

Proceedings of the
**2019 Cornell AgriTech
Summer Research Scholars Program**

Research Poster Session

July 26, 2019

Geneva, NY



Cornell AgriTech
New York State Agricultural Experiment Station

These abstracts report the results of research performed by the Summer Scholars participating in the *2019 Cornell University Geneva Summer Scholars Program*

This program was funded by:

Cornell University College of Agriculture and Life Sciences Alumni Association

Canandaigua Wine Company Inc.

Marilyn Hicks, Hicks Nursery, Westbury, NY

HM Clause, Inc., Davis, CA

Gordon B. Carruth Scholarship

Shaulis Scholarship Fund

M. Nolan Enology and Viticulture Fellowship

Peter and Tacie Saltonstall Fund for Enology and Viticulture

USDA Federal Capacity Funds; *Agricultural Research Internship Opportunities for Undergraduates* awarded to L. Smart

USDA NIFA CAP Project 2018-68005-27925 awarded to L. Smart

NIFA USDA Specialty Crop Research Initiative 123535 G003383 awarded to D. Gadoury

National Science Foundation Plant Genome Research Program grant IOS-1339211 awarded to K. Xu

New York State Farm Viability Specialty Crop Block Grant Program SCB 18 008 awarded to A. Khan

USDA NIFA grant 2016-67032-25009; *Undergraduate Research and Ext. Experiential Learning Fellowships* awarded to C. Smart

[1] **Morphological traits of resistance of *Salix* spp. to *Melampsora americana***

Patrick W. McMullen^{1,2}, Chase R. Crowell², Christine D. Smart²

¹Dept. of Biology, Lebanon Valley College, Annville PA 17003-1400

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva NY 14456

Shrub willow (*Salix* spp.), an important bioenergy crop in the northern U.S., can face significant defoliation and reduction in crop yield due to the rust pathogen *Melampsora* spp. This study aimed to understand the morphological traits of willow that lead to higher susceptibility to rust. Stomatal density and trichome coverage of 12 cultivars of willow was analyzed using microscopy and compared to AUDPC data of these cultivars. Cultivars with higher trichome densities tended to be more resistant to rust. Cultivars with fewer stomata had a slight resistance to rust. *Melampsora* spores require stomata to form appressoria and penetrate the host. To determine the time when appressoria form, *S. purpurea* leaves were inoculated with *M. americana* and allowed to germinate in a growth chamber. The percentage of spores forming appressoria was recorded for each two-hour interval up to 18hpi. Prior to 18 hpi, a significantly lower percentage of spores formed appressoria compared to 18 hpi. Scanning electron microscopy was utilized to visualize appressorial formation over stomata, pustule formation, and single uredospores. The time of germination and appressoria formation will allow us to further study the pathogenicity at this initial interaction of the pathogen with the host. A better understanding of the leaf surface characteristics of willow and their relation to rust resistance can aid willow breeders in developing resistant cultivars.

[2] **Digital Phenotyping to Characterize Genetic Variations in Open Pollinated Progeny of Apples**

Angela Chen^{1,2}, Richard Tegtmeier², and Awais Khan²

¹Department of Life Sciences, University of California, Los Angeles (UCLA), Los Angeles, CA 90024

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, NY 14456

Accurate and high-throughput evaluation of crop responses to biotic and abiotic stresses is necessary for breeders for genetic improvement and farmers to make crop management decisions. The traditional methods of plant phenotyping are manual, highly time-consuming, and subjective. Innovations in sensor technology have presented proven methods to capture plant responses to biotic and abiotic factors in both visible and invisible light spectra for monitoring crop growth and health. The objective of this study was to evaluate 300 F1 open-pollinated progeny of ‘Cox’s Orange Pippin’ for genetic differences in phenotypic traits like height, chlorophyll content, and leaf area using digital phenotyping tools. Plants were grown in a greenhouse where an adjustable overhead camera frame was set up to take imaging data in RGB (red, green, blue) and NDVI (Normalized Difference Vegetation Index). Ground-truthing was performed manually; plant height (cm) was measured with a ruler, chlorophyll content with a handheld SPAD 502+ Chlorophyll Meter, and leaf area (cm²) with the LeafScan iOS Application. Camera images were processed with ImageJ Pixel Inspector for color quantification and ImageJMacro scripting language for leaf area. The imaging data supported the feasibility of using camera imaging as a non-destructive way to capture and process large amounts of phenotypic data quickly. Future applications of these phenotyping techniques include developing high-throughput imaging protocols for precise evaluation of apple diseases for genetic mapping.

[3] **Comparative analysis of DNA extractions using Whatman FTA cards and a high throughput DNA extraction method for determining sex of hemp plants**

William Gura^{1,2}, Ali Cala², Christine D. Smart², Jacob Toth³, Craig H. Carlson³, Lawrence B. Smart³.

¹Plant Sciences Major, School of Integrative Plant Sciences, Cornell University, Ithaca NY 14850

²Plant Pathology and Plant Microbe Biology Section

³Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell Agritech, Geneva NY 14456

Hemp (*Cannabis sativa*) is a dioecious species that has been increasing in popularity in New York State for its various applications, especially in the production of cannabidiol (CBD). When pollinated, CBD levels in female hemp flowers decrease. Male plants must be removed from CBD production fields to ensure pollination does not occur. A PCR protocol using fluorescent markers for the X and Y chromosomes was developed for efficient sex determination. This protocol was developed using a standard DNA extraction protocol with a throughput of ~400 samples per day per person. This study compares this DNA extraction method to an alternate DNA extraction method, Whatman FTA Cards, to determine the most cost effective, accurate, efficient, and practical method for sex determination for removal of males. DNA from three cultivars of hemp plants was extracted using the standard DNA extraction process and Whatman FTA Cards. The DNA was then used in the PCR protocol for sex determination and results were compared. FTA cards proved to be more efficient and practical but was not as accurate as the standard method. Possibly due to various forms of contamination FTA cards could prove to be a better method for DNA extraction, but until accuracy is above 80% the method is not as successful as the standard DNA extraction. Changes to the FTA card protocol will be made to increase overall accuracy. Pricing is also compared to further assess the two methods.

[4] **Expert-annotated image database of foliar diseases of apples for automated diagnosis through computer vision**

Zachary R. Guillian^{1,2}, Awais Khan²

¹College of Agriculture and Life Sciences, University of Vermont, Burlington, VT 05401

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva NY 14456

Rapid and accurate disease diagnosis is critical in commercial apple orchards for timely control. As disease symptoms vary widely due to age of infected tissues, genetic variation, and light conditions within trees, it is challenging for computer vision models to accurately distinguish between diseases. Large datasets of high-quality images are critical to train computer vision models. Apple scab (*Venturia inaequalis*) and cedar apple rust (*Gymnosporangium juniperi-virginianae*) are two economically important common fungal diseases of apples across New York State. The objective of this study was to develop an image database of apple scab and cedar apple rust as they appear on the leaves of diverse apple cultivars. Photos were taken using a Canon Rebel T5i DSLR and smartphones under different light conditions, angles, and at different stages of developing disease symptoms. A total of 1,534 photos were taken of apple scab, 1030 of cedar apple rust, and 1135 of healthy leaves. This image database is currently being used to train a computer vision model to diagnose diseases on apple leaves. So far, an accuracy of 82% has been achieved with the model. This database can be extended by adding data collected from unmanned aerial vehicles (UAVs) and the computer vision model can be used to develop apps for disease scouting and precision orchard management tools.

[5] Identifying genes regulating pathogenicity and cercosporin production in *Cercospora beticola*

Christopher Rivera-Torres^{1,2}, Sandeep Sharma², Sarah Pethybridge²

¹Dept. of Agro-Environmental Sciences, University of Puerto Rico-Mayaguez, Puerto Rico, PR 00681

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell AgriTech at NYSAES, Cornell University, Geneva NY 14456

Cercospora beticola, is an important pathogen of table beet, sugar beet and Swiss chard in the United States. Yield is significantly reduced due to foliar necrosis leading to defoliation, making it impossible to harvest with top pulling machinery. Fungicides are the dominant control strategy. However, due to high genetic diversity within the *C. beticola* population, resistance to single-site modes of action threaten the durability of this approach. Thus efficient alternative management strategies are urgently needed which require knowledge of pathogen biology and pathogenicity. This project had two major objectives: 1) To generate a population of random insertional mutants using *Agrobacterium tumefaciens*-mediated transformation in *Cercospora beticola* Tb14-085 (a New York wild-type isolate), and 2) Screen the mutants' ability to cause disease and/or produce cercosporin; a phytotoxin poorly understood but may be involved in pathogenicity. Around 700 random insertional mutants were generated and screened for pathogenicity, ability to produce cercosporin, and abnormal phenotypes. Four avirulent mutants, and three mutants with increased cercosporin production were identified and compared to Tb14-085. Two of the avirulent mutant isolates also displayed a different phenotype on artificial media. Eventually, interesting mutants from different screens will be sequenced to identify the genomic mutation/s associated with the phenotypes. Knowledge from this project will enable the identification of novel genes as prospective targets for disease control, especially through RNAi approaches.

[6] Phenotypic analysis and comparison of *Phytophthora capsici* isolates from Ontario County NY in 2013 and 2017

Carolina Puentes Silva^{1,2}, Gregory Vogel^{2,3}, and Christine D. Smart²

¹Biological Sciences Department, Universidad de los Andes, Bogotá, Colombia

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

³Plant Breeding and Genetics Section, School of Integrative Plant Science, Cornell University, Ithaca, NY 14853

Phytophthora capsici is an oomycete plant pathogen that causes stem, root, and fruit rots on vegetable crops such as eggplant, squash and pepper. One interesting characteristic about the biology of *Phytophthora* species is the genetic variation between and within clonal lineages. The aim of this project was to obtain and analyze phenotypic information on 46 *Phytophthora capsici* isolates collected from one farm in Ontario county, NY, 2013 and associate phenotypic differences between isolates with genetic differences, previously determined with genotyping-by-sequencing. Furthermore, these data were compared with isolates collected in the same field in 2017. Mefenoxam sensitivity and mating type assays were conducted on all isolates. All of the 2013 isolates were sensitive to mefenoxam except one intermediately resistant, whereas two of the 2017 isolates were resistant and two intermediately sensitive. Regarding the mating type results, in 2013, 65% of the isolates were A1 while in 2017 the percentage of isolates that were A1 was 48%. Three clonal lineages in 2013 and two in 2017 featured phenotypic differences between isolates belonging to that lineage. Finally, the results show that in the same field there is a sexual population of *P. capsici* as well as a difference in sensitivity to mefenoxam between the two years.

[7] **Differences in susceptibility of ethylene mutant tomato plants and fruit to *Clavibacter michiganensis* subsp. *michiganensis*, *Xanthomonas gardneri* and *Pseudomonas syringae* pv. *tomato***

Brigithe Tatiana Ortiz Sanabria^{1,2}, F. Christopher Peritore-Galve², Juan L. Gonzalez Girón², Christine D. Smart²

¹Department of Biological Sciences, Universidad de los Andes, Bogotá, Colombia, 111711

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY, 14456

Tomato (*Solanum lycopersicum*) is susceptible to infections by bacterial plant pathogens, which can cause significant economic loss. Three bacterial pathogens important to New York tomato production include *Clavibacter michiganensis* subsp. *michiganensis* (*Cmm*), which causes bacterial canker and "bird's-eye" lesions on the fruit, *Xanthomonas gardneri* (*Xg*), which causes bacterial spot characterized as deep, large fruit lesions and *Pseudomonas syringae* pv. *tomato* (*Pst*), which is responsible for bacterial speck of tomato, appearing as black specks on fruit. Ethylene is a diffusible phytohormone with an important role in diverse developmental processes such as seed germination, fruit ripening, and senescence. It has been reported that ethylene produced by the plant can play an important role in susceptibility of the tomato plants to *Cmm* and *Xg* but not to *Pst*. The goal of this study was to determine plant and fruit susceptibility of six mutant tomato genotypes impaired in ethylene perception, signaling, and production to *Cmm*, *Xg*, and *Pst*. We inoculated stems and leaves with *Cmm* and *Pst*, respectively and symptoms were measured to determine susceptibility. Tomato fruit 0.5-2.5 cm in diameter were inoculated with *Cmm*, *Xg*, and *Pst*, and the number of lesions per fruit were counted fifteen days post inoculation. This study will provide us with insights into the role of ethylene during disease of fruit (for all three pathogens) and plants (*Cmm* and *Pst*) caused by bacterial pathogens.

[8] **Suppression of Canada thistle (*Cirsium arvense*) using organic weed management**

Colden Proe¹, Zachary J. Stansell^{1,2}, Thomas Björkman^{1,2}

¹Cornell University College of Agriculture and Life Sciences, Ithaca, NY 14851

²Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, NY 14456

Canada thistle (*Cirsium arvense*) is a common perennial weed in agricultural systems worldwide, from its native North America to Italy and New Zealand. In organically managed farms, Canada thistle is increasingly difficult to manage due to the prohibition of conventional herbicides and resistance of deep rhizomes to tillage. Current organic management therefore requires a combination of several types of weed management practices for elimination or economic control. We evaluated *C. arvense* stem diameter, plant height, biomass, and abundance under both bi-weekly mowing and cover crop suppression using a sorghum sudangrass (*Sorghum bicolor* x *S. bicolor* var. *sudanese*) 'Greengrazer V' in organic field trials in western New York over an 8-week period in the summer of 2019. Although complete elimination was not achieved during the study period, both treatments reduced thistle shoot abundance by 50% from original levels (mowing: 23 shoots/m² to 11 shoots/m²; cover crop: 21 shoots/m² to 10.7 shoots/m²). Final biomass of thistle in treated plots was reduced by 80 to 90% compared to the control plots (mowing: 37g/m²; cover crop: 20g/m²; control: 198g/m²). Shoot abundance and biomass reduction between mowing and cover crop treatments was not statistically significant, indicating that mowing and cover crops are both effective treatment recommendations. This work presents effective *C. arvense* management alternatives suitable to organic production in the northeast United States.

[9] **Ultraviolet Light Treatment Causes Delayed Development of Immature *Tetranychus urticae***

Nia Riggins¹, Karen S. Wentworth², Molly Erin Cappiello³, Rey O. Cotto-Rivera⁴, and Jan Peter Nyrop⁵

Dept. of Entomology, Cornell University, Geneva NY 14456

Tetranychus urticae, two spotted spider mites (TSSM), are common crop pests that attack plants grown worldwide. Ultraviolet (UV) light treatments have been shown to be an effective way of killing TSSM eggs. A five second treatment of one hundred joules will kill most eggs but not have a large effect on the host plant. While killing eggs is useful, killing larval and nymphal stages of the mites would produce a greater suppressive effect on TSSM populations. The effects on motile states were explored through UV light bioassays that followed mite development after treatment. Larvae and nymphs were monitored each day to record if the organism could move, had molted or had died. UV light treatment reduced motility of treated mites, caused delayed molting, and ultimately led to death. Unlike with eggs, mites did not die until several days after exposure. Of the few survivors, those that did molt and mature were mostly male. As well as testing if UV light treatment affected motile mites, the effect of treatment timing was examined by comparing mite development when treatments were made at night versus during the day. We also attempted to measure oxidative stress of DNA in UV-treated immature mites to observe any difference between these mites and those that were not treated.

[10] **Investigating the Transmission and Movement of Grapevine Red Blotch Virus in *Phaseolus vulgaris***

Brandon G. Roy^{1,2}, Maddie Flasco², and Marc Fuchs²

¹Dept. of Biochemistry and Molecular Biology, Lebanon Valley College, Annville, PA 17003

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

Grapevine red blotch virus (GRBV) infects *Vitis* spp., has a single-stranded DNA genome, and belongs to the genus *Grabovirus* in the family *Geminiviridae*. GRBV infection results in irregular foliar red blotches on red-berried grape cultivars and poor fruit quality. The virus is transmitted from vine to vine by the three-cornered alfalfa hopper, *Spissistilus festinus*. A host of GRBV outside of grape has yet to be identified. This study investigated common bean, *Phaseolus vulgaris*, as a systemic herbaceous host of GRBV. Repeated pin prick agro-inoculation experiments of bean plants with infectious clones showed that the virus moves at least 0.5 cm, and as far as 3 cm away from the inoculation site by two weeks post-inoculation, as shown by reverse transcription-polymerase chain reaction (PCR). Further movement of GRBV inconsistently reached 4 cm away from the inoculation site in subsequent weeks with apical leaves testing negative. *S. festinus* was found to transmit the virus with a one-week acquisition access period on GRBV-infected bean plants and a four-day inoculation access period on healthy, detached bean leaves. The initial inoculated plants, insects, and detached leaves used in the transmission assay were all confirmed to have GRBV through multiplex PCR. This study showed that *P. vulgaris* is a suitable host to advance our understanding of GRBV-host-vector interactions. The resulting knowledge will influence further studies, leading to disease management strategies.

[11] **Genetic Control of Flowering Time in Interspecific Grapevine Families**

Hannah E. Levengood^{1,2}, Avinash Karn², and Bruce I. Reisch²

¹Purdue University, West Lafayette, IN 47907

²Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, NY 14456

Flowering, likely a complex trait in grapevines, is controlled by both genetic and environmental factors. Although the effects of the environment on grapevines have been widely studied, the genetic control of flowering has rarely been examined in vines used in breeding programs in North America. A better understanding of the genetic control of flowering time can be useful in developing grape cultivars that are adapted to the changing climate. We studied two grapevine populations, one that descends from an early flowering species (*V. rupestris* B38 × ‘Horizon’ (RH); 151 vines) and one that descends from a late flowering species (‘Horizon’ × *V. cinerea* B9 (HC); 127 vines). Our analyses in the RH population indicate that the onset and end of bloom are highly heritable, while the length of the blooming period has low heritability, indicating that the latter trait is influenced by environmental factors. From composite interval mapping, two significant Quantitative Trait Loci (QTL) for the end of bloom were identified on chromosomes 5 and 19 explaining 15.6 and 8.8% of the phenotypic variation, respectively. Compared to 2018, the bloom period in 2019 was unusually wet and cool. It is likely that additional replicates of flowering time data will be required to re-confirm results. Additional results from the HC population will be presented in the poster.

[12] **Effect of Powdery Mildew Resistance on Phenolic Content of Inoculated *Vitis* Leaves**

Lindsay Brown¹, Kyra Battaglia², Molly Carroll², Lindsay Lesniak² and Ben Gutierrez²

¹School of Integrative Plant Science & Viticulture and Enology, Cornell University, Ithaca, NY 14853

²USDA-ARS, Plant Genetics Resources Unit, Cornell AgriTech, Geneva, NY 14456

Genetic resistance to the economically damaging powdery mildew (*Erysiphe necator*) can improve the sustainability of viticultural control measures as demonstrated through the Ren3 and Ren9 resistance genes. These genes trigger a hypersensitive response in tissues affected by powdery mildew and associated changes in the concentration of phenolic compounds. Phenolics are defensive compounds which may prevent the spread of powdery mildew throughout the impacted vines. However, the post inoculation relationship between the genotypes of interest and the phenolics is not fully understood. This experiment analyzed the phenolic concentrations of leaf tissue samples from an interspecific hybrid population of 103 individuals with both, either, or neither of these resistance genes at 8 days post inoculation with HPLC to examine the relationship between the phenolic concentration and the genotypes. HPLC showed three main peaks: a catechin, a hydroxycinnamic acid derivative, and a quercetin. The impact of the genotype on the phenolic content was analyzed and will be discussed in the poster. Moving forward, HPLC analysis with time trials consistent to the main points of phenolic change in the literature would prove most effective to fully understand the metabolite changes related to the Ren3 and Ren9 genotypes.

[13] **Characterization of 30 CBD hemp cultivars in New York State**

Mariana I. Marrero González^{1,2}, Craig H. Carlson², George M. Stack², Jacob A. Toth², and Lawrence B. Smart²

¹Agro-environmental Science Department, Faculty of Agricultural Sciences, University of Puerto Rico, Mayagüez campus, Mayagüez, PR 00680

²Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, NY 14456

Hemp (*Cannabis sativa*, <0.3% Δ^9 -THC) is a versatile crop grown to produce a variety of materials such as cannabidiol (CBD), oil, grain, and fiber. While the amount of available information on hemp is growing, there is limited phenotypic data for hemp cultivars in New York State. To address this, we characterized 30 hemp cultivars grown for CBD production in two locations in upstate New York, Geneva and Ithaca. The cultivars came from several sources, and included plants started from cuttings, feminized seed, and dioecious seed. Because the trial was meant for CBD production, dioecious hemp cultivars were screened using a Y-specific sex marker to identify females. Only females were planted, because pollination of inflorescences negatively impacts CBD yields. Over the course of seven weeks, we measured traits including plant height, floral phenology, chlorophyll content, and leaf area. We found clear phenotypic differences between cultivars. We will relate this data to other important plant traits including cannabinoid type, cannabinoid yield, disease resistance, nutrient uptake, and root establishment. Phenotypic characterization of cultivars used in this trial will better inform New York hemp growers and breeders of the diverse phenotypes of CBD hemp.

[14] **Pooled genome sequencing analysis of genetic dwarf in apple**

Elizaveta Makarova^{1,2}, Laura Dougherty¹, Susan Brown¹ and Kenong Xu¹

¹Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell Agritech, Geneva NY 14456

²Dept. of Biology, Lafayette College, Easton PA 18042

Development of dwarf and semi-dwarf corn, rice and wheat cultivars in the 1950s and 1960s drastically increased the crop yield. This landmark accomplishment has been known as the Green Revolution. To reduce overall tree size especially height in apple orchards, dwarfing root stocks have been developed and used widely for commercial apple production. Although much has been learned about the dwarfing effect of rootstocks on scions, information about genetic dwarf in apple scions, which is a recessive trait, remains scarce. To gain insight into genetic dwarf in apple, a non-grafted F₁ population of 365 progeny, segregating for the dwarf trait was investigated using pooled genome sequencing approach. Two genomic DNA pools, 'Dwarf' and 'Tall' were created with dwarf and tall progeny, respectively. Deep sequencing of the two genomic pools and subsequent DNA variant analysis identified three genomic regions putatively associated with the dwarf trait, which are located on chromosomes 1, 8 and 17, respectively. To confirm the findings, multiple simple sequence repeat (SSR) markers in the three regions were screened and analyzed in the entire F₁ population. The data indicated that the loci on chromosomes 1 and 8 were linked to the genetic dwarf trait.

[15] Novel Approach for Biomass Estimation in Complex Canopy Structure (Shrub Willow)

Daniel Klimkowski¹, Justin Heavey¹, Timothy Volk¹

¹Willow Project: SUNY College of Environmental Science and Forestry, Syracuse NY 13210

Above Ground biomass (AGB) is an important metric in bioenergy crops such as shrub willow. In lieu of destructive sampling and/or collecting diameter data and using allometric equations to estimate biomass, subjective visual assessments of crop parameters like AGB are often used for management decisions. The ability to accurately estimate AGB with low time and labor inputs would be beneficial to the development of commercial shrub willow crops. This research tested a novel approach for non-destructively estimating AGB using an unmanned aerial system (UAS), multispectral imagery, and photogrammetric image processing. Multispectral georeferenced images of commercial-scale shrub willow in Solvay, NY were collected and processed to create a multi-band orthomosaic, and historical elevation datasets were utilized to create a canopy height model (CHM). By incorporating two multispectral vegetation indices with the CHM, a correlation was established with biomass estimations using allometric equations with a R^2 of 30%. Incorporation of field specific plant density measurements improved this model to an R^2 of 63%. Future efforts to improve these estimates using this technique should involve the incorporation of multi-level ground control points for CHM improvements, computer vision algorithms for isolation of canopy reflectance and individual stool recognition, and comparisons of plant density measurement techniques.

[16] Locating the genetic locus associated with weeping phenotype in *Malus domestica*

Haoguang Yang¹, Laura Dougherty¹, and Kenong Xu¹

¹Horticulture Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

Weeping growth habit, which is characterized by downward growing branches, is a unique tree architecture form in woody plants. In *Malus*, weeping is present in domestic apples although it is mostly observed in crabapples. A previous study on the weeping trait in crabapples identified a major weeping locus (*W*) on chromosome 13. In this study, we intend to map the weeping growth habit in *M. domestica* using a half-sib family of 200 seedling trees derived from open pollinated seeds of a weeping apple cultivar. The progenies were phenotyped according to their growth habits (weeping and normal), and their DNA was also extracted. Two weeping and two normal gDNA pools each comprising ten individuals were created and were screened with various simple sequence repeat (SSR) markers covering the apple genome. Markers that showed putative linkage were confirmed further in the whole population, leading to mapping the weeping trait to another locus on chromosome 13. Analysis of more SSR markers narrowed the new weeping locus to a 900 kb region in the apple reference genome. These results provide crucial genetic information for identifying the weeping causal gene in *M. domestica*.

[17] Monitoring SDHI resistance development in *Venturia inaequalis* as a result of fungicide application rate.

April Moffett^{1, 2}, Katrin Ayer², Mei-Wah Choi², Kerik Cox²

¹Dept. of Biology, Hobart and William Smith Colleges, Geneva, NY 14456

²Plant Pathology, Cornell AgriTech Center, Geneva, NY 14456

Venturia inaequalis, the fungal causal agent of apple scab, produces lesions on both leaves and fruit of apple, often rendering fruit unmarketable. Management therefore requires growers to use frequent fungicide applications to control the disease. This can lead to the development of fungicide resistance, resulting in management failures. Succinate dehydrogenase inhibitors (SDHI) are a class of fungicides that target cell respiration in fungi, and there are currently no known SDHI-resistant populations of *V. inaequalis*. Maintenance of SDHI-sensitive populations is important for continued management of this disease. To address the question of how fungicide application rate influences resistance development, two different treatments of the SDHI fungicide, fluxapyroxad, were applied to two orchards over four years in a repeated measures experiment. Treatments included high (7.0 fl. oz/acre) and low (3.5 fl. oz/acre) fluxapyroxad rates, as well as an untreated control. Each treatment had four replicates that were distributed in a random complete block design. Fifteen-twenty lesions were collected from each replicate for a total of 50 isolates per treatment. Conidia were isolated from lesions and plated on discriminatory doses of fluxapyroxad. After a week of incubation, conidial germination was measured, and relative growth was calculated. Results will have immediate impacts on growers' best practices regarding fungicide resistance management.

[18] Measurement of *Salix* spp. fertilizer response with unmanned aerial systems

Jonathan M. Berlinger^{1, 2}, Eric S. Fabio², Lawrence B. Smart²

¹Agricultural Sciences Major, Cornell University, Ithaca, NY 14850

²Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva NY 14456

Unmanned aerial systems (UAS) provide a quick and effective method for monitoring pest and disease pressure, heat stress, and nutrient deficiencies across large areas, and can generate savings and consumer benefit by informing management decisions and breeding programs. One potentially useful application of UAS technology in agricultural research would be to replace time-consuming ground-based measurements of plant nutritional status through the development of vegetative indices (VI) that serve as proxies. Previous research on shrub willow (*Salix* spp.) nutrition showed a strong positive correlation between non-destructive chlorophyll meter readings and foliar nitrogen content. In the current research, multispectral reflectance data of shrub willow canopy obtained via UAS platform were correlated with ground-based measurements of chlorophyll content and plant height. We aimed to determine fertilizer response/N-status in each of three research trials which all received fertilization treatments, but which varied in the genotypes present and in plot size (225, 11 and 3 m²). Several VI were used in correlations with ground-based measurements of soil and plant analysis development (SPAD) in order to determine the best choice to use as a proxy for chlorophyll content/ N-status. In addition, an index representing the degree of reflectance in the red region of visible light was derived as a proxy for anthocyanin content at one trial site. These data may correlate with plant stress tolerance and will be used in future trait mapping experiments. Differences in the fertilizer response of cultivars are under genetic control and could be mapped using this technology.

[19] **Screening for QoI Resistance in *Podosphaera leucotricha* and *Podosphaera xanthii* Isolates from New York State**

Jamie Spychalla^{1,2}, David Strickland², Margaret Tuttle McGrath³, and Kerik Cox²

¹Dept. of Integrative Biology, University of Wisconsin-Madison, Madison, WI 53706

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva NY 14456

³Department of Plant Pathology, Long Island Horticultural Research and Extension Center, Cornell University, 3059 Sound Avenue, Riverhead, New York, 11901

Powdery mildew is a fungal disease that affects many agriculturally important crops and ornamentals. While resistant cultivars of these crops are available, conventional fungicide management programs are commonly used to control powdery mildew. Growers often utilize single-site fungicides due to their high level of efficacy and minimal off-target effects compared to multisite fungicides. However, overuse of single-site fungicides may promote resistance in pathogen populations by selecting for subsets of the population with point mutations that confer resistance. Quinone outside inhibitors (QoIs) are one class of single-site fungicide often used for powdery mildew management. These fungicides inhibit cellular respiration in the mitochondria. However, point mutations at codons 129, 137, and 143 in the mitochondrial *cytochrome b* gene confer resistance. We designed a PCR assay to screen isolates of two powdery mildew species - *P. leucotricha* (apple) and *P. xanthii* (cucurbit) – collected in New York State for these mutations. Seventeen and twenty-one isolates were screened, respectively. Resistance to QoIs has been reported in *P. xanthii* in New York and elsewhere in the United States. To date, no resistance has been reported in *P. leucotricha* globally, however continued unrestricted use has the potential for resistance development. Our assay rapidly screens for point mutations known to confer QoI fungicide resistance, allowing us to better study and inform sustainable chemical management practices with this valuable single-site fungicide, preserving its efficacy.

[20] **The Price is Blight: Effects of Prebloom Prohexadione-Calcium Programs on Fire Blight Control and Plant Vigor in Apple Trees**

John Spafford¹, Anna Wallis², Kerik Cox²

¹Hobart and William Smith Colleges, Geneva NY, 14456

²Dept. Plant Pathology, Cornell University, Geneva NY, 14456

Fire blight, caused by the bacteria *Erwinia amylovora*, is one of the most destructive diseases of commercial pome fruit. Presently, the most effective means of management rely on applications of the antibiotic streptomycin. However, there is increased pressure from the government and public sector to find alternative management strategies to control fire blight infection. Prohexadione-calcium (PhCa; trade name Apogee), a gibberellic acid inhibitor, was found to reduce the incidence of fire blight infections in apples at the expense of tree vigor when applied after bloom. Little is known about the impact of pre-bloom applications of PhCa on fire blight suppression or tree vigor. To shed light on the impact of pre-bloom PhCa programs, field trials were conducted in several apple orchards across two major apple production regions in New York and Vermont. At each location management programs were applied and the development of fire blight and host vigor were assessed. Data and results will be used to inform farmers of optimal fire blight management practices.

[21] **Sensory Evaluation of Vignoles (*Vitis spp Vignoles*) Clones Selected For Loose Cluster Phenotype**

Jennifer M. Neubauer¹, Timothy Martinson², Anna Katherine Mansfield³

¹Dept. of Viticulture & Wine Technology, Finger Lakes Community College, Canandaigua, NY 14424

² Sr. Ext. Assoc., School of Integrated Plant Science, Cornell AgriTech, Geneva, NY 14456

³Assoc. Prof. of Enology, Dept. Food Science, Cornell AgriTech, Geneva, NY 14456.

Vignoles is a grape cultivar used in cool climate wine production; its tight cluster morphology increases the incidence and severity of disease. For several years, looser-clustered Vignoles clones have been selected in an effort to decrease disease pressure, increase spray effectiveness, and increase fruit quality and yield. To assess the sensory profiles of wines made from Vignoles clones, wines made in 2018 from tight-clustered Clone R53 v30 was compared to wines from four loose cluster phenotypes. Using a 9-point difference-from control scale, 37 panelists compared both aroma and flavor of Clone R53 v30 to four treatment clones and a blind control. A significant difference was found in aroma between the control and one treatment (R65v83), but no other differences were found. To establish that wines made from each clone are statistically similar, additional sensory evaluations should be performed with a larger panel and over several vintages.

[22] **Behavioral responses of *Drosophila suzukii* to food odors as affected by changing temperature and fly phenotype**

Diego Sotomayor¹, Dara Stockton², Gregory Loeb³

¹University of Puerto Rico, Agroenvironmental Science Department Mayagüez, PR 00680

^{2,3}Dept. of Entomology, Cornell University, Cornell AgriTech, Geneva, NY 14456

Invasive Spotted wing *Drosophila* (SWD) is an economically important pest of small fruit. Phenotypic plasticity in response to cold temperatures and short day length (e.g. wintermorph phenotype) gives SWD an advantage in surviving harsh winters within central NY compared to the summermorph phenotype. Here we compared attractiveness of artificial diet, activity level and mortality for both summer and wintermorph flies at different temperatures to assess whether the efficiency of monitoring traps using food odor bait differs between phenotypes. An additional assay was directed towards measuring fly activity in response to temperature for both phenotypes. Flies were released into closed arenas containing a trap baited with fly diet which produces attractive odors within environmental chambers set at five different temperatures in a no-choice assay. Their response was measured after 24 and 48 hours. Activity levels were measured through visual assessment at 24 hours on a 4 point scale. Results indicate that wintermorphs remain active at lower temperatures compared to summermorphs. However, summermorphs were more likely to be captured in traps than wintermorphs, even at the lower temperatures. Survival was higher for wintermorphs than summermorphs at the lower temperatures. These findings indicate that wintermorphs have the capacity of being active during cool spring conditions. However, they may not be strongly attracted to standard trapping systems baited with food odors potentially leading to an underestimation of their population.

[23] **Overnight cold gives hop powdery mildew a hangover**

Owen Washam^{1,2}, Bill Weldon², Camille Sisto², David Gadoury²

¹Dept. of Horticulture, North Carolina State University, Raleigh, NC 27607

²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva NY 14456

Podosphaera macularis is a biotrophic pathogen that causes powdery mildew of hop (*Humulus lupulus*). Acute cold events (ACE) (<8C) have been shown to suppress disease development through a phenomenon termed stress-induced disease resistance (SIDR) in grape, Arabidopsis and hop powdery mildew pathosystems. However, the degree to which cold events are mediated through the host vs direct effects upon a biotrophic pathogen can only be determined when a cold event precedes inoculation, and this project aims to explore this pre-inoculation response. We exposed young hop leaves to 4C for 6 hours before inoculating with *P. macularis*, resulting in a mild reduction of pathogen growth. To further test the response across variable temperatures, leaf disks cut from young hop leaves were subjected to 2C, 4C, and 8C for 4 hours, inoculated, cleared of their chlorophyll, stained, and imaged with a high-throughput phenotyping robot. X-Y hyphal transect counts were recorded for each disk as a measure of pathogen growth, which failed to indicate a cold SIDR response for ACEs of 4 hours. Therefore, we conclude that a) acute cold SIDR in hop is most relevant in post inoculation scenarios and b) the cold SIDR response is different among hosts and merits further investigation.

[24] **Understanding grapevine (*Vitis*) domestication and variation between *Vitis* species through analysis of polyphenolic and aromatic compounds**

Lindsay M Lesniak^{1,2}, Ben Gutierrez²

¹Hobart and William Smith Colleges, Geneva, NY 14456²USDA-ARS Plant Genetic Resources Unit, Geneva, NY 14456

The evolution of grapes (*Vitis* species) has resulted in nearly sixty species of *Vitis* worldwide, varying in physical and chemical characteristics, including, disease resistance, antioxidant concentration, color, sweetness, acidity and the focus of this research, aromas. Human use of grapes has narrowly focused on the domesticated grapevine, *Vitis vinifera*. Wild North American species *Vitis labrusca* are used for grape breeding with distinct foxy aromas (such as ‘Concord’), but not always favored in wine production. *V. vinifera* cultivars however, have promised more successful hybrid crosses because of their floral and apple-like aromas due to the presence of aromatic compounds such as, 2-Hezenal and acetic acid. By studying aromatic compounds in a diverse collection of grapes from the USDA grape collection in Geneva, New York and the UC Davis Grape Repository in Davis, California, the complex domestication history and how *Vitis* species differ at the biochemical level can be better understood. The accessions were preselected based on foxy or Muscat aromas and analyzed by grouping into *V. vinifera*, *V. labrusca*, and *Vitis* hybrids. GC-MS indicated the presence of major aromatics in conjunction with titratable acidity and soluble solids (Brix) to measure pH and sugar content of individual accessions. This study can aid the wine and table grape industry in yielding the best quality product that not only have favorable and diverse physical properties but also beneficial nutritional properties. Additionally, it provides a bridge between the *V. vinifera* species grown in Western United States at UC Davis and the hybrid accessions bred in the Northeast at the Geneva repository.

[25] **Screening *Cannabis sativa* cultivars for resistance to powdery mildew caused by *Golovinomyces spadicus***

Nathalia A. Portilla¹, Ali Cala², Christine D. Smart², Surya Sapkota², Lawrence Smart³, George Stack³, Jacob Toth³, Craig Carlson³, Lance Cadle-Davidson²

¹Departamento de ciencias biológicas, Universidad de los Andes, Bogotá 111711, Colombia

²Plant Pathology and Plant-microbe Biology Section, School of integrative Plant Science, Cornell University, Geneva, NY 14456

³Horticulture Section, School of integrative Plant Science, Cornell University, Geneva, NY 14456

Powdery Mildew, caused by *Golovinomyces spadicus* is an obligate biotrophic disease that causes significant economic damage to industrial hemp (*Cannabis sativa*). Because hemp is an emerging industry in New York, there is a lack of information about the susceptibility to powdery mildew. Thirty cultivars of high cannabinoid (CBD) hemp were analyzed for resistance with imaging assay that uses 5-millimeter leaf discs. The adaxial surface of discs were spray inoculated with powdery mildew conidia and ten discs per genotype were imaged three times. Area under the disease progress curves (AUDPC) for each of the cultivars were calculated and compared to determine the differences in susceptibility to the pathogen. This information will be useful for the hemp breeding program and will expand our *Cannabis sativa* host-pathogen knowledge. From this assay and possibly future assays like this one, we will be able to work with the breeding program to identify regions of the hemp genome that are involved in resistance to powdery mildew.

[26] **Comparison of Bioassays for Monitoring Onion Thrips Susceptibility to Insecticides**

Isabella Magna Yannuzzi¹, Erica Moretti², Brian Nault²

¹Plant Science, CALS, Cornell University, Ithaca NY 14853

²Dept. of Entomology, Cornell University, Cornell AgriTech, Geneva NY 14456

Onion thrips (*Thrips tabaci* Lindeman) is the most damaging insect pest of onion, and can cause yield reductions between 30%-60%. While they are managed primarily with insecticides, thrips are highly proficient at developing resistance across insecticide classes. To monitor population resistance in the field, bioassays can be used to analyze onion thrips susceptibility to insecticides. Three lab bioassays have been documented in the literature for use with onion thrips: TIBS (contact assay), feeding-only assays, and leaf dips (contact + feeding assay). The purpose of this study was to (1) understand how insecticide exposure, via these different assays influences mortality, (2) determine which bioassay is most representative of field conditions, and (3) discover which assay was the easiest to execute. We tested these three bioassays, in addition to a field simulation using a susceptible colony of onion thrips with spinetoram (Radiant[®]), a commonly used insecticide. Results indicated (1) that each bioassay generated a unique mortality curve and LC₅₀(the concentration of pesticide resulting in 50% population mortality), (2) all three lab assays showed 100% mortality at 100 ppm while the field assay only exhibited 91%, and (3) the feeding-only assay was preferred due to ease of set up and monitoring, cost, and minimal waste. These data will assist with making bioassays more applicable to growers and extension educators as a monitoring tool for onion thrips resistance.

[27] **Characterization of the USDA Tart Cherry (*Prunus cerasus*) Collection in Geneva, NY**

Kyra Battaglia¹, Molly Carroll¹, Ben Gutierrez¹

¹USDA-ARS PGRU Geneva, NY

The sweet cherry, *Prunus avium*, and tart cherry, *Prunus cerasus*, are the two major species grown commercially. In comparison to sweet cherries, tart cherries have high acidity and softer fruit. Additionally, the tart cherry anthocyanins (red pigments in fruit) differ from sweet cherry and have reported benefits to human health. This experiment looked at the various characteristics of cherry fruit quality important for commercial purposes, including fruit weight, flesh to pit ratio, acidity, total soluble solids, aromatic compounds, and anthocyanin content. To evaluate diversity of fruit quality, ripe cherries were collected from the USDA Tart Cherry Collection in Geneva, NY in 2011, 2013, 2014, and 2019. The USDA collection maintains 130 tart cherry accessions across 7 species. Cherries were weighed, de-pitted, and weighed without pits. The cherries were juiced to determine the total soluble solids (TSS) using a refractometer, the malic acid concentration, and the presence of different aromatic compounds using gas chromatography-mass spectrometry (GC-MS). The samples were also prepared and processed using High Performance Liquid Chromatography (HPLC) to determine the anthocyanin concentration. This diversity project showed the relationship of other cherry species in relation to Montmorency, the main cherry sold for commercial purposes, with others containing more favorable traits. Analysis also showed characteristic and phenolic comparisons between tart and sweet cherries. This information will be publicly available through the Germplasm Resources Information Network (GRIN-Global), providing accession data for future research and development of cultivars with optimal characteristics.

[28] **Mating Type Distribution and Formation of Chasmothecia on Grapevine by *Erysiphe necator* in the Northeastern United States.**

James Belton^{1,2}, Breanne Kisselstein², and David Gadoury²

¹Dept. of Environmental and Forest Biology, SUNY College of Environmental Science and Forestry, Syracuse, NY 13210

²Plant Pathology and Plant-Microbe Biology Section, Cornell University, Geneva, NY 14456

Erysiphe necator causes grapevine powdery mildew and threatens sustainable grape production worldwide. Pathogen populations are heterothallic, and two mating types generally exist in a 1:1 distribution throughout the growing season. Ascocarps are initiated immediately upon hyphal contact between opposite (i.e., compatible) mating types. However, a recent report from Oregon described an unequal temporal distribution of mating types, as well as delayed initiation of ascocarps in colonies comprised of both mating types. As a precursor to reexamining the process of ascocarp formation in Washington and Oregon in comparison to that reported elsewhere, we optimized the performance of MAT1-1 and MAT1-2 primers. We determined mating types within *E. necator* colonies from Finger Lakes Wine Region commercial vineyards and regional wild *Vitis riparia* and *Vitis labrusca* grapevines using DNA extraction and a multiplexed qPCR assay. Clonal lab isolates were crossed on detached surface-sterilized grape leaves to ensure proper function of the PCR-based assays. All locations and grapevine species sampled showed the expected 1:1 ratio of mating types over the growing season. Departures from a 1:1 ratio were only observed in single site timepoints with small sample sizes (n<30).

[29] **Differences in progression of *Melampsora* rust disease in a segregating *Salix purpurea* mapping population**

Diego A. Hernandez^{1,2}, Dustin G. Wilkerson², Chase R. Crowell³, Patrick McMullen³, Lawrence B. Smart², and Christine D. Smart³

¹Dept of Biological Science, Universidad de los Andes, Bogota, Colombia 111711

²Horticulture Section and ³Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, NY 14456

Melampsora americana is a phytopathogenic fungus involved in rust disease in shrub willow (*Salix* spp.). Symptoms of the disease are the formation of small (1-2 mm), orange to yellow pustules of urediniospores on the lower surface of the leaf. Some of the effects are premature defoliation, increased susceptibility against secondary pest and disease infection, and a reduction in total biomass yield, all negatively affecting industrial bioenergy production. Leaf disc assays have the advantage of requiring little space, high throughput, and ease of inoculation. The objective of this project was to develop and test a leaf disk assay that can detect the differences in the progression of the disease in susceptible and resistance genotypes inoculated with *M. americana*. Leaf samples were collected from genotypes that were previously identified as resistant or susceptible in a F₂ mapping population of *S. purpurea* from a field trial in Geneva, NY. Leaf disks (1 cm) were inoculated with *M. americana* urediniospores using a settling tower, and then transferred to Pyrex plates for imaging. Photos were taken at 0, 6, 9, and 13 DPI using a PMBot imaging robot. Photo processing was conducted using ImageJ to detect the percent area of disease. Data was collected on the same set of disks for repeated measures analysis using R Studio. There was a reduction in the progression measure of the disease after 6 days post-inoculation. This is due to loss of the orange color of the spores during germination.

[30] **Quantitative determination of anthocyanin compounds during tart cherry maturation**

Molly Carroll^{1,2}, Lindsay Brown², Lindsay Lesniak², Kyra Battaglia², Benjamin Gutierrez²

¹Dept. of Food Science, Purdue University, West Lafayette, IN 47906

²Plant Genetic Resource Unit, United States Department of Agriculture, Agricultural Research Service, Geneva NY 14456

With increasing interest in foods with antioxidant, anti-inflammatory, and other health properties, fruit with rich phenolic and anthocyanin profiles are in greater demand by consumers. Tart cherries (*Prunus cerasus*) have unique nutritional qualities, relative to sweet cherries, which contribute to human health. However, dietary consumption of tart cherries as juice or processed fruit in the U.S. is largely based on one variety, 'Montmorency'. Studying the diversity of the tart cherry species would allow for more insight into how this fruit can be better used to improve human health and preserve the genetic variance within the species. High Performance Liquid Chromatography (HPLC) was used to track anthocyanin and phenolic compounds in 19 varieties of tart cherry, during maturation. Samples of leaves and fruit were collected at four increments throughout the ripening period of the fruit to analyze how anthocyanin production progresses. It was found that relevant anthocyanin compounds to the tart cherry profile were accumulated or degraded, depending on the compound, throughout the ripening process. This change in quantity was constant. The phenolic profile of the leaves had very small changes throughout fruit maturation, so therefore serve as a control. This study serves as the beginning of a much larger exploration into the genetic and phenolic diversity of tart cherries.

[31] Collembola abundances interact with fertilizer amendments to alter microbial activity and impact crop development

Perla Carmenate^{1,2}, Ashley Jernigan², Kyle Wickings²

¹Dept. of Agronomy, Iowa State University, Ames, IA 50011

²Dept. of Entomology, Cornell University, Cornell AgriTech, Geneva, NY 14456

Microarthropods (collembola and mites) have been shown to accelerate rates of decomposition and promote nutrient mineralization. Our objective was to test how microarthropod abundances influence soil microbial metrics and to determine whether they impact crop development under different fertilizer treatments. The greenhouse experiment included twelve combinations of three collembola treatments (none, low, high) and four organic fertilizer treatments (no fertilizer, compost, alfalfa green manure, synthetic Chilean nitrate) with four replicates (96 pots). Plant phenology was recorded weekly and half of the pots were destructively harvested for plant biomass and microbial metrics after twenty-eight days. The oat growth stage was accelerated by alfalfa green manure and compost at different times in early oat development in the absence of collembola, however, this effect disappeared in the presence of collembola. Shoot biomass was unaffected by treatments, however, root biomass was greater in the no fertilizer treatment compared to the Chilean nitrate treatment. Within the no collembola treatment, alfalfa green manure and compost stimulated the enzymes that break down amino acids and organic phosphorus. Within the high collembola treatment, the enzyme that breaks down lignin was more abundant in the compost treatment than in the no fertilizer treatment. This suggests that soil microarthropods modify interactions between soil microbes and fertilizer amendments. When microarthropods are present they appear to mediate the effects of the fertilizer, making fertilizer type less significant.

[32] Willow Leaf Beetle and Shrub Willow Biomass Yield

Allison P. Koehle^{1,2}, Felipe Montes², Sarah Wurzbacher³, Armen R. Kemanian²

¹The Pennsylvania State University, Department of Plant Science, 116 ASI Building, University Park, PA 16803

²Juniata College, Department of Biology, 1700 Moore Street, Huntingdon, PA 16652

³Penn State Extension, Williamsport, PA

Pest infestation, specifically imported willow leaf beetle (*Plagiodera versicolora* Laicharting), is one determinant of the success of the shrub willow (*Salix* spp.), a crop with promising potential as a feedstock for bioenergy production. In this study, the presence of this pest was assessed to determine the impact on growth and ultimately yield of the shrub willow. A stratified sampling method was used to observe the willow leaf beetle population at two fields, Rockview and Rock Spring, in Central Pennsylvania to compare the genotypic differences of defoliation due to herbivory and growth differences. The willow leaf beetles demonstrate selectivity due to higher populations within specific cultivars. A higher population of beetles within Preble cultivars shows an impact on the growth with lower than average height for this genotype. A higher population within the nitrogen fertilized plots also demonstrates nutrient selectivity of the willow leaf beetle. These findings along with future proximal sensing data will help to mitigate the impact of the willow leaf beetle, along with several other pests, and increase the feedstock potential of the willow shrub.