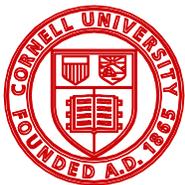


Proceedings of the
2012 Summer Scholars Program
Undergraduate Research Poster Session
July 31, 2012
Geneva, NY



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
2012 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 *Translational Research Opportunities for Undergraduates at Cornell University's New
York State Agricultural Experiment Station*

Additional funds were provided by Cornell's NY State Agricultural Experiment Station Director's
Excellence Fund and College of Agriculture and Life Sciences

Students were also funded by grants awarded to individual faculty mentors

These proceedings can be found on-line at

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

[1] *Phytophthora capsici*, an oomycete pathogen in New York surface irrigation water: biological threshold and results of ultraviolet treatment

Megan N. Daniels^{1,2}, Lisa A. Jones², and Christine D. Smart²

¹SUNY Binghamton, Vestal, NY 13854. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Surface irrigation waters, widely used for irrigation by New York state growers, can serve as reservoirs for human and plant pathogens. *Phytophthora capsici*, the causal agent of Phytophthora Blight, is a widespread oomycete plant pathogen capable of infecting many plants including tomatoes and all cucurbits. It has been isolated from surface water sources in New York State as part of a surface irrigation water pathogen survey. A greenhouse experiment was conducted using highly susceptible squash plants that were irrigated with water infested with *P. capsici* zoospores at concentrations ranging from 10^1 to 10^3 L⁻¹, to determine the biological threshold of zoospores necessary in irrigation water to cause disease. In a second related experiment, an ultraviolet light liquid processing unit, the UV CiderSure 3500, was used to treat water infested with zoospore concentrations from 10^3 to 10^5 L⁻¹. The long-term project goals are to better understand the risks of using infested irrigation water and to determine if UV light can be used effectively to treat surface irrigation water, that may be too turbid and alkaline for other methods of sterilization.

[2] Constructing Plasmids for Producing Type I Pili Gene Mutants and Protein of Type IV Pili in *Xylella fastidiosa*

Ranata DeGennaro¹, Cheryl Galvani¹, Thomas J. Burr², Patricia Mowery¹

¹Hobart and William Smith Colleges, Geneva, NY 14456 ²Department of Plant Pathology and Plant-Microbe Biology, NYSAES Cornell University, Geneva, NY 14456

Xylella fastidiosa is a gram-negative plant pathogen that expresses both type I and type IV pili. Both pili play important roles in the progression of Pierce's disease in grapevines. My projects involved creating constructs to better explore the role of the pili in disease progression. First, I successfully made a plasmid that will be used to knock-out the *fimA* gene responsible for type I pili production. Second, I created a complementation plasmid for the *fimA* mutant. The product had mutations and more constructs will be screened and sequenced. Third, I constructed a plasmid for expressing the major protein responsible for type IV pili production for antibody production. This product needs to be confirmed by sequencing. Overall, a better understanding of these two pili may aid in the studies of the economically devastating Pierce's disease.

[3] Effect of process conditions (ratio of solids to liquid, brine temperature, and blanching) on the lethality of thermally processed pickled carrots

Corinna A. Noel¹, Oscar G. Acosta², Olga I. Padilla-Zakour²

¹Saint Joseph's University, Philadelphia, PA 19131. ²Cornell University, Department of Food Science, Geneva, NY 14456.

Pickling is a longstanding method of preserving fruits and vegetables, including carrots. Based on FDA regulations, acidified (pickled) foods must be thermally processed after packing to ensure their safety and stability. A 2³ factorial experiment was performed with carrots in brine (2 cm maximum diameter), packaged in 8 oz glass jars, to determine the effect of three processing conditions: (a) ratio of solids to liquid at 35/65 or 65/35, (b) brine temperature at 25 or 75°C, and (c) blanching or no blanching prior to filling. Seven jars were used per trial, and processed in boiling water until internal temperature of cold spot reached the designated temperature from 140 to 200 °F at 10-degree intervals, resulting in at least 18 data points per treatment. All trials were performed in triplicate. Multiple linear regression analysis (using a natural log transformation of lethality as the response variable) showed that only hot-filling with low solids to liquid ratio significantly increased the rate of lethality accumulation (p<0.001). All other conditions followed the same rates. The results obtained and additional trials will be used to establish optimized processing guidelines for production of safe and stable pickled foods.

[4] Root-Galling Severity Incited by the Northern and Southern Root-Knot Nematodes on Cucumbers, Peas and Soybeans Under Greenhouse Conditions

Renate Loomis^{1,2} and George S. Abawi²

¹Armstrong Atlantic State University, Savannah, GA, 31419. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Root-knot nematodes are major pathogens on many crops, including vegetables, and are capable of greatly reducing the quality and quantity of marketable yield. Currently, the northern root-knot nematode (*Meloidogyne hapla*) is the only species found occurring outdoors in New York State. The southern root-knot nematode (*Meloidogyne incognita*) is unable to overwinter in New York and similar regions, but with changing climates, it may be able to survive through mild winters. Peas, soybeans, and cucumbers were grown in the greenhouse and were inoculated with three replications of five levels of *M. hapla* and *M. incognita* eggs (0, 5, 10, 20, or 40 eggs/cc of soil) immediately after seeding. After 32 days, the plants were washed free of soil, counted and weighed. The roots were then rated for root-galling severity on a scale of 1 (no galls observed) to 9 (>80% of root system galled). Results show that as the initial population of eggs increased, root-galling severity also increased. Cucumbers were the most susceptible to both species, followed by peas, then soybeans. *M. incognita* also exhibited larger and more galls than *M. hapla* in these crops, showing potential to further constrain the production of these and other vegetables with climate change trends.

[5] Life Table Study of Virgin Females: Thelytokous and Arrhenotokous *Thrips tabaci*

Leanne M. Combs¹, Jozsef Fail², and Anthony M. Shelton³

¹Alfred University, Alfred, NY 14802. ²Corvinus University of Budapest, H-1118 Budapest, Hungary.

³Cornell University, New York Agricultural Experiment Station, Geneva, NY 14456.

Onion thrips (OT), *Thrips tabaci* Lindeman, is a global pest of many crops, and its feeding may result in stunting and death of plants. OT have a high reproductive capacity and can reproduce with and without mating. We investigated the life table parameters of the thelytokous and arrhenotokous OT, whose virgin females primarily lay diploid female eggs and haploid male eggs, respectively. The objective of our study was to compare developmental rates and fecundity of the thelytokous and arrhenotokous OT. We found significant differences in time spent in the larva 1, larva 2, prepupa, pupa, and preoviposition stages between arrhenotokous and thelytokous OT, but no significant differences in the egg stage, or the fecundity of the adult females. There were significant differences in longevity, in the time required from egg to adult emergence, and from egg to first oviposition. Because some plant viruses are primarily acquired in the larva 1 stage, and because the arrhenotokous OT spent ~ 30% more time than thelytokous OT in that stage, they may have a higher virus acquisition rate. Mathematical models should be developed to determine which mode of reproduction would result in a higher risk of feeding injury and virus transmission in OT.

[6] Effect of clone, stem contact, and fermentation yeast strain on Pinot noir phenolics

Kadeem F. Hinton¹, David C. Manns², and Anna Katharine Mansfield²

¹ Alabama Agricultural and Mechanical University, Department of Food and Animal Sciences, Normal, Alabama 35762 ² Cornell University, Department of Food Science, New York State Agricultural Experiment Station, Geneva, New York 14456

Wine phenolics, such as anthocyanins and polymeric tannins, are generally low in Pinot noir (*Vitis vinifera* L.) grapes. Because these phenolic compounds impact wine color and sensory characteristics, developing Pinot noir wines with acceptable sensory characteristics is often a challenge. The phenolic profile of select Pinot noir clones and winemaking treatments were examined in samples taken after alcoholic and malolactic fermentation. Individual anthocyanin and tannins concentrations were measured by high-performance liquid chromatography (HPLC) following solid phase extraction (SPE). Variation in color profile and total phenolic content were determined by measuring select wavelength maxima using spectrophotometric analysis. Selected clones displayed a higher concentration of polymeric tannin over control wines, while displaying a much lower concentration of monomeric anthocyanins. While overall tannin concentration varied between clone and stem exposure treatments, there were no significant differences observed in their mean degree of polymerization, suggesting that while select clones produce and/or extract greater amounts of tannins, the same class of tannins are extracted. This research suggests that in addition to increased tannin yield, total phenolic content and color stability of Pinot noir can be improved by fermenting in the presence of >50% stem content, along with pairing select clones with specific yeast strains for fermentation.

[7] Monitoring Fungicidal Effects on *Botrytis cinerea* Infection during Flowering in a Vignoles Vineyard

Grady Zuiderveen¹, Seiya Saito², Wayne Wilcox²

¹Grand Valley State University, Allendale, MI 49401. ²Cornell University, Department of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Botrytis cinerea is one of the major grapevine diseases worldwide, and results in significant losses in both yield and quality every year. *B. cinerea* is a fungus that causes bunch rot on grape berries, subsequently causing significant economical losses. Botrytis disease is generally controlled by fungicide applications; however, it has been known to develop fungicide resistance. The objective of this study was to determine which fungicides are most effective in inhibiting Botrytis infection. Toward that objective, 400 clusters of ‘Vignoles’ (*Vitis* interspecific hybrid) were inoculated with a *B. cinerea* spore suspension at full bloom. Two days after inoculation, the clusters were sprayed with three different fungicides commonly used for Botrytis control (Elevate, Merivon, and Vanguard). The samples were collected, placed on PDA plates, and inoculated for 4 days, after which sporulation was used to measure the prevalence of infection. Data was subject to ANOVA with a post hoc Tukey’s HSD test. Under trial conditions, Vanguard and Elevate resulted in roughly 60% and 40% reductions of Botrytis respectively, while Merivon made no statistical difference. This research indicates that growers in New York State should consider using Vanguard in their fungicide rotation to control Botrytis if they are not already doing so.

[8] Tracking genetic structure changes through fingerprinting of an isolated population of *Phytophthora capsici*

Stephen R. Bruening^{1,2}, Amara R. Dunn², and Christine D. Smart²

¹Hobart and William Smith Colleges, Geneva, NY 14456

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

The oomycete, *Phytophthora capsici*, causes Phytophthora blight, a serious problem for many commercial vegetable growers in New York State. *P. capsici* causes fruit and root rot on all cucurbit and many solanaceous vegetables as well as snap beans and lima beans. The pathogen can be moved between fields via soil, infected plants, or water, but not by wind. Previous research has shown that *P. capsici* populations throughout New York are diverse but largely isolated, with little gene flow between fields or regions. The goal of this study is to track how the population structure of this pathogen can change over time when no new isolates are introduced following the initial establishment. An in-field and an *in vitro* population were started from the same two New York isolates in the fall of 2008. Progeny in both populations are being characterized using microsatellite markers. In 2012, isolates have been collected from the in-field study and characterization is in progress. Additionally, *in vitro* progeny have been characterized and 11 unique genotypes have been identified among 14 individuals. This project will help us understand how a *P. capsici* population in a single field changes over time, and will ultimately contribute to improved disease management.

[9] Evaluation of plant defense activators and bactericides for the control of black rot in cabbage

Kristen L. Andersen^{1,2}, Holly W. Lange², Christine D. Smart²

¹SUNY Cobleskill, Cobleskill, NY 12043. ²Cornell University, Dept. of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Black rot, caused by the bacterium *Xanthomonas campestris* pv. *campestris* (Xcc) is a major disease of cabbage and other cruciferous crops and can infect plants at any stage of growth spreading easily during warm, wet conditions. A black rot outbreak can leave cabbage growers with an unmarketable crop, an issue of economic impact in New York State. A trial was conducted to determine the effectiveness of plant defense activators and bactericides for black rot control in the greenhouse and field, and to ensure that these strategies do not alter plant yield. Treatments were applied to cabbage seedlings in the greenhouse and half were inoculated with Xcc 24 hours later. Two additional sprays were applied prior to transplant to the field. After planting, weekly sprays and ratings of disease incidence and severity were conducted. After the final rating, five heads were harvested from each of the four repetitions per treatment and weighed to determine if there was any influence on production. The heads were also cut open to rate internal black rot symptoms. The results were analyzed to determine if there were any significant differences between treatments.

[10] Identification of the *Grapevine fanleaf virus* silencing suppressor

Libby Cieniewicz¹, John Gottula², and Marc Fuchs²

¹Lebanon Valley College, Annville, PA 17003. ²Cornell University, Department of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Grapevine fanleaf virus (GFLV) is responsible for fanleaf degeneration, one of the most damaging viral diseases of grapevines worldwide. GFLV has a bipartite, single stranded plus sense RNA genome, and is spread from grapevine to grapevine by the nematode vector *Xiphinema index*. One of the major plant defense systems against viruses, RNA silencing, is combatted by viral silencing suppressors. The GFLV gene responsible for silencing suppression has not yet been determined. In a twist on a common assay for silencing suppression, *Nicotiana benthamiana* plants expressing enhanced Green Fluorescent Protein (eGFP) were infected with a viral vector that silences eGFP. After virus-induced eGFP knockdown, the plants were subsequently agroinfiltrated with individual GFLV genes and proper controls to determine the viral gene responsible for suppression of RNA silencing. The leaves agroinfiltrated with the GFLV 1B gene showed increased eGFP fluorescence, comparable to the levels of known viral silencing suppressors, which indicates silencing suppressor activity. The likely silencing suppression mechanism and point of interference in the RNA silencing pathway can be deduced by homology to other silencing suppressors.

[11] Assessing the effects of local and landscape factors on the abundance of *Tipula paludosa* Meigen in turfgrass habitats

Suzanne Yocom¹ and Matthew Petersen²

¹Millersville University, Millersville, PA 17551. ²Cornell University, Department of Entomology, Geneva, NY 14456

Tipula paludosa is an invasive species that has quickly become established as a major pest in North American turfgrass, causing economic loss across both commercial and residential settings. Patchy distributions are displayed by *T. paludosa* both locally (i.e., within a site) and across the landscape (i.e., between sites), suggesting that factors working at multiple scales are impacting distributions and abundance patterns. Our objective was to determine why *T. paludosa* is abundant at some sites but not others by modeling larval abundance in relation to local and landscape factors. Results indicated that local factors of soil texture, acting as a bottom up effect, and the abundance of endemic entomopathogenic nematodes present at a site, acting as a top down effect, best predicted *T. paludosa* abundance. Landscape factors within a 0.5 km radius of a site including total grass area, impervious surface area and average patch size had negligible effects. To further elucidate the impact of endemic biotic controls, we conducted a bioassay to determine the efficacy of entomopathogenic nematodes (*Heterorhabditis* sp.) collected from the research sites against *T. paludosa*. Results showed that endemic *Heterorhabditis* sp. are capable of infecting *T. paludosa* and limit larval abundance.

[12] Supplemented Honey Bees and Bumble Bees Lack Fidelity to Pumpkin Flowers

Elizabeth Miller¹, Jessica D. Petersen², Brian A. Nault²

¹Saint Vincent College, Latrobe, PA 15650. ²Cornell University, Department of Entomology, Geneva, NY 14456

Many food crops, such as cucurbits, require pollination by bees to produce fruit. Vegetable growers commonly rent honey bee (*Apis mellifera*) hives to supplement pollination activity in cucurbit fields. The cost of renting honey bee hives continues to increase and growers are interested in using an alternative pollinator like the common eastern bumble bee (*Bombus impatiens*). Although previous studies have shown that *B. impatiens* is an excellent pollinator of pumpkin, a study in 2011 revealed that supplementing pumpkin fields with colonies of *B. impatiens* did not increase their visitation to the pumpkin flowers. Our objective was to quantify the fidelity of *B. impatiens* and *A. mellifera* from colonies placed within pumpkin fields. Pumpkin fields were stocked with *A. mellifera* at a standard density (1 hive/3 acres; n=3 fields), *B. impatiens* at a standard density (4 hives/2 acres; n=3 fields), and *B. impatiens* at three times the standard stocking density (12 hives/2 acres; n=3 fields). For each field, ten bees carrying pollen were captured and then the pollen was identified. Preliminary results indicate that none of the *B. impatiens* or *A. mellifera* sampled were carrying pumpkin pollen. Rather, these bees were carrying pollen from white clover, chicory, corn, and nightshade.

[13] Infection of Apple Rootstocks by *Erwinia amylovora*

Kristie Goughenour¹, Kiersten Bekoscke², and Herb Aldwinckle²

¹Ohio Wesleyan University, Delaware, OH 43015. ²Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456²

Fire blight, caused by the bacterium *Erwinia amylovora* (Ea) is a significant threat to apple growers. Infection of the rootstock, usually leads to loss of the tree due to girdling of the rootstock. Susceptible rootstocks, and streptomycin-resistant strains of Ea, have led to an increased focus on breeding fire blight-resistant rootstocks. The route of infection of rootstocks was investigated, with infection of the scion, damage from borer insects and direct infection by contaminated rainwater considered as potential routes. The susceptibility of new and established rootstocks was investigated by inoculating the scions of young 'Gala' trees grafted on various rootstocks with Ea and observing rootstock infection. Another plot of trees simulated damage from borer insects carrying Ea. A third plot compared inoculation of blossoms, shoots, and rootstock shanks as modes of rootstock infection. Samples were collected, Ea was identified, and virulence of isolated strains was tested. Only 9 out of 20 rootstocks showed any rootstock infection and rootstock 70-06-08 appeared most susceptible with B-51-11, EMLA26, and EMLA9 also showing high susceptibility. Borer insect damage was a frequent route of rootstock infection. Blossom infection was the most common route of rootstock infection, although direct spraying of rootstock shanks with simulated contaminated rainwater did cause some infections. This indicates that contaminated rain could infect the rootstock, but probably only when the rootstock was damaged.

[14] The fight against blight: a Q-PCR-based assay to detect the arrival of *Phytophthora infestans*

Anjali Merchant¹, Matthew A. Tancos², and Christine D. Smart²

¹Middlebury College, Middlebury, VT 05753. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Phytophthora infestans ranks amongst the most economically devastating oomycete plant pathogens, affecting members of the family Solanaceae. Management of late blight accordingly depends upon the regular application of fungicides. Given the expense and often-contentious environmental ramifications of fungicide usage, this experiment sought to validate a Q-PCR based disease-forecasting system for late blight, thereby providing an early warning system for growers. Using spore traps, the system takes advantage of the fact that airborne sporangia facilitate the spread of *P. infestans*. Biweekly samples were collected from spore traps from June 3, 2012 to July 20, 2012 and subsequently assayed for the presence of *P. infestans*. Analysis of rods collected on July 17, 2012 revealed the potential presence of *P. infestans* sporangia at one of the two monitored fields. Continued sampling by spore traps and monitoring of plants will be necessary to validate the presence of *P. infestans* within the area.

[15] Comparative attractiveness of a single-component isomer vs. the racemic blend of a mating pheromone in *Prionus* root-boring beetle traps

Dylan A. Tussey¹ and Arthur M. Agnello²

¹University of North Carolina at Asheville, Asheville, NC 28804. ²Cornell University, Dept of Entomology, Geneva, NY 14456

The broadnecked root borer (Coleoptera: Cerambycidae, *Prionus laticollis*) is one of the largest insects that pose a risk to apple orchards. This native species typically lives in hardwood forests but may occasionally infest apple orchards. Larvae of this beetle live in the soil and feed on tree roots for up to three years. The damage caused is substantial enough for one larva to kill a previously healthy small apple tree. Due to the specific life history these beetles, traditional pesticides are often ineffective. Aside from preventive insecticide sprays, the best method of protection is by mass trapping or mating disruption during the brief adult stage of the *Prionus* beetle. I compared the effectiveness of two sex-pheromone lures at attracting adult male *P. laticollis*. The first was a synthetic racemic blend of multiple isomers, called prionic acid (PA). More recently, a single isomer in this pheromone blend was found to be the specific pheromone for a close relative of *P. laticollis*; this isomer is known as 3R,5S-dimethyldodecanoic acid (3R). Although the 3R isomer was successful at attracting male *P. laticollis*, it did not appear to be consistently more effective than the commercial blend.

[16] Investigations into *eIF4E* as a resistance gene for *Grapevine fanleaf virus*

Larissa Osterbaan¹, John Gottula², Marc Fuchs²

¹Calvin College, Grand Rapids, MI 49546. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Genetic resistance is the most effective means for virus protection in crops. The 4E family of eukaryotic initiation factors (eIFs) is a critical component of the RNA translation machinery and a crucial host factor for the replication of RNA viruses. The 4E family is also a source of recessive resistance genes to several plant viruses. *Grapevine fanleaf virus* (GFLV) is a nepovirus that causes damage to grapevines for which no source of resistance is known. The aim of this study was to investigate *eIF4E* as a possible resistance gene for GFLV. The model species *Nicotiana tabacum* and *Nicotiana benthamiana* are known to be resistant and susceptible to GFLV, respectively, while a F₁ hybrid of the two species is susceptible, indicating that *N. tabacum* harbors one or more recessive resistance genes. Using specific primers, we amplified *eIF4E* sequences from 13 *Nicotiana* species, including the F₁ hybrid. Sequence alignments of *Nicotiana* and a wide array of crop species revealed a SNP within *eIF4E* associated with GFLV resistance, resulting in an amino acid change from an isoleucine (susceptible) to valine (resistant). Functional characterization of the role of eIF4E in GFLV infection using virus-induced gene silencing and stable transformations with *eIF4E* is on-going.

[17] Influence of modern fungicides and growth regulators in the development of fruit russet caused by *Aureobasidium pullulans* in NY plantings of ‘Sweetango’ apples

Shawn Lyons¹, Sara Villani², and Kerik Cox²

¹University of Georgia, Department of Horticulture, Athens, GA 30306. ²Cornell University, Department of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Apple fruit russet is a physiological disorder in apple crops characterized by patches of brown, scaly suberized epidermal tissue on the surface of the fruit. The onset of apple fruit russet is caused by a combination of environmental factors and the presence of certain yeasts, most notably *Aureobasidium pullulans*, on the surface of the fruit early in its development. Two experiments, a field trial and an *in vitro* relative inhibition assays, were designed to evaluate the effectiveness of selected apple scab fungicides and growth regulators for controlling *A. pullulans*. *In vitro* relative inhibition assays were conducted by plating isolates on media amended with one of six technical grade fungicides difenoconazole, cyprodinil, penthiopyrad, fluopyram, trifloxystrobin, and benomyl at a logarithmic scale of concentrations. A trial was established in a “Sweetango” orchard at the NYSAES to evaluate the effect of fungicide and growth regulator programs on the development of fruit russet. In the field trial the application of Captozeb or ProVide significantly reduced the incidence of fruit russet, while difenoconazole demonstrated the highest activity *in vitro*.

[18] Differential tannin binding to grape alcohol insoluble residues: *V. vinifera* vs. non-*vinifera* varieties

Emily Defnet¹, Lindsay F. Springer², and Gavin L. Sacks²

¹Lafayette College, Easton, PA 18042. ²Cornell University, Dept of Food Science, Geneva, NY 14456

Condensed tannins are a class of polyphenolic compounds found in grapes that contribute to several critical organoleptic characteristics in red wine, particularly astringency and color stability. Regional winemakers have noted that wines produced from non-*vinifera* containing hybrid grapes are very low in tannins, making them inappropriate for premium red wine production. However, these hybrid grapes have comparable tannin concentrations to classic *V. vinifera* species, suggesting that variation in wine tannin results from differences in extractability due to binding of tannins to cell wall material during fermentation. To investigate this hypothesis, alcohol insoluble residues (AIRs) from the skins, flesh, and seeds of *vinifera* and non-*vinifera* grape varieties were isolated, and tannin fining experiments with AIRs were performed in triplicate using model wine supplemented with a commercial tannin preparation, and repeated with a representative Cabernet Sauvignon. Tannin concentrations in wines were measured using the Adams-Harbertson protein precipitation assay. On a w/w basis, non-*vinifera* AIRs were able to bind up to 4-fold more tannin than *vinifera* AIRs, which would explain differences in observed tannin extractability. Understanding the chemical or physical mechanisms for the greater binding capacity of non-*vinifera* species should facilitate breeding of new grape varieties with improved tannin extractability.

[19] Mefenoxam sensitivity of recently predominant clonal lineages of *Phytophthora infestans* in the United States

Dov Camuzeaux¹, Richard Childers¹, Giovanna Danies, Ian Small, Kevin Myers and Bill Fry

College of Agriculture and Life Sciences, Ithaca NY 14853, Cornell University, Dept of Plant Pathology and Plant Microbe Biology

Phytophthora infestans, the causal agent of late blight disease, is one of the most devastating pathogens of potato and tomato. In the 1970's and 1980's *P. infestans* could be effectively controlled through the use of fungicides containing the active ingredient metalaxyl/mefenoxam. Unfortunately in the late 1980's populations of *P. infestans* displaying resistance to mefenoxam began to emerge. Due to the simple population structure of *P. infestans* in the United States, isolates have been grouped into clonal lineages based on genetic and phenotypic markers. Since the mid-1990s, populations of *P. infestans* on potato in the United States have been dominated by clonal lineage US8, which is resistant to mefenoxam. More recent clonal lineages, US22, US23 and US24, however, have been shown to be generally sensitive to mefenoxam when tested on mefenoxam-amended plates. This shift in the population of *P. infestans* suggests the possibility of utilizing fungicides containing metalaxyl/mefenoxam for the control of late blight. Samples have been collected throughout the United States and isolates representing clonal lineages US8, US11, US23 and US24, are being tested against low and high concentrations of mefenoxam both in an *in vitro* and an *in vivo* assay, to determine their sensitivity levels. Results are to be announced.

[20] Growing with light: the ontogeny of sporulation in *Erysiphe necator*

Tyler McCann¹, David M. Gadoury², Lance Cadle-Davidson², and Robert C. Seem²

¹University of Florida, Gainesville, FL 32612. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Erysiphe necator, which causes grapevine powdery mildew, generally grows for 5-10 days before colonies can support spore production; *i.e.*, they become "sporulation competent". Previous work indicated that complete darkness inhibits conidiation, and sporulation competent colonies will not initiate conidiation until after sunrise. However, the precise sequence of growth events and their dependency on light and/or darkness was poorly understood. Detached, susceptible leaves from Chardonnay vines were inoculated and maintained in chambers with a 12/12 hr day/night cycle. A sample of colonies containing only hyphae were kept in darkness for 24 hrs preceding sporulation competency. Colonies formed conidiophores, but not conidia during darkness. Thus, only the final step (conidiation) requires light. In vineyard and lab experiments, conidiophores produced a single physiologically mature conidium (capable of detachment) approximately five hours after light exposure. Conidiation then ceased until the next day, but resumed in light. Conidiation did not increase in 6/6 hr day/night cycles. In preliminary studies, conidiation stopped after the first sporulation cycle in continuous light. This study suggests several useful methods involving light as a tool for studying genetics of sporulation, and provides an alternative explanation for correlations of airborne conidial dose and various environmental factors observed in previous reports.

[21] Variation in susceptibility to potato leafhopper (*Empoasca fabae*) among shrub willow (*Salix* spp.) genotypes: Feeding insensitivity or host choice?

Jane E. Petzoldt^{1,2}, Fred E. Gouker², Gregory M. Loeb³, and Lawrence B. Smart²

¹Wesleyan University, Middletown, CT 06459. ²Dept. of Horticulture, ³Dept. of Entomology, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

Shrub willows (*Salix* spp.) are an emerging bioenergy crop by virtue of their rapid growth, ease of propagation, and sustainability. Variable susceptibility to potato leafhopper (*Empoasca fabae*) has been observed among taxa in the field, but the mechanism of resistance is poorly understood. Potato leafhopper injects saliva during phloem feeding, resulting in a complex of symptoms known as “hopperburn,” characterized by shoot tip necrosis, leaf curling, general chlorosis, and reduced internodal growth, which negatively impact biomass yield. A choice feeding assay was conducted to test whether susceptibility observed in the field could be replicated under controlled conditions. Leafhoppers were caged on three genotypes: *Salix viminalis* ‘Jorr’ (susceptible), *S. viminalis* x *S. miyabeana* ‘Tully Champion’ (intermediate), and *S. purpurea* 94006 (resistant). The genotypes exhibited hopperburn symptoms and reduced relative growth rate as observed in the field, demonstrating this assay could enable accurate phenotyping of resistance. A no-choice experiment was conducted by caging potato leafhoppers on individual shoots of either ‘Tully Champion’, 94006, or *S. viminalis* x (*S. sachalinensis* x *S. miyabeana*) ‘Preble’ (resistant) using nylon mesh bags. Preliminary results suggest hopperburn symptoms can be induced on resistant genotypes, implying that susceptibility is based in part on host choice.

[22] Transformation of Greensleeves Using the MYB10 Gene

Deborah LeGendre¹, Ewa Borejsza-Wysocka², and Herb Aldwinckle²

¹Department of Biological Sciences, University of Cincinnati, Cincinnati, OH, 45221. ²Department of Plant Pathology and Plant Microbe Biology, Cornell University, Geneva, NY 14456

Anthocyanins that give apple their characteristic red color are a product of the flavonoid biosynthetic pathway. This pathway is regulated by MYB transcription factors, which regulate anthocyanin accumulation by controlling transcription of the pathway enzymes. The transcription factor MYB10 determines leaf and flesh color in apple and when this gene is over expressed, those tissues exhibit a red coloration. To explore the effects of MYB10 on apple, the apple cultivar ‘Greensleeves’ was transformed by following the Aldwinckle Lab *Agrobacterium* Transformation protocol. The transformation was performed by use of *Agrobacterium tumefaciens* carrying the construct p35SMdMYB10 without the use of the kanamycin resistance gene. In total three transformation experiments were performed. Regeneration has just started to occur and a 20% efficiency of transformation has been observed. When apple is successfully transformed by using a MYB10 construct, the regenerant tissue have accumulated anthocyanin. The noticeable red color enables the MYB10 gene to be used as a reporter gene in genetic transformation and eliminates the need for PCR to tell if the procedure was successful.

[23] Phylogenetic Analysis of Putative Vacuolar Malate Transporters in the ALMT1 Gene Family: Structural Comparisons and Functional Implications

Bonnie L. Bernard¹, Kenong Xu²

¹Centenary College of Louisiana, Shreveport, LA 71104. ²Cornell University, Dept of Horticulture, Geneva, NY 14456

Apple acidity greatly affects fruit flavor, and in mature apple fruit, malic acid is most prevalent. Several studies have demonstrated that variation in apple fruit acidity is primarily controlled by the quantitative trait locus (QTL) *Ma* (malic acid). Recently, detailed characterization of the *Ma* locus has identified *Mal*, an aluminum-activated malate transporter (ALMT)-like gene, as the primary factor controlling apple fruit acidity. The founding member of the ALMT1 family, TaALMT1, is a plasma membrane protein in wheat that confers soil aluminum toxicity tolerance. The *Mal* protein, however, is more closely related to *Arabidopsis* vacuolar malate transporters (e.g., AtALMT9 and AtALMT6), which function in maintaining cellular malate homeostasis. To investigate whether *Mal* orthologs may regulate acidity levels in other fruit species, we conducted a phylogenetic analysis of the ALMT1 gene family among nine fruits, with *Arabidopsis* as a reference. We then examined the genome organization, structure, and sequence variation of the putative vacuolar ALMT genes most closely related to *Mal*, including genes from peach, strawberry, grape and tomato. Although these *Mal* orthologs may or may not be involved in fruit acidity, they provide a list of interesting targets for future studies.

[24] Potentially important natural enemies of onion thrips in onion fields

Martin C. Holdrege¹, Elaine J. Fok², and Brian A. Nault²

¹SUNY College of Environmental Science and Forestry, Syracuse, NY 13210. ²Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456.

Onion thrips, *Thrips tabaci* (Thysanoptera: Thripidae), is a major pest of onions in New York and can cause substantial reductions in onion bulb size. Recently, thrips management has shifted away from broad-spectrum insecticides to more selective ones timed using action thresholds rather than calendar dates. Consequently, natural enemies of onion thrips are more common in onion fields. The objective of this study was to determine whether and to what extent three commonly encountered natural enemies, *Orius insidiosus* (Hemiptera: Anthracoridae), *Chrysoperla rufilabris* (Neuroptera: Chrysopidae), and *Coleomegilla maculata* (Coleoptera: Coccinellidae) will consume onion thrips. Bioassays were conducted in Petri dishes and on caged onion plants in exclusion cages to determine predation rates and feeding damage by onion thrips. In Petri dishes, all three predators significantly reduced numbers of thrips (39% to 73%). *C. rufilabris* and *O. insidiosus* also reduced thrips feeding damage. In exclusion cages, *C. rufilabris* significantly reduced numbers of thrips (59%) relative to numbers in the control, but *O. insidiosus* did not; *C. maculata* was not included in exclusion cage experiment. Our results clearly indicate that these natural enemies consume onion thrips, but more research is needed to determine their impact on onion thrips populations in onion fields.

[25] Identity and Effectiveness of Bacterial Biocontrols in Organic Tomato Growth

Alexandra M. Curtis^{1,2}, Carly F. Summers², Christine D. Smart²

¹University at Buffalo The State University of New York, Buffalo, NY 14260. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Cover crops have been shown to influence soil microbe diversity, in some cases providing general suppression of plant pathogens. Soil microbes which produce antimicrobial compounds, parasitize plant pathogens, support plant health, or activate plant disease resistance are used by organic growers as biocontrols. This study tests whether cover crops, specific bacterial biocontrols, or the interactions between cover crops and biocontrols improve tomato yield and vigor. Five different inoculant treatments were tested: *Mitsuaria* spp. isolated from NY and OH fields, 2 commercial strains – Serenade and Actinovate – and water as control. A rye-vetch cover crop mixture and bare ground control were tested with each inoculant. To identify and quantify the biocontrols in the rhizosphere following inoculation we developed primers specific to the *Mitsuaria* sp. ITS1 region. Preliminary results show that plots inoculated with OH inoculant produced significantly taller plants than water control in a research field and taller plants than Actinovate in a grower-collaborator field. Our primers provided sequences of the ITS1 region, but amplified the ITS1 region of other bacterial strains and cannot be used for quantification at this time. Disease rating and yield measurements this season will determine if treatments favorably affect tomato crop health.

[26] Effects of pre-inoculation host stress on infection and establishment of the grapevine powdery mildew pathogen *Erysiphe necator*

Ashley C. Williams¹, David Gadoury², and Robert Seem²

¹Southern University A&M, Baton Rouge, LA 70813. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

In recent studies involving European wine grapes (*Vitis vinifera*), acute cold events (2°C to 8°C) induced resistance to the grape powdery mildew pathogen, *Erysiphe necator*. In the present study, our objective was to determine if the effect of acute cold could be duplicated by other environmental stress. We treated young susceptible leaves of *V. vinifera* ‘Chardonnay’ at 40°C (heat), 24°C (control) or 4°C (cold) for 15 to 60 min. To avoid direct effects of heat and cold upon the pathogen, we delayed inoculation until 24 h after treatment. Furthermore, to avoid confounding temperature effects with moisture stress, in addition to incubation in air, we submerged leaves in water at either 4 or 40°C. Conidial germination and appressorial formation were unaffected by heat and cold treatments, but both treatments suppressed primary and secondary hyphal development by 47 to 68%, indicating that both acute heat and cold induced resistance that was still significant 24 h after treatment. Notably, resistance was induced in ordinarily susceptible tissues. Punctuated episodes of acute cold and heat have previously unrecognized effects on grapevine powdery mildew, and possibly epidemics in other powdery mildew pathosystems, and their inclusion may improve accuracy in a broad range of forecast models.

[27] Efficacy of Biochar Amended Soil for Suppression of Alternaria Leaf Spot on *Brassica oleracea*

Amanda K. Hastings¹, Susan Scheufele², and Dr. Helene R. Dillard²

Appalachian State University, Boone, NC 28608¹; Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456²

Cabbage is an important economic crop in New York State with 10,900 acres planted and a value of \$87 million. Among the variety of insects and diseases that depress Brassica crop yield and quality, *Alternaria brassicicola* has been identified as a prevalent fungal pathogen responsible for Alternaria leaf spot in *Brassica oleracea*. The purpose of this study was to investigate the efficacy of biochar-amended soils for suppression of Alternaria leaf spot. Amtrak cabbage seedlings grown in soils intermixed with varying rates of biochar (0%, 0.2%, 2.0%, and 20% by weight) were inoculated with an 1.67×10^6 Alternaria spore/ mL solution. Control and treatment plants were rated for disease incidence and percent diseased leaf area was calculated. Overall plant health was assessed with measurements of plant height and fresh weight biomass. In each of the completed measures, there were no statistically significant differences found between treatments. Biochar has been shown to suppress disease in pepper and tomato cropping systems; however, beneficial effects were not observed in this study. Further studies are needed to identify suppressive biochar formulations, potentially using soils with extant bacterial communities and/or alternative organic materials.

[28] Evaluating the potential impact of brown marmorated stink bug (*Halyomorpha halys*) on grape production

Jeffrey Smith¹, Greg Loeb²

¹University of Delaware, Newark, DE 19716. ²Cornell University, Department of Entomology, Geneva, NY 14456

Our study aims to determine how *Halyomorpha halys* may affect grape production if the invasive insect becomes well established in the Finger Lakes. We measured the impact of density, gender and life stage of *H. halys* on Concord and Chardonnay grapevines. We confined insects on a single grape cluster using a fine mesh bag, which we replicated five times each for Concord and Chardonnay. Each replicate consisted of the following treatments: a bag lacking insects; 2nd instar nymphs in densities of 5, 10, and 20; adult females in densities of 1, 2, and 5; and adult males in densities of 1, 2, and 5. The insects remained caged on the clusters for 2 weeks, after which damaged and undamaged berries were enumerated. We found a strong positive correlation between density and number and percentage of berries damaged for both nymphal and adult feeding. The raw number of damaged berries per cluster was greater on Chardonnay grapes compared to Concord and higher after feeding by adult females than males on both varieties. While these data provide preliminary evidence of significant impact, the more telling data will come at harvest when it will be possible to measure yield and incidence of disease.

[29] Understanding Grape Crown Gall (*Agrobacterium vitis*): Distribution in Grape and Biocontrol Potential

Heather Cronin¹, Kameka Johnson², Desen Zheng² and Thomas Burr²

¹Colby College, Waterville, Me 04901. ²Cornell University, Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Agrobacterium vitis, the causal agent of crown gall is an important pathogen in the grape industry. It can be a particular problem because infected, yet asymptomatic vines may be used to propagate new planting material, acting as the primary source in spreading crown gall. Recently, a new, more sensitive method for detecting *A. vitis* was developed in our laboratory using magnetic capture hybridization (MCH) and real-time PCR. This method was used to determine the distribution of *A. vitis* in dormant canes and in a limited number of green shoots of symptomatic Chardonnay vines. Two dormant canes, sectioned into nodal and internodal segments, and two shoot tips and basal green internodes of each vine were tested. *A. vitis* was found to be distributed throughout node and internode sections of dormant canes with significantly more detections made in nodes. The pathogen was also detected on one basal node and one tip of different green shoots. A second part of this research investigated siderophore loci in *A. vitis* that were found by mutation to be associated with biological control activity of strain F2/5. Mutations in each of the three loci resulted in reduced siderophore production indicating the relationship of these molecules to biological control.

[30] The ability of a decision support system to optimize fungicide application for the management of potato and tomato late blight

Christopher Chang, Ian Small, William Earl Fry

Dept of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853

For years, fungicides such as chlorothalonil have been used to control outbreaks of potato and tomato late blight, caused by the oomycete pathogen *Phytophthora infestans*. If conditions are favorable for late blight, the weathering of contact fungicides makes regular reapplication necessary; however, frequently administering fungicides incurs economic and environmental costs. These costs create a need for a Decision Support System (DSS), a tool by which growers can determine their relative risk of a *P. infestans* outbreak through the analysis of local weather data, both observed and predicted, in combination with disease forecast systems Simcast and Blitecast. Growers can use the DSS to explore several management scenarios through LATEBLIGHT (LB2004 version), a *P. infestans* simulator which predicts the development of *P. infestans* epidemics up to seven days into the future, taking into account predicted weather and host resistance, as well as user-determined fungicide application. With this information, growers will be able to make an informed decision regarding the application of fungicides, therefore optimizing limited resources and minimizing costs. Using disease progress data from field experiments in 2010 and 2011, DSS recommended fungicide application schedules were compared against time dependent application regimens to determine the cost mitigating capabilities of a DSS.

[31] Adapting a bioluminescence-based assay to assess sodium-dependent cytotoxicity in human embryonic kidney (HEK293) cells engineered to express voltage-gated sodium channels

Will Agnew-Svoboda¹, David Soderlund²

¹Willamette University, Salem, OR 97301. ²Cornell University, Department of Entomology, Geneva, NY 14456

Voltage gated sodium channels play an essential role in the generation of action potentials. Human embryonic kidney (HEK293) cells can be easily transfected to express working forms these critical channels, making them a powerful tool in ion channel study. The buildup of sodium in HEK293 cells is known to be cytotoxic. In this study, the cytotoxicity of cytoplasmic sodium build up was measured using bioluminescence. Proteases from dead cells cleave a synthetic peptide, creating a substrate for luciferase. The subsequent reaction produces measurable light. HEK293 cells transfected with mammalian sodium channel Na_v1.6 and subunits β₁ and β₂ were treated with either monensin or veratridine to create either a sodium specific pore or persistently open sodium channels. All assays were preformed in ouabain to block energy dependent cytoplasmic sodium removal. Luminescence readings from control cells, cells treated with either veratridine or monensin, and cells treated with digitonin (which disrupts the membrane leading to cell death) were taken after 24 hours. Both treatments lead to a significant increase in cytoplasmic sodium that led to cell death. Future studies will use this method to assess sodium dependent cytotoxicity caused by pyrethroid insecticides, which effect sodium channels in a qualitatively similar way to veratridine.

[32] Red Cabbage Anthocyanins as a Source of Natural Colors

Sarah Beatty¹, Kaileigh Ahlquist², David Manns², Anna Katherine Mansfield², and Phillip Griffiths²

¹Lebanon Valley College, Annville, PA 17003. ²Cornell University, Department of Horticulture, Geneva, NY 14456

The use of red cabbage for the production of natural colors could provide the basis for significant opportunities for NY cabbage growers and affiliated industries. The food industry is searching for natural color alternatives to artificial colors due to recent negative press based on research linking artificial colors with ADHD and potential carcinogenic activity. Red cabbage has unique properties for natural color production, in that it is high yielding and provides stable sources of both blue and red colors through pH variation. In this study, pigments were extracted from acylated anthocyanins concentrated in the epidermal leaf tissues of red cabbage. Colorimetry comparisons illustrated the variety of color found in red cabbage tissues over different stages of development. Variations in extracted individual acylated anthocyanins and total anthocyanin content of commercial cultivars were observed between seedling, twelve week, and mature tissue using HPLC. Seedling and adult cabbage tissue had 100x the anthocyanin concentration as the 12-week cabbage samples. Selection and breeding of the optimal red cabbage genotypes in future studies could enable development of cultivars selected and adapted for significant characteristics such as color, high anthocyanin content, and high yields of natural colors relative to total plant tissue harvested.

[33] Exploration of the field distribution and selection pressures on *Grapevine fanleaf virus* satellite RNAs

Keiran Cantilina¹, John Gottula², Marc Fuchs²

Cornell University, ¹Ithaca, NY 14853 and ²Dept of Plant Pathology and Plant-Microbe Biology, Geneva, NY 14456

Grapevine fanleaf virus (GFLV) is a nepovirus that has become one of the most serious threats to grape production worldwide. A satellite RNA is associated with some GFLV strains. Satellite RNAs are small, non-essential subviral components of an RNA virus that may or may not affect the helper virus. The GFLV satellite RNA produces a protein of unknown function. The goal of this study was to further understand the ecology and diversity of the GFLV satellite RNA by investigating its distribution within a GFLV-infected vineyard and examining the selection pressure on the satellite RNA relative to particular GFLV and *Arabis Mosaic Virus* (ArMV) genes. To study the distribution of the satellite RNA, selected sections of an experimental vineyard were screened for both GFLV and the satellite RNA by using Immunocapture-Reverse-Transcription-PCR (IC-RT-PCR) and specific primers to amplify both the satellite RNA sequence and the coat protein gene sequence from GFLV, and then analyzing the DNA products via gel electrophoresis. Computational analysis methods were used on a variety of GFLV and ArMV gene sequences (including satellite RNA sequences) to evaluate selection pressures on the GFLV satellite. This study sheds light on the ecology, diversity, and evolution of a mysterious subviral agent.

[34] Rye as an overwinter crop: suppression of germination and vegetative growth of Bodacious sweet corn

Tamara McClung¹, Joseph W. Shail², Thomas Bjorkman²

¹University of Arizona, Tucson, AZ 85719, ²Cornell University, Department of Horticulture, Geneva, NY 14456

Cover crops are used to help manage fields when not producing a crop by helping to prevent erosion, add organic matter, improve aggregate stability, suppress weeds, and prevent leaching loss of nitrogen from the soil. Winter grain cover crops are used in New York because they grow late into the fall and resume growth early in the spring. Previous studies have shown some cereal cover crops, killed at the boot stage, to inhibit germination and/or growth of vegetable crops planted the following season by approximately 20%. In this experiment, rye was killed at five different maturity stages to test whether killing the rye earlier in the spring reduces inhibition. The rye was incorporated at the last killing treatment and sweet corn was sown in two plantings, four and six weeks after incorporation. Germination was not inhibited by any treatment. Chlorophyll concentration of corn was measured by SPAD meter and was lower in plots that had incorporated more mature rye by 6.3% (2 SPAD meter points, or 36 $\mu\text{mol}/\text{m}^2$ chlorophyll). Despite these results, vigorous growth of the corn measured by fresh weight at 40d was not inhibited by any treatment. Less inhibition by rye was observed this year than previously, but was not reduced by killing the rye earlier in the spring.

[35] RNA-interference (RNAi) of four embryonically expressed genes in the codling moth *Cydia pomonella*

Stephen C. Ireland^{1,2}, Luiqi Gu², Douglas C. Knipple²

¹Michigan State University, Department of Entomology, East Lansing, MI 48824

²Cornell University, Department of Entomology, New York State Agricultural Experiment Station, Geneva, NY 14456

The codling moth is a major worldwide pest of apple, other tree fruits and nuts. In this project we are using RNAi to inhibit the expression of specific codling moth genes in order to evaluate their functions and explore the potential use of this approach for future control strategies. We previously cloned four cDNAs from codling moth embryos that are homologous to *Drosophila melanogaster* genes with known functions (*cullin*, *Deformed*, *musashi*, and *pumilio*). I synthesized dsRNAs specific to these four cDNAs for use in RNAi knockdown experiments. I first designed gene-specific primers for the four cDNAs and a *green fluorescent protein* control cDNA incorporating T7 promoter sequences. The primers were commercially synthesized and I used them to make template preparations from the embryonic cDNAs using the polymerase chain reaction (PCR). The specificity of each PCR reaction was evaluated by gel electrophoresis and PCR parameters were optimized as necessary. The templates were then transcribed using T7 RNA polymerase to produce double-stranded RNA (dsRNA). The purity and concentrations of the dsRNAs were evaluated by gel electrophoresis and spectrophotometry. These dsRNA will be used to inject codling moth embryos in order to evaluate their effects on embryonic development and survival.

[36] Variation in shrub willow biomass traits based on genotype and environment

Kayleigh E. Hogan^{1,2}, Michelle J. Serapiglia², Arthur J. Stipanovic³, and Lawrence B. Smart²

¹University of Rochester, Rochester, NY 14627. ²Dept. of Horticulture, Cornell University, New York State Agricultural Experiment Station, Geneva, NY 14456

³Dept. of Chemistry, SUNY College of Environmental Science and Forestry, Syracuse, NY 13210

Understanding the genotype by environment interactions among commercial cultivars of shrub willow (*Salix* spp.) will provide growers with the knowledge to choose appropriate cultivars with greatest yield potential for differing marginal or underutilized farmland. Wood properties of different cultivars of shrub willow were characterized across six different locations in the Northeast U.S. Wood density, biomass composition, and percent bark content were determined and variation was correlated with soil type, soil nutrients, rainfall, and temperature data for the different locations to determine to what extent site characteristics affect the development of above ground biomass. Site contributes to variation in wood density and differences in density are consistent across sites for all cultivars. Wood density after the first, second and third growing seasons was also characterized for 76 genotypes grown in a selection trial in Geneva, NY to better understand developmental patterns throughout the harvest rotation, especially in novel hybrids being selected for high yield. Density was also determined for stems harvested from the second three-year harvest rotation from two sites, Tully and Belleville, NY, to compare any differences in density from the first harvest cycle.

[37] Confirmation and elucidation of the mechanism of acquired resistance to mefenoxam in sensitive isolates of *Phytophthora infestans*

Richard Childers, Giovanna Danies, Christopher Chang and William Earl Fry

Dept of Plant Pathology and Plant-Microbe Biology, Cornell University, Ithaca, NY 14853

The systemic fungicide mefenoxam is an important fungicide in the control of late blight disease caused by *Phytophthora infestans*. The susceptibility or resistance of *P. infestans* to mefenoxam is commonly assessed *in vitro* through measuring the mycelial growth of the pathogen in response to increasing concentrations of the fungicide in amended media. However, recent observations suggest that the prior exposure of an isolate in culture to mefenoxam can cause a rapid increase in the observed pathogen resistance in subsequent mefenoxam resistance assays. This change has thus far been observed in several isolates from clonal lineages US-23 and US-24, with significantly increased resistance occurring after a single transfer. This acquired resistance might pose a challenge to accurate *in vitro* mefenoxam sensitivity assays, and, more importantly, as an effective resistance mechanism for previously sensitive isolates in the field. A genetic basis for this acquired resistance seems unlikely, given the speed of the change. Thus exploration of various possible physiological or epigenetic mechanisms using a variety of molecular techniques (Southern blot, RT-PCR, RNA-Seq might prove fruitful in elucidating the underlying mechanism.

[38] Thermal and acid stability of Thuricin H, a unique bacteriocin produced by *Bacillus thuringiensis* SF361

Breanna McArthur^{1,2}, Gaoyan Wang², and Randy W. Worobo²

¹Alabama A&M University, ²Cornell University, Department of Food Science, Geneva, NY 14456

The demand for “natural” preservatives to enhance the microbiological safety and quality continues to increase due to consumer demands for foods containing no chemical preservatives. Bacteriocins are antimicrobial peptides produced by bacteria that inhibit other bacteria that include spoilage and foodborne pathogens. Thurincin H is a bacteriocin produced by *Bacillus thuringiensis* SF361. It showed strong inhibitive activity against many Gram-positive food-borne pathogens and food spoilage microorganisms, such as *Listeria monocytogenes* and *B. cereus*. Thurincin H, a 31 amino acid peptide, has been shown to have a unique 3D structure that contains four sulfur to α -carbon crosslinks. The mode of action and stability to thermal processing and acidic conditions of thurincin H were investigated. Thurincin H was shown to inactivate 90% of *B. cereus* within 1 hour of exposure. The antimicrobial activity of thurincin H was partially lost after being treated with different temperatures ranging from 90°C, 80°C, 70°C, 60°C, and 50°C. The activity of thurincin H gradually decreased to 25% and 12.5% at 70°C and 60°C, respectively. The antimicrobial activity of thurincin H was slightly lost when exposed to a range of pH conditions between 2 and 10. These results suggest that thurincin H has potential as a “natural” preservative for enhancing the microbiological quality and safety of foods.