economically significant damage to berries and other small fruit crops through oviposition in ripening fruit. Here we investigated how aversive odors can be used to reduce damage through disruption of host finding and oviposition behaviors. Several caged behavioral assays were conducted in the greenhouse to characterize the effect of aversive odors on the behavioral response of SWD to attractive chemical and visual stimuli. First, lab-reared female SWD were released into cages containing store-bought raspberries in no-choice experiments to assess oviposition and visitation rates in the presence and absence of a novel aversive odor. Both volatile compounds tested significantly reduced oviposition rates. One compound significantly reduced visitation 20 and 50 minutes after assay initiation. Additional experiments of longer duration confirmed the necessary role of both odorous and visual cues in SWD landing on artificial fruit models. However, when we used these models in place of real raspberries, we found that aversive odor did not affect the influence of either attractive visual or odorous cues on landing for reasons not yet understood. Still, experimental decoupling of host-associated chemical and visual stimuli could help anticipate interactions between repellants and chemical or visual attractants in push-pull systems. The significant behavior modification by both experimental compounds when presented alongside real fruit suggests potential efficacy as oviposition deterrents in field situations.

[29] Assessing susceptibility levels of spinetoram in onion thrips (*Thrips tabaci*) populations in New York onion fields

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Onion thrips (*Thrips tabaci*) is a serious piercing-sucking pest of onions that causes leaf damage and transmits several fungal and bacterial diseases. Thrips cause reduced photosynthetic potential, which leads to smaller bulbs and economic loss. Insecticides are the main method of control for onion thrips and Radiant SC (spinetoram) is currently one of the most widely used and effective products. However, in recent years onion growers from Elba, NY have reported a decrease in control with Radiant SC and have to use the highest recommended rates to manage infestations. Radiant SC has also been evaluated in efficacy trials every year in Elba from 2005-2015 and control has decreased by 30%. Decreasing thrips mortality in these studies suggest that populations in Elba may be developing resistance. To test this hypothesis, thrips from two onion fields in the Elba muck were collected and assayed for levels of susceptibility to Radiant SC in comparison to a population from a small, isolated organic farm in Phelps, NY where insecticides have never been used. A new method of oral ingestion bioassay was developed with formulated insecticide in 10% sucrose diet. The methods developed in this project will be used for future research on many more populations in NY to determine the extent of resistance.

[30] Evaluation of prohexadione-calcium, a plant growth regulator, biological SARs, and other biological and chemical management practices on the development of fire blight and apple productivity

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Fire blight, caused by the bacterial pathogen *Erwinia amylovora*, results in considerable production losses from blossom blight and planting losses from shoot blight. Management of blossom blight relies on timed antibiotic applications, and shoot blight is best managed by the growth regulator prohexadione-calcium. However, the use of prohexadione-calcium impedes the vigor and productivity of the orchard. A trial was conducted in a 16-year-old 'Gala' orchard to explore the possibility of bloom time applications of prohexadione-calcium and biological SARs as a means of managing blossom blight in the absence of antibiotics. Treatments were applied from pink to early shoot elongation with *E. amylovora* inoculation at 80% bloom. The development of fire blight and tree productivity were evaluated 14 days after inoculation and on a weekly basis, respectively. All treatments provided some level of blossom and shoot blight control, with antibiotic standards providing the most control, and Regalia (a natural SAR inducer) providing the least control. Streptomycin, Regalia, and BmJ (a natural SAR inducer) treatments resulted in low number of fruit, but fruit size was similar among all treatments. Prohexadione-calcium applied at petal fall had reduced shoot growth compared to prohexadione-calcium applications at pink. Overall, early prohexadione-calcium treatments were effective at managing blossom blight without compromising tree productivity.