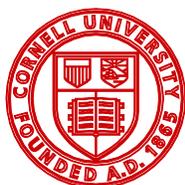


Proceedings of the
2015 Summer Scholars Program
Undergraduate Research Poster Session
July 31, 2015
Geneva, NY



Cornell University
College of Agriculture and Life Sciences
New York State Agricultural Experiment Station

These abstracts report the results of research performed by the Summer Scholars participating in the
2015 Cornell University Summer Scholars Program

This program was funded by

USDA Federal Formula Funds administered by the NY State Agricultural Experiment Station through
a grant entitled *Agriculture and Food Production Summer Internship Opportunities for
Undergraduates: A Cross-Departmental Summer Scholars Program at Cornell University's New York
State Agricultural Experiment Station*

Additional funds were provided by

New York State Agricultural Experiment Station Director's Excellence Fund
College of Agriculture and Life Sciences Alumni Association
The New York State Agricultural Society Foundation
Genesee Valley Regional Market Authority
Hicks Nursery, Westbury, NY
Students were also funded by grants awarded to individual faculty mentors

*Special thanks to Dr. Christine de Denus, Dr. Patricia Mowery and Hobart and William Smith
Colleges for providing the venue for the poster session.*

These proceedings can be found on-line at

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

[1] **Ambrosia Beetle: An Invasive Pest Invading New York Apple Orchards from Forest Exteriors**

Abigail E. Davis^{1,2}, Tessa Lessord², and Arthur M. Agnello²

¹Roanoke College, Salem, Virginia 24202; ²Dept. of Entomology, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

The state of New York is ranked second in the nation for apple production, thus making the crop a crucial economic commodity. In recent years, an invasive species of ambrosia beetle called the black stem borer (*Xylosandrus germanus*) has been threatening apple orchards in New York (Agnello et al., 2015). The objective of this study was to assess the distribution and damage of *X. germanus* in Wayne County, NY. Furthermore, the efficacy of insecticides or biologicals was assessed to control either *X. germanus* or its fungal symbiont, *Ambrosiella hartigii*. Specimens were collected using bottle traps with ethanol lures and a soap and water solution in 14 commercial orchards. Insecticide efficacy was tested on 2 known infested sites with different insecticide treatments and one control. The number of *X. germanus* individuals peaked mid-season for both exterior and interior traps. There was a statistically significant difference between Warrior (lambda-cyhalothrin)-handgun and Lorsban (chlorpyrifos)-airblast in potted trees at Roberts Farm, and Lorsban (chlorpyrifos)-airblast for orchard trees on Furber Farm. Results indicate that *X. germanus* have scheduled flight times corresponding to their life cycle, and that they invade an orchard from an exterior forest habitat. Additionally, efficacy of insecticides may not be correlated with spray coverage.

[2] **Heterologous Expression of the *Bacillus thuringiensis* SF361 protein, YvgO**

Janeth Perez-Garza^{1,2}, Abigail Synder², and Randy Worobo²

¹Facultad de Ciencias Biologicas, Universidad Autonoma de Nuevo Leon. 124-F. San Nicolas, N.L. 66451 Mexico; ²Department of Food Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Many species of Bacilli are known producers of antimicrobial peptides, antibiotics and bacteriocins, which in total exhibit a broad inhibition spectrum against bacteria, yeast, and fungi. Particularly, *Bacillus thuringiensis* SF361 produces an antifungal protein with filamentous fungi and yeast as principal targets. Since fungal species are food spoilage microorganisms, development of novel antifungal proteins could improve food quality. The purpose of this study was to heterologously express the *Bacillus thuringiensis* protein, YvgO, using *Escherichia coli*, to provide large quantities of the pure protein needed to further characterize YvgO, or determine its potential as a natural antifungal agent for foods. A *Bacillus thuringiensis* SF361 culture was used for YvgO DNA extraction for cloning into pTrc99a, a vector that contains a 6 His tag to facilitate purification. The cloning results were satisfactory, in that the DNA and plasmid products were quantified using the NanoDrop and visualized using agarose gel electrophoresis. Transformants were plated on TSA + ampicillin so only the colonies that had the plasmid could grow. The transformants were screened for the correct insert and used for large scale expression and purification of the YvgO protein.

[3] Relationship between phenotype and genotype among New York *Sclerotinia sclerotiorum* isolates

Tilly I. Bartelt^{1,2}, Amara R. Dunn², and Sarah J. Pethybridge²

¹Macalester College, St. Paul, MN 55105; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

White mold caused by the fungus, *Sclerotinia sclerotiorum*, is an important disease of many vegetables. The phenotypes of 25 isolates with a predetermined multilocus genotype using microsatellite loci collected from fields across New York between 1982 and 2014 were characterized by aggressiveness on snap beans (*Phaseolus vulgaris*) in a greenhouse bioassay, mycelial growth rate, and mycelial compatibility grouping (MCG). Significant differences were observed in isolate aggressiveness when lesion lengths on stems of snap bean plants were measured after one day. Isolates of the same MCG were a like multilocus genotype (91.7%), with the exception of isolates -14151-02 and 14246-03. In addition, isolate 43 C was compatible with isolates from multiple MCGs. Mycelial growth rate on potato dextrose agar had low but significant ($P < 0.001$) variability among isolates (28.20 to 35.64 mm/day, for all but three isolates) and no significant correlation was observed between rate of growth and lesion length ($r = 0.30$; $P = 0.22$). Understanding the phenotypic variability among genotypes of *S. sclerotiorum* isolates within New York State may improve our ability to test the effectiveness of management practices for this disease.

[4] Development of Species-Specific PCR primers and Assessment of DNA Extraction Techniques for the Detection of *Meloidogyne hapla* in Soil

Austin Lien^{1,2}, Adrienne Gorny², and Sarah J. Pethybridge²

¹University of Minnesota-Crookston, Crookston, MN 56723; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Effective management of plant-parasitic nematodes relies on the correct identification of the pest before planting. Prediction of damage from soilborne diseases may be substantially improved by the provision and adaption of pre-plant soil tests that are highly sensitive and specific. Using *Meloidogyne hapla* (Northern root-knot nematode) in vegetables as a model system, PCR primers were designed and tested for specificity. Further, three different methods for the extraction of DNA from soil were assessed for their efficacy. A commercially available Mo Bio PowerLyzer[®] PowerSoil[®] DNA Isolation kit acted as a 'gold standard' for testing alternative protocols in extracting DNA from soil isolation methods. The primers developed in this study and the modified protocol of the phenol extraction, hydroxyapatite purification DNA isolation method from Purdy et al. 1996 will be utilized in future qPCR tests for quantification and to assess risk of crop damage or loss from *M. hapla*.

[5] Characterization of Fungicide Resistance to Promote Integration of Disease Management Practices in Strawberry Nurseries and Fruit Production Fields

Rebecca Hall^{1,2}, David Gadoury², Bruna Forcelini³, and Lance Cadle-Davidson^{2,4}

¹Clarion University of Pennsylvania, Clarion, PA 16214; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456; ³University of Florida, Gainesville, FL 32611; ⁴USDA-ARS Grape Genetics Research Unit, Geneva, NY 14456.

Strawberry Powdery Mildew (*Podosphaera aphanis*) is a devastating disease that is particularly destructive in high tunnel production systems. Resistance to available fungicides is a recurring issue, made more difficult by a lack of coordination between fungicide use in nurseries and the use in fruit production fields. We studied the phenotypic nature of fungicide resistances of quinoxyfen and the demethylation inhibitors (DMI) fungicides, and investigated molecular methods to assess resistance. The grape powdery mildew pathogen (*Erysiphe necator*) was used as a model system, due to extensive prior research and availability of molecular tools for study. Although quinoxyfen purportedly inhibits appressorial formation, this response was not consistently observed. The DMI fungicide myclobutanil exhibited both fungitoxic and fungistatic effects. Both myclobutanil, quinoxyfen, and two additional respiration inhibitor fungicides (boscalid and azoxystrobin) did not exhibit vapor activity, an important consideration for bioassays in closed in-vitro systems. Two mutations in the *cyp51* gene were associated with many, but not all phenotypic expressions of resistance to myclobutanil. These preliminary results are part of an international project that seeks to coordinate fungicide management programs of strawberry nurseries with those used in fruit production fields.

[6] Characterizing Ornamental Crabapple Progenies for Plant Habit and Leaf Size, Color, and Lobing

Caitlyn Fleischman^{1,2} and Susan K. Brown²

¹University of Wisconsin Stevens Point, Stevens Point, WI 54481; ²Horticulture Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Weeping tree habit, leaf color and leaf lobing are valued ornamental traits in *Malus*. However, weeping is the least studied growth habit in apple and leaf lobing also has not been researched extensively. A better understanding of both these traits would be useful in breeding new crabapples for landscaping. In this study, one-year-old plants from four different progenies were characterized for these traits. These progenies helped confirm the dominant gene for weeping, the dominant gene for red coloration of foliage and indicated greater variability for leaf size outside of the parental means. Leaf lobing was inherited and expressed much more strongly than in previous studies on this trait with different germplasm. These results demonstrate the potential for creating new crabapples with weeping habit, attractive red/purple leaf types and deeply lobed leaves.

[7] Phenotypic characterization of a New York *Phytophthora capsici* field population

Kimberly N. D’Arcangelo^{1,2}, Maryn O. Carlson², and Christine D. Smart²

¹Adrian College, Adrian, Michigan 49221; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

Phytophthora capsici is the oomycete pathogen responsible for Phytophthora blight. This vegetable disease causes significant losses to crops in the Solanaceae, Cucurbitaceae and Fabaceae families. Flooding events in the northeast, in recent years, have introduced *P. capsici* into growers’ fields with no prior history of this pathogen. In addition, many growers are no longer able to use mefenoxam, a commonly used fungicide, to control *P. capsici*, due to an increase in the prevalence of pathogen insensitivity to this chemistry. Seventy isolates had been previously collected from a New York grower’s field of mixed cucurbits that was infested with *P. capsici* for the first time. We assessed these isolates for several phenotypic traits: 1) sensitivity to mefenoxam; 2) growth rate; and 3) mating type. In addition, population structure was assessed using principle component analysis on genotypic data derived from genotyping-by-sequencing. Of the 70 isolates tested for sensitivity to mefenoxam, fifty-nine were sensitive, 3 intermediately sensitive, and 8 isolates were insensitive to the fungicide. Genotypic clustering was primarily consistent with mefenoxam sensitivity classification.

[8] RNA Interference to Engineer Resistance Against *Grapevine fanleaf virus*: mRNA Expression vs. Rate of Infection

Emily Donaldson^{1,2}, Patricia Marsella-Herrick², and Marc F. Fuchs²

¹Harvard University, Cambridge, MA 02138; ²Plant Pathology and Plant Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Grapevine fanleaf virus (GFLV) severely affects the grape and wine industry worldwide. No resistance to GFLV is known in *Vitis* spp, therefore researchers have turned to genetic engineering in the hopes of creating a grapevine rootstock resistant to GFLV. Since genetically distinct strains of GFLV exist, unique constructs were created using combinations of eight regions that are conserved across the genome of multiple strains with the hopes of using RNA interference to engineer resistance against as many strains as possible. The objective of this project was to investigate (1) which constructs in genetically engineered *Nicotiana benthamiana* fair better against the virus and (2) how the level of transgene expression affects viral resistance. The experimental approach consisted of inoculating *N. benthamiana* with different constructs and wild-type control-plants with three distantly related strains of GFLV. Viral presence was monitored by DAS-ELISA in all plants over time and RT-qPCR was performed with total RNA from selected plants to determine the effect of mRNA expression on infection rates. Our results revealed the relationship between mRNA expression and viral infection, and the significant effect of the constructs on infection rate, suggesting RNA interference as a valid method for protecting *Vitis* spp from GFLV.

[9] Anthocyanin Color Perception and Degradation of Red Cabbage Genotypes

Emma Weidman^{1,2}, Didier Socquet-Juglard², Alexandra Bennett², and Phillip Griffiths²

¹Webster University, Saint Louis, MO, 63119; ²Horticulture Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY, 14456

Anthocyanins are water-soluble pigments found in plants that produce a range of colors including red, purple, green and blue when placed in solutions with pH values ranging from 1-12. These pigments generally degrade at high pH, high temperatures, and in presence of light. Larger, more complex, and stable anthocyanins can be used as food additives when they resist degradation. This study aimed to evaluate the pigment perception and degradation in 88 different genotypes of juvenile red cabbage at pH2 and pH7. Anthocyanins were extracted from each sample and diluted to a concentration of 0.02g/ml. A colorimeter was used to calculate the Chroma and Hue angle of each genotype and to measure anthocyanin degradation 6, 24, and 48 hours after initial measurements. Considering all measurements at pH7, a range of Hue angles from 197° (Slate Gray) to 252° (Sky Blue) was observed. In pH2, solutions produced a range of Hue angles from 346° (Light Pink) to 358° (Hot Pink). The findings from this work will help develop new lines of red cabbage with high anthocyanin yields producing stable, natural colors that can be used in the food industry to replace synthetic additives.

[10] Sensitivity of New York isolates of *Alternaria brassicicola* to azoxystrobin

Anna J. Muhich^{1,2}, Rachel A. Kreis², and Christine D. Smart²

¹Gonzaga University, Spokane, WA 99258; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

Alternaria brassicicola is a fungal pathogen that causes *Alternaria* leaf spot in brassica crops. Growers of brassica crops in New York have expressed concerns regarding the possibility of increased resistance of *A. brassicicola* to commonly used fungicides, such as azoxystrobin. Azoxystrobin, an inhibitor of fungal respiration, leads to lower germination rates in *A. brassicicola* when applied. Thirty-two *A. brassicicola* isolates drawn from several areas of New York State were exposed to 9 concentrations of azoxystrobin: water agar control, SHAM control (60 µg/mL), 0.001 µg/mL, 0.01 µg/mL, 0.1 µg/mL, 1.0 µg/mL, 10.0 µg/mL, 25.0 µg/mL, and 100.0 µg/mL. Percent germination was determined at each the 9 concentrations. The 50% effective concentration (EC₅₀) was calculated for each isolate. Twenty-three isolates exhibited EC₅₀ values between 0 and 10.0 µg/mL; these were classified as high sensitivity and medium sensitivity to azoxystrobin. 6 isolates exhibited EC₅₀ values between 10.0 and 100.0 µg/mL; these were classified as low sensitivity. Two outlying isolates exhibited very high EC₅₀ values, lying above 100.0 µg/mL. Further testing is required to determine with more certainty if these isolates are highly insensitive to azoxystrobin application.

[11] Identification of a Grapevine red blotch-associated virus Insect Vector

Hannah Sweet^{1,2}, Elizabeth Cieniewicz², and Marc F. Fuchs²

¹University of Minnesota Morris, Morris, MN 56267; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Grapevine red blotch-associated virus (GRBaV) is a recently recognized geminivirus implicated in red blotch disease. GRBaV has been detected in vineyards across the United States and Canada, and is of concern to the grape and wine industry. The transmission of GRBaV is not well understood; the main objective of this study is to identify possible insect vectors of GRBaV. We are conducting a survey of insects visiting a vineyard in California, where within-vineyard spread of GRBaV is suspected. Insect traps were placed throughout the vineyard and rotated weekly. Insect populations of orders Thysanoptera, Diptera, and Apocrita caught on traps dominated throughout May. Individual insects were collected from traps and tested for GRBaV presence by PCR using appropriate primers. The majority of insects tested negative for GRBaV, with a few exceptions in the family Miridae. These individuals are unlikely transmitters, indicating that the May survey did not reveal any likely vector candidates. Therefore, insect survey and virus detection will continue through the 2015 grape-growing season. Once vector candidates are identified, greenhouse transmission assays will be conducted to confirm a vector species. Understanding GRBaV transmission will help growers implement optimal management strategies to minimize the spread of GRBaV.

[12] Effects of Antibiotic Applications on the Bacterial Community Structure in the Apple Phyllosphere

Jason Hagel^{1,2}, Kiersten Bekoscke², Catherine Miller³, Kerik D. Cox²

¹Millersville University, Department of Biology, Millersville, PA; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, New York State Agricultural Experiment Station, Cornell University, Geneva NY; ³William Smith College, Geneva NY

Erwinia amylovora is a bacterium that causes fire blight in apple and pear. Fire blight moves systematically through the tree and can destroy an entire orchard if left untreated. Streptomycin is the most effective method of preventing fire blight; however, streptomycin resistance (SmR) is a growing problem in NY. The *strA/strB* gene pair is the most common determinant of resistance. This gene pair is also found in commonly epiphytes, such as *Pantoea agglomerans* and *Pseudomonas species*. Oddly enough, all recent reports of the gene pair in resistant *E. amylovora* have been found on a nonconjugative plasmid, pEa29. Groups of Idared apple trees were treated with increasing applications of streptomycin or kasugamycin to observe the changes that occur in the epiphytic community. Representative samples of the bacterial community were collected and cultured on different media to observe the microbial community and antibiotic resistance. Trees treated with kasugamycin exhibited a decrease in SmR bacteria, while those treated with streptomycin exhibited an increase in SmR bacteria. Streptomycin treatment favored the survival of *Pseudomonas sp.*, whereas the kasugamycin treatment favored the survival of *P. agglomerans*. Such changes in the community structure could have an impact on the mobilization of the *strA/strB* gene pair.

[13] Characterizing a Symptom Determinant Region of *Grapevine fanleaf virus* (GFLV)

Jessica Carpenter^{1,2}, Larissa Osterbaan², Marc F. Fuchs²

¹University of Wisconsin – River Falls, River Falls, WI 54022; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Grapevine fanleaf virus (GFLV) continues to be a major threat to the grapevine industry. GFLV causes fanleaf degeneration of grapevines; symptoms include leaf deformities, poor fruit set, shortened internodes, and premature death of vines. GFLV is a nematode-vectored, bipartite positive-sense RNA virus. Two strains of GFLV were used in this study: GHu and F13. Though both strains cause symptoms on grapevines, only GFLV-GHu causes symptoms (vein-clearing) on the model species *Nicotiana benthamiana*, while GFLV-F13 produces an asymptomatic infection. GFLV-GHu has a symptom determinant region at the 3' end of the RNA1-encoded 1E^{pol} (408nt long) coding region that is the focus of this study. Binary vectors based on the GFLV genome included fragments of the GFLV-GHu symptom determinant region, which were used for agroinfection of three-week old *N. benthamiana* seedlings. The intent was to narrow down the minimal sequence necessary to produce vein-clearing symptoms in *N. benthamiana*. Double Antibody Sandwich (DAS) Enzyme-Linked Immunosorbent Assay (ELISA) was used to screen agroinfected *N. benthamiana* for GFLV infection; this screening detected no GFLV-positive plants throughout this study. Following troubleshooting, future studies will include more agroinfections in order to continue the characterization of the GFLV-GHu symptom determinant region.

[14] Molecular mapping confirms the location of the weeping trait in the apple genome

Joyce Wu^{1,2}, Raksha Singh², and Kenong Xu²

¹University of Wisconsin-Madison, Madison, WI 53715; ²Horticulture Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

The weeping growth habit is a unique tree architectural trait. Although an early study reported that the trait is controlled by a dominant gene *W* (weeping) in apple, there exists little research at molecular levels. An in-depth investigation into the genetic and molecular mechanisms of the weeping growth habit would help understand the overall mechanisms regulating woody plant growth patterns, which is essential for the improvement of tree forms. Using a pooled genome sequencing approach, two pools of genomes, representing 16 and 18 standard and weeping progeny respectively, from cross Evereste (*ww*) × Cheal's Weeping, (*Ww*) were sequenced with a coverage of 27-30×. A series of variant detection and analyses between the two pools putatively mapped *W* to a five (6.5-11.5) Mb region on chromosome 13. To validate the mapping, a set of 24 SSR (short sequence repeats) and SNP (single nucleotide polymorphisms) markers were designed within the *W* region and evaluated for polymorphisms between the two parents, Evereste and Cheal's Weeping. Assessing three polymorphic SSR and two SNP markers with 38 individual progeny from the cross indicated that they are all tightly linked with the weeping growth habit, confirming the genetic mapping of *W* by pooled genome sequencing.

[15] Genetic and physical characterization of the *MaQ8* locus important for apple fruit acidity

Lauren McLain^{1,2}, Laura Dougherty², and Kenong Xu²

¹Truman State University, Kirksville, MO 63501; ²Horticulture Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

The sweet or tart taste of apple is directly associated with fruit acidity levels. Previous studies demonstrated that apple fruit acidity is controlled by the major QTL (quantitative trait locus) *Ma* and several other QTLs, including *MaQ8*. This QTL has been shown to play a critical role on fruit acidity; however, the effect is unstable, varying from a major QTL to a minor QTL depending on studies. We have recently isolated the *Ma* QTL and identified its causal gene *Ma1* that encodes an aluminum-activated malate transporter (ALMT) –like protein. With this development, we introduced the F₁ population ('Fiesta' × 'Discovery') in which *MaQ8* was originally detected to characterize the *MaQ8* QTL. Genetic analysis using *Ma1*-based functional marker CAPS₁₄₅₅ indicated that the F₁ population was derived from a cross between *Mama* ('Fiesta') × *MaMa* ('Discovery'). When fruit acidity levels were analyzed within the same genotype group *MaMa* or *Mama* in the progeny, the effect of *MaQ8*, as determined by linked markers, is clearly detectable and highly significant. By developing new markers and identifying bacterial artificial chromosome (BAC) clones, we mapped the *MaQ8* QTL to a genetic interval of 4.8 cM that physically spans 2.1 Mb in apple genome on chromosome 8.

[16] Bacteria and fungi associated with the black stem borer, *Xylosandrus germanus*

Katrin M. Ayer^{1,2}, Sarah M. Villani², and Kerik D. Cox²

¹Department of Biology, Hobart and William Smith Colleges, Geneva, NY 14456; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456.

Severe tree decline and death during Spring 2013 led to the identification of the black stem borer (BSB), *Xylosandrus germanus*, as an emerging pest in western NY apple orchards. The BSB bores into stressed trees, tunnels to form a gallery and lay eggs, and farms fungi for larval food sources. These fungi can colonize vascular tissue leading to wilting and death of the tree. This study aimed to identify bacteria and fungi associated with BSB and symptomatic wood following infestation in apples. For fungal isolates, PCR and sequencing of the ITS region was conducted for identification. Of the eight fungal species isolated from symptomatic wood, the majority were identified as *Ambrosiella xylebori*, a fungus that has previously been associated with BSB. Conversely, *Nectria haematococca*, which has also been associated with BSB was most frequently found on *X. germanus*. Bacteria were also identified using PCR and differential media, but neither *Pseudomonas* nor *Erwinia amylovora* detected on the insect. The presence of *A. xylebori* and *N. haematococca*, in apple vascular tissue indicates that the insect can establish fungal farms within the host and may have detrimental effects to the tree.

[17] Optimizing Tannin Content, Sweetness and Carbonation of Cider Made from Dessert Apples for Consumer Acceptability

Meaghan Sugrue^{1,2}, Christopher Gerling², Cortni McGregor¹, Anna-Katherine Mansfield², Olga Padilla-Zakour^{1,2}

¹Department of Food Science, Cornell University, Ithaca NY 14853; ²Department of Food Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

In the United States hard cider sales are skyrocketing. This popularity could benefit New York (NY) agriculture. However, due to a lack of standards, a range of apples are used, thereby producing beverages with different flavors and composition. Through chemical and sensory analysis, we discovered which aspects of ciders lead to an enjoyable product. From this knowledge, we predicted a NY dessert apple cider with high consumer appeal could be made if carbonated and supplemented with additional tannins and sugar. Tasting of commercial NY hard ciders showed that moderate carbonation and sugar as well as high acidity and phenolic content were preferred. The chemical compositions of those commercial ciders were compared to those of four experimental dessert apple ciders. Sensory tests were performed to determine the optimized specifications for yeast fermentation (DV10), commercial tannin choice (Enartis Tan UVA), carbonation (4 g/L), tannin addition (75-300 ppm) and sugar level (4 % w/w) to use in final ciders. From these results it was inferred that NY dessert apples can produce a quality cider when supplemented with sugar and tannins. In order to create ciders with natural tannins, future research could examine a traditional cider apple.

[18] Characterizing Non-Tumorigenic Strains of *Agrobacterium vitis*, the Causal Agent for Crown Gall in Grapevine

Molly Sheppard^{1,2}, Didem Canik Orel², Desen Zheng², and Thomas J. Burr²

¹Austin Peay State University, Clarksville, TN; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

Agrobacterium vitis is the bacterium known to cause crown gall in grape vines. Crown gall can cause significant economic loss in both nurseries and vineyards. Tumorigenicity of agrobacteria is determined by the presence of Tumor-inducing (Ti) plasmid in their genome. The tumorigenic strains have the gall forming gene *virD2*, while the non-tumorigenic do not. The aim of this study is determine if non-tumorigenic (NT) strains of *A. vitis* from different locations carried *virD2* gene and also reveal the efficiency and reliability of *virD2* based MCH method as a tool of *A. vitis* determination. Sixty nine strains were tested for the *virD2* and polygalacturonase (PG) gene (*pehA*, gene 5759) to determine if they were *A. vitis*. Hypersensitive response and shoot necrosis were also done to further identify the strains. Twelve out of 69 NT strains were *pehA* negative and five out of twelve strains were found negative for carrying of both PG genes. HR results on tobacco showed four of the negative strains were HR negative, too. Two of the strains caused heavy necrosis, two of them weak necrosis on young grapevine shoots. Future studies could be done to identify what the role of polygalacturonase is in *A. vitis*.

[19] Parthenocarpy in Summer Squash Varies Among Varieties

Sean Murphy^{1,2} and Stephen Reiners²

¹Morrisville State College, Morrisville, NY 13408; ²Horticulture Section, School of Integrative Plant Science, Cornell University, Geneva, NY 14456

With honeybee populations in decline across North America, growers that rely on these insects to pollinate their crops are concerned. For decades, squash growers rented hives to ensure adequate pollination but fewer hives are available now and the price to acquire the hives is high. A parthenocarpic squash, one that can produce a marketable fruit without pollination, would overcome these obstacles. Prior research has shown that summer squash (*Cucurbita pepo* L.) varieties vary a great deal in this trait, but no evaluation has been conducted that tests current varieties for parthenocarpy. A study was conducted at the NYS Agricultural Experiment Station in 2015 on 12 commonly grown varieties. Female flowers were covered and secured with a bag prior to opening to exclude pollinators. Bags were removed after seven days and fruit determined to be marketable were deemed parthenocarpic. Those with no marketable fruit were considered non-parthenocarpic. Green zucchini and yellow round types generally seemed to have the highest levels of parthenocarpy. Growers may want to consider using these varieties where pollinator availability is low.

[20] The Genetic Basis of Sex Determination in the Purple Osier Willow (*Salix purpurea*)

Jeremy D. Pardo^{1,2}, Craig H. Carlson², Fred E. Gouker², and Lawrence B. Smart²

¹Cornell University, Ithaca, NY, 14853; ²Horticulture Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

The species of the two genera (*Populus* and *Salix*) in the family Salicaceae are dioecious, which provides an opportunity to study the genetic mechanisms of sex determination. The members of the genus *Salix* studied thus far are of particular interest because they use the relatively uncommon ZW system (females are heterogametic), while some *Populus* use an XY and others use a ZW system. Markers linked with loci controlling sex will aid the breeding of *Salix* species as a biofuel crop. Previous work has revealed several regions on chromosome 15 in *Salix purpurea* and *S. viminalis* that correlate with sex. The goal of this study was to identify potential candidate genes responsible for sex determination in *S. purpurea*. A total of 26 PCR primer pairs were designed in order to amplify, sequence, and analyze coding sequences of genes within regions mapped for sex determination from DNA of four individuals (two male, two female) in a mapping pedigree of *S. purpurea*. Of five genes associated with sex, only three had divergent predicted amino acid sequence. Future studies will focus on screening a larger number of segregating individuals in order to confirm the association of these polymorphisms with sex.

[21] Using linkage maps to develop molecular markers for black rot resistance in grapevines

Anne C. Repka^{1,2}, Elizabeth M. Takacs², and Bruce I. Reisch²

¹Cornell University, Ithaca, NY 14853; ²Horticulture Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456.

Black rot is a fungal disease of grapevines caused by *Guignardia bidwellii*, which is native to North America. While some American grapevine species, such as *Vitis rupestris* and *V. cinerea*, have genetic resistance to the disease, widely-grown Eurasian grape species such as *V. vinifera* are extremely susceptible. As black rot is poorly controlled by organic fungicides, successful organic cultivation in high-disease pressure regions such as New York hinges on the development of resistant cultivars through grape breeding programs. As grape breeding is a lengthy process, the discovery of significant Quantitative Trait Loci (QTLs) and their corresponding molecular markers for use in marker-assisted selection is crucial. In a mapping population of 137 progeny of *V. rupestris* B38 x 'Horizon' (a susceptible interspecific hybrid), we inoculated three clusters per vine with a solution of *G. bidwellii* pycnidiospores to assess genetic resistance to black rot. The subsequent QTL analysis revealed two significant QTLs, one each on chromosomes 11 and 17 of 'Horizon', which suggest the presence of susceptibility loci. These QTLs can be used as the starting point to develop molecular markers for marker-assisted selection.

[22] Electronic Sensors for Measuring Deposition in Fruit Crops

Andrew D. Schulman^{1,2}, Andrew J. Landers², and Tomas Palleja Cabre²

¹Cornell University, Ithaca, NY, 14853; ²Dept. of Entomology, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

This research proposes a real-time method, based on an array of electronic moisture sensors, to estimate deposition in apple orchards and vineyards for field application of pesticides. This estimation could be used as a reference to adjust the canopy spraying machine parameters with the aim of improving deposition and avoiding drift. Two sets of experiments were carried out, the first one in the Cornell Spray Laboratory (NYSAES) and the second one under real working conditions in the field. Electronic sensors were sprayed indoors in the first experiment with a controlled temperature of 25°C and 15% humidity to determine how signal behavior correlates to coverage (%). A wooden mast configured with a sensor array composed of 5 resistor rain sensors and 3 optical rain sensors was used in the field trials. A sprayer fixed with an air-diverting louvre sprayed this mast for three treatments: With the mast placed in the vineyard, in the apple orchard, and on a metal post (Control). Louvre settings were adjusted to 25%, 50%, and 100% for 5 spray trials in each treatment. Results showed that the signal obtained is highly correlated with the deposition recorded by traditional water sensitive cards placed adjacent to corresponding sensors.

[23] Investigation of a plant-like expansin in *Clavibacter michiganensis* subsp. *michiganensis*

Shaun P. Stice^{1,2}, Matthew A. Tancos², and Christine D. Smart²

¹University of Portland, Portland, OR 97203; ²Plant Pathology and Plant-Microbe Biology Section, School of Integrative Plant Science, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Expansins are non-enzymatic plant proteins that are involved in the relaxation of cell walls through an uncharacterized pH-dependent mechanism. Interestingly, several vascular-colonizing phytopathogenic bacteria possess plant-like expansins, but their role in pathogenicity remains unexplored. Therefore, the putative expansin (*CmEXLX2*) in *C. michiganensis* subsp. *michiganensis* was disrupted with a gentamicin insert, which led to earlier and more severe symptoms characterized by large cankers. We hypothesized that the lack of the putative expansin limits the lateral spread of *C. michiganensis* subsp. *michiganensis* between vascular bundles. To test this hypothesis, the *CmEXLX2* knockout and wild-type 0317 parental strains were transformed to express a green-fluorescent protein for visualization in tomato stem tissue. Infected tomato plants were harvested at 5, 7, and 9 days post inoculation. Cross sections of stems were analyzed in 1-3 cm increments above and below the inoculation sites while the number of infected protoxylem, vascular bundles, and parenchyma cells were recorded. Scanning electron microscopy was used to observe differences in plant cells infected with the *CmEXLX2* knockout and wild-type 0317 strains. Preliminary results suggest that the putative expansin does not influence the ability of *C. michiganensis* subsp. *michiganensis* to laterally spread into living parenchyma tissue. Future studies will look at host response to the *CmEXLX2* mutant as an explanation for why the mutant is significantly more aggressive.

[24] Evaluation of Onion Cultivars for Resistance to Onion Thrips (*Thrips tabaci*) in the Field

Sierra Short^{1,2} and Brian Nault²

¹Mary Baldwin College, Staunton, VA 24401; ²Dept. of Entomology, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Onion thrips, *Thrips tabaci*, is a pest of onion, *Allium cepa*, found worldwide, and is an important vector for *Iris yellow spot virus* and other pathogens. Because thrips management in onion is heavily reliant on insecticide use and insecticide resistance has been a major problem in the past, alternative methods of management are needed, particularly the development of onion thrips-resistant cultivars. Seven onion cultivars, produced in breeding programs in New Mexico and Wisconsin, are purported to show mild thrips resistance and were compared alongside two thrips-susceptible cultivars in a replicated field study. Thrips densities were assessed weekly, and plant size assessments were made once every three weeks. Results indicated that all mildly resistant cultivars had significantly lower thrips densities than the susceptible cultivars, Bradley and Milestone. However, only USDA 5336A x 5351C and New Mex Fabian Garcia showed similar foliar characteristics to Bradley and Milestone; the other cultivars evaluated were significantly smaller and do not appear suitable for New York. USDA 5336A x 5351C and New Mex Fabian Garcia may be viable, mildly thrips-resistant alternatives to currently used thrips-susceptible onion cultivars in New York.

[25] Entomopathogenic fungi display sensitivity to fungicide practices in golf turf

Bennett Thompson^{1,2}, Huijie Gan², and Kyle Wickings²

¹Swarthmore College, Swarthmore, PA 19081; ²Dept. of Entomology, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Entomopathogenic fungi (EPFs) such as *Beauveria bassiana* and *Metarrhizium anisopliae* show promise as biocontrol agents against insect pests in turfgrass systems. In order to improve EPF effectiveness, however, it is necessary to understand how soil and turf management practices affect them *in situ*. We surveyed EPF abundance across eight golf courses with varying soil characteristics and fungicide application histories. Using soil collected in 2015, we employed the *Galleria* bait method to estimate EPF abundance. We found EPFs, primarily of genus *Metarrhizium*, in soils from all but one golf course. Fairways exhibited significantly lower EPF abundance than roughs, which are less intensively managed ($p = 0.018$). Golf courses with lower fungicide rates tended to have greater EPF abundance, and there was a significant negative relationship between fungicide rates and EPF abundance over all sites ($p = 0.034$). EPFs were not affected by soil characteristics including pH, moisture, clay, and carbon content. Future work will involve directly varying fungicide application rates on a single site, in order to reduce noise from site variation. For now, the data suggest that EPFs benefit from lower fungicide rates and reduced management intensity, though the benefits of EPFs must be balanced against managing fungal pathogens.

[26] Potential for three bee genera to vector the pathogen *Botrytis cinerea* to strawberry flowers

Nolan D. Amon^{1,2}, Heather L. Connelly², and Gregory M. Loeb²

¹Cornell University, Ithaca, NY 14853; ²Dept. of Entomology, New York State Agricultural Experiment Station, Geneva, NY 14456

A growing body of research has made it clear that on some occasions, naive pollinators (bees, syrphid flies, some thrips) are vectors of disease to agricultural crops. Given both the environmental and economic consequences of both pollination and disease in agriculture, it is surprising that we lack information on which behavioral and morphological traits contribute to an insect pollinator's capacity to vector diseases like *Monilinia vaccinii-corymbosi*, *Erwinia amylovora*, and *Botrytis cinerea*. Here, three bee genera (*Bombus*, *Osmia*, and *Lasioglossum*) were tested for their efficacy in vectoring *B. cinerea* to strawberry flowers. Disease transmission was quantified by detecting the amount of *B. cinerea* biomass moved by each bee species, using a quantitative enzyme-linked immunosorbent assay (ELISA). Results are still being analyzed, but it appears that morphological traits like pilosity and body size will be more important traits in determining vector potential for *B. cinerea* to strawberries than behavioral traits, such as sociality. By identifying traits that allow us to predict disease vector ability in pollinators, management of pollination to crops like strawberry can be guided to better utilize solitary native bees like *Lasioglossum* spp, in order to prevent or reduce both disease outbreak and fungicide applications during the growing season.